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Jellyfish Research Literatures

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Abstract: Jellyfish and sea jellies are the informal common names given to the medusa-phase of certain gelatinous members of the subphylum Medusozoa, a major part of the phylum Cnidaria. Jellyfish are mainly free-swimming marine animals with umbrella-shaped bells and trailing tentacles, although a few are not mobile, being anchored to the seabed by stalks. The bell can pulsate to provide propulsion and highly efficient locomotion. The tentacles are armed with stinging cells and may be used to capture prey and defend against predators. Jellyfish have a complex life cycle; the medusa is normally the sexual phase, the planula larva can disperse widely and is followed by a sedentary polyp phase. This article introduces recent research reports as references in the related studies.
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Key words: cancer; life; research; literature; cell

1. Introduction

Jellyfish and sea jellies are the informal common names given to the medusa-phase of certain gelatinous members of the subphylum Medusozoa, a major part of the phylum Cnidaria. Jellyfish are mainly free-swimming marine animals with umbrella-shaped bells and trailing tentacles, although a few are not mobile, being anchored to the seabed by stalks. The bell can pulsate to provide propulsion and highly efficient locomotion. The tentacles are armed with stinging cells and may be used to capture prey and defend against predators. Jellyfish have a complex life cycle; the medusa is normally the sexual phase, the planula larva can disperse widely and is followed by a sedentary polyp phase.

Jellyfish have a complex life cycle which includes both sexual and asexual phases, with the medusa being the sexual stage in most instances. Sperm fertilize eggs, which develop into larval planulae, become polyps, bud into ephyrae and then transform into adult medusae. In some species certain stages may be skipped. Upon reaching adult size, jellyfish spawn regularly if there is a sufficient supply of food. In most species, spawning is controlled by light, with all individuals spawning at about the same time of day, in many instances this is at dawn or dusk. Jellyfish are usually either male or female (with occasional hermaphrodites). In most cases, adults release sperm and eggs into the surrounding water, where the unprotected eggs are fertilized and develop into larvae. In a few species, the sperm swim into the female's mouth, fertilizing the eggs within her body, where they remain during early development stages. In moon jellies, the eggs lodge in pits on the oral arms, which form a temporary brood chamber for the developing planula larvae.

The following introduces recent reports as references in the related studies.

A, T. B., et al. (2000). "The synthesis of mycosporine-like amino acids (MAAs) by cultured, symbiotic dinoflagellates." J Exp Mar Bio Ecol **249**(2): 219-233.

We tested the hypothesis that there is a relation between phylotypes (phylogenetic types, as determined by restriction fragment length polymorphism (RFLP) and partial sequence analysis of the small subunit ribosomal RNA gene (SSUrDNA)) and the synthesis of mycosporine-like amino acids (MAAs) by symbiotic dinoflagellates under the influence of ultraviolet radiation (UV-B/A) and photosynthetically active radiation (PAR). We exposed 27 isolates of symbiotic dinoflagellates simultaneously to UV-B/A and PAR, and subsequently determined the MAAs present in cell extracts and in the media. The algae used included 24 isolates of Symbiodinium spp. originating from jellyfishes, sea anemones, zoanthids, scleractinians, octocorals, and bivalves, and three others in the genera Gymnodinium, Gloeodinium and Amphidinium from a jellyfish, an hydrocoral and a flatworm, respectively. In this study, all of the phylotype A Symbiodinium spp. synthesized up to three identified MAAs. None of the 11 cultured phylotypes B and C Symbiodinium spp. synthesized MAAs. The three non-Symbiodinium symbionts also

synthesized up to three MAAs. The results support a conclusion that phylotype A Symbiodinium spp. have a high predilection for the synthesis of MAAs, while phylotypes B and C do not. Synthesis of MAAs by symbiotic dinoflagellates in culture does not appear to relate directly to depths or to the UV exposure regimes from which the consortia were collected.

Abe, Y., et al. (1999). "Present status of the total artificial heart at the University of Tokyo." Artif Organs **23**(3): 221-228.

At the University of Tokyo, various types of total artificial heart (TAH) systems have been studied since 1959. At the present time, 2 types of implantable TAH have been developed. One is an undulation pump TAH (UPTAH) and the other is a flow transformed pulsatile TAH (FTPTAH). Using the UPTAH, 14 cases of implantation were performed in goats and 10 days' survival obtained. The new type of FTPTAH is under a prototype study. To prevent ring thrombus, a polyurethane membrane valve, a jellyfish valve, has been developed. The longest in vivo experiences with this valve in the TAH blood pump have been 312 days in the left side blood pump and 414 days in the right side blood pump. Conductance and arterial pressure based control (1/R control) can realize the physiological control of the TAH. Using 1/R control, 532 days of survival could be obtained in a goat with a paracorporeal TAH. The technique required to apply this control method to a implantable TAH is under development. We have proposed a new 5 year research project of the implantable TAH entitled "Comprehensive Basic Research on the Development of a Japanese Original Implantable Total Artificial Heart" to The Ministry of Welfare.

Abrams, M. J., et al. (2015). "Self-repairing symmetry in jellyfish through mechanically driven reorganization." Proc Natl Acad Sci U S A **112**(26): E3365-3373.

What happens when an animal is injured and loses important structures? Some animals simply heal the wound, whereas others are able to regenerate lost parts. In this study, we report a previously unidentified strategy of self-repair, where moon jellyfish respond to injuries by reorganizing existing parts, and rebuilding essential body symmetry, without regenerating what is lost. Specifically, in response to arm amputation, the young jellyfish of Aurelia aurita rearrange their remaining arms, recenter their manubria, and rebuild their muscular networks, all completed within 12 hours to 4 days. We call this process symmetrization. We find that symmetrization is not driven by external cues, cell proliferation, cell death, and proceeded even when foreign arms were grafted on. Instead, we find that forces generated by the muscular network are essential. Inhibiting pulsation using muscle relaxants completely, and reversibly, blocked symmetrization. Furthermore, we observed that decreasing pulse frequency using muscle relaxants slowed symmetrization, whereas increasing pulse frequency by lowering the magnesium concentration in seawater accelerated symmetrization. A mathematical model that describes the compressive forces from the muscle contraction, within the context of the elastic response from the mesoglea and the ephyra geometry, can recapitulate the recovery of global symmetry. Thus, self-repair in Aurelia proceeds through the reorganization of existing parts, and is driven by forces generated by its own propulsion machinery. We find evidence for symmetrization across species of jellyfish (Chrysaora pacifica, Mastigias sp., and Cotylorhiza tuberculata).

Abrams, M. J. and L. Goentoro (2016). "Symmetrization in jellyfish: reorganization to regain function, and not lost parts." Zoology (Jena) **119**(1): 1-3.

We recently reported a previously unidentified strategy of self-repair in the moon jellyfish Aurelia aurita. Rather than regenerating lost parts, juvenile Aurelia reorganize remaining parts to regain essential body symmetry. This process that we called symmetrization is rapid and frequent, and is not driven by cell proliferation or cell death. Instead, the swimming machinery generates mechanical forces that drive symmetrization. We found evidence for symmetrization across three other species of jellyfish (Chrysaora pacifica, Mastigias sp., and Cotylorhiza tuberculata). We propose reorganization to regain function without recovery of initial morphology as a potentially broad class of self-repair strategy beyond radially symmetrical animals, and discuss the implications of this finding on the evolution of self-repair strategies in animals.

Abul-Hassan, K., et al. (2000). "Optimization of non-viral gene transfer to human primary retinal pigment epithelial cells." Curr Eye Res **20**(5): 361-366.

PURPOSE: To optimise the high efficiency, non-viral transfer of DNA to retinal pigment epithelial (RPE) cells in vitro. METHODS: A mammalian expression vector (pcDNA3.1) containing a firefly luciferase (luc) cDNA was used to transfect RPE cells using different chemical methods; calcium phosphate, DEAE-dextran and, liposomes-based transfection techniques. Transfection was optimised for both dose and time of exposure. The efficiency of gene transfer and cytotoxicity was measured 48 hours post-transfection using luciferase and MTT assays, respectively. The percentage of transfected cells (using optimal conditions) was determined with a construct

expressing a jellyfish green fluorescent protein (GFP) using flow cytometery. RESULTS: Calcium phosphate and DEAE-dextran techniques failed to transfect the vector and led to high cytotoxicity. Liposomes-based methods successfully transferred the vector to RPE cells, but the efficiency varied for different liposomes; Tfx-50 > Lipofectin > Lipofectamine > Cellfectin > DMRIE-C. No significant cytotoxicity was observed with any of the liposome treatments. Optimal transfection was achieved with Tfx-50 at a 3:1 ratio of DNA:liposome; between 12-15% of cells being transfected. CONCLUSIONS: Efficient and non-toxic transfer of functional genes into primary RPE cells in vitro can be successfuly achieved by liposomes-based techniques. Tfx-50 appears to be a promising non-viral vector for RPE gene transfer.

Abu-Nema, T., et al. (1988). "Jellyfish sting resulting in severe hand ischaemia successfully treated with intra-arterial urokinase." Injury **19**(4): 294-296.

Acebo, P., et al. (2000). "Quantitative detection of Streptococcus pneumoniae cells harbouring single or multiple copies of the gene encoding the green fluorescent protein." Microbiology **146 (Pt 6)**: 1267-1273.

A modified gfp gene from Aequorea victoria, encoding a variant of the green fluorescent protein (GFP), was subcloned into the mobilizable plasmid pMV158. gfp was placed under the control of the inducible P (M) promoter of the Streptococcus pneumoniae gene malM, cloned in plasmid pLS70. The P (M) promoter is regulated by the product of the pneumococcal malR gene, which is inactivated by growing the cells in maltose-containing media. By homologous recombination, the P (M)-gfp construction was integrated into the host chromosome in a single copy. In both conditions (single and multiple copies), the pneumococcal cells were able to express GFP in an inducible or constitutive form, depending on whether the S. pneumoniae strain harboured a wild-type or a mutant malR gene. Quantification of the levels of GFP expressed by cultures supplemented with sucrose or maltose as carbon sources was feasible by fluorescence spectroscopy. Phase-contrast and fluorescence microscopy allowed pneumococcal cells expressing GFP in mixed cultures to be distinguished from those not carrying the gfp gene.

Acevedo, M. J., et al. (2019). "Revision of the genus Carybdea (Cnidaria: Cubozoa: Carybdeidae): clarifying the identity of its type species Carybdea marsupialis." Zootaxa **4543**(4): 515-548.

While records of Carybdea marsupialis in the literature suggest a worldwide distribution of this species, the validity of some of these records has been questioned recently, as has the validity of some nominal Carybdea species. We inspected material of all known species of Carybdea from multiple locations (i.e. Spain, Algeria, Tunisia, Puerto Rico, California, Hawaii, Australia, South Africa, and Japan) using morphological and genetic tools to differentiate Carybdea species as well as understand their evolutionary relationships. We observed morphological differences between adult medusae of Mediterranean and Caribbean C. marsupialis; the most obvious differences were the structure of the phacellae, the structure of the pedalial canal knee bend, and the number and structure of the velarial canals. The characters of the adult Mediterranean specimens agree with the description provided by Claus (1878) for individuals of C. marsupialis from the Adriatic Sea (Italy); specimens from the Caribbean (Puerto Rico) agreed with the description of C. xaymacana by Conant (1897). Significant differences between both species were also observed in the newly released medusa stage. Further, we resolved a discord about the undefined polyp culture originating from Puerto Rico that was long considered Carybdea marsupialis but should be referred to as C. xaymacana. Although C. marsupialis is currently considered the only species of Cubozoa to occur in the Mediterranean, specimens collected in Algeria and Tunisia suggest that species of Alatinidae may also be present in the Mediterranean. Our investigations indicate that Carybdea spp. are more restricted in their geographical distribution than has been recognized historically. These findings confirm that Carybdea arborifera Maas, 1897 from Hawaii, Carybdea branchi, Gershwin Gibbons, 2009 from South Africa, Carybdea brevipedalia Kishinouye, 1891 from Japan, Carybdea confusa Straehler-Pohl, Matsumoto Acevedo, 2017 from California, Carybdea marsupialis Linnaeus, 1758 from the European Mediterranean Sea, Carybdea rastonii Haacke, 1886 from South Australia, and Carybdea xaymacana, Conant, 1897 from the Caribbean Sea are valid names representing distinct species, rather than synonyms. A taxonomic key for all valid species is provided, and a neotype for C. marsupialis is designated.

Acuna, J. L., et al. (2011). "Faking giants: the evolution of high prey clearance rates in jellyfishes." Science **333**(6049): 1627-1629.

Jellyfishes have functionally replaced several overexploited commercial stocks of planktivorous fishes. This is paradoxical, because they use a primitive prey capture mechanism requiring direct contact with the prey, whereas fishes use more efficient visual detection. We have compiled published data to show that, in spite of their primitive life-style, jellyfishes exhibit similar instantaneous prey clearance

and respiration rates as their fish competitors and similar potential for growth and reproduction. To achieve this production, they have evolved large, water-laden bodies that increase prey contact rates. Although larger bodies are less efficient for swimming, optimization analysis reveals that large collectors are advantageous if they move through the water sufficiently slowly.

Adamicova, K., et al. (2016). "[Skin cell response after jellyfish sting]." Cesk Patol **52**(1): 55-60.

INTRODUCTION: Jellyfish burning is not commonly part of the professional finding in the central Europe health care laboratory. Holiday seaside tourism includes different and unusual presentations of diseases for our worklplaces. Sea water-sports and leisure is commonly connected with jellyfish burning and changes in the skin, that are not precisely described. AIM: Authors focused their research on detection of morphological and quantitative changes of some inflammatory cells in the skin biopsy of a 59-years-old woman ten days after a jellyfish stinging. Because of a comparison of findings the biopsy was performed in the skin with lesional and nonlesional skin. METHODS: Both excisions of the skin were tested by imunohistochemical methods to detect CD68, CD163, CD30, CD4, CD3, CD8, CD20 a CD1a, to detect histiocytes, as well as several clones of lymphocytes and Langerhans cells (antigen presenting cells of skin), CD 117, toluidin blue and chloracetase esterase to detect mastocytes and neutrophils. Material was tested by immunofluorescent methods to detect IgA, IgM, IgG, C3, C4, albumin and fibrinogen. Representative view-fields were documented by microscope photocamera Leica DFC 420 C. Registered photos from both samples of the skin were processed by morphometrical analysis by the Vision Assistant software. A student t-test was used for statistical analysis of reached results. RESULTS: Mean values of individual found cells in the sample with lesion and without lesion were as follows: CD117 -2.64/0.37, CD68-6.86/1.63, CD163-3.13/2.23, CD30-1.36/0.02, CD4-3.51/0.32, CD8-8.22/0.50, CD3-10.69/0.66, CD20-0.56/0.66, CD1a-7.97/0.47 respectively. Generally mild elevation of eosinofils in lesional skin was detected. Increased values of tested cells seen in excision from lesional skin when compared with nonlesional ones were statistically significant in eight case at the level $p = 0.033$ to 0.001. A not statistically significant difference was found only in the group of CD163+ histiocytes. CONCLUSION: Authors detected numbers of inflammatory cells in lesional skin after the stinging by a jellyfish and compared them with the numbers of cells in the nonlesional skin of the same patient. Statistically significant differences were seen in the level of selected inflammation cells and numerically documented changes of cellularity in the inflammatory focus were caused by a hypersensitivity reaction after jellyfish injury in the period of 10 days after attack.

Addad, S., et al. (2011). "Isolation, characterization and biological evaluation of jellyfish collagen for use in biomedical applications." Mar Drugs **9**(6): 967-983.

Fibrillar collagens are the more abundant extracellular proteins. They form a metazoan-specific family, and are highly conserved from sponge to human. Their structural and physiological properties have been successfully used in the food, cosmetic, and pharmaceutical industries. On the other hand, the increase of jellyfish has led us to consider this marine animal as a natural product for food and medicine. Here, we have tested different Mediterranean jellyfish species in order to investigate the economic potential of their collagens. We have studied different methods of collagen purification (tissues and experimental procedures). The best collagen yield was obtained using Rhizostoma pulmo oral arms and the pepsin extraction method (2-10 mg collagen/g of wet tissue). Although a significant yield was obtained with Cotylorhiza tuberculata (0.45 mg/g), R. pulmo was used for further experiments, this jellyfish being considered as harmless to humans and being an abundant source of material. Then, we compared the biological properties of R. pulmo collagen with mammalian fibrillar collagens in cell cytotoxicity assays and cell adhesion. There was no statistical difference in cytotoxicity ($p > 0.05$) between R. pulmo collagen and rat type I collagen. However, since heparin inhibits cell adhesion to jellyfish-native collagen by 55%, the main difference is that heparan sulfate proteoglycans could be preferentially involved in fibroblast and osteoblast adhesion to jellyfish collagens. Our data confirm the broad harmlessness of jellyfish collagens, and their biological effect on human cells that are similar to that of mammalian type I collagen. Given the bioavailability of jellyfish collagen and its biological properties, this marine material is thus a good candidate for replacing bovine or human collagens in selected biomedical applications.

Adonin, L. S., et al. (2009). "[The plate in the zone of oocyte and germinal epithelium contact in scyphomedusa Aurelia aurita binds antibodies to ZP-domain-containing protein mesoglein]." Tsitologiia **51**(5): 435-441.

Cnidaria are lower multicellular animals with the body consisting of two epithelial layers. An extracellular substance--mesoglea--is situated between epidermal and gastrodermal layers of these animals.

Mesoglein is one of the major mesogleal proteins of adult medusa of Scyphozoan jellyfish Aurelia aurita. Search for the known domains in mesoglein amino acid sequence reveals prominent zona pellucida (ZP) domain (which was found at first in the mammal oocyte zona pellucida proteins), so the protein belongs to ZP family of extracellular matrix proteins and it is an early metazoan member of ZP-domain-containing protein family. However, nothing is known about oogenesis related ZP-domain proteins in the lower multicellular animals. Oogenesis in Scyphozoa is described poorly. In this work morphological features of the zone in contact area between the oocyte and the germinal epithelium were investigated in semi-fine sections: To make it more convenient we identified seven stages according to the oocyte size and the structure found in this area was named the plate. It was shown that the components of the plate bound specifically the antibodies against mesoglein. So it seems the plate material contains ZP-domain proteins. Electrophoresis and immunoblot results give evidence that the proteins immunologically related to mesoglein have a higher molecular mass. It might be due to either the posttranslational modifications of the precursors or that they represent other proteins of ZP-domain family in Cnidaria.

Adonin, L. S., et al. (2012). "[Morphodynamics of the contract plate in the course of oocyte maturation in the scyphozoan Aurelia aurita (Cnidaria: Semaeostomae)]." Ontogenez **43**(1): 20-27.

The structure forming in the area of contact between the oocyte and the germinal epithelium in the course of oocyte maturation of the scyphozoan Aurelia aurita is termed the contact plate. This study traces the successive stages of contact plate formation in the course of oocyte maturation at the light microscopic and ultrastructural levels. At early stages ofoocyte development, the appearance of granules is observed in the peripheral cytoplasm of the oocyte; these granules accumulate at the pole, which retains its connection with the germinal epithelium of the gonads. Two types of these granules are recognized: (1) granules with homogeneous content and (2) granules containing loose shapeless material in the form of thick cords. The transformation of type two granules into larger structures, as well as the consolidation of type one and type two granules at later stages of oocyte development, are probably the processes that lead to the formation of the characteristic structure and contact plate, visible in paraffin and semithin sections. It remains unclear where exactly the contact plate is localized at the moment of fertilization: inside or outside the oocyte. The content of granules and components of the plate specifically bind the antibodies (RA47) against mesoglein, the ZP domain-containing protein of the mesoglea of A. aurita. The contact plate, covering only the anomalous pole of the oocyte but detected by the presence of ZP domain-containing proteins, may prove to be the simplest egg membrane of the zona pellucida type.

Adonin, L. S., et al. (2012). "Aurelia aurita (Cnidaria) oocytes' contact plate structure and development." PLoS One **7**(11): e46542.

One of the A. aurita medusa main mesoglea polypeptides, mesoglein, has been described previously. Mesoglein belongs to ZP-domain protein family and therefore we focused on A.aurita oogenesis. Antibodies against mesoglein (AB RA47) stain the plate in the place where germinal epithelium contacts oocyte on the paraffin sections. According to its position, we named the structure found the "contact plate". Our main instrument was AB against mesoglein. ZP-domain occupies about half of the whole amino acid sequence of the mesoglein. Immunoblot after SDS-PAGE and AU-PAGE reveals two charged and high M (r) bands among the female gonad germinal epithelium polypeptides. One of the gonads' polypeptides M (r) corresponds to that of mesogleal cells, the other ones' M (r) is higher. The morphological description of contact plate formation is the subject of the current work. Two types of AB RA47 positive granules were observed during progressive oogenesis stages. Granules form the contact plate in mature oocyte. Contact plate of A.aurita oocyte marks its animal pole and resembles Zona Pellucida by the following features: (1) it attracts spermatozoids; (2) the material of the contact plate is synthesized by oocyte and stored in granules; (3) these granules and the contact plate itself contain ZP domain protein (s); (4) contact plate is an extracellular structure made up of fiber bundles similar to those of conventional Zona Pellucida.

Afendra, A. S., et al. (2004). "Gene transfer and expression of recombinant proteins in moderately halophilic bacteria." Methods Mol Biol **267**: 209-223.

Moderately halophilic bacteria (MHB) of the genera Halomonas and Chromohalobacter have been used as hosts for the expression of heterologous proteins of biotechnological interest, thus expanding their potential to be used as cell factories for various applications. This chapter deals with the methodology for the construction of recombinant plasmids, their transfer to a number of MHB, and the assaying of the corresponding heterologous proteins activity. The transferred genes include (1) inaZ, encoding the ice nucleation protein of the plant pathogen Pseudomonas syringae, (2) gfp, encoding a green fluorescent protein from the marine bioluminescent jellyfish Aequorea victoria, and (3) the alpha-amylase gene from the

hyperthermophilic archeon Pyrococcus woesei. Vector pHS15, which was designed for expression of heterologous proteins in both E. coli and MHB, was used for the subcloning and transfer of the above genes. The recombinant constructs were introduced to MHB by assisted conjugal transfer from E. coli donors. The expression and function of the recombinant proteins in the MHB transconjugants is described.

Aglieri, G., et al. (2014). "First evidence of inbreeding, relatedness and chaotic genetic patchiness in the holoplanktonic jellyfish Pelagia noctiluca (Scyphozoa, Cnidaria)." PLoS One **9**(6): e99647.

Genetic drift and non-random mating seldom influence species with large breeding populations and high dispersal potential, characterized by unstructured gene pool and panmixia at a scale lower than the minimum dispersal range of individuals. In the present study, a set of nine microsatellite markers was developed and used to investigate the spatio-temporal genetic patterns of the holoplanktonic jellyfish Pelagia noctiluca (Scyphozoa) in the Southern Tyrrhenian Sea. Homozygote excess was detected at eight loci, and individuals exhibited intra-population relatedness higher than expected by chance in at least three samples. This result was supported by the presence of siblings in at least 5 out 8 samples, 4 of which contained full-sib in addition to half-sib dyads. Having tested and ruled out alternative explanations as null alleles, our results suggest the influence of reproductive and behavioural features in shaping the genetic structure of P. noctiluca, as outcomes of population genetics analyses pointed out. Indeed, the genetic differentiation among populations was globally small but highlighted: a) a spatial genetic patchiness uncorrelated with distance between sampling locations, and b) a significant genetic heterogeneity between samples collected in the same locations in different years. Therefore, despite its extreme dispersal potential, P. noctiluca does not maintain a single homogenous population, but rather these jellyfish appear to have intra-bloom localized recruitment and/or individual cohesiveness, whereby siblings more likely swarm together as a single group and remain close after spawning events. These findings provide the first evidence of family structures and consequent genetic patchiness in a species with highly dispersive potential throughout its whole life cycle, contributing to understanding the patterns of dispersal and connectivity in marine environments.

Agmon, N. (2005). "Proton pathways in green fluorescence protein." Biophys J **88**(4): 2452-2461.

Proton pathways in green fluorescent protein (GFP) are more extended than previously reported. In the x-ray data of wild-type GFP, a two-step exit pathway exists from the active site to the protein surface, controlled by a threonine switch. A proton entry pathway begins at a glutamate-lysine cluster around Glu-5, and extends all the way to the buried Glu-222 near the active site. This structural evidence suggests that GFP may function as a portable light-driven proton-pump, with proton emitted in the excited state through the switchable exit pathway, and replenished from Glu-222 and the Glu-5 entry pathway in the ground state.

Agungpriyono, D. R., et al. (2000). "Green fluorescent protein gene insertion of Sendai Virus infection in nude mice: possibility as an infection tracer." J Vet Med Sci **62**(2): 223-228.

The green fluorescent protein (GFP) marker from jellyfish Aequorea victoria is considered to have potential use in the study of host-pathogen relationships, by tracing infections in living cells, organs and animals. We compared the pathogenicity of Sendai virus with an inserted GFP gene (GFP-SeV) with that of its wild-type (Wt-SeV) to determine the usefulness of the recombinant virus in long-term infection of BALB/c nude (nu/nu) mice. The results indicated that the presence of GFP in infected cells could be analyzed easily and sensitively. GFP helped in identifying and in understanding the cellular sites of viral replication in vitro and in vivo. However, the GFP insertion into the Wt-SeV genome, led to decreased pathogenicity, altering the in vivo viral kinetics.

Ahlborn, B. K., et al. (2006). "Frequency tuning in animal locomotion." Zoology (Jena) **109**(1): 43-53.

In locomotion that involves repetitive motion of propulsive structures (arms, legs, fins, wings) there are resonant frequencies f (*) at which the energy consumption is a minimum. As animals need to change their speed, they can maintain this energy minimum by tuning their body resonances. We discuss the physical principles of frequency tuning, and how it relates to forces, damping, and oscillation amplitude. The resonant frequency of pendulum-type oscillators (e.g. swinging arms and legs) may be changed by varying the mass moment of inertia, or the vertical acceleration of the pendulum pivot. The frequency of elastic vibrations (e.g. the bell of a jellyfish) can be tuned with a non-linear modulus of elasticity: soft for low deflection amplitudes (low resonant frequency), and stiff for large displacements (high resonant frequency). Tuning of elastic oscillations can also be achieved by changing the effective length or cross-sectional area of the elastic members, or by allowing springs in parallel or in series to become active. We propose that swimming and flying animals generate oscillating propulsive forces from precisely placed

shed vortices and that these tuned motions can only occur when vortex shedding and the simple harmonic motion of the elastic elements of the propulsive structures are in resonance.

Ahn, E. Y., et al. (2018). "Upcycling of jellyfish (Nemopilema nomurai) sea wastes as highly valuable reducing agents for green synthesis of gold nanoparticles and their antitumor and anti-inflammatory activity." Artif Cells Nanomed Biotechnol **46**(sup2): 1127-1136.

Due to its tentacle poison and huge body, giant jellyfish (Nemopilema nomurai) poses challenging issues to the environment and ecosystems. Here we developed, upcycling a giant jellyfish extract as a reducing agent, a green synthetic method of gold nanoparticles (JF-AuNPs) which possess biological activities. The colloidal solutions of JF-AuNPs were blue, violet, purple and pink depending on the extract concentration. UV-visible spectra exhibited two surface plasmon resonance bands at 5 4 0 approximately 550 nm and 810 nm. Spherical shapes with an average size of 35.2 +/- 8.7 nm and triangular nanoplates with an average height of 70.5 +/- 30.3 nm were observed. A face-centered cubic structure was confirmed by high-resolution X-ray diffraction. JF-AuNPs exhibited significant cytotoxic effect against HeLa cancer cells but not against normal cells such as NIH-3T3 and Raw 264.7 cells. In HeLa cells, JF-AuNPs decreased the phosphorylation of AKT and ERK, which are crucial for cell proliferation. Also, JF-AuNPs decreased NO secretion and iNOS expression levels, resulting in anti-inflammatory effects in LPS-inflamed macrophages. Collectively, we established a green synthesis of anti-tumorigenic and anti-inflammatory JF-AuNPs using the extract of jellyfish sea wastes. Thus, beneficial effects of JF-AgNPs must be weighed in further studies in vivo and it can be potent nanomedicine for future applications.

Ai, H. W., et al. (2006). "Directed evolution of a monomeric, bright and photostable version of Clavularia cyan fluorescent protein: structural characterization and applications in fluorescence imaging." Biochem J **400**(3): 531-540.

The arsenal of engineered variants of the GFP [green FP (fluorescent protein)] from Aequorea jellyfish provides researchers with a powerful set of tools for use in biochemical and cell biology research. The recent discovery of diverse FPs in Anthozoa coral species has provided protein engineers with an abundance of alternative progenitor FPs from which improved variants that complement or supersede existing Aequorea GFP variants could be derived. Here, we report the engineering of the first monomeric version of the tetrameric CFP (cyan FP) cFP484 from Clavularia coral. Starting from a designed synthetic gene library with mammalian codon preferences, we identified dimeric cFP484 variants with fluorescent brightness significantly greater than the wild-type protein. Following incorporation of dimer-breaking mutations and extensive directed evolution with selection for blue-shifted emission, high fluorescent brightness and photostability, we arrived at an optimized variant that we have named mTFP1 [monomeric TFP1 (teal FP 1)]. The new mTFP1 is one of the brightest and most photostable FPs reported to date. In addition, the fluorescence is insensitive to physiologically relevant pH changes and the fluorescence lifetime decay is best fitted as a single exponential. The 1.19 A crystal structure (1 A=0.1 nm) of mTFP1 confirms the monomeric structure and reveals an unusually distorted chromophore conformation. As we experimentally demonstrate, the high quantum yield of mTFP1 (0.85) makes it particularly suitable as a replacement for ECFP (enhanced CFP) or Cerulean as a FRET (fluorescence resonance energy transfer) donor to either a yellow or orange FP acceptor.

Akashi, K., et al. (1998). "Potential dual targeting of an Arabidopsis archaebacterial-like histidyl-tRNA synthetase to mitochondria and chloroplasts." FEBS Lett **431**(1): 39-44.

A cDNA clone encoding a histidyl-tRNA synthetase (HisRS) was characterized from Arabidopsis thaliana. The deduced amino acid sequence (AtHRS1) is surprisingly more similar to HisRSs from archaebacteria than those from eukaryotes and prokaryotes. AtHRS1 has an N-terminal extension with features characteristic of mitochondrial and chloroplast transit peptides. Transient expression assays in tobacco protoplasts clearly demonstrated efficient targeting of a fusion peptide consisting of the first 71 amino acids of AtHRS1 joined to jellyfish green fluorescent protein (GFP) to both mitochondria and chloroplasts. These observations suggest that the AtHisRS1 cDNA encodes both mitochondrial and chloroplast histidyl-tRNA synthetases.

Al-Ajmi, A. M., et al. (2013). "Isolated severe median mononeuropathy caused by a jellyfish sting." J Clin Neuromuscul Dis **14**(4): 188-193.

Neuropathies caused by jellyfish stings are extremely rare and poorly studied. A 20-year-old female patient was stung on the volar aspect of the right forearm by an unidentified species of jellyfish. Local cutaneous reaction was followed within few days by severe median mononeuropathy, involving the motor and sensory branches to the hand and forearm but sparing the palmar branch. The patient had

neuropathic pain relieved by pregabaline. Electrodiagnostic studies confirmed a demyelinating lesion. Ultrasound and magnetic resonance imaging of the median nerve revealed uniform swelling with mild uptake of contrast along the forearm. Within 2 months, strength improved significantly, pain subsided, and numbness partially resolved. Literature review and discussion of the possible mechanisms and implications of this rare effect of marine animal envenomation is presented. Jellyfish sting may cause focal mononeuropathies most probably because of the local effects of the toxins.

Alam, M. J. and K. U. Ashraf (2013). "Prediction of an Epitope-based Computational Vaccine Strategy for Gaining Concurrent Immunization Against the Venom Proteins of Australian Box Jellyfish." Toxicol Int **20**(3): 235-253.

BACKGROUND: Australian Box Jellyfish (C. fleckeri) has the most rapid acting venom known to in the arena of toxicological research and is capable enough of killing a person in less than 5 minutes inflicting painful, debilitating and potentially life-threatening stings in humans. It has been understood that C. fleckeri venom proteins CfTX-1, 2 and HSP70-1 contain cardiotoxic, neurotoxic and highly dermatonecrotic components that can cause itchy bumpy rash and cardiac arrest. SUBJECTS AND METHODS: As there is no effective drug available, novel approaches regarding epitope prediction for vaccine development were performed in this study. Peptide fragments as nonamers of these antigenic venom proteins were analyzed by using computational tools that would elicit humoral and cell mediated immunity, were focused for attempting vaccine design. By ranking the peptides according to their proteasomal cleavage sites, TAP scores and IC50<250 nM, the predictions were scrutinized. Furthermore, the epitope sequences were examined by in silico docking simulation with different specific HLA receptors. RESULTS: Interestingly, to our knowledge, this is the maiden hypothetical immunization that predicts the promiscuous epitopes with potential contributions to the tailored design of improved safe and effective vaccines against antigenic venom proteins of C. fleckeri which would be effective especially for the Australian population. CONCLUSION: Although the computational approaches executed here are based on concrete confidence which demands more validation and in vivo experiments to validate such in silico approach.

Albert, D. J. (2011). "What's on the mind of a jellyfish? A review of behavioural observations on Aurelia sp. jellyfish." Neurosci Biobehav Rev **35**(3): 474-482.

Aurelia sp. (scyphozoa; Moon Jellies) are one of the most common and widely distributed species of jellyfish. Their behaviours include swimming up in response to somatosensory stimulation, swimming down in response to low salinity, diving in response to turbulence, avoiding rock walls, forming aggregations, and horizontal directional swimming. These are not simple reflexes. They are species typical behaviours involving sequences of movements that are adjusted in response to the requirements of the situation and that require sensory feedback during their execution. They require the existence of specialized sensory receptors. The central nervous system of Aurelia sp. coordinates motor responses with sensory feedback, maintains a response long after the eliciting stimulus has disappeared, changes behaviour in response to sensory input from specialized receptors or from patterns of sensory input, organizes somatosensory input in a way that allows stimulus input from many parts of the body to elicit a similar response, and coordinates responding when stimuli are tending to elicit more than one response. While entirely different from that of most animals, the nervous system of Aurelia sp. includes a brain that creates numerous adaptive behaviours that are critical to the survival of these phylogenetically ancient species.

Alder, H. and V. Schmid (1987). "Cell cycles and in vitro transdifferentiation and regeneration of isolated, striated muscle of jellyfish." Dev Biol **124**(2): 358-369.

Isolated, mononucleated, cross-striated muscle cells of a medusa can transdifferentiate in vitro to various new cell types and even form a complex regenerate. The transdifferentiation events follow a strict pattern. The first new cell type resembles smooth muscle and is formed without a preceding DNA replication. This cell type behaves like a stem cell and by quantal cell cycles produces all other new cell types. Some preparations develop an inner and an outer layer separated by a basal lamella. Formation of these layers does not depend on DNA replication. When layers do not form, each division results in nerve cells and smooth muscle cells. If separation into layers occurs, then a regenerate will be formed, and in the course of only two cell cycles all necessary cell types to form a functional regenerate will differentiate.

al-Ebrahim, K., et al. (1995). "Jellyfish-venom-induced deep venous thrombosis. A case report." Angiology **46**(5): 449-451.

The authors describe a case of jellyfish sting that resulted in deep venous thrombosis of the leg and thigh of a thirty-five-year-old healthy man. The authors found no mention of this complication from jellyfish sting in the literature. Successful treatment

measures are described.

Alexander, D. R. and J. G. Armstrong (1987). "Explosive vaporization of aerosol drops under irradiation by a CO (2) laser beam." Appl Opt **26**(3): 533-538.

Experimental results on the explosive breakup of water aerosols in response to high-energy CO (2) laser radiation are presented for optical size parameters ranging from 6 to 15. The maximum power density used in this work was ~1.5 MW/cm (2). A pulsed N (2) laser imaging system coupled to a digital image processing system was used to observe visually the behavior of the drops on breakup. A phase/Doppler particle analyzer system was used to determine the simultaneous size and velocity of expelled particles at a distance of 2 mm from the drops. Results indicate that the incident irradiance affects the average size of particles expelled, but the average velocity of the expelled particles is not a strong function of the incident irradiance. Drop explosions resembling jellyfish are reported, we believe, for the first time in this work.

Al-Garib, S. O., et al. (2003). "Tissue tropism in the chicken embryo of non-virulent and virulent Newcastle diseases strains that express green fluorescence protein." Avian Pathol **32**(6): 591-596.

The tissue tropism of non-virulent and virulent Newcastle disease virus (NDV) was investigated using 8-day-old and 14-day-old embryonating chicken eggs (ECE), inoculated with an infectious clone of the non-virulent La Sota strain (NDFL-GFP) or its virulent derivative (NDFLtag-GFP). Both strains expressed the gene encoding jellyfish green fluorescence protein (GFP) as a marker. The GFP was readily expressed in chicken embryo cells infected with the NDV strains indicating virus replication. Whereas both strains replicated in the chorioallantoic membrane (CAM) and infected the skin of 8-day-old ECE, only the virulent strain (NDFLtag-GFP) spread to internal organs (pleura/peritoneum). In 14-day-old ECE, the initial target organs appeared to be the CAM and the lungs for both strains. At 48 h after inoculation, the virulent strain (NDFLtag-GFP) had also spread to the spleen and heart and was detected in a wide-range of embryonic cell types. The kinetics of virus replication and spread in the CAM closely resembled each other in both the 8-day-old and 14-day-old ECE. Infection of 8-day-old and 14-day-old ECE forms a convenient model to investigate tissue tropism of NDV, as well as the kinetics of viral infection. The advantage of using GFP is that samples can be easily screened by direct fluorescence microscopy without any pre-treatment.

Aljbour, S. M., et al. (2018). "Metabolic and oxidative stress responses of the jellyfish Cassiopea to pollution in the Gulf of Aqaba, Jordan." Mar Pollut Bull **130**: 271-278.

Physiological responses of jellyfish to pollution are virtually overlooked. We measured the activity of two glycolytic enzymes (pyruvate kinase (PK) and lactate dehydrogenase (LDH)), lipid peroxidation (LPO), protein and chlorophyll a content in the jellyfish Cassiopea sp. from polluted and reference sites along the Gulf of Aqaba, Jordan. In jellyfish from polluted sites, low PK/LDH ratios and high LDH activity clarify their reliance on anaerobic metabolism. PK and LDH were positively correlated in the jellyfish. While medusae from polluted sites showed no signs of oxidative stress damage, protein content was significantly lower. This might suggest protein utilization for energy production needed for maintenance. Unchanged LPO in polluted sites indicates the ability of jellyfish to keep reactive oxygen species under control. Overall these results suggest that the jellyfish seems to tolerate the current levels of pollution at the studied sites and they might be anaerobically poised to live at such habitats.

Allavena, A., et al. (1998). "In vitro evaluation of the cytotoxic, hemolytic and clastogenic activities of Rhizostoma pulmo toxin (s)." Toxicon **36**(6): 933-936.

Cytotoxic, hemolytic and clastogenic activities of Rhizostoma pulmo toxin (s) contained in the jelly tissue free of nematocysts were investigated in mammalian cells with in vitro procedures. At the concentration of 37.6 microg/ml the tissue protein produced the death of 50% V79 cells; a similar potency was observed in terms of hemolytic activity. The toxin (s) was not clastogenic for human lymphocytes in culture at the concentration of 5 microg/ml.

Al-Rubiay, K., et al. (2009). "Skin and systemic manifestations of jellyfish stings in iraqi fishermen." Libyan J Med **4**(2): 75-77.

BACKGROUND: Jellyfish stings are common worldwide with an estimated 150 million cases annually, and their stings cause a wide range of clinical manifestations from skin inflammation to cardiovascular and respiratory collapse. No studies on jellyfish stings have been carried out in Basra, Iraq. OBJECTIVES: To describe the immediate and delayed skin reactions to White Jellyfish (Rhizostoma sp.) stings and the types of local treatment used by fishermen. METHODS AND MATERIALS: 150 fishermen were enrolled at three Marine stations in Basra, Iraq. Demographic data, types of skin reactions, systemic manifestations and kinds of treatments were collected. RESULTS: Overall, 79% of fishermen in all three Marine stations gave a history of having been

stung. The common sites of sings were the hands and arms followed by the legs. Most fishermen claimed that stings led to skin reactions within 5 minutes. The presenting complaints were itching, burning sensation, and erythematic wheals. A few days after the sting, new groups of painless and itchy erythematous monomorphic papular rashes developed at the site of the sting in 62% of cases as a delayed type of skin reaction that resolved spontaneously. The local remedies commonly used by the fishermen were seawater, tap water and ice. A few fishermen considered stings as insignificant and did not think there was a need to seek medical help. CONCLUSIONS: We conclude that jellyfish causes many stings among fishermen in the Basra region. Their stings lead to immediate and delayed skin reactions. Self-treatment by topical remedies is common.

Alvarez Silva, C., et al. (2003). "[Morphologic variations in Blackfordia virginica (hydroidomedusae: Blackfordiidae) in coastal lagoons of Chiapas, Mexico]." Rev Biol Trop **51**(2): 409-412.

Blackfordia virginica is an important hydromedusae in the zooplankton of coastal lagoons at Mexico. In order to contribute to their study, morphological variations of these species were analyzed in the system of coastal lagoons of Chiapas, Mexico. A total of 503 jellyfish were studied their sizes varied from 6.1 to 9.9 mm of umbrelar diameter. The number of marginal tentacles varied from 86 to 125. A 67.7% females and 30.2% males were recognized. Only 31 jellyfish (26 females and five males) presented morphological variations of ten different types and affected the number and form of the handles, radial channels and gonads. The size of the jellyfish and the number of tentacles reflected a correlation of 0.74.

Amsterdam, A., et al. (1996). "Requirements for green fluorescent protein detection in transgenic zebrafish embryos." Gene **173**(1 Spec No): 99-103.

We have generated transgenic (Tg) lines of zebrafish in which the green fluorescent protein (GFP)-encoding gfp cDNA is driven by the Xenopus laevis ef1 alpha enhancer/promoter; Tg embryos from most of these lines show detectable fluorescence throughout their body. We have investigated the copy number of the Tg genes in fluorescent and non-fluorescent lines, in order to determine how this affects the production of detectable levels of GFP in the zebrafish embryo. Additionally, we have injected purified recombinant GFP into embryos to determine the intracellular GFP concentration required for detection, both when all of the cells in the embryo contain GFP and when only a few do.

An, L. Y., et al. (2012). "Generation of human lactoferrin transgenic cloned goats using donor cells with dual markers and a modified selection procedure." Theriogenology **78**(6): 1303-1311.

The objective was to use dual markers to accurately select genetically modified donor cells and ensure that the resulting somatic cell nuclear transfer kids born were transgenic. Fetal fibroblast cells were transfected with dual marking gene vector (pCNLF-ng) that contained the red-shifted variant of the jellyfish green fluorescent protein (LGFP) and neomycin resistance (Neo) markers. Cell clones that were G418-resistant and polymerase chain reaction-positive were subcultured for several passages; individual cells of the clones were examined with fluorescence microscopy to confirm transgenic integration. Clones in which every cell had bright green fluorescence were used as donor cells for nuclear transfer. In total, 86.7% (26/30) cell clones were confirmed to have transgenic integration of the markers by polymerase chain reaction, 76.7% (23/30) exhibited fluorescence, but only 40% (12/30) of these fluorescent cell clones had fluorescence in all cell populations. Moreover, through several cell passages, only 20% (6/30) of the cell clones exhibited stable LGFP expression. Seven transgenic cloned offspring were produced from these cells by nuclear transfer. Overall, the reconstructed embryo fusion rate was 76.6%, pregnancy rates at 35 and 60 days were 39.1% and 21.7%, respectively, and the offspring birth rate was 1.4%. There were no significant differences between nuclear transfer with dual versus a single (Neo) marker (overall, 73.8% embryo fusion rate, 53.8% and 26.9% pregnancy rates, and 1.9% birth rate with five offspring). In conclusion, the use of LGFP/Neo dual markers and an optimized selection procedure reliably screened genetically modified donor cells, excluded pseudotransgenic cells, and led to production of human lactoferrin transgenic goats. Furthermore, the LGFP/Neo markers had no adverse effects on the efficiency of somatic cell nuclear transfer.

An, S., et al. (2017). "Bio-inspired, colorful, flexible, defrostable light-scattering hybrid films for the effective distribution of LED light." Nanoscale **9**(26): 9139-9147.

Bioluminescent jellyfish has a unique structure derived from fiber/polymer interfaces that is advantageous for effective light scattering in the dark, deep sea water. Herein, we demonstrate the fabrication of bio-inspired hybrid films by mimicry of the jellyfish's structure, leading to excellent light-scattering performance and defrosting capability. A haze value reaching 59.3% and a heating temperature of up to 292 degrees C were achieved with the films.

Accordingly, the developed surface constitutes an attractive optical device for lighting applications, especially for street or vehicle luminaries for freezing Arctic-climate countries. The morphological details of the hybrid films were revealed by scanning electron microscopy. The light-scattering properties of these films were examined by ultraviolet-visible-infrared spectrophotometry and anti-glare effect analyses. The defrosting performance of the hybrid films was evaluated via heating tests and infra-red observations.

Andersen, J. B., et al. (1998). "New unstable variants of green fluorescent protein for studies of transient gene expression in bacteria." Appl Environ Microbiol **64**(6): 2240-2246.

Use of the green fluorescent protein (Gfp) from the jellyfish Aequorea victoria is a powerful method for nondestructive in situ monitoring, since expression of green fluorescence does not require any substrate addition. To expand the use of Gfp as a reporter protein, new variants have been constructed by the addition of short peptide sequences to the C-terminal end of intact Gfp. This rendered the Gfp susceptible to the action of indigenous housekeeping proteases, resulting in protein variants with half-lives ranging from 40 min to a few hours when synthesized in Escherichia coli and Pseudomonas putida. The new Gfp variants should be useful for in situ studies of temporal gene expression.

Anderson, P. A. (1985). "Physiology of a bidirectional, excitatory, chemical synapse." J Neurophysiol **53**(3): 821-835.

Neurons of the motor nerve net of the jellyfish Cyanea are connected by chemical synapses that, from their ultrastructure, appear to be bidirectional chemical synapses. These synapses were examined physiologically, by recording intracellularly from synaptically connected cells, with the whole cell configuration of the patch-clamp recording technique. Subthreshold depolarizations produced neither small voltage responses indicative of electrical coupling, nor unitary depolarizations suggestive of excitatory postsynaptic potentials (EPSP). Synaptic transmission was affected only when the presynaptic cell was depolarized above spike threshold. The synaptic delay was slightly less than 1 ms at room temperature. The postsynaptic response was initially suprathreshold, resulting in an action potential, but with time this gave way to a large 60 mV amplitude EPSP that did not produce action potentials. The amplitude of the EPSP was directly related to the postsynaptic membrane potential and extrapolated to a reversal potential close to zero mV. Reversal of the EPSP was never observed, even in the presence of intracellular tetrathylammonium (TEA). The relationship between presynaptic depolarization and postsynaptic response was difficult to examine in normal conditions, but in the presence of extracellular lidocaine, which blocked the Na+ and K+ channels in these membranes, a distinct relationship was apparent. The synapse was physiologically nonpolarized and conducted equally well in either direction with a constant synaptic delay.

Anderson, P. A. and U. Grunert (1988). "Three-dimensional structure of bidirectional, excitatory chemical synapses in the jellyfish Cyanea capillata." Synapse **2**(6): 606-613.

Neurons in the ectoderm of the perirhopalial tissue of the jellyfish Cyanea capillata were exposed and fixed for electron microscopy under conditions designed to minimize exocytosis of synaptic vesicles. The structure of the bidirectional chemical synapses that connect neurons was examined and the three-dimensional organization of these synapses was determined from reconstructions of serial sections. Synapses were characterized by the accumulation of a relatively few, large synaptic vesicles. These lie in a single layer against the terminal membrane of each terminal. The cytoplasmic side of the vesicles in any one terminal was covered by a single, large, perforated cisternal sheet. In addition, there were numerous smaller, bulbous cisternae that intermingled with the vesicles in the terminal. The structure of any one terminal was mirrored by that of the opposite terminal of the pair. The organization of these synapses is discussed from the viewpoint of cnidarian synapses in general.

Anderson, P. A., et al. (1993). "Deduced amino acid sequence of a putative sodium channel from the scyphozoan jellyfish Cyanea capillata." Proc Natl Acad Sci U S A **90**(15): 7419-7423.

Members of the phylum Cnidaria are the lowest extant organisms to possess a nervous system and are the first that are known to contain cells that produce action potentials carried exclusively by Na+ ions. They thus occupy an important position in the evolution of Na+ channels. A cDNA encoding a 198-kDa protein with high sequence identity to known Na+ channels was isolated from the scyphozoan jellyfish Cyanea capillata. The similarity between this and other Na+ channels is greatest in the transmembrane segments and the putative pore region and less so in the cytoplasmic loops that link the four domains of the protein. Phylogenetic analysis of the deduced protein reveals that it is closely related to known Na+ channels, particularly those of squid and Drosophila, and more distantly separated from Ca2+ channels. Scrutiny of the Cyanea channel in regions corresponding to those purported to form the tetrodotoxin receptor and selectivity filter of Na+ channels in higher animals

reveals several anomalies that suggest that current models of the location of the tetrodotoxin binding site and Na+ channel selectivity filter are incomplete.

Anderson, P. A. and G. O. Mackie (1977). "Electrically coupled, photosensitive neurons control swimming in a jellyfish." Science **197**(4299): 186-188.

Central neurons in Polyorchis (Hydromedusae) were impaled with microelectrodes, and conventional resting potentials were obtained. The waveform of action potentials recorded concurrently with swimming events shows evidence of electrotonic coupling between these neurons, which are also directly photosensitive and receive excitatory synaptic input from other conduction systems.

Anderson, P. A., et al. (1992). "The presence and distribution of Antho-RFamide-like material in scyphomedusae." Cell Tissue Res **267**(1): 67-74.

The nervous systems of the scyphomedusae Chrysaora hysoscella, Cyanea capillata and Cyanea lamarckii (Phylum Cnidaria) were stained using an anti-serum against the anthozoan neuropeptide Antho-RFamide. Staining was widespread in all three species. In Chrysaora, the antiserum revealed nerve nets in the subumbrella and exumbrella ectoderm, in both faces of the oral lobes, and in the endoderm lining the subumbrella and exumbrella surfaces of the gastric cavity. The most prominent staining occurred in a dense plexus of neurons in the ectoderm at the base of the tentacles. This nerve net sent projections into the subumbrella ectoderm. For the most part, staining in the two species of Cyanea was similar to that in Chrysaora, with a few exceptions. These include the presence, in Cyanea, of an obvious tentacular nerve tract and nerve nets associated with clusters of cnidocytes in the tentacles. Radioimmunoassays of extracts from Chrysaora and Cyanea lamarkii revealed that both species contain large amounts of Antho-RFamide-like material (up to 55 nmol/animal). The results indicate that Antho-RFamide-like neuropeptides are widespread in scyphomedusae.

Asakawa, H., et al. (2017). "Microscopic Observation of Living Cells Stained with Fluorescent Probes." Cold Spring Harb Protoc **2017**(10): pdb prot079848.

Fluorescence imaging of living cells provides a unique opportunity to follow dynamic behavior of specific molecules under physiological conditions. In the fission yeast Schizosaccharomyces pombe, expression of a target protein genetically fused with a fluorescent protein such as the jellyfish green fluorescent protein (GFP) is widely used. In addition, fluorescent chemical reagents are also used to stain specific molecules (e.g., Hoechst 33324 to stain DNA). Specimens of S. pombe cells for live cell imaging are prepared by either of two methods: sandwiching the cells between glass coverslips and by mounting the cells on a glass-bottom culture dish. For time-lapse observation, it is necessary to immobilize fission yeast cells on the glass surface of the glass-bottom dish because they are nonadherent and tend to move easily as a result of stage movement, convection flow of culture medium, and the contact and pushing of neighboring cells during cell growth. Either concanavalin A or soybean lectin, which bind to S. pombe cell walls, can be used for immobilization. Considerations for sample preparations and observation conditions are described.

Audano, P. and F. Vannberg (2014). "KAnalyze: a fast versatile pipelined k-mer toolkit." Bioinformatics **30**(14): 2070-2072.

MOTIVATION: Converting nucleotide sequences into short overlapping fragments of uniform length, k-mers, is a common step in many bioinformatics applications. While existing software packages count k-mers, few are optimized for speed, offer an application programming interface (API), a graphical interface or contain features that make it extensible and maintainable. We designed KAnalyze to compete with the fastest k-mer counters, to produce reliable output and to support future development efforts through well-architected, documented and testable code. Currently, KAnalyze can output k-mer counts in a sorted tab-delimited file or stream k-mers as they are read. KAnalyze can process large datasets with 2 GB of memory. This project is implemented in Java 7, and the command line interface (CLI) is designed to integrate into pipelines written in any language. RESULTS: As a k-mer counter, KAnalyze outperforms Jellyfish, DSK and a pipeline built on Perl and Linux utilities. Through extensive unit and system testing, we have verified that KAnalyze produces the correct k-mer counts over multiple datasets and k-mer sizes. AVAILABILITY AND IMPLEMENTATION: KAnalyze is available on SourceForge: https://sourceforge.net/projects/kanalyze/.

Auerbach, P. S. and J. T. Hays (1987). "Erythema nodosum following a jellyfish sting." J Emerg Med **5**(6): 487-491.

At least 100 of the approximately 9,000 species of coelenterates are dangerous to humans. The most common syndrome following an envenomation is an immediate intense dermatitis, with characteristic skin discoloration, local pain, and systemic symptoms. In this case report, we describe a case of erythema nodosum with articular manifestations following envenomation with an unknown jellyfish. Serological testing of the victim revealed marked elevation of

immunoglobulins G and M directed against Physalia physalis, the Portuguese man-of-war. The patient's condition did not respond to conventional topical therapy for coelenterate envenomation, but was successfully managed with systemic corticosteroid therapy. This case demonstrates that the emergency physician should consider a delayed reaction to a marine envenomation in any victim who presents with an acute dermatological disease following immersion in marine coastal waters.

Aumento, F., et al. (2005). "Transuranium radionuclide pollution in the waters of the La Maddalena National Marine Park." J Environ Radioact **82**(1): 81-93.

Following the grounding and subsequent explosion, in October 2003, of a nuclear submarine in the waters of the La Maddalena National Marine Park, fears arose of possible radioactive leakages. However, isotopic analyses on algae showed that the gamma-ray emitting artificial radionuclides that one might expect to leak from a damaged nuclear reactor (such as U-235, I-131, Cs-137) were absent, and that U-238/U-234 activities were in equilibrium with values typical of sea water; this excluded any direct anthropogenic contamination as a result of the accident. We used alpha autoradiographic techniques to detect possible traces of transuranium radionuclides; 160 samples of algae, granites, sea urchins, gastropods, limpets, cuttlefish and jellyfish were collected from the area, as well as from other Mediterranean coastlines and the Baltic Sea. All samples were autoradiographed, and selected samples further analysed by alpha spectrometry. There were no alpha track concentrations above background levels in our control Mediterranean specimens. In the samples from the La Maddalena and Baltic areas two different track distributions were observed: --those homogeneously distributed over the surfaces examined; --groups (10 to over 500) of radially distributed alpha tracks (forming "star" bursts, or "hot spots") emanating from point sources. By comparing radionuclide activities measured by alpha spectroscopy with alpha track densities, we extrapolated Pu activities for all samples. About 74% of algae had Pu activities of less than 1 Bq/kg and 0.25 Bq/kg, 16% had accumulated Pu to levels between 1 and 2 Bq/kg, and a very few specimens had concentrations between 2 and 6 Bq/kg. Plots showed that alpha tracks and stars concentrate around the northern and eastern margins of the Rada (Basin) di Santo Stefano, sites facing the nuclear submarine base on the eastern shore of the island of Santo Stefano. What is the source of these nuclides: last century's atmospheric nuclear testing, Chernobyl or a local source? Their concentrated, extremely localised occurrence seems difficult to explain in terms of left-over worldwide nuclear pollution. A local source seems more plausible.

Avian, M., et al. (1995). "Nematocysts of Rhopilema nomadica (Scyphozoa: Rhizostomeae), an immigrant jellyfish in the eastern mediterranean." J Morphol **224**(2): 221-231.

Rhopilema nomadica-a recently discovered scyphomedusa in the eastern Mediterranean-is considered a lessepsian migrant. Its nematocysts were extracted from the scapular and mouth-arm tentacles and examined using light and electron microscopy techniques. The morphometric parameters of the nematocysts were measured before and after complete discharge. Three categories of nematocysts were identified: heterotrichous isorhiza haploneme, holotrichous isorhiza haploneme, and heterotrichous microbasic eurytele. The relative abundance of the nematocysts and their occurrence in tissues of the jellyfish were noted. A brief discussion concerning the classification of certain types of nematocysts is given. A comparison with the available data on other Rhopilema species revealed that the nematocyst categories of R. nomadica are more similar to those of the Atlantic R. verrilli than to those of the Western Pacific R. esculentum. A brief comparison of the injuries caused by these species is given. (c) 1995 Wiley-Liss, Inc.

Ayed, Y., et al. (2014). "Cell death in relation to DNA damage after exposure to the jellyfish Pelagia noctiluca nematocysts." Environ Toxicol **29**(3): 337-344.

Studies on the toxicity of Mediterranean jellyfish have gained attention owing to their weak toxic properties. Our research has been mainly performed on the Scyphomedusae. Pelagia noctiluca is a scyphozoan jellyfish which causes a danger to sea bathers and fishery damages in the Mediterranean Sea. To check whether the cytotoxicity of Pelagia noctiluca nematocysts was associated to DNA lesions, we have looked for DNA fragmentation by means of the Comet and chromosome aberration assays. To specify cell death pathway, we have investigated caspase-3 activation. Our results have shown that nematocysts reduced cell viability and induced DNA fragmentation in a concentration-dependent manner with a maximum effect at 150 000 nematocysts mL (-1). The high percentage of chromosome aberrations also emphasized the genotoxic character of Pelagia noctiluca nematocysts in Vero cells. This fragmentation was correlated to apoptosis induction which was confirmed by caspase-3 activation. In conclusion, the present report has suggested that Pelagia noctiluca nematocysts were able to promote apoptosis in Vero cells and therefore may be useful in

cancer therapy.

Ayed, Y., et al. (2012). "Impairment of the cell-to-matrix adhesion and cytotoxicity induced by the Mediterranean jellyfish Pelagia noctiluca venom and its fractions in cultured glioblastoma cells." Lipids Health Dis **11**: 84.

BACKGROUND: The biodiversity of the marine environment and the associated chemical diversity constitute a practically unlimited source of new active substances in the field of the development of bioactive products. In our study, we have investigated the efficiency of the venom from the Mediterranean jellyfish, Pelagia noctiluca and its fractions for anti-proliferative and anti-cell adhesion to cell-extracellular matrix activities. RESULTS: Our experiments have indicated that the separation of the Mediterranean jellyfish Pelagia noctiluca crude venom extract by sephadex G-75 chromatography led to four fractions (F1, F2, F3, and F4). Among the four fractions F1 and F3 were cytotoxic against U87 cells with IC50 values of 125 and 179 mug/ml respectively. The venom, F1, F2 and F 3 showed significant anti-proliferative activity in time-dependent manner. Our results also suggest that these fractions and the venom are able to inhibit cell adhesion to fibrinogen in dose-dependent manner. This inhibition is reliant on its ability to interact with integrins. CONCLUSIONS: To conclude, we have demonstrated for the first time that Pelagia noctiluca venom and its fractions especially (F1 and F2) display potent anti-tumoral properties. Separation by sephadex G-75 chromatography give rise to more active fractions than the crude venom extract. The purification and the determination of chemical structures of compounds of these active fractions are under investigation. Overall, Pelagia noctiluca venom may has the potential to serve as a template for future anticancer-drug development.

Ayed, Y., et al. (2011). "Induction of cytotoxicity of Pelagia noctiluca venom causes reactive oxygen species generation, lipid peroxydation induction and DNA damage in human colon cancer cells." Lipids Health Dis **10**: 232.

BACKGROUND: The long-lasting and abundant blooming of Pelagia noctiluca in Tunisian coastal waters compromises both touristic and fishing activities and causes substantial economic losses. Determining their molecular mode of action is, important in order to limit or prevent the subsequent damages. Thus, the aim of the present study was to investigate the propensity of Pelagia noctiluca venom to cause oxidative damage in HCT 116 cells and its associated genotoxic effects. RESULTS: Our results indicated an overproduction of ROS, an induction of catalase activity and an increase of MDA generation. We looked for DNA fragmentation by means of the comet assay. Results indicated that venom of Pelagia noctiluca induced DNA fragmentation. SDS-PAGE analysis of Pelagia noctiluca venom revealed at least 15 protein bands of molecular weights ranging from 4 to 120 kDa. CONCLUSION: Oxidative damage may be an initiating event and contributes, in part, to the mechanism of toxicity of Pelagia noctiluca venom.

Ayed, Y., et al. (2013). "Is cell death induced by nematocysts extract of medusa Pelagia noctiluca related to oxidative stress?" Environ Toxicol **28**(9): 498-506.

Pelagia noctiluca, a jellyfish widely distributed in the Mediterranean waters, especially in coastal areas of Tunisia, has garnered attention because of its stinging capacity and the resulting public health hazard. Crude extracts of P. noctiluca nematocysts have been tested for their cytotoxicity on Vero cells. Our results clearly showed that nematocysts induced cell mortality in a dose- and time-dependent manner. A cytoprotective effect against cell mortality was obtained when Vero cells were treated with Vitamin E. This process was further confirmed by the generation of reactive oxygen species (ROS) and the induction of Hsp 70 and 27 protein expressions. Thus, our findings suggested that oxidative stress is involved in the toxicity of pelagia nematocysts and may therefore constitute the major mechanism of this medusa nematocysts toxicity.

Azari, P., et al. (2011). "Pathophysiology of the spreading of complex regional pain syndrome revisited: a case report." Neuromodulation **14**(5): 428-431; discussion 431.

OBJECTIVE: To determine if there is a relationship in our patient developing complex regional pain syndrome from a jellyfish and its subsequent spread to the contralateral side. METHODS: Data bases were searched using PubMed and Ovid. Keywords searched include "complex regional pain syndrome,""jelly fish," and "pathophysiology." RESULTS: This patient was successfully treated with a spinal cord stimulator implantation with bilateral lead placement at thoracic spine (T9) stimulating her lower extremities in addition to the leads that had already been placed in her cervical spine for her upper extremities. CONCLUSION: Definite knowledge of the pathophysiology of complex regional pain syndrome would allow better identification of risk factors for the development of this condition after trauma. This patient is at higher risk of developing complex regional pain syndrome and should avoid surgeries (such as knee and wrist surgeries) and high risk physical activities.

Azila, N., et al. (1991). "Haemolytic, oedema and haemorrhage inducing activities of tentacular extract of the blubber jellyfish (Catostylus mosaicus)." Comp Biochem Physiol C **99**(1-2): 153-156.

1. An extract prepared from the tentacle of the jellyfish (CE), Catostylus mosaicus exhibited haemolytic, oedema and haemorrhage-inducing activities. 2. Acetone treatment of the tentacle extract produced an acetone soluble extract (AE) which showed an increase in specific haemolytic and haemorrhagic activities by 25- and 120-fold respectively; the minimum oedema dose was reduced by 30-fold. 3. The AE caused a rapid onset of oedema in the mouse foot pad. The effect was long-lasting, reaching a maximum in about 30 min after injection and sustained up to 4 hr. 4. Fractionation of the AE on Q-Sepharose gave 4 bound fractions which induced oedema and haemorrhage; however only 3 of the fractions exhibited haemolytic activity.

Azuma, H., et al. (1986). "Calcium-dependent contractile response of arterial smooth muscle to a jellyfish toxin (pCrTX: Carybdea rastonii)." Br J Pharmacol **88**(3): 549-559.

The purpose of the present experiments was to investigate the pharmacological mechanisms of the vasoconstriction caused by the toxin (pCrTX) which had been partially purified from the tentacles of the jellyfish Carybdea rastonii ('Andonkurage'). pCrTX (0.1 to 10 micrograms ml-1) produced a tonic contraction of rabbit aortic strips, which was nearly abolished in Ca2+-free medium and was significantly reduced by verapamil or diltiazem. pCrTX stimulated 45Ca2+-influx and this effect was markedly attenuated by verapamil. pCrTX-induced vasoconstriction was significantly attenuated by phentolamine, 6-hydroxydopamine (6-OHDA) and in low Na+-medium, but not by bretylium, guanethidine, reserpinization or tetrodotoxin (TTX). pCrTX continuously and significantly increased the 3H-efflux from [3H]-noradrenaline preloaded aortic strips and this effect was completely inhibited by pretreatment with 6-OHDA and in Ca2+-free medium, but not by phentolamine, bretylium, guanethidine or TTX. A single exposure to pCrTX for 30 min greatly reduced the contractile responses to tyramine, nicotine and transmural electrical stimulation, but not those to noradrenaline or KC1. In addition, incorporation of [3H]-noradrenaline was reduced. Pretreatments with chlorphenylamine or indomethacin failed to modify the contractile response to pCrTX. These results suggest that the pCrTX-induced vasoconstriction is caused by a presynaptic action, releasing noradrenaline from the intramural adrenergic nerve terminals, and by a postsynaptic action, which consists at least in part of stimulation of the transmembrane calcium influx. Both pre- and postsynaptic actions depend on the external calcium concentration. The data further suggest that pCrTX damages the noradrenaline uptake and/or storage mechanisms without damaging postsynaptic contractile systems.

Azuma, H., et al. (1986). "Platelet aggregation caused by Carybdea rastonii toxins (CrTX-I, II and III) obtained from a jellyfish, Carybdea rastonii." Proc Soc Exp Biol Med **182**(1): 34-42.

The pharmacological mechanisms of platelet aggregation induced by highly toxic proteins (CrTX-I, CrTX-II, and CrTX-III) obtained from tentacles of a jellyfish, Carybdea rastonii, were investigated. When the partially purified toxin (pCrTX) and CrTXs were added to the citrated platelet-rich plasma (PRP), aggregation was produced in a concentration-dependent manner. The activity of CrTXs was approximately 100 times more potent than pCrTX. The CrTXs-induced aggregation was little affected by indomethacin and quinacrine at concentrations sufficient to inhibit arachidonic acid- and collagen-induced aggregation. The CrTXs-induced aggregation in washed platelets was significantly augmented in the presence of Ca2+. The pretreatment with verapamil failed to modify this augmentation of aggregation. The concentration of cytoplasmic-free calcium ([Ca2+]i) of platelets was increased by CrTXs at the same concentrations that produced aggregation. This effect of CrTXs was again little affected by verapamil. CrTXs at the same concentrations as those that produced aggregation and increased [Ca2+]i caused depolarization of platelets, which was unchanged after pretreatment with sodium or potassium transport inhibitors. CrTX-I significantly increased the 22Na flux into platelets and this effect of CrTX-I was unaffected by tetrodotoxin. The CrTX-I-induced aggregation, depolarization, and increase in [Ca2+]i were all significantly attenuated in the low Na+ medium. These results suggest that CrTXs cause a massive depolarization by increasing cation permeability and this generalized depolarization permits an inward movement of Ca2+ down its electrochemical gradient which, in turn, triggers platelet aggregation.

Azuma, H., et al. (1986). "Platelet aggregation caused by a partially purified jellyfish toxin from Carybdea rastonii." Toxicon **24**(5): 489-499.

A partially purified toxin (pCrTX) was obtained from the tentacles of the jellyfish, Carybdea rastonii. When pCrTX (3 X 10(-8) - 3 X 10(-7) g/ml) was added to citrated platelet-rich plasma, aggregation was produced in a concentration-dependent manner. Scanning electron microscopic examination revealed

that both pCrTX and collagen produced aggregates of platelets possessing many pseudopods. The concentration which produced 50% aggregation for pCrTX was 1.8 X 10(-7) g/ml, as compared to 2.3 X 10(-6) g/ml for collagen. The pCrTX-induced aggregation was only slightly inhibited by indomethacin and quinacrine in concentrations sufficient to inhibit arachidonic acid- and collagen-induced aggregation. pCrTX was less active in washed platelets suspended in Ca2+ free medium, whereas the pCrTX-induced aggregation was significantly augmented in the presence of Ca2+. The augmentation of aggregation by Ca2+ was only slightly attenuated by pretreatment with 100 microM verapamil. pCrTX significantly increased the concentration of cytoplasmic free Ca2+ ([Ca2+]i) and depolarized the platelet membrane in concentrations that produced aggregation. The increase in [Ca2+]i caused by pCrTX was little affected by verapamil. The depolarization by pCrTX was unchanged in the presence or absence of Ca2+, or by sodium or potassium transport inhibitors. The movement of 22Na+ into platelets was significantly increased by pCrTX. This increase in the movement of 22N+ into platelets was unaffected by tetrodotoxin. On the other hand, pCrTX-induced aggregation, depolarization and the increase in [Ca2+]i were all significantly attenuated in low Na+ medium. These results suggest that pCrTX causes a massive depolarization by increasing cation permeability indiscriminately and this generalized depolarization permits an inward movement of calcium down an electrochemical gradient which, in turn triggers platelet aggregation.

Badre, S. (2014). "Bioactive toxins from stinging jellyfish." Toxicon **91**: 114-125.

Jellyfish blooms occur throughout the world. Human contact with a jellyfish induces a local reaction of the skin, which can be painful and leave scaring. Systemic symptoms are also observed and contact with some species is lethal. A number of studies have evaluated the in vitro biological activity of whole jellyfish venom or of purified fractions. Hemolytic, cytotoxic, neurotoxic or enzymatic activities are commonly observed. Some toxins have been purified and characterized. A family of pore forming toxins specific to Medusozoans has been identified. There remains a need for detailed characterization of jellyfish toxins to fully understand the symptoms observed in vivo.

Bae, S. K., et al. (2017). "In vitro characterization of jellyfish venom fibrin (ogen)olytic enzymes from Nemopilema nomurai." J Venom Anim Toxins Incl Trop Dis **23**: 35.

BACKGROUND: Because jellyfish are capable of provoking envenomation in humans, they are considered hazardous organisms. Although the effects of their toxins are a matter of concern, information on the venom components, biological activity and pathological mechanisms are still scarce. Therefore, the aim of the present study was to investigate a serine protease component of Nemopilema nomurai jellyfish venom (NnV) and unveil its characteristics. METHODS: To determine the relationship between fibrinolytic activity of NnV and the serine protease, fibrin zymography was performed using metalloprotease and serine protease inhibitors. The biochemical characterization of serine proteases of NnV were determined by the amidolytic assay. Fractions with fibrinolytic activity were obtained by DEAE cation exchange column. RESULTS: NnV displayed fibrinolytic activities with molecular masses of approximately 70, 35, 30, and 28 kDa. The fibrinolytic activity of NnV was completely obliterated by phenylmethylsulfonyl fluoride, a prototype serine protease inhibitor. Based on amidolytic assays using chromogenic substrates specific for various kinds of serine proteases, NnV predominantly manifested a chymotrypsin-like feature. Its activity was completely eliminated at low pH (< 6) and high temperatures (> 37 degrees C). Some metal ions (Co (2+), Cu (2+), Zn (2+) and Ni (2+)) strongly suppressed its fibrinolytic activity, while others (Ca (2+) and Mg (2+)) failed to do so. Isolation of a serine protease with fibrionolytic activity from NnV revealed that only p3 showed the fibrinolytic activity, which was completely inhibited by PMSF. CONCLUSION: The present study showed that N. nomurai jellyfish venom has a chymotrypsin-like serine protease with fibrinolytic activity. Such information might be useful for developing clinical management of jellyfish envenomation and pharmacological agents with therapeutic potential for thrombotic diseases in the future.

Baek, D., et al. (2004). "Bax-induced cell death of Arabidopsis is meditated through reactive oxygen-dependent and -independent processes." Plant Mol Biol **56**(1): 15-27.

An Arabidopsis protoplast system was developed for dissecting plant cell death in individual cells. Bax, a mammalian pro-apoptotic member of the Bcl-2 family, induces apoptotic-like cell death in Arabidopsis. Bax accumulation in Arabidopsis mesophyll protoplasts expressing murine Bax cDNA from a glucocorticoid-inducible promoter results in cytological characteristics of apoptosis, namely DNA fragmentation, increased vacuolation, and loss of plasma membrane integrity. In vivo targeting analysis monitored using jellyfish green fluorescent protein (GFP) reporter indicated full-length Bax was localized to the mitochondria, as it does in animal cells. Deletion

of the carboxyl-terminal transmembrane domain of Bax completely abolished targeting to mitochondria. Bax expression was followed by reactive oxygen species (ROS) accumulation. Treatment of protoplasts with the antioxidant N -acetyl- -cysteine (NAC) during induction of Bax expression strongly suppressed Bax-mediated ROS production and the cell death phenotype. However, some population of the ROS depleted cells still induced cell death, indicating that there is a process that Bax-mediated plant cell death is independent of ROS accumulation. Accordingly, suppression of Bax-mediated plant cell death also takes place in two different processes. Over-expression of a key redox-regulator, Arabidopsis nucleoside diphosphate kinase 2 (AtNDPK2) down-regulated ROS accumulation and suppressed Bax-mediated cell death and transient expression of Arabidopsis Bax inhibitor-1 (AtBI-1) substantially suppressed Bax-induced cell death without altering cellular ROS level. Taken together, our results collectively suggest that the Bax-mediated cell death and its suppression in plants is mediated by ROS-dependent and -independent processes.

Bailes, H. J., et al. (2012). "Reproducible and sustained regulation of Galphas signalling using a metazoan opsin as an optogenetic tool." PLoS One **7**(1): e30774.

Originally developed to regulate neuronal excitability, optogenetics is increasingly also used to control other cellular processes with unprecedented spatiotemporal resolution. Optogenetic modulation of all major G-protein signalling pathways (Gq, Gi and Gs) has been achieved using variants of mammalian rod opsin. We show here that the light response driven by such rod opsin-based tools dissipates under repeated exposure, consistent with the known bleaching characteristics of this photopigment. We continue to show that replacing rod opsin with a bleach resistant opsin from Carybdea rastonii, the box jellyfish, (JellyOp) overcomes this limitation. Visible light induced high amplitude, reversible, and reproducible increases in cAMP in mammalian cells expressing JellyOp. While single flashes produced a brief cAMP spike, repeated stimulation could sustain elevated levels for 10s of minutes. JellyOp was more photosensitive than currently available optogenetic tools, responding to white light at irradiances >/=1 microW/cm (2). We conclude that JellyOp is a promising new tool for mimicking the activity of Gs-coupled G protein coupled receptors with fine spatiotemporal resolution.

Bailey, P. M., et al. (2003). "Jellyfish envenoming syndromes: unknown toxic mechanisms and unproven therapies." Med J Aust **178**(1): 34-37.

Interest in envenoming syndromes caused by Australian jellyfish has been intense since the deaths in early 2002 of two tourists in Queensland, attributed to the Irukandji syndrome. We review current knowledge of these envenoming syndromes, mechanisms of venom action and therapy, focusing on the deadly box jellyfish, Chironex fleckeri, and the array of jellyfish thought to cause the Irukandji syndrome. Current understanding of jellyfish venom activity is very limited, and many treatments are unproven and based on anecdote.

Bajar, B. T., et al. (2016). "Improving brightness and photostability of green and red fluorescent proteins for live cell imaging and FRET reporting." Sci Rep **6**: 20889.

Many genetically encoded biosensors use Forster resonance energy transfer (FRET) to dynamically report biomolecular activities. While pairs of cyan and yellow fluorescent proteins (FPs) are most commonly used as FRET partner fluorophores, respectively, green and red FPs offer distinct advantages for FRET, such as greater spectral separation, less phototoxicity, and lower autofluorescence. We previously developed the green-red FRET pair Clover and mRuby2, which improves responsiveness in intramolecular FRET reporters with different designs. Here we report the engineering of brighter and more photostable variants, mClover3 and mRuby3. mClover3 improves photostability by 60% and mRuby3 by 200% over the previous generation of fluorophores. Notably, mRuby3 is also 35% brighter than mRuby2, making it both the brightest and most photostable monomeric red FP yet characterized. Furthermore, we developed a standardized methodology for assessing FP performance in mammalian cells as stand-alone markers and as FRET partners. We found that mClover3 or mRuby3 expression in mammalian cells provides the highest fluorescence signals of all jellyfish GFP or coral RFP derivatives, respectively. Finally, using mClover3 and mRuby3, we engineered an improved version of the CaMKIIalpha reporter Camuialpha with a larger response amplitude.

Bakayan, A., et al. (2017). "Fluorescent Protein-photoprotein Fusions and Their Applications in Calcium Imaging." Photochem Photobiol **93**(2): 448-465.

Calcium-activated photoproteins, such as aequorin, have been used as luminescent Ca (2+) indicators since 1967. After the cloning of aequorin in 1985, microinjection was substituted by its heterologous expression, which opened the way for a widespread use. Molecular fusion of green fluorescent protein (GFP) to aequorin recapitulated the nonradiative energy transfer process that occurs in the

jellyfish Aequorea victoria, from which these two proteins were obtained, resulting in an increase of light emission and a shift to longer wavelength. The abundance and location of the chimera are seen by fluorescence, whereas its luminescence reports Ca (2+) levels. GFP-aequorin is broadly used in an increasing number of studies, from organelles and cells to intact organisms. By fusing other fluorescent proteins to aequorin, the available luminescence color palette has been expanded for multiplexing assays and for in vivo measurements. In this report, we will attempt to review the various photoproteins available, their reported fusions with fluorescent proteins and their biological applications to image Ca (2+) dynamics in organelles, cells, tissue explants and in live organisms.

Bakayan, A., et al. (2011). "Red fluorescent protein-aequorin fusions as improved bioluminescent Ca2+ reporters in single cells and mice." PLoS One **6**(5): e19520.

Bioluminescence recording of Ca (2+) signals with the photoprotein aequorin does not require radiative energy input and can be measured with a low background and good temporal resolution. Shifting aequorin emission to longer wavelengths occurs naturally in the jellyfish Aequorea victoria by bioluminescence resonance energy transfer (BRET) to the green fluorescent protein (GFP). This process has been reproduced in the molecular fusions GFP-aequorin and monomeric red fluorescent protein (mRFP)-aequorin, but the latter showed limited transfer efficiency. Fusions with strong red emission would facilitate the simultaneous imaging of Ca (2+) in various cell compartments. In addition, they would also serve to monitor Ca (2+) in living organisms since red light is able to cross animal tissues with less scattering. In this study, aequorin was fused to orange and various red fluorescent proteins to identify the best acceptor in red emission bands. Tandem-dimer Tomato-aequorin (tdTA) showed the highest BRET efficiency (largest energy transfer critical distance R (0)) and percentage of counts in the red band of all the fusions studied. In addition, red fluorophore maturation of tdTA within cells was faster than that of other fusions. Light output was sufficient to image ATP-induced Ca (2+) oscillations in single HeLa cells expressing tdTA. Ca (2+) rises caused by depolarization of mouse neuronal cells in primary culture were also recorded, and changes in fine neuronal projections were spatially resolved. Finally, it was also possible to visualize the Ca (2+) activity of HeLa cells injected subcutaneously into mice, and Ca (2+) signals after depositing recombinant tdTA in muscle or the peritoneal cavity. Here we report that tdTA is the brightest red bioluminescent Ca (2+) sensor reported to date and is, therefore, a promising probe to study Ca (2+) dynamics in whole organisms or tissues expressing the transgene.

Balamurugan, E., et al. (2010). "Antitumor and antioxidant role of Chrysaora quinquecirrha (sea nettle) nematocyst venom peptide against Ehrlich ascites carcinoma in Swiss Albino mice." Mol Cell Biochem **338**(1-2): 69-76.

This investigation aims to evaluate the antitumor and antioxidant potential of Chrysaora quinquecirrha (sea nettle) nematocyst venom on Ehrlich ascites carcinoma (EAC) tumor model. Tumor was induced in mice by intraperitoneal injection of EAC cells. The antitumor effect of sea nettle nematocyst venom (SNV) peptide was evaluated by assessing in vitro cytotoxicity, survival time, hematological, and antioxidant parameters. Intraperitoneal injection of SNV peptide increased the survival time of the EAC-bearing mice. The SNV peptide brought back the altered levels of the hematological and antioxidant parameters in a dose dependent manner in EAC-bearing mice. The results were comparable to that of the result obtained from the animals treated with the standard drug 5-fluorouracil (20 mg/kg bw). Thus, present study revealed that SNV peptide possessed significant antitumor and antioxidant activity.

Balasubramanian, P. G., et al. (2012). "Proteome of Hydra nematocyst." J Biol Chem **287**(13): 9672-9681.

Stinging cells or nematocytes of jellyfish and other cnidarians represent one of the most poisonous and sophisticated cellular inventions in animal evolution. This ancient cell type is unique in containing a giant secretory vesicle derived from the Golgi apparatus. The organelle structure within the vesicle comprises an elastically stretched capsule (nematocyst) to which a long tubule is attached. During exocytosis, the barbed part of the tubule is accelerated with >5 million g in <700 ns, enabling a harpoon-like discharge (Nuchter, T., Benoit, M., Engel, U., Ozbek, S., and Holstein, T. W. (2006) Curr. Biol. 16, R316-R318). Hitherto, the molecular components responsible for the organelle's biomechanical properties were largely unknown. Here, we describe the proteome of nematocysts from the freshwater polyp Hydra magnipapillata. Our analysis revealed an unexpectedly complex secretome of 410 proteins with venomous and lytic but also adhesive or fibrous properties. In particular, the insoluble fraction of the nematocyst represents a functional extracellular matrix structure of collagenous and elastic nature. This finding suggests an evolutionary scenario in which exocytic vesicles harboring a venomous secretome assembled a sophisticated predatory structure from extracellular matrix motif proteins.

Balhara, K. S. and A. Stolbach (2014). "Marine envenomations." Emerg Med Clin North Am **32**(1): 223-243.

This article describes the epidemiology and presentation of human envenomation from marine organisms. Venom pathophysiology, envenomation presentation, and treatment options are discussed for sea snake, stingray, spiny fish, jellyfish, octopus, cone snail, sea urchin, and sponge envenomation. The authors describe the management of common exposures that cause morbidity as well as the keys to recognition and treatment of life-threatening exposures.

Baliarsingh, S. K., et al. (2016). "Environmental dynamics of red Noctiluca scintillans bloom in tropical coastal waters." Mar Pollut Bull **111**(1-2): 277-286.

An intense bloom of red Noctiluca scintillans (NS) occurred off the Rushikulya estuarine region along the east coast of India, an important site for mass nesting events of the vulnerable Olive Ridley sea turtle. At its peak, densities of NS were 3.3x10(5) cells-l (-1), with low relative abundance of other phytoplankton. The peak bloom coincided with high abundance of gelatinous planktivores which may have facilitated bloom development by their grazing on other zooplankton, particularly copepods. Ammonium concentrations increased by approximately 4-fold in the later stages of bloom, coincident with stable NS abundance and chlorophyll concentrations in the nano- and microplankton. This increase likely was attributable to release of intracellular ammonium accumulated through NS grazing. Dissolved oxygen concentrations decreased in sub-surface waters to near hypoxia. Micro-phytoplankton increasingly dominated chlorophyll-a biomass as the bloom declined, with diminishing picoplankton abundance likely the result of high predation by the ciliate Mesodinium rubrum. Together, these data illustrate factors that can disrupt ecosystem balance in this critically important Indian coastal region.

Ballantine, J. A., et al. (1976). "Marine sterols. III--The sterol compositions of oceanic jellyfish. The use of gas chromatographic mass spectrometric techniques to identify unresolved components." Biomed Mass Spectrom **3**(1): 14-20.

The sterol compositions of three oceanic jellyfish have been determined using gas chromatographic mass spectrometric techniques involving the use of two separate gas chromatographic column systems. The components in overlapping peaks have been identified by comparison of the mass spectra of peaks in the two column systems using subtractive techniques. A mid-water animal, Periphylla periphylla, was found to contain a very complex and unusual sterol profile including rare 5alpha-stanols, whereas two other oceanic jellyfish Pelagia noctiluca and Atolla wyvillei contained similar mixtures of delta5 sterols to those previously isolated from coastal species.

Bally, A. and V. Schmid (1988). "The jellyfish and its polyp: a comparative study of gene expression monitored by the protein patterns, using two-dimensional gels with double-label autoradiography." Cell Differ **23**(1-2): 93-102.

The life cycle of Podocoryne carnea (Coelenterata, Anthomedusae) shows several distinct stages which differ considerably in terms of their ecology, morphology, cellular composition, and ultrastructure. Previously these stages had even been described as separate species. Using two-dimensional gel electrophoresis and a new method of double-label autoradiography, we show here for the first time for metagenic hydrozoans that only minor differences in gene expression exist between the various life cycle stages. Our results demonstrate the high resolution power of these techniques and show that the different life stages of P. carnea remain rather similar on the protein level. Most of the prominent spots of the two-dimensional gel protein patterns are common to all stages studied. These data show that the hydrozoan life cycle and development are regulated by only minor distinctions in gene expression which possibly explains the great morphogenetic repertoire of these animals described in many studies.

Balqis, A. R. S., et al. (2016). "Seasonal variations of zooplankton biomass and size-fractionated abundance in relation to environmental changes in a tropical mangrove estuary in the Straits of Malacca." J Environ Biol **37**(4 Spec No): 685-695.

Seasonal variations of zooplankton community in terms of biomass and size-fractionated densities were studied in a tropical Sangga Kechil river, Matang, Perak from June 2010 to April 2011. Zooplankton and jellyfish (hydromedusae, siphonophores and ctenophores) samples were collected bimonthly from four sampling stations by horizontal towing of a 140-?m plankton net and 500?m bongo net, respectively. A total of 12 zooplankton groups consisting of six groups each of mesozooplankon (0.2 mm-2.0 mm) and macrozooplankton (2.0 mm-20.0 cm) were recorded. The total zooplankton density (12375?3339 ind m (-3)) and biomass (35.32?14.56 mg m (-3)) were highest during the northeast (NE) monsoon and southwest (SW) monsoon, respectively, indicating the presence of bigger individuals in the latter season. Mesozooplankton predominated (94%) over the macrozooplankton (6%) during all the seasons, and copepods contributed 84% of the total mesozooplankton abundance. Macrozooplankton was

dominated by appendicularians during most of the seasons (43%-97%), except during the NE monsoon (December) when chaetognaths became the most abundant (89% of the total macrozooplankton). BIO-ENV analysis showed that total zooplankton density was correlated with turbidity, total nitrogen and total phosphorus, which in turn was positively correlated to chlorophyll a. Cluster analysis of the zooplankton community showed no significant temporal difference between the SW and NE monsoon season during the study period (> 90% similarity). The present study revealed that the zooplankton community in the tropical mangrove estuary in the Straits of Malacca was dominated by mesoplankton, especially copepods.

Bamstedt, U. and M. B. Martinussen (2000). "Estimating digestion rate and the problem of individual variability, exemplified by a scyphozoan jellyfish." J Exp Mar Bio Ecol **251**(1): 1-15.

Short-term (h) and long-term (days) individual variability and the effects of momentary change in feeding intensity on digestion time were studied in the scyphomedusa Aurelia aurita as a basis for developing a method to experimentally measure the digestion rate with a high precision. Ten individual medusae showed only small, non-significant differences in average digestion time (range, 2.1-2.5 h at 10 degrees C) over a 9-day experiment, whereas variability within and between days and between individuals at a given occasion was high. When medusae were manually kept at a constant feeding intensity, stomach fullness showed high variability both between individuals and within an individual over time. With a feeding intensity of, respectively, 1, 2, 4 and 8 prey h (-1) over a 5-h experimental period, stomach fullness of most individuals corresponded to a theoretical digestion time of 1-3 h, whereas single meals of the same size usually gave somewhat higher digestion time. Medusae subject to a switching from a low to a high feeding intensity tended to increase the variability, but most individuals showed a digestion time of 1-3 h. An opposite switching tended to increase the digestion time and its variability. It is concluded that the digestion time of A. aurita is randomly variable over time within given limits for a given food and environmental condition. This variability is non-synchronised in the population, causing high variability between individuals, and changes in the feeding intensity cause additional variability. However, the average digestion time of A. aurita in a physically and nutritionally stable environment is robust, and changes in the feeding intensity give predictable effects. The use of field collected data on stomach contents and laboratory determined digestion times is therefore an attractive method to calculate predation rate, but the inherent high variability in digestion time must be taken into consideration when designing the digestion experiments. Based on these findings a simple experimental method to determine the digestion time of aquatic animals is outlined and evaluated. The digestion time is simply given as the ratio between number of prey in stomach and total number of prey eaten, times the incubation time, assuming that the feeding intensity is constant.

Banuelos, O., et al. (2002). "Subcellular localization of the homocitrate synthase in Penicillium chrysogenum." Mol Genet Genomics **266**(5): 711-719.

There are conflicting reports regarding the cellular localization in Saccharomyces cerevisiae and filamentous fungi of homocitrate synthase, the first enzyme in the lysine biosynthetic pathway. The homocitrate synthase (HS) gene (lys1) of Penicillium chrysogenum was disrupted in three transformants (HS (-)) of the Wis 54-1255 pyrG strain. The three mutants named HS1(-), HS2(-) and HS3(-) all lacked homocitrate synthase activity and showed lysine auxotrophy, indicating that there is a single gene for homocitrate synthase in P. chrysogenum. The lys1 ORF was fused in frame to the gene for the green fluorescent protein (GFP) gene of the jellyfish Aequorea victoria. Homocitrate synthase-deficient mutants transformed with a plasmid containing the lys1-GFP fusion recovered prototrophy and showed similar levels of homocitrate synthase activity to the parental strain Wis 54-1255, indicating that the hybrid protein retains the biological function of wild-type homocitrate synthase. Immunoblotting analysis revealed that the HS-GFP fusion protein is maintained intact and does not release the GFP moiety. Fluorescence microscopy analysis of the transformants showed that homocitrate synthase was mainly located in the cytoplasm in P. chrysogenum; in S. cerevisiae the enzyme is targeted to the nucleus. The control nuclear protein StuA was properly targeted to the nucleus when the StuA (targeting domain)-GFP hybrid protein was expressed in P. chrysogenum. The difference in localization of homocitrate synthase between P. chrysogenum and S. cerevisiae suggests that this protein may play a regulatory function, in addition to its catalytic function, in S. cerevisiae but not in P. chrysogenum.

Barath Kumar, S., et al. (2017). "Impingement of marine organisms in a tropical atomic power plant cooling water system." Mar Pollut Bull **124**(1): 555-562.

A one-year impingement monitoring was conducted at Madras Atomic Power Station (MAPS), Kalpakkam, southeastern coast of India and identified a total of 67 species of marine organisms in the cooling water system. Estimates of total annual

impingement contributed about 1.47x10(6) individuals and 142.5t of biomass. Jellyfish contributed about 6.8x10(5) individuals and 135.6t of biomass. Crabs, shrimps and fish were the most vulnerable organisms contributing about 4.29x10(5) individuals, 1.39x10(5) individuals and 2.16x10(5) individuals respectively. Commercially important species namely Trichiurus lepturus, Sardinella longiceps and Portunus pelagicus were found to be impinged 1.88% and 0.29% by number and weight of the total biomass respectively. Out of ~327 fish species recorded at Kalpakkam, only about 9.4% of species were impinged at MAPS. Multispecies impingement at MAPS poses the problem of finding the best mitigation options for tropical conditions.

Barker, H., et al. (2001). "Evidence for RNA-mediated defence effects on the accumulation of Potato leafroll virus." J Gen Virol **82**(Pt 12): 3099-3106.

In plants infected with Potato leafroll virus (PLRV), or other luteoviruses, infection is very largely confined to cells in the vascular system. Even in tobacco plants transformed with PLRV full-length cDNA, in which all mesophyll cells should synthesize infectious PLRV RNA transcripts, only a minority of the mesophyll cells accumulate detectable amounts of virus. We have explored this phenomenon further by transforming a better PLRV host, Nicotiana benthamiana, with the same transgene, by superinfecting transformed plants with Potato virus Y and by producing tobacco plants in which cells contained both PLRV cDNA and DNA encoding the P1/HC-Pro genes of the potyvirus Tobacco etch virus. A greater proportion of cells in superinfected plants or in doubly transgenic plants accumulated PLRV than did in singly transgenic tobacco plants. However, most cells in these plants did not accumulate virus. To investigate restriction of the multiplication of viruses containing PLRV sequences, transgenic plants were infected with a chimeric virus that consisted of Tobacco mosaic virus (TMV) containing genes for either the coat protein (CP) of PLRV or jellyfish green fluorescent protein (GFP) in place of the TMV coat protein. The virus that encoded PLRV CP spread more slowly and accumulated less extensively than did the virus that expressed GFP. The results support the suggestion that an RNA-mediated form of resistance that resembles post-transcriptional gene silencing operates in non-vascular cells and may be part of the mechanism that restricts PLRV to vascular tissue in conventionally infected plants.

Barnett, F. I., et al. (2005). "Management of Irukandji syndrome in northern Australia." Rural Remote Health **5**(3): 369.

INTRODUCTION: Irukandji syndrome, a potentially life-threatening condition that follows the sting of small carybdeid jellyfish, occurs along the northern Australian coastline from Broome, Western Australia in the west to Rockhampton, Queensland in the east. Much of this area is classified rural or remote. Because correct patient management is essential to avoid unnecessary fatality, and stings are relatively uncommon in any specific location, it was considered important to document current approaches to Irukandji syndrome management throughout coastal northern Australia, comparing urban and more rural health facilities, and to assess the availability of management guidelines for health staff. METHODS: A telephone survey of the clinicians responsible for Irukandji syndrome patient management at 34 coastal northern Australian health facilities that might encounter this patient presentation was conducted during November and December 2003. Healthcare providers responsible for Irukandji syndrome management on the day of survey were interviewed using a structured, standardized questionnaire, which included a description of a hypothetical patient with Irukandji syndrome. This was used to stimulate a spontaneous description of the usual response of the particular health facility to such a patient presentation. Additional vignettes were used to investigate further specific aspects of patient management, including first aid, and pain and blood pressure management. Respondents were also asked about the existence of Irukandji treatment guidelines at their facility. RESULTS: All 34 facilities contacted agreed to participate. Five health facilities were in urban centres with a population of 50,000 or greater, four were within 50 km of such centres, 20 were more remote and five facilities were on islands. Basic clinical monitoring (blood pressure, pulse, respiratory rate and oxygen saturation) was generally adequately practised. Topical application of vinegar as a first aid measure was described by 79% of respondents, with spontaneous mention of vinegar significantly associated with increasing remoteness ($p = 0.023$). Other sting site management was variable, with uncertainty about the use of pressure immobilisation bandaging. Intravenous opiate analgesia was administered at 91% of facilities, and magnesium sulphate, a treatment that is still being evaluated for its role in Irukandji syndrome-related pain and hypertension, was mentioned by 12% of respondents for pain relief. Twelve different pharmacological treatments were used for syndrome-associated hypertension, with magnesium sulphate being mentioned by 21% of respondents. Of the 22 facilities with guidelines, 14 used either the Primary Clinical Care Manual or the Central Australian Rural Practitioners Association Standard Treatment Manual.

The remaining guidelines were independently produced protocols. The availability of guidelines was associated with appropriate use of intravenous opiate for adequate pain relief (p = 0.037). Although all urban health centres and 75% of health facilities <50 km away had guidelines, only 56% of more remote or island facilities reported the availability of guidelines. CONCLUSIONS: Although monitoring and pain management of patients with Irukandji syndrome were generally appropriate, a variety of inappropriate first aid and hypertension management approaches were found. In general, appropriate practice was associated with the presence of guidelines but, unfortunately, guidelines were less often present in remote health facilities. This is particularly important because the majority of respondents who reported no experience of managing Irukandji syndrome were located in more remote settings. There is a need for uniform, evidence-based guidelines, and mechanisms for effective dissemination of these guidelines with training for all health staff who may be required to manage Irukandji syndrome, particularly in remote areas of northern Australia.

Barry, J. K. and W. A. Miller (2002). "A -1 ribosomal frameshift element that requires base pairing across four kilobases suggests a mechanism of regulating ribosome and replicase traffic on a viral RNA." Proc Natl Acad Sci U S A **99**(17): 11133-11138.

Programmed -1 ribosomal frameshifting is necessary for translation of the polymerase genes of many viruses. In addition to the consensus elements in the mRNA around the frameshift site, we found previously that frameshifting on Barley yellow dwarf virus RNA requires viral sequence located four kilobases downstream. By using dual luciferase reporter constructs, we now show that a predicted loop in the far downstream frameshift element must base pair to a bulge in a bulged stem loop adjacent to the frameshift site. Introduction of either two or six base mismatches in either the bulge or the far downstream loop abolished frameshifting, whereas mutations in both sites that restored base pairing reestablished frameshifting. Likewise, disruption of this base pairing abolished viral RNA replication in plant cells, and restoration of base pairing completely reestablished virus replication. We propose a model in which Barley yellow dwarf virus uses this and another long-distance base-pairing event required for cap-independent translation to allow the replicase copying from the 3' end to shut off translation of upstream ORFs and free the RNA of ribosomes to allow unimpeded replication. This would be a means of solving the "problem," common to positive strand RNA viruses, of competition between ribosomes and replicase for the same RNA template.

Barthmaier, P. and E. Fyrberg (1995). "Monitoring development and pathology of Drosophila indirect flight muscles using green fluorescent protein." Dev Biol **169**(2): 770-774.

We describe the use of a green fluorescent protein (GFP) reporter construct to monitor indirect flight muscle development in normal and mutant Drosophila melanogaster strains. We used polymerase chain reaction to amplify a portion of the Act88F actin gene that includes 1420 nucleotides of flanking DNA, the transcription start, first intron, and initiator codon, incorporating the fragment into the Drosophila germ line transformation vector pCaSpeR. We fused the fragment to the gene encoding green fluorescent protein of the bioluminescent jellyfish Aequorea victoria. We could detect GFP protein in transgenic strains and found that its accumulation, conveniently visualized in living flies using epifluorescence microscopy, was limited to the indirect flight muscles. GFP fluorescence can be used to visualize all stages of flight muscle development subsequent to myoblast fusion nad facilitates the detection of morphological changes in fibers caused by particular mutations.

Barzideh, Z., et al. (2014). "ACE Inhibitory and Antioxidant Activities of Collagen Hydrolysates from the Ribbon Jellyfish (Chrysaora sp.)." Food Technol Biotechnol **52**(4): 495-504.

Collagen isolated from the ribbon jellyfish (Chrysaora sp.) was hydrolysed using three different proteases (i.e. trypsin, alcalase and Protamex) to obtain bioactive peptides. Angiotensin-I-converting enzyme (ACE) inhibitory activity and antioxidant activities (i.e. ferric reducing antioxidant power (FRAP) and 2,2-diphenyl-1-picrylhydrazyl (DPPH) radical scavenging activity) of the peptides were measured and compared, and the effect of the duration of hydrolysis on the bioactivity (ACE inhibitory and antioxidant activities) of peptides was also evaluated. FRAP activity was the highest in Protamex-induced (25-27 mM) and trypsin-induced hydrolysates (24-26 mM) at 7 and 9 h, respectively. Conversely, hydrolysates produced by trypsin for 1 and 3 h showed the highest DPPH radical scavenging activities (94 and 92%, respectively). Trypsin-induced hydrolysates (at 3 h) also showed the highest ACE inhibitory activity (89%). The peptide sequences with the highest activities were identified using tandem mass spectrometry, and the results show that the hydrolysates had a high content of hydrophobic amino acids as well as unique amino acid sequences, which likely contribute to their biological activities.

Basso, L., et al. (2019). "Jellyfish summer

outbreaks as bacterial vectors and potential hazards for marine animals and humans health? The case of Rhizostoma pulmo (Scyphozoa, Cnidaria)." Sci Total Environ **692**: 305-318.

Jellyfish represent an important component of marine food webs characterized by large fluctuations of population density, with the ability to abruptly form outbreaks, followed by rarity periods. In spite of considerable efforts to investigate how jellyfish populations are responding globally to anthropogenic change, available evidence still remains unclear. In the last 50years, jellyfish are seemingly on the rise in a number of coastal areas, including the Mediterranean Sea, where jellyfish blooms periodically become an issue to marine and maritime human activities. Their impacts on marine organism welfare have been poorly quantified. The jellyfish, Rhizostoma pulmo, is an outbreak-forming scyphomedusa whose large populations spread across the Mediterranean, with increasing periodicity and variable abundance. Studies on cnidarian jellyfish suggested being important vectors of bacterial pathogens. In the present study, by combination of conventional culture-based methods and a high-throughput amplicon sequencing (HTS) approach, we characterized the diversity of the bacterial community associated with this jellyfish during their summer outbreak. Three distinct jellyfish compartments, namely umbrella, oral arms, and the mucus secretion obtained from whole specimens were screened for specifically associated microbiota. A total of 17 phyla, 30 classes, 73 orders, 146 families and 329 genera of microbial organisms were represented in R. pulmo samples with three major clades (i.e. Spiroplasma, Mycoplasma and Wolinella) representing over 90% of the retrieved total sequences. The taxonomic microbial inventory was then combined with metabolic profiling data obtained from the Biolog Eco-Plate system. Significant differences among the jellyfish compartments were detected in terms of bacterial abundance, diversity and metabolic utilization of 31 different carbon sources with the highest value of abundance and metabolic potential in the mucus secretion compared to the umbrella and oral arms. Results are discussed in the framework of the species ecology as well as the potential health hazard for marine organisms and humans.

Baubet, V., et al. (2000). "Chimeric green fluorescent protein-aequorin as bioluminescent Ca2+ reporters at the single-cell level." Proc Natl Acad Sci U S A **97**(13): 7260-7265.

Monitoring calcium fluxes in real time could help to understand the development, the plasticity, and the functioning of the central nervous system. In jellyfish, the chemiluminescent calcium binding aequorin protein is associated with the green fluorescent protein and a green bioluminescent signal is emitted upon Ca (2+) stimulation. We decided to use this chemiluminescence resonance energy transfer between the two molecules. Calcium-sensitive bioluminescent reporter genes have been constructed by fusing green fluorescent protein and aequorin, resulting in much more light being emitted. Chemiluminescent and fluorescent activities of these fusion proteins have been assessed in mammalian cells. Cytosolic Ca (2+) increases were imaged at the single-cell level with a cooled intensified charge-coupled device camera. This bifunctional reporter gene should allow the investigation of calcium activities in neuronal networks and in specific subcellular compartments in transgenic animals.

Baulcombe, D. C., et al. (1995). "Jellyfish green fluorescent protein as a reporter for virus infections." Plant J **7**(6): 1045-1053.

The gene encoding green fluorescent protein (GFP) of Aequorea victoria was introduced into the expression cassette of a virus vector based on potato virus X (PVX). Host plants of PVX inoculated with PVX.GFP became systemically infected. Production of GFP in these plants was detected initially between 1 and 2 days postinoculation by the presence of regions on the inoculated leaf that fluoresced bright green under UV light. Subsequently, this green fluorescence was evident in systemically infected tissue. The fluorescence could be detected by several methods. The simplest of these was by looking at the UV-illuminated plants in a darkened room. The PVX.GFP-infected tissue has been analysed either by epifluorescence or confocal laser scanning microscopy. These microscopical methods allow the presence of the virus to be localized to individual infected cells. It was also possible to detect the green fluorescence by spectroscopy or by electrophoresis of extracts from infected plants. To illustrate the potential application of this reporter gene in virological studies a derivative of PVX.GFP was constructed in which the coat protein gene of PVX was replaced by GFP. Confocal laser scanning microscopy of the inoculated tissue showed that the virus was restricted to the inoculated cells thereby confirming earlier speculation that the PVX coat protein is essential for cell-to-cell movement. It is likely that GFP will be useful as a reporter gene in transgenic plants as well as in virus-infected tissue.

Baumstark-Khan, C., et al. (2001). "Enhanced green fluorescent protein (EGFP) for space radiation research using mammalian cells in the International Space Station." Phys Med **17 Suppl 1**: 210-214.

In the endeavour to assess radiation risks for humans in space the concerted action of all stimuli (e.g. radiation and microgravity) has to be known already at

a cellular level. The introduction of reporter genes into mammalian cells which allows the visualisation of modified gene expression levels, signal transduction rates and cell metabolism activities will supply basic information on the cellular response to space radiation. The cloning of the gene for green fluorescent protein (GFP) from the jellyfish Aequorea victoria and its subsequent expression in heterologous systems has established GFP as a unique genetic reporter system for use in a variety of organisms. Unlike other reporters, GFP fluorescence emerges in the absence of substrates or cofactors and allows for non-invasive monitoring in living and in paraformaldehyde-fixed cells. Enhancement of wild-type GFP by human codon optimisation and fluorophore mutation (EGFP) resulted in higher expression levels in mammalian cells and brighter fluorescence. The suitability of EGFP for gene expression studies to be performed on the ISS is shown for recombinant mammalian cells in response to UVC exposure.

Baxter, E. J., et al. (2011). "Gill damage to Atlantic salmon (Salmo salar) caused by the common jellyfish (Aurelia aurita) under experimental challenge." PLoS One **6**(4): e18529.

BACKGROUND: Over recent decades jellyfish have caused fish kill events and recurrent gill problems in marine-farmed salmonids. Common jellyfish (Aurelia spp.) are among the most cosmopolitan jellyfish species in the oceans, with populations increasing in many coastal areas. The negative interaction between jellyfish and fish in aquaculture remains a poorly studied area of science. Thus, a recent fish mortality event in Ireland, involving Aurelia aurita, spurred an investigation into the effects of this jellyfish on marine-farmed salmon. METHODOLOGY/PRINCIPAL FINDINGS: To address the in vivo impact of the common jellyfish (A. aurita) on salmonids, we exposed Atlantic salmon (Salmo salar) smolts to macerated A. aurita for 10 hrs under experimental challenge. Gill tissues of control and experimental treatment groups were scored with a system that rated the damage between 0 and 21 using a range of primary and secondary parameters. Our results revealed that A. aurita rapidly and extensively damaged the gills of S. salar, with the pathogenesis of the disorder progressing even after the jellyfish were removed. After only 2 hrs of exposure, significant multi-focal damage to gill tissues was apparent. The nature and extent of the damage increased up to 48 hrs from the start of the challenge. Although the gills remained extensively damaged at 3 wks from the start of the challenge trial, shortening of the gill lamellae and organisation of the cells indicated an attempt to repair the damage suffered. CONCLUSIONS: Our findings clearly demonstrate that A. aurita can cause severe gill problems in marine-farmed fish. With aquaculture predicted to expand worldwide and evidence suggesting that jellyfish populations are increasing in some areas, this threat to aquaculture is of rising concern as significant losses due to jellyfish could be expected to increase in the future.

Bayha, K. M., et al. (2017). "Multigene phylogeny of the scyphozoan jellyfish family Pelagiidae reveals that the common U.S. Atlantic sea nettle comprises two distinct species (Chrysaora quinquecirrha and C. chesapeakei)." PeerJ **5**: e3863.

BACKGROUND: Species of the scyphozoan family Pelagiidae (e.g., Pelagia noctiluca, Chrysaora quinquecirrha) are well-known for impacting fisheries, aquaculture, and tourism, especially for the painful sting they can inflict on swimmers. However, historical taxonomic uncertainty at the genus (e.g., new genus Mawia) and species levels hinders progress in studying their biology and evolutionary adaptations that make them nuisance species, as well as ability to understand and/or mitigate their ecological and economic impacts. METHODS: We collected nuclear (28S rDNA) and mitochondrial (cytochrome c oxidase I and 16S rDNA) sequence data from individuals of all four pelagiid genera, including 11 of 13 currently recognized species of Chrysaora. To examine species boundaries in the U.S. Atlantic sea nettle Chrysaora quinquecirrha, specimens were included from its entire range along the U.S. Atlantic and Gulf of Mexico coasts, with representatives also examined morphologically (macromorphology and cnidome). RESULTS: Phylogenetic analyses show that the genus Chrysaora is paraphyletic with respect to other pelagiid genera. In combined analyses, Mawia, sampled from the coast of Senegal, is most closely related to Sanderia malayensis, and Pelagia forms a close relationship to a clade of Pacific Chrysaora species (Chrysaora achlyos, Chrysaora colorata, Chrysaora fuscescens, and Chrysaora melanaster). Chrysaora quinquecirrha is polyphyletic, with one clade from the U.S. coastal Atlantic and another in U.S. Atlantic estuaries and Gulf of Mexico. These genetic differences are reflected in morphology, e.g., tentacle and lappet number, oral arm length, and nematocyst dimensions. Caribbean sea nettles (Jamaica and Panama) are genetically similar to the U.S. Atlantic estuaries and Gulf of Mexico clade of Chrysaora quinquecirrha. DISCUSSION: Our phylogenetic hypothesis for Pelagiidae contradicts current generic definitions, revealing major disagreements between DNA-based and morphology-based phylogenies. A paraphyletic Chrysaora raises systematic questions at the genus level for Pelagiidae; accepting the validity of the recently erected genus Mawia, as well as past genera, will require the creation of additional pelagiid

genera. Historical review of the species-delineating genetic and morphological differences indicates that Chrysaora quinquecirrha Desor 1848 applies to the U.S. Coastal Atlantic Chrysaora species (U.S. Atlantic sea nettle), while the name C. chesapeakei Papenfuss 1936 applies to the U.S. Atlantic estuarine and Gulf of Mexico Chrysaora species (Atlantic bay nettle). We provide a detailed redescription, with designation of a neotype for Chrysaora chesapeakei, and clarify the description of Chrysaora quinquecirrha. Since Caribbean Chrysaora are genetically similar to Chrysaora chesapeakei, we provisionally term them Chrysaora c.f. chesapeakei. The presence of Mawia benovici off the coast of Western Africa provides a potential source region for jellyfish introduced into the Adriatic Sea in 2013.

Bayha, K. M. and M. N. Dawson (2010). "New family of allomorphic jellyfishes, Drymonematidae (Scyphozoa, Discomedusae), emphasizes evolution in the functional morphology and trophic ecology of gelatinous zooplankton." Biol Bull **219**(3): 249-267.

Molecular analyses have revealed many cryptic species in the oceans, often permitting small morphological differences to be recognized as diagnosing species, but less commonly leading to consideration of cryptic ecology. Here, based on analyses of three nuclear DNA sequence markers (ribosomal 18S, 28S, and internal transcribed spacer 1 [ITS1]), two mitochondrial DNA markers (cytochrome c oxidase subunit I [COI] and ribosomal 16S), and 55 morphological features, we revise the classification of the enigmatic jellyfish genus Drymonema. We describe a new scyphozoan family, Drymonematidae, elevating the previous subfamily Drymonemidae to accommodate three species: the type species D. dalmatinum from the Mediterranean region, for which we identify a neotype; the western South Atlantic species D. gorgo; and a new species, D. larsoni from the western Atlantic and Caribbean, which also is described here. This revision emphasizes the remarkable morphological disparity of Drymonematidae from all other scyphomedusae, including allometric growth of the bell margin distal of the rhopalia, an annular zone of tentacles on the subumbrella, and ontogenetic loss of gastric filaments. Anatomical innovations are likely functionally related to predatory specialization on large gelatinous zooplankton, most notably the phylogenetically younger moon jellyfish Aurelia, indicating evolution of the feeding niche in Drymonematidae. This family-level revision contributes to the growing body of evidence that scyphomedusae are far more taxonomically rich, their biogeography is a more detailed mosaic, and their phenotypes are more nuanced than traditionally thought. Ecological and evolutionary responses to environmental change, past or future, are likely to be commensurately diverse.

Bayha, K. M., et al. (2010). "Evolutionary relationships among scyphozoan jellyfish families based on complete taxon sampling and phylogenetic analyses of 18S and 28S ribosomal DNA." Integr Comp Biol **50**(3): 436-455.

A stable phylogenetic hypothesis for families within jellyfish class Scyphozoa has been elusive. Reasons for the lack of resolution of scyphozoan familial relationships include a dearth of morphological characters that reliably distinguish taxa and incomplete taxonomic sampling in molecular studies. Here, we address the latter issue by using maximum likelihood and Bayesian methods to reconstruct the phylogenetic relationships among all 19 currently valid scyphozoan families, using sequence data from two nuclear genes: 18S and 28S rDNA. Consistent with prior morphological hypotheses, we find strong evidence for monophyly of subclass Discomedusae, order Coronatae, rhizostome suborder Kolpophorae and superfamilies Actinomyariae, Kampylomyariae, Krikomyariae, and Scapulatae. Eleven of the 19 currently recognized scyphozoan families are robustly monophyletic, and we suggest recognition of two new families pending further analyses. In contrast to long-standing morphological hypotheses, the phylogeny shows coronate family Nausithoidae, semaeostome family Cyaneidae, and rhizostome suborder Daktyliophorae to be nonmonophyletic. Our analyses neither strongly support nor strongly refute monophyly of order Rhizostomeae, superfamily Inscapulatae, and families Ulmaridae, Catostylidae, Lychnorhizidae, and Rhizostomatidae. These taxa, as well as familial relationships within Coronatae and within rhizostome superfamily Inscapulatae, remain unclear and may be resolved by additional genomic and taxonomic sampling. In addition to clarifying some historically difficult taxonomic questions and highlighting nodes in particular need of further attention, the molecular phylogeny presented here will facilitate more robust study of phenotypic evolution in the Scyphozoa, including the evolution characters associated with mass occurrences of jellyfish.

Beadnell, C. E., et al. (1992). "Management of a major box jellyfish (Chironex fleckeri) sting. Lessons from the first minutes and hours." Med J Aust **156**(9): 655-658.

OBJECTIVE: To report the management of a serious box jellyfish (Chironex fleckeri) envenomation from the first minutes of bystander first aid and treatment by ambulance personnel to subsequent treatment in hospital. CLINICAL FEATURES: A 14-

year-old girl sustained a serious Chironex fleckeri sting. There was no loss of consciousness, but the patient suffered severe pain, myocardial irritability, acute pulmonary oedema and mild systemic hypotension, due to the direct toxic effects of the venom. Thirst was a dominant symptom. INTERVENTION AND OUTCOME: Management involved rapid bystander action and call for ambulance assistance; and early intervention with oxygen/nitrous oxide administration, compression bandaging, antivenom administration and electrocardiographic monitoring at the site by ambulance personnel. Echocardiography in hospital three hours after the sting showed a normal myocardium. In hospital management resulted in recovery. Nocturnal itching of the sting persisted for six weeks. CONCLUSIONS: (i) Vinegar dousing may irritate freshly stung skin, but as a nematocyst inhibitor vinegar remains an essential part of the first aid treatment for cubozoan jellyfish stings. (ii) Compression/immobilisation bandaging was not associated with long-term harm to the sting area. (iii) The pain of an intramuscular antivenom injection may not be felt by a chirodropid sting victim, so safe injection protocols must be strictly observed. (iv) Ambulance services in other States whereas there is a risk of box jellyfish (Chironex fleckeri or Chiropsalmus quadrigatus) stings should be similarly trained and equipped to deal with serious jellyfish envenomations.

Beauchemin, C., et al. (2005). "Simultaneous production of two foreign proteins from a polyvirus-based vector." Virus Res **112**(1-2): 1-8.

With the aim of developing a biotechnological tool for the production of foreign proteins in plants, we first engineered an infectious turnip mosaic virus (TuMV) cDNA that contained the jellyfish green fluorescent protein (GFP) gene or the bacterial beta-glucuronidase (GUS) gene (uidA). Two insertion sites were assessed, either between P1 and HCPro cistrons or Pol and CP cistrons. In each construct, the junctions flanking the inserted gene coded for P1 and/or VPg-Pro cleavage recognition site sequences, to produce free GUS or GFP. After transfection by particle bombardment on Brassica perviridis, characteristic symptoms for TuMV infection appeared and Western blot analyses showed that GFP and GUS had been excised from the viral polyprotein. No significant differences in expression level were noticed between the two insertion sites. By RT-PCR, gfp was found to be stable over 30 days post-transfection (dpt) while uidA was gradually lost at 15 dpt. We also created two constructs containing either gene at each insertion sites on the same molecule. Attenuated systemic symptoms were observed after particle bombardment on B. perviridis and Western blot analyses showed that both foreign proteins were produced. Also, the same stability/instability as for the single-gene constructs were observed. These results indicate that it is possible to produce at least two foreign proteins simultaneously in a TuMV-based vector.

Bebenek, I. G., et al. (2004). "sine oculis in basal Metazoa." Dev Genes Evol **214**(7): 342-351.

We report the recovery of homologs of Six1/2/sine oculis (so), a homeodomain-containing member of the Six-gene family, from a diverse set of basal Metazoa, including representatives of the poriferan classes Demospongia, Calcarea and Hexactinellida, the cnidarian classes Hydrozoa, Scyphozoa and Anthozoa, as well as a ctenophore. so sequences were also recovered from a platyhelminth, an echiurid and two bivalve molluscs, members of the super-phyletic group Lophotrochozoa. In the case of the platyhelminth, multiple distinct so sequences were recovered, as well as a member of the related group Six4/5/D-Six4. Extended sequences of the so gene were recovered from the demosponge, Haliclona sp., and the scyphozoan Aurelia aurita via PCR, and 3' RACE. The affinities of all recovered sequences were assessed using a parsimony analysis based on both nucleic and amino acid sequence and using successive character weighting. Our results indicate that so is highly conserved across the animal kingdom. Preliminary expression data for Aurelia reveal that transcripts of the so homolog are present in the manubrium as well as in the rhopalia, which contain the statocyst and eyes, in the free-swimming ephyra and juvenile stages of these jellyfish.

Becerra-Amezcua, M. P., et al. (2016). "In vivo analysis of effects of venom from the jellyfish Chrysaora sp. in zebrafish (Danio rerio)." Toxicon **113**: 49-54.

The jellyfishes of the genus Chrysaora are present in all of the world's oceans, but the toxicity of their venoms has not yet been thoroughly characterized. The zebrafish as a toxicology model can be used for general toxicity testing of drugs and the investigation of toxicological mechanisms. The aim of this study was to evaluate the effect of crude venom from jellyfish Chrysaora sp., a species of jellyfish observed in the tropical lagoons of the Gulf of Mexico, on the zebrafish Danio rerio. Juvenile zebrafish were injected with different concentrations of venom from Chrysaora sp. via intraperitoneal and subcutaneous injections. The effects of the venom were determined by histopathological analysis and through the measurement of hemolytic and phospholipase A2 activities. The crude venom was examined by SDS-PAGE. The effect of sublethal concentrations of crude venom from Chrysaora sp. on D. rerio was

hemorrhaging in the eyes, while the histopathological analysis demonstrated that the primary organs targeted were the pseudobranch, which displayed hyperemia, and the gill, which displayed hyperplasia and hypertrophy. The blood analysis exhibited hemolysis, nuclear abnormalities, and echinocytes by the action of phospholipase A2, which was determined to have 596 units of activity/mg of protein in the venom. The crude venom has proteins with molecular weights ranging from 250 to 6 kDa, with more density in the bands corresponding to 70, 20 and 15 kDa. The venom of Chysaora sp. caused disturbances in circulation associated with vascular dilation due to the localized release of inflammatory mediators. The hemolysis of erythrocytes was caused by the action of phospholipase A2. These findings not only provide an excellent study model but also have a great pharmacological potential for designing new drugs and for the elucidation of the mechanisms of action of and treatment against stings.

Becker, A., et al. (2005). "Calcium sulfate hemihydrate is the inorganic mineral in statoliths of Scyphozoan medusae (Cnidaria)." Dalton Trans (8): 1545-1550.

Scyphomedusae use inorganic crystals (statoliths) for gravity sensing. The organs which contain the statoliths are called rhopalia. Rhopalia of five different species of the three different orders of the class Scyphozoa were studied with high-end solid-state chemical methods to elucidate the crystallographic nature of the biomineral: synchrotron powder diffraction, synchrotron single-crystal diffraction, synchrotron microtomography, scanning electron microscopy, and energy dispersive X-ray spectroscopy. Each rhopalium contains a large number of statoliths in an ordered way. The statoliths of all species consist of calcium sulfate hemihydrate, a water-deficient phase. This is remarkable for sea-living organisms consisting mostly of water. The phylogenetic relationships within the class Scyphozoa are discussed.

Bedry, R. and L. de Haro (2007). "[Venomous and poisonous animals. V. Envenomations by venomous marine invertebrates]." Med Trop (Mars) **67**(3): 223-231.

Epidemiological information about marine envenomation is generally less extensive in Europe than in tropical countries where this type of injury is more severe and the need for medical attention is more frequent. For this reason use of the regional poison control centers in the areas where envenomation occurs must be encouraged. The purpose of this review is to describe envenomation by poisonous marine invertebrates (cephalopods, sea urchins, cone shells, jellyfish, anemones, star-fish, corals, and worms). Understanding of these envenomation syndromes is important not only in tropical areas but also in Europe where importation of dangerous species has increased in recent years.

Beier, K. T., et al. (2016). "Anterograde or Retrograde Transsynaptic Circuit Tracing in Vertebrates with Vesicular Stomatitis Virus Vectors." Curr Protoc Neurosci **74**: 1 26 21-21 26 27.

Viruses have been used as transsynaptic tracers, allowing one to map the inputs and outputs of neuronal populations, due to their ability to replicate in neurons and transmit in vivo only across synaptically connected cells. To date, their use has been largely restricted to mammals. In order to explore the use of such viruses in an expanded host range, we tested the transsynaptic tracing ability of recombinant vesicular stomatitis virus (rVSV) vectors in a variety of organisms. Successful infection and gene expression were achieved in a wide range of organisms, including vertebrate and invertebrate model organisms. Moreover, rVSV enabled transsynaptic tracing of neural circuitry in predictable directions dictated by the viral envelope glycoprotein (G), derived from either VSV or rabies virus (RABV). Anterograde and retrograde labeling, from initial infection and/or viral replication and transmission, was observed in Old and New World monkeys, seahorses, jellyfish, zebrafish, chickens, and mice. These vectors are widely applicable for gene delivery, afferent tract tracing, and/or directional connectivity mapping. Here, we detail the use of these vectors and provide protocols for propagating virus, changing the surface glycoprotein, and infecting multiple organisms using several injection strategies.

Beilei, W., et al. (2012). "Direct cardiac toxicity of the tentacle-only extract from the jellyfish Cyanea capillata demonstrated in isolated rat heart." J Cardiovasc Pharmacol **59**(4): 331-338.

Previous studies in our laboratory have shown that the cardiotoxicity is the main reason for rat death caused by tentacle-only extract from jellyfish Cyanea capillata. However, the direct cardiotoxicity in vitro and its mechanisms of toxic action remain unclear. The current studies were performed by using the Langendorff-perfused isolated heart model, which showed a dose-dependent hemodynamic and electrocardiogram changes. Heart injury-related enzymes increased. Histopathological analysis showed early ischemic damage in the myocardium. The Ca channel blockers nifedipine and verapamil led to a marked improvement in recovery of cardiac function, including heart rate, left ventricular developed pressure, positive and negative first derivatives of intraventricular pressure, coronary flow, left

ventricular end-diastolic pressure, and electrocardiogram changes. Tentacle-only extract-induced cardiac dysfunction could be partly improved by the pretreatments of both propranolol and phentolamine, but not by either atropine or neostigmine at all. In conclusion, we have verified the direct cardiotoxicity of tentacle-only extract from jellyfish C. capillata by the Langendorff isolated heart model, which consisted of 3 separate parts: sinoatrial node malfunction, cardiomyocyte injury, and coronary spasm. The potential mechanism might be attributed to the overactivation of L-type Ca channel, beta- and alpha-adrenergic receptors, but not cholinergic receptors.

Bellaud, G., et al. (2013). "[Marine envenomation by box-jellyfish in a tourist in Cambodia]." Bull Soc Pathol Exot **106**(4): 229-232.

We report a case of box-jellyfish related envenomation in a 40 year old tourist that occurred in Sihanoukville, Cambodia, in the Gulf of Thailand. Symptoms that appeared within a few minutes associated intense pain, hand edema and large edematous and erythematous flagellations in the stung skin areas. Antibiotics and corticosteroids were delivered. Inflammatory signs and skin lesions disappeared within 15 days followed by crusts then scars. Jellyfish at risk for humans are generally found in tropical seas and their geographic distribution seems to spread. As it is difficult to prevent this kind of accident, travelers should be aware of the first acts to perform, such as appropriate cleaning of the wound, the interest of vinegar usage, the administration of analgesics and corticosteroids in case of significant inflammatory signs.

Bellucci, M., et al. (2003). "Jellyfish green fluorescent protein as a useful reporter for transient expression and stable transformation in Medicago sativa L." Plant Cell Rep **22**(5): 328-337.

The aim of the experiments reported herein was to transiently test different gene constructs using green fluorescent protein (GFP) as a reporter gene for a future localization of the maize beta-zein in the chloroplast of alfalfa (Medicago sativa L.). The transient expression of two GFP genes was compared in alfalfa leaves to determine which of these two mutants is the easier to detect. Based on the intensity of fluorescence emitted, the GFP S65C gene was used to assemble a chloroplast-targeted GFP to verify the efficiency of the transit peptide for chloroplast targeting. A chloroplast-targeted fusion protein between beta-zein and GFP was then assembled, and this protein was observed to accumulate in small aggregates into the chloroplasts of transiently transformed cells. To the best of our knowledge, this is the first report of the GFP S65C gene being used to obtain transformed alfalfa plants expressing GFP.

Belogurova, N. V., et al. (2008). "Spectral components of bioluminescence of aequorin and obelin." J Photochem Photobiol B **92**(2): 117-122.

Complex bioluminescence spectra of photoproteins from marine coelenterates - jellyfish Aequorea victoria and hydroid Obelia longissima, and photoluminescence spectra of the bioluminescent reaction products (Ca (2+)-discharged photoproteins) were deconvolved into components. The bioluminescence spectra of aequorin were found to include three, the bioluminescence spectra of obelin - four, and the photoluminescence spectra of the Ca (2+)-discharged photoproteins - only two components. The spectral components were assigned to one unionized and three ionized forms of coelenteramide. The changes in acidity of the excited coelenteramide molecule are discussed. The differences in bioluminescence and photoluminescence spectra are considered, with protonic environment of coelenteramide taken into account.

Benedetti-Cecchi, L., et al. (2015). "Deterministic Factors Overwhelm Stochastic Environmental Fluctuations as Drivers of Jellyfish Outbreaks." PLoS One **10**(10): e0141060.

Jellyfish outbreaks are increasingly viewed as a deterministic response to escalating levels of environmental degradation and climate extremes. However, a comprehensive understanding of the influence of deterministic drivers and stochastic environmental variations favouring population renewal processes has remained elusive. This study quantifies the deterministic and stochastic components of environmental change that lead to outbreaks of the jellyfish Pelagia noctiluca in the Mediterranen Sea. Using data of jellyfish abundance collected at 241 sites along the Catalan coast from 2007 to 2010 we: (1) tested hypotheses about the influence of time-varying and spatial predictors of jellyfish outbreaks; (2) evaluated the relative importance of stochastic vs. deterministic forcing of outbreaks through the environmental bootstrap method; and (3) quantified return times of extreme events. Outbreaks were common in May and June and less likely in other summer months, which resulted in a negative relationship between outbreaks and SST. Cross- and along-shore advection by geostrophic flow were important concentrating forces of jellyfish, but most outbreaks occurred in the proximity of two canyons in the northern part of the study area. This result supported the recent hypothesis that canyons can funnel P. noctiluca blooms towards shore during upwelling. This can be a general, yet unappreciated

mechanism leading to outbreaks of holoplanktonic jellyfish species. The environmental bootstrap indicated that stochastic environmental fluctuations have negligible effects on return times of outbreaks. Our analysis emphasized the importance of deterministic processes leading to jellyfish outbreaks compared to the stochastic component of environmental variation. A better understanding of how environmental drivers affect demographic and population processes in jellyfish species will increase the ability to anticipate jellyfish outbreaks in the future.

Bengtson, K., et al. (1991). "Sudden death in a child following jellyfish envenomation by Chiropsalmus quadrumanus. Case report and autopsy findings." JAMA **266**(10): 1404-1406.

Sudden death following coelenterate envenomation is not uncommon in Australia where the Pacific box jellyfish is indigenous. However, few cases of sudden fatal reactions have been reported in the Northern Hemisphere, and those that have occurred have all been attributed to the Portuguese man-of-war, Physalia physalis. We report the case of a child who died within 40 minutes of accidental envenomation with tentacles of a jellyfish, Chiropsalmus quadrumanus, and describe the findings at autopsy. This coelenterate may be of special danger to small children.

Bentlage, B., et al. (2018). "Loss of metagenesis and evolution of a parasitic life style in a group of open-ocean jellyfish." Mol Phylogenet Evol **124**: 50-59.

Loss or stark reduction of the free-swimming medusa or jellyfish stage is common in the cnidarian class Hydrozoa. In the hydrozoan clade Trachylina, however, many species do not possess a sessile polyp or hydroid stage. Trachylines inhabiting freshwater and coastal ecosystems (i.e., Limnomedusae) possess a metagenetic life cycle involving benthic, sessile polyp and free-swimming medusa. In contrast, the paradigm is that open ocean inhabiting, oceanic trachylines (in the orders Narcomedusae and Trachymedusae) develop from zygote to medusa via a free-swimming larva, forgoing the polyp stage. In some open-ocean trachylines, development includes a sessile stage that is an ecto- or endoparasite of other oceanic organisms. We expand the molecular-based phylogenetic hypothesis of trachylines significantly, increasing taxon and molecular marker sampling. Using this comprehensive phylogenetic hypothesis in conjunction with character state reconstructions we enhance understanding of the evolution of life cycles in trachyline hydrozoans. We find that the polyp stage was lost at least twice independently, concurrent with a transition to an oceanic life style. Further, a sessile, polypoid parasitic stage arose once, rather than twice as current classification would imply, in the open ocean inhabiting Narcomedusae. Our results also support the hypothesis that interstitial species of the order Actinulida are directly descended from direct developing, oceanic trachylines.

Bentolila, L. A., et al. (2005). "Quantum dots for molecular imaging and cancer medicine." Discov Med **5**(26): 213-218.

Extract: The past few decades have witnessed technical advances that have introduced cell biologists and physicians to a new, dynamic, subcellular world where genes and gene products can be visualized to interact in space and time and in health and disease. The accelerating field of molecular imaging has been critically dependent on indicator probes which show when and where genetically or biochemically defined molecules, signals or processes appear, interact and disappear, with high spatial and temporal resolution in living cells and whole organisms. For example, the use of radionuclide tracers combined with 3-dimensional (3-D) imaging systems such as Positron Emission Tomography (PET) and Single Photon Emission Computed Tomography (SPECT) are now helping clinicians to characterize the molecular status of tumors deep within patients. Other types of imaging probes rely on the bioluminescence and fluorescence of genetically encoded proteins (originally found in fireflies and jellyfish, respectively) or entirely synthetic fluorochromes, or a combination of both. New powerful biological fluorescence microscopes provide the ability to study single molecules within single cells. Multiphoton confocal microscopy has been developed to allow for the capturing of high-resolution, 3-D images of living tissues that have been tagged with highly specific fluorophores.

Berking, S. (2007). "Generation of bilateral symmetry in Anthozoa: a model." J Theor Biol **246**(3): 477-490.

Polyps of Anthozoa usually display bilateral symmetry with respect to their mouth opening, to their pharynx, and in particular to the arrangement of their mesenteries. Mesenteries, which are endodermal folds running from the apical to the basal end of the body, subdivide the gastric cavity into pouches. They form in a bilateral symmetric sequence. In this article I propose that early in polyp development the endoderm subdivides successively into three different types of compartments. A mesentery forms at the border between compartments. Two of the compartments are homologous to those of Scyphozoa. They form by mutual activation of cell states that locally exclude each other. The third compartment leads to siphonoglyph formation and is an evolutionary

innovation of the Anthozoa. The mechanism that controls the number and spatial arrangement of the third type of compartment changes the radial symmetry into a bilateral one and occasionally into a different one. The dynamics of its formation indicate an activator-inhibitor mechanism. Computer models are provided that reproduce decision steps in the generation of the mesenteries.

Berking, S., et al. (2005). "A newly discovered oxidant defence system and its involvement in the development of Aurelia aurita (Scyphozoa, Cnidaria): reactive oxygen species and elemental iodine control medusa formation." Int J Dev Biol **49**(8): 969-976.

In Aurelia aurita, applied iodine induces medusa formation (strobilation). This process also occurs when the temperature is lowered. This was found to increase oxidative stress resulting in an increased production of iodine from iodide. One polyp produces several medusae (initially termed ephyrae) starting at the polyp's oral end. The spreading of strobilation down the body column is controlled by a feedback loop: ephyra anlagen decrease the tyrosine content in adjacent polyp tissue by producing melanin from tyrosine. Endogenous tyrosine is able to remove iodine by forming iodiferous tyrosine compounds. The reduced level of tyrosine causes the ephyra-polyp-border to move towards the basal end of the former polyp. We argue that an oxidant defence system may exist which makes use of iodide and tyrosine. Like other marine invertebrates, polyps of Aurelia contain iodide ions. Inevitably produced peroxides oxidise iodide into iodine. The danger to be harmed by iodine is strongly decreased by endogenous tyrosine which reacts with iodine to form iodiferous tyrosine compounds including thyroxin. Both substances together, iodide and tyrosine, form an efficient oxidant defence system which shields the tissue against damage by reactive oxygen species. In the course of evolution (from a species at the basis of the animal kingdom like Aurelia to a highly evolved species like man) the waste product thyroxin (indicating a high metabolic rate) has developed into a hormone which controls the metabolic rate.

Berking, S. and K. Herrmann (2007). "Compartments in Scyphozoa." Int J Dev Biol **51**(3): 221-228.

Polyps of Scyphozoa have a cup-shaped body. At one end is the mouth opening surrounded by tentacles, at the other end is an attachment disc. The body wall consists of two tissue layers, the ectoderm and the endoderm, which are separated by an extracellular matrix, the mesoglea. The polyp's gastric cavity is subdivided by septa running from the apical end to the basal body end. The septa consist of two layers of endoderm and according to biology textbooks the number of septa is four. However, in rare circumstances Aurelia produces polyps with zero, two, six, or eight septa. We found that the number was always even. Therefore we propose that two types of endoderm exist, forming alternating stripes running from the oral body end to the aboral end. The stripes have some properties of developmental compartments. Where cells of different compartments meet, they form a septum. We also propose that the ectoderm is subdivided into compartments. The borders of the ectodermal and endodermal compartments are perpendicular to each other. Tentacles of the polyp and rhopalia (sense organs) of the ephyra (young medusa), respectively, develop at the border between two ectodermal compartments. The number can be even or odd. Rhopalia formation is particularly favored where two ectodermal and two endodermal compartments meet.

Berline, L., et al. (2013). "Modeling jellyfish Pelagia noctiluca transport and stranding in the Ligurian Sea." Mar Pollut Bull **70**(1-2): 90-99.

Jellyfish blooms are generally attributed to a biological response to the environment, neglecting the role of transport patterns in redistributing existing populations. Here, we use high-resolution (1.25km) ocean modeling to examine the role of transport in the onshore arrival and abundance of the pelagic stinging jellyfish Pelagia noctiluca on the Ligurian Sea coast. Jellyfish are modeled as Lagrangian particles with a 0-300-m diel vertical migration typical of P. noctiluca. Over the course of a year, onshore arrivals are not restricted to the summer. Arrivals are concentrated at capes, but abundance can reach maxima in bays and in the lee of capes. Two factors impact jellyfish arrivals at the coast: the position of the Northern Current and the wind. A comparison of summer 2006 and available onshore jellyfish observations suggests a correct capture of the main stranding events by the model. These results have implications for understanding long-term fluctuations.

Berling, I. and G. Isbister (2015). "Marine envenomations." Aust Fam Physician **44**(1-2): 28-32.

BACKGROUND: Marine stings are common but most are minor and do not require medical intervention. Severe and systemic marine envenoming is uncommon, but includes box jellyfish stings, Irukandji syndrome, major stingray trauma and blue-ringed octopus envenoming. Almost all marine injuries are caused by jellyfish stings, and penetrating injuries from spiny fish, stingrays or sea urchins. OBJECTIVE: This article describes the presentation and management of marine envenomations and injuries that may occur in Australia. DISCUSSION: First aid

for jellyfish includes tentacle removal, application of vinegar for box jellyfish, and hot water immersion (45 degrees C for 20 min) for bluebottle jellyfish stings. Basic life support is essential for severe marine envenomings that result in cardiac collapse or paralysis. Irukandji syndrome causes severe generalised pain, autonomic excess and minimal local pain, which may require large amounts of analgesia, and, uncommonly, myocardial depression and pulmonary oedema occur. Penetrating marine injuries can cause significant trauma depending on location of the injury. Large and unclean wounds may have delayed healing and secondary infection if not adequately irrigated, debrided and observed.

Bernhardt, A., et al. (2018). "Biphasic Scaffolds from Marine Collagens for Regeneration of Osteochondral Defects." Mar Drugs **16**(3).

BACKGROUND: Collagens of marine origin are applied increasingly as alternatives to mammalian collagens in tissue engineering. The aim of the present study was to develop a biphasic scaffold from exclusively marine collagens supporting both osteogenic and chondrogenic differentiation and to find a suitable setup for in vitro chondrogenic and osteogenic differentiation of human mesenchymal stroma cells (hMSC). METHODS: Biphasic scaffolds from biomimetically mineralized salmon collagen and fibrillized jellyfish collagen were fabricated by joint freeze-drying and crosslinking. Different experiments were performed to analyze the influence of cell density and TGF-beta on osteogenic differentiation of the cells in the scaffolds. Gene expression analysis and analysis of cartilage extracellular matrix components were performed and activity of alkaline phosphatase was determined. Furthermore, histological sections of differentiated cells in the biphasic scaffolds were analyzed. RESULTS: Stable biphasic scaffolds from two different marine collagens were prepared. An in vitro setup for osteochondral differentiation was developed involving (1) different seeding densities in the phases; (2) additional application of alginate hydrogel in the chondral part; (3) pre-differentiation and sequential seeding of the scaffolds and (4) osteochondral medium. Spatially separated osteogenic and chondrogenic differentiation of hMSC was achieved in this setup, while osteochondral medium in combination with the biphasic scaffolds alone was not sufficient to reach this ambition. CONCLUSIONS: Biphasic, but monolithic scaffolds from exclusively marine collagens are suitable for the development of osteochondral constructs.

Bertucci, E., et al. (2019). "The Jellyfish Sign: A New Sonographic Cervical Marker to Predict Maternal Morbidity in Abnormally Invasive Placenta Previa." Ultraschall Med **40**(1): 40-46.

PURPOSE: To investigate the value of a new cervical sonographic sign, called the jellyfish sign (JS), for predicting the risk of maternal morbidity in cases of abnormally invasive placenta (AIP) previa totalis. MATERIALS AND METHODS: Retrospective evaluation of transvaginal (TV) and transabdominal (TA) scans performed in all singleton pregnancies with placenta previa totalis. JS, i. e. the absence of the normal linear demarcation between the placenta previa and the cervix, was evaluated by TV scans. The presence/severity of AIP and outcomes of maternal morbidity were related to this sign. RESULTS: JS was noted in 8/39 (20.5 %) patients. The two analyzed groups, i. e. with and without JS, were similar. The specificity of JS in AIP diagnosis, histological findings of accreta/increta/percreta, need for caesarean hysterectomy or blood loss > 2000 ml ranges between 92 % and 96.2 %, with the PPV and NPV ranging between 71.4 % and 85.7 % and 61.3 % and 80.6 %, respectively. The JS group had a significant increase in blood loss (ml) ($p = 0.003$), transfusions (%) ($p = 0.016$), red blood cells ($p = 0.002$) and plasma ($p = 0.002$), admission to an postoperative intensive care unit (ICU) (%) ($p = 0.002$), hospitalization length ($p < 0.001$) and the need of cesarean hysterectomy (%) ($p < 0.001$). JS was independently correlated to cesarean hysterectomy (OR 25.6; 95 % CI 2.0:322.3, $p = 0.012$) and blood loss > 2000 ml (OR 16.6; 95 % CI 1.5:180.1, $p = 0.021$) also in a logistic regression model. CONCLUSION: JS is useful in predicting the increase in maternal morbidity: massive transfusion, admission to the ICU and cesarean hysterectomy related to intraoperative bleeding in patients with a previa AIP.

Beverly, K. N., et al. (2008). "The Tim8-Tim13 complex has multiple substrate binding sites and binds cooperatively to Tim23." J Mol Biol **382**(5): 1144-1156.

The Tim8-Tim13 complex, located in the mitochondrial intermembrane space, functions in the TIM22 import pathway that mediates the import of the mitochondrial carriers Tim23, Tim22, and Tim17 into the mitochondrial inner membrane. The Tim8-Tim13 complex assembles as a hexamer and binds to the substrate Tim23 to chaperone the hydrophobic Tim23 across the aqueous intermembrane space. However, both structural features of the Tim8-Tim13 complex and the binding interaction to Tim23 remain poorly defined. The crystal structure of the yeast Tim8-Tim13 complex, reported here at 2.6 A resolution, reveals that the architecture of the Tim8-Tim13 complex is similar to those of other chaperones such as Tim9-Tim10, prefoldin, and Skp, in which long helices extend from a central body like tentacles from a jellyfish. Surface plasmon resonance was applied to investigate

interactions between the Tim8-Tim13 complex and Tim23. The Tim8-Tim13 complex contained approximately six binding sites and showed a complex binding interaction indicative of positive cooperativity rather than a simple bimolecular interaction. By combining results from the structural and binding studies, we provide a molecular model of the Tim8-Tim13 complex binding to Tim23. The regions where the tentacle helices attach to the body of the Tim8-Tim13 complex contain six hydrophobic pockets that likely interact with specific sequences of Tim23 and possibly other substrates. Smaller hydrophobic patches on the tentacles themselves likely interact nonspecifically with the substrate's transmembrane helices, shielding it from the aqueous intermembrane space. The central region of Tim23, which enters the intermembrane space first, may serve to nucleate the binding of the Tim8-Tim13 complex, thereby initiating the chaperoned translocation of Tim23 to the mitochondrial inner membrane.

Bhosale, S. H., et al. (2002). "Antifouling potential of some marine organisms from India against species of Bacillus and Pseudomonas." Mar Biotechnol (NY) **4**(2): 111-118.

Crude methanolic extracts of 37 marine organisms (16 species of flora, 21 species of fauna) were screened for antibacterial properties against 5 strains of bacteria isolated from marine environments. Of these, 10 plant and 9 animal extracts exhibited antibacterial activity against at least one bacterial strain. The extracts of 6 species were active against all the strains: i.e., Stoechospermum marginatum (brown algae), Cymodocea rotundata (seagrass), Petrosia sp. and Psammaplysilla purpurea (sponges), Sinularia compressa (soft coral), and Cassiopeia sp. (jellyfish). Among the plants, Padina tetrastromatica (brown algae) extract exhibited significant activity (9-11-mm inhibition zone at 500 microg per 6-mm disc) against Bacillus pumilus and Pseudomonas vesicularis, while the extracts of Petrosia, Psammaplysilla, and Cassiopeia were strongly active (11-13-mm inhibition zone at 500 microg per 6-mm disc) against B. circulans and P. putida. It was further confirmed that the attachment of bacterial strains on glass slides was inhibited remarkably with increasing concentrations of bioextracts of Petrosia sp. and Psammaplysilla purpurea. The present findings could form the basis for exploring the antibacterial potential of bioactive molecules from some of the marine organisms that exhibited moderate to strong antibacterial properties.

Binnetoglu, F. K., et al. (2013). "Severe digital necrosis in a 4-year-old boy: primary Raynaud's or jellyfish sting." BMJ Case Rep **2013**.

Raynaud's phenomena is a common disorder which may be primary or secondary to some connective tissue disorders such as systemic sclerosis and systemic lupus erythematosus. Jellyfish sting is a rare but life-threatening cause of Raynaud's phenomena. Digital gangrene is reported in 3% of children with secondary Raynaud's phenomena but does not occur in children with primary Raynaud's phenomena. We report a case of a 4-year-old boy who initially presented with episodes of pain and bluish to blackish discolouration and necrosis affecting the fingers on both hands after a jellyfish sting without any sign of connective tissue disorder.

Birsa, L. M., et al. (2010). "Evaluation of the effects of various chemicals on discharge of and pain caused by jellyfish nematocysts." Comp Biochem Physiol C Toxicol Pharmacol **151**(4): 426-430.

Jellyfish tentacles in contact with human skin can produce pain swelling and redness. The pain is due to discharge of jellyfish nematocysts and associated toxins and discharge can be caused by a variety of mechanical and chemical stimuli. A series of tests were carried out with chemicals traditionally used to treat jellyfish stings e.g. acetic acid ammonia meat tenderizer baking soda and urea to determine if these chemicals stimulated or inhibited nematocyst discharge and if they brought relief to testers who were exposed to jellyfish tentacles. Chrysaora quinquecirrha (sea nettle) Chiropsalmus quadrumanus (sea wasp) and Physalia physalis (Portuguese man-of-war) were used in the study. It was found that many of the chemicals traditionally used to treat jellyfish stings stimulated nematocyst discharge and did not relieve the pain. However there was immediate relief when a common anesthetic lidocaine was sprayed on the skin of testers in contact with jellyfish tentacles. Initial exposure of tentacle suspensions to lidocaine prevented the nematocyst discharge by subsequent exposure to acetic acid ethanol ammonia or bromelain. Thus lidocaine in addition to acting as an anesthetic on skin in contact with jellyfish tentacles inhibited nematocyst discharge possibly by blocking sodium and/or calcium channels of the nematocytes.

Black, R. E. and L. Bloom (1984). "Heat shock proteins in Aurelia (Cnidaria, Scyphozoa)." J Exp Zool **230**(2): 303-307.

Heat shock proteins (hsp) in Aurelia identified by one-dimensional SDS-PAGE are of sizes 93,83,70,68,45, and 39 kD, the most rapidly labeled being hsp 70 in all developmental stages. Labeled hsp in the polyp are found mostly in the epidermis; gastrodermal nuclei are also labeled. The minimum temperature for induction of the proteins is about the same (27 degrees to 28 degrees C), regardless of whether polyps have been cultured at 15 degrees or 24

degrees C. Adults and planulae taken from natural water at 28 degrees C do not show accumulation of hsp 70. Induction of strobilation by raising polyps from 15 degrees to 25 degrees C is not associated with appreciable labeling of hsp. Polyps transferred to higher or lower salinity have decreased protein synthesis but do not synthesize stress proteins.

Black, R. E. and G. K. Riley (1985). "Dissociation and reaggregation of cells of Chrysaora quinquecirrha (Cnidaria, Scyphozoa)." J Exp Zool **233**(3): 369-375.

Cells of scyphistomae, strobilae, and ephyrae were dissociated with trypsin and reaggregated. Clumping was inhibited in low Ca++ and by puromycin, but not by collagenase or sugars. Reaggregates from the oral end of the polyp developed tentacles and mouths first and basal structures later, whereas the opposite sequence occurred with cells from the lower gastric region. Nile-blue-stained cells from hypostome or peduncle did not form specific structures in the reconstructed polyp, but were distributed throughout the animal. Ephyra cell aggregates showed little morphogenesis, whereas cells from presumptive ephyra tissue gave rise to structures with tentacles and multiple oral openings. Mixed reaggregates containing equal proportions of polyp and ephyra cells formed irregular structures with transparent outer layer and opaque inner cell mass, suggesting stage-specific sorting.

Blackband, S. J. and M. K. Stoskopf (1990). "In vivo nuclear magnetic resonance imaging and spectroscopy of aquatic organisms." Magn Reson Imaging **8**(2): 191-198.

NMR imaging and localized 1H spectroscopy of a variety of aquatic organisms in vivo is described for the first time. The practical consideration of life support, water volume, salinity, and anesthesia are discussed and solutions presented. Such animal studies shape our understanding of physiology, biochemistry, and biology, and provide models of human disease and normal function. These studies also have economic and ecological importance.

Blanazs, A., et al. (2011). "Mechanistic insights for block copolymer morphologies: how do worms form vesicles?" J Am Chem Soc **133**(41): 16581-16587.

Amphiphilic diblock copolymers composed of two covalently linked, chemically distinct chains can be considered to be biological mimics of cell membrane-forming lipid molecules, but with typically more than an order of magnitude increase in molecular weight. These macromolecular amphiphiles are known to form a wide range of nanostructures (spheres, worms, vesicles, etc.) in solvents that are selective for one of the blocks. However, such self-assembly is usually limited to dilute copolymer solutions (<1%), which is a significant disadvantage for potential commercial applications such as drug delivery and coatings. In principle, this problem can be circumvented by polymerization-induced block copolymer self-assembly. Here we detail the synthesis and subsequent in situ self-assembly of amphiphilic AB diblock copolymers in a one pot concentrated aqueous dispersion polymerization formulation. We show that spherical micelles, wormlike micelles, and vesicles can be predictably and efficiently obtained (within 2 h of polymerization, >99% monomer conversion) at relatively high solids in purely aqueous solution. Furthermore, careful monitoring of the in situ polymerization by transmission electron microscopy reveals various novel intermediate structures (including branched worms, partially coalesced worms, nascent bilayers, "octopi", "jellyfish", and finally pure vesicles) that provide important mechanistic insights regarding the evolution of the particle morphology during the sphere-to-worm and worm-to-vesicle transitions. This environmentally benign approach (which involves no toxic solvents, is conducted at relatively high solids, and requires no additional processing) is readily amenable to industrial scale-up, since it is based on commercially available starting materials.

Blanchet, M., et al. (2015). "Changes in bacterial community metabolism and composition during the degradation of dissolved organic matter from the jellyfish Aurelia aurita in a Mediterranean coastal lagoon." Environ Sci Pollut Res Int **22**(18): 13638-13653.

Spatial increases and temporal shifts in outbreaks of gelatinous plankton have been observed over the past several decades in many estuarine and coastal ecosystems. The effects of these blooms on marine ecosystem functioning and particularly on the dynamics of the heterotrophic bacteria are still unclear. The response of the bacterial community from a Mediterranean coastal lagoon to the addition of dissolved organic matter (DOM) from the jellyfish Aurelia aurita, corresponding to an enrichment of dissolved organic carbon (DOC) by 1.4, was assessed for 22 days in microcosms (8 l). The high bioavailability of this material led to (i) a rapid mineralization of the DOC and dissolved organic nitrogen from the jellyfish and (ii) the accumulation of high concentrations of ammonium and orthophosphate in the water column. DOM from jellyfish greatly stimulated heterotrophic prokaryotic production and respiration rates during the first 2 days; then, these activities showed a continuous decay until reaching

those measured in the control microcosms (lagoon water only) at the end of the experiment. Bacterial growth efficiency remained below 20%, indicating that most of the DOM was respired and a minor part was channeled to biomass production. Changes in bacterial diversity were assessed by tag pyrosequencing of partial bacterial 16S rRNA genes, DNA fingerprints, and a cultivation approach. While bacterial diversity in control microcosms showed little changes during the experiment, the addition of DOM from the jellyfish induced a rapid growth of Pseudoalteromonas and Vibrio species that were isolated. After 9 days, the bacterial community was dominated by Bacteroidetes, which appeared more adapted to metabolize high-molecular-weight DOM. At the end of the experiment, the bacterial community shifted toward a higher proportion of Alphaproteobacteria. Resilience of the bacterial community after the addition of DOM from the jellyfish was higher for metabolic functions than diversity, suggesting that jellyfish blooms can induce durable changes in the bacterial community structure in coastal lagoons.

Bleve, G., et al. (2019). "Identification of Safety and Quality Parameters for Preparation of Jellyfish Based Novel Food Products." Foods **8**(7).

Edible jellyfish are mainly consumed and marketed in Southeastern Countries, generally produced by a multi-phase drying process, using mixtures of salt and alum. Recently, jellyfish have become very attractive also for Western food markets. They are novel food in Europe and no recognized handling/processing steps have been set up yet. Moreover, no specific food safety and quality parameters are available. In this study, we identified a set of safety and quality parameters for jellyfish, based on standards and process hygiene criteria used in Europe for other products. These assays were tested on three different jellyfish preparations that can be used as raw materials for subsequent food processing. All jellyfish samples revealed the absence of pathogens (Salmonella spp. and Listeria monocytogenes), Enterobacteriaceae and Pseudomonas spp., even if a limited presence of Staphylococci was observed. No biogenic amine histamine was detected and negligible levels of total volatile basic nitrogen (TVB-N) were revealed. Total bacterium, yeast and mold counts were negligible or undetectable by conventional accredited methods, and conversely the results were higher when optimized saline conditions were used. This study, for the first time, established a set of quality and safety parameters necessary for first-operations and subsequent processing of jellyfish as novel food. Highlights: Jellyfish can represent a novel food in Europe. Identification of safety and quality parameters for jellyfish food products. Saline conditions are essential for improving safety and quality assessment of jellyfish as food.

Blyth, D. J., et al. (1996). "Calcium biosensing with a sol-gel immobilized photoprotein." Analyst **121**(12): 1975-1978.

Aequorin, the bioluminescent protein found in the jellyfish Aequorea sp., has been immobilized in a porous sol-gel glass environment. The luminescence from this protein is specifically triggered by the presence of calcium ions, thus offering exciting possibilities for the development of an optical biosensor for this cationic species. The luminescence emission spectrum has been measured from the aequorin protein after interaction with calcium ions. The intensity of the luminescence, measured at the peak maximum of 470 nm, for the encapsulated protein has been calibrated against calcium ion concentration. The characterization of the protein within the sol-gel matrix has been reported together with biosensing experiments using human sera and milk samples. The results suggest that the sol-gel encapsulated aequorin protein offers potential as a one shot bioluminescence based biosensor for the determination of calcium ions in such complex matrices.

Bock, O. (2013). "Cajal, Golgi, Nansen, Schafer and the neuron doctrine." Endeavour **37**(4): 228-234.

The Nobel Prize for Physiology or Medicine of 1906 was shared by the Italian Camillo Golgi and the Spaniard Santiago Ramon y Cajal for their contributions to the knowledge of the micro-anatomy of the central nervous system. In his Nobel Lecture, Golgi defended the going-out-of-favour Reticular Theory, which stated that the nerve cells--or neurons--are fused together to form a diffuse network. Reticularists like Golgi insisted that the axons physically join one nerve cell to another. In contrast, Cajal in his lecture said that his own studies confirmed the observations of others that the neurons are independent of one another, a fact which is the anatomical basis of the now-accepted Neuron Doctrine (Theory). This much is well documented. Less well known, however, is the fact that evidence against the Reticular Theory had been mounting for some time prior to the Nobel Lecture. The Norwegian Fridtjof Nansen had reported in 1887 that, in his studies of the primitive creatures he studied in the sea near Bergen, he found no connections between the processes of the ganglion cells in their nervous systems. Nor is it adequately appreciated that ten years earlier, in 1877, the Englishman Edward Schafer had similarly described seeing no connections between the nerve elements in the mantles of the jellyfish. This paper begins by charting the research that led directly to the

awarding of the 1906 Nobel Prize. It then shows that long before the ultimate vindication of the Neuron Doctrine, researchers in several countries had been accumulating evidence that undermined or contradicted the Reticular Theory.

Boco, S. R., et al. (2019). "Extreme, but not moderate climate scenarios, impart sublethal effects on polyps of the Irukandji jellyfish, Carukia barnesi." Sci Total Environ **685**: 471-479.

Ocean acidification and warming, fueled by excess atmospheric carbon dioxide, can impose stress on marine organisms. Most studies testing the effects of climate change on marine organisms, however, use extreme climate projection scenarios, despite moderate projections scenarios being most likely to occur. Here, we examined the interactive effects of warming and acidification on reproduction, respiration, mobility and metabolic composition of polyps of the Irukandji jellyfish, Carukia barnesi, to determine the responses of a cubozoan jellyfish to moderate and extreme climate scenarios in Queensland, Australia. The experiment consisted two orthogonal factors: temperature (current 25 degrees C and future 28 degrees C) and pH (current (8.0) moderate (7.9) and extreme (7.7)). All polyps survived in the experiment but fewer polyps were produced in the pH7.7 treatment compared to pH7.9 and pH8.0. Respiration rates were elevated in the lowest pH treatment throughout most of the experiment and polyps were approximately half as mobile in this treatment compared to pH7.9 and pH8.0, regardless of temperature. We identified metabolites occurring at significantly lower relative abundance in the lowest pH (i.e. glutamate, acetate, betaine, methylguanidine, lysine, sarcosine, glycine) and elevated temperature (i.e. proline, trigonelline, creatinine, mannose, acetate, betaine, methylguanidine, lysine, sarcosine) treatments. Glycine was the only metabolite exhibiting an interactive effect between pH and temperature. Our results suggest that C. barnesi polyps are unaffected by the most optimistic climate scenario and may tolerate even extreme climate conditions to some extent.

Bodio, M. and T. Junghanss (2009). "[Accidents with venomous and poisonous animals in Central Europe]." Ther Umsch **66**(5): 349-355.

Central Europe is largely safe from accidents with venomous and poisonous animals. The regions where European vipers are regularly found are shrinking. Today accidents with jellyfish and stings of venomous fish afflicted during leisure activities at the sea side play the dominant role. Life threatening accidents in Europe are mainly due to exotic snakes held in captivity. A system useful in daily medical practice is explained to classify and stage accidents due to poisonous and venomous animals. The important poisonous and venomous animals of Central Europe and the specific therapeutics, the antivenoms, are covered. The antivenom depot "Antivenin-CH" of the Swiss Toxicology Information Centre in Zurich and the MRITox in Munich with the antivenom registry Munich AntiVenom INdex (MAVIN) are presented.

Boero, F., et al. (2013). "A salp bloom (Tunicata, Thaliacea) along the Apulian coast and in the Otranto Channel between March-May 2013." F1000Res **2**: 181.

Between March-May 2013 a massive Salpa maxima bloom was recorded by a citizen science study along the Ionian and Adriatic coast of the Salento peninsula (Italy). Citizen records were substantiated with field inspections along the coast and during an oceanographic campaign in the Otranto Channel. Salps clogged nets, impairing fishing activities along the coast. Swimmers were scared by the gelatinous appearance of the salps, and thought they were jellyfish. At the end of the bloom the dead bodies of the colonies, that were up to 6-7 m long, were accumulated along the coast and stirred by the waves, forming foams along dozens of kilometers of coast. The bloom also occurred at the Tremiti Islands, north of the Gargano Peninsula. The possible impacts of such events on the functioning of pelagic systems are discussed.

Boero, F. and G. Bernardi (2014). "Phenotypic vs genotypic approaches to biodiversity, from conflict to alliance." Mar Genomics **17**: 63-64.

Taxonomy has traditionally been based on morphological characters. Such a "phenotypic taxonomy" has steadily been replaced by the advent of molecular approaches, culminating with the rapid sequencing of genetic barcodes. The convenience of barcoding and its relative ease has relegated "phenotypic taxonomy" to a historical status. The use of genetics is undeniably powerful. It has relatively few biases and DNA can be extracted from challenging groups, where forms are fragile, such as jellyfish, or where early life stages are difficult to connect with adult forms. The problem is that resources are finite, and the rise of one powerful method came with the demise of traditional taxonomy. In addition, genetic methods may be very sophisticated, requiring acute expertise to master its techniques. These two points in combination have resulted in less funding and attraction for traditional approaches. This is doubly unfortunate because, first we are quickly losing experts in organisms that have incredibly complex lifestyles, and second because in order to fully appreciate a molecular taxonomy, one needs to understand the organisms. In a time of rapid loss of

biodiversity, time is ripe for traditional and molecular taxonomists to unite in order to better appreciate and understand the complexity of life forms.

Bogs, J., et al. (1998). "Colonization of Host Plants by the Fire Blight Pathogen Erwinia amylovora Marked with Genes for Bioluminescence and Fluorescence." Phytopathology **88**(5): 416-421.

ABSTRACT To follow the movement of Erwinia amylovora in plant tissue without dissection, this bacterium was marked with either the lux operon from Vibrio fischeri or the gfp gene from the jellyfish Aequorea victoria, both carried on multicopy plasmids and expressed under the control of the lac promoter from Escherichia coli. Movement of the pathogen was visualized in leaves, stems, and roots of apple seedlings, and migration of E. amylovora was traced from inoculation sites in the stem to as far as the roots. Green fluorescent E. amylovora cells were observed in the xylem and later appeared to break out of the vessels into the intercellular spaces of the adjacent parenchyma. Inoculation in the intercostal region of leaves caused a zone of slow necrosis that finally resulted in bacterial invasion of the xylem vessels. Labeled bacteria could also be seen in association with the anchor sites of leaf hairs. Distortion of the epidermis adjacent to leaf hairs created openings that were observed by scanning electron microscopy. As the intercostal region, the bases of leaf hairs provided E. amylovora access to intact xylem vessels, which allowed further distribution of the pathogen in the host plant.

Boonstra, J. L., et al. (2015). "Milbemycin oxime (Interceptor) treatment of amphipod parasites (Hyperiidae) from several host jellyfish species." J Zoo Wildl Med **46**(1): 158-160.

Wild-caught crystal jellyfish (Aequorea victoria) arrived at the John G. Shedd Aquarium infested with hyperiid amphipods (Hyperia medusarum), which were inadvertently introduced into a system containing several jellyfish species. Affected systems were treated with milbemycin oxime (Interceptor tablets for dogs 51-100 lbs, Novartis Animal Health US, Inc., Greensboro, North Carolina 27408, USA), a treatment prescribed for red bug (Tegastes acroporanus) infestation in corals. Two treatments using one 25-mg aliquot of Interceptor per 10 gallons of tank water administered 6-7 days apart were completed. Overall, treatment to eradicate the parasite from the affected systems was successful. Further studies evaluating the tolerance of jellyfish to milbemycin oxime, particularly in small juvenile Eutonina indicans and Aurelia aurita, are warranted. Based on clinical observations, there were more negative effects associated with the treatment in the hydrozoans than in the scyphozoans.

Bordehore, C., et al. (2015). "Use of an Inverse Method for Time Series to Estimate the Dynamics of and Management Strategies for the Box Jellyfish Carybdea marsupialis." PLoS One **10**(9): e0137272.

Frequently, population ecology of marine organisms uses a descriptive approach in which their sizes and densities are plotted over time. This approach has limited usefulness for design strategies in management or modelling different scenarios. Population projection matrix models are among the most widely used tools in ecology. Unfortunately, for the majority of pelagic marine organisms, it is difficult to mark individuals and follow them over time to determine their vital rates and built a population projection matrix model. Nevertheless, it is possible to get time-series data to calculate size structure and densities of each size, in order to determine the matrix parameters. This approach is known as a "demographic inverse problem" and it is based on quadratic programming methods, but it has rarely been used on aquatic organisms. We used unpublished field data of a population of cubomedusae Carybdea marsupialis to construct a population projection matrix model and compare two different management strategies to lower population to values before year 2008 when there was no significant interaction with bathers. Those strategies were by direct removal of medusae and by reducing prey. Our results showed that removal of jellyfish from all size classes was more effective than removing only juveniles or adults. When reducing prey, the highest efficiency to lower the C. marsupialis population occurred when prey depletion affected prey of all medusae sizes. Our model fit well with the field data and may serve to design an efficient management strategy or build hypothetical scenarios such as removal of individuals or reducing prey. TThis This sdfsdshis method is applicable to other marine or terrestrial species, for which density and population structure over time are available.

Bosch-Belmar, M., et al. (2016). "Concurrent environmental stressors and jellyfish stings impair caged European sea bass (Dicentrarchus labrax) physiological performances." Sci Rep **6**: 27929.

The increasing frequency of jellyfish outbreaks in coastal areas has led to multiple ecological and socio-economic issues, including mass mortalities of farmed fish. We investigated the sensitivity of the European sea bass (Dicentrarchus labrax), a widely cultured fish in the Mediterranean Sea, to the combined stressors of temperature, hypoxia and stings from the jellyfish Pelagia noctiluca, through measurement of oxygen consumption rates (MO2), critical oxygen levels (PO2crit), and histological analysis of tissue damage.

Higher levels of MO2, PO2crit and gill damage in treated fish demonstrated that the synergy of environmental and biotic stressors dramatically impair farmed fish metabolic performances and increase their health vulnerability. As a corollary, in the current scenario of ocean warming, these findings suggest that the combined effects of recurrent hypoxic events and jellyfish blooms in coastal areas might also threaten wild fish populations.

Bosch-Belmar, M., et al. (2016). "Jellyfish Stings Trigger Gill Disorders and Increased Mortality in Farmed Sparus aurata (Linnaeus, 1758) in the Mediterranean Sea." PLoS One **11**(4): e0154239.

Jellyfish are of particular concern for marine finfish aquaculture. In recent years repeated mass mortality episodes of farmed fish were caused by blooms of gelatinous cnidarian stingers, as a consequence of a wide range of hemolytic, cytotoxic, and neurotoxic properties of associated cnidocytes venoms. The mauve stinger jellyfish Pelagia noctiluca (Scyphozoa) has been identified as direct causative agent for several documented fish mortality events both in Northern Europe and the Mediterranean Sea aquaculture farms. We investigated the effects of P. noctiluca envenomations on the gilthead sea bream Sparus aurata by in vivo laboratory assays. Fish were incubated for 8 hours with jellyfish at 3 different densities in 300 l experimental tanks. Gill disorders were assessed by histological analyses and histopathological scoring of samples collected at time intervals from 3 hours to 4 weeks after initial exposure. Fish gills showed different extent and severity of gill lesions according to jellyfish density and incubation time, and long after the removal of jellyfish from tanks. Jellyfish envenomation elicits local and systemic inflammation reactions, histopathology and gill cell toxicity, with severe impacts on fish health. Altogether, these results shows P. noctiluca swarms may represent a high risk for Mediterranean finfish aquaculture farms, generating significant gill damage after only a few hours of contact with farmed S. aurata. Due to the growth of the aquaculture sector and the increased frequency of jellyfish blooms in the coastal waters, negative interactions between stinging jellyfish and farmed fish are likely to increase with the potential for significant economic losses.

Bose, A. P. H., et al. (2019). "Freshwater hydrozoan blooms alter activity and behaviour of territorial cichlids in Lake Tanganyika." R Soc Open Sci **6**(11): 191053.

Blooms of gelatinous zooplankton can represent dramatic environmental perturbations for aquatic ecosystems. Yet, we still know little about how blooms impact fitness-related behaviours of fish caught within their areas of effect, especially for freshwater systems. Here, we documented the behavioural impacts of freshwater hydrozoan (Limnocnida tanganjicae) blooms on a territorial cichlid (Variabilichromis moorii), as well as on the wider community of cichlids in a shallow-water rocky habitat of Lake Tanganyika. Compared with non-bloom conditions, V. moorii individuals in the midst of blooms reduced their swimming and territory defence activities (each by approx. 50%) but not their foraging or affiliative behaviours. Despite this reduction in activity, V. moorii could not entirely avoid being stung and preferred to remain closer to the rocky substrata as opposed to the more open demersal zone. Many other fishes similarly hid among the benthic substrata, changing the composition of the fish community in the demersal zone during bloom conditions. Reductions in activity could have multiple fitness-related implications for individual fish. Establishing the consequences of these behavioural changes is important for understanding the effects of gelatinous zooplankton blooms in freshwater systems.

Bouchard, C., et al. (2019). "A SLC6 transporter cloned from the lion's mane jellyfish (Cnidaria, Scyphozoa) is expressed in neurons." PLoS One **14**(6): e0218806.

In the course of recent comparative genomic studies conducted on nervous systems across the phylogeny, current thinking is leaning in favor of more heterogeneity among nervous systems than what was initially expected. The isolation and characterization of molecular components that constitute the cnidarian neuron is not only of interest to the physiologist but also, on a larger scale, to those who study the evolution of nervous systems. Understanding the function of those ancient neurons involves the identification of neurotransmitters and their precursors, the description of nutrients used by neurons for metabolic purposes and the identification of integral membrane proteins that bind to those compounds. Using a molecular cloning strategy targeting membrane proteins that are known to be present in all forms of life, we isolated a member of the solute carrier family 6 from the scyphozoan jellyfish Cyanea capillata. The phylogenetic analysis suggested that the new transporter sequence belongs to an ancestral group of the nutrient amino acid transporter subfamily and is part of a cluster of cnidarian sequences which may translocate the same substrate. We found that the jellyfish transporter is expressed in neurons of the motor nerve net of the animal. To this end, we established an in situ hybridization protocol for the tissues of C. capillata and developed a specific antibody to the jellyfish transporter. Finally, we showed that the gene that codes for the jellyfish

transporter also expresses a long non-coding RNA. We hope that this research will contribute to studies that seek to understand what constitutes a neuron in species that belong to an ancient phylum.

Boulware, D. R. (2006). "A randomized, controlled field trial for the prevention of jellyfish stings with a topical sting inhibitor." J Travel Med **13**(3): 166-171.

BACKGROUND: Jellyfish stings are a common occurrence among ocean goers worldwide with an estimated 150 million envenomations annually. Fatalities and hospitalizations occur annually, particularly in the Indo-Pacific regions. A new topical jellyfish sting inhibitor based on the mucous coating of the clown fish prevents 85% of jellyfish stings in laboratory settings. The field effectiveness is unknown. The objective is to evaluate the field efficacy of the jellyfish sting inhibitor, Safe Sea. METHODS: A double-blind, randomized, placebo-controlled trial occurred at the Dry Tortugas National Park, FL, USA and Sapodilla Cayes, Belize. Participants were healthy volunteers planning to snorkel for 30 to 45 minutes. Ten minutes prior to swimming, each participant was directly observed applying a blinded sample of Safe Sea (Nidaria Technology Ltd, Jordan Valley, Israel) to one side of their body and a blinded sample of Coppertone (Schering-Plough, Kenilworth, NJ, USA) to the contralateral side as placebo control. Masked 26 g samples of both Safe Sea SPF15 and Coppertone SPF15 were provided in identical containers to achieve 2 mg/cm (2) coverage. Sides were randomly chosen by participants. The incidence of jellyfish stings was the main outcome measure. This was assessed by participant interview and examination as subjects exited the water. RESULTS: A total of 82 observed water exposures occurred. Thirteen jellyfish stings occurred during the study period for a 16% incidence. Eleven jellyfish stings occurred with placebo, two with the sting inhibitor, resulting in a relative risk reduction of 82% (95% confidence interval: 21%-96%; p= 0.02). No seabather's eruption or side effects occurred. CONCLUSIONS: Safe Sea is a topical barrier cream effective at preventing >80% jellyfish stings under real-world conditions.

Bouyer-Monot, D., et al. (2017). "Retrospective study of jellyfish envenomation in emergency wards in Guadeloupe between 2010 and 2016: When to diagnose Irukandji syndrome?" Toxicon **137**: 73-77.

BACKGROUND: In Guadeloupe (French West Indies), many marine envenomation cases by jellyfish are observed. Some of them might induce an Irukandji syndrome (IS). The aim of this study was to analyse the clinical features of IS from the envenomation cases in the two public hospitals in Guadeloupe, and to compare them to non-IS stings. METHODS: All jellyfish envenomation cases between the 1st of January 2010 and the 1st of September 2016, from the emergencies data-base, have been extracted. The primary endpoint was the existence of an IS defined by a jellyfish sting followed by one of the symptoms among: severe lumbosacral, thoracic or abdominal pain, muscle cramps of the four limbs, profuse sweating, anxiety, restlessness, nausea, or vomiting. RESULTS: Two hundred and eleven envenomation cases have been extracted, 45.0% of them happened between the 22nd and the 26th day of the lunar phase during a period from June to September. Ninety five patients had an IS. Three of them had Quincke's edema and one a cardiopulmonary failure. Other clinical signs have been associated with IS compared to other sting cases, including hypertension (51.6% vs 18.1%, $p < 0.001$), tremor (32.6% vs 14.7%, $p = 0.0014$), paresthesia (20.0% vs. 10.3%, $p = 0.049$), dyspnea (13.7% vs 3.4%, $p = 0.006$), and the pain evaluation by the visual analogue pain scale (7.5 +/- 2.6 and 6.0 +/- 2.6, $p = 0.001$). CONCLUSION: Jellyfish envenomation is frequently associated with IS in Guadeloupean emergency wards. The IS cases were probably due to the species Alatina alata, and their periodicity can be determined according to the cycle of the moon. If patients showed symptoms slightly less severe than those in Australian studies, a case of cardiac decompensation, the first out of the Pacific, was observed. Based on our results, new definition of IS and severe IS are proposed.

ouzaiene, M., et al. (2007). "Immunohistochemical localization of a retinoic acid-like receptor in nerve cells of two colonial anthozoans (Cnidaria)." Tissue Cell **39**(2): 123-130.

Retinoic acid is known to induce vertebrate stem cells to differentiate into a variety of cell types, including neurons. Although retinoic acid was reported to affect morphogenetic pattern specification in the hydrozoan Hydractinia (Muller, W.A., 1984. Retinoids and pattern formation in a hydroid. J. Embryol. Exp. Morph. 81, 253-271) and a retinoid RXR receptor was cloned in the jellyfish Tripedalia (Kostrouch, Z., Kostrouchova, M., Love, W., Jannini, E., Piatigorsky, J., Rall, J.E., 1998. Retinoic acid X receptor in the diploblast, Tripedalia cystophora. Proc. Natl. Acad. Sci. U.S.A. 95, 13442-13447), the cellular targets of retinoids were not investigated. We used Western immunoblotting and immunohistochemistry to investigate the presence and cellular distribution of a RXR-like receptor in the sea pansy Renilla koellikeri and in the staghorn coral Acropora millepora (Cnidaria, Anthozoa). Western blots revealed a 64 kDa protein from a sea pansy extract in a band that co-migrated with a RXR protein from the rat brain. Using

antibodies raised against an epitope of human alpha RXR, we visualized putative ectodermal sensory cells in the polyp column of the adult sea pansy. Immunoreactivity was absent in staghorn coral larvae but present in the polyp column of adult colonies in the form of clusters of neuron-like cells in the basiectoderm near the ectoderm-mesoglea interface. These observations suggest that a RXR-like receptor is involved in epithelial nerve cell specification in adult anthozoans and that this role is conserved throughout evolution.

Breen, P., et al. (2017). "New insights into ocean sunfish (Mola mola) abundance and seasonal distribution in the northeast Atlantic." Sci Rep **7**(1): 2025.

The ocean sunfish, Mola mola, is the largest teleost fish in the world. Despite being found in all oceans of the world, little is known about its abundance and factors driving its distribution. In this study we provide the first abundance estimates for sunfish in offshore waters in the northeast Atlantic and the first record of extensive sunfish presence in these waters year-round. Abundance estimates and predictive distributions for sunfish in approximately 300,000 km (2) of the northeast Atlantic were derived from large scale offshore aerial surveys in 2015-2016 using distance sampling techniques. Generalized additive models of sunfish density were fitted to survey data from 17,360 km of line transect effort resulting in minimum abundance estimates of 12,702 (CI: 9,864-16,357) in the summer (Density = 0.043 ind/km (2)) and 8,223 individuals (CI: 6,178-10,946) (Density = 0.028 ind/km (2)) in the winter. Density surface models predicted seasonal shifts in distribution and highlighted the importance of the mixed layer depth, possibly related to thermoregulation following deep foraging dives. The abundance estimate and estimated daily consumption of 2,600 tonnes of jellyfish in the northeast Atlantic highlights the need to re-assess the importance of this species in the pelagic ecosystem, and its role in top-down control of jellyfish blooms.

Breitbart, M., et al. (2015). "Discovery, Prevalence, and Persistence of Novel Circular Single-Stranded DNA Viruses in the Ctenophores Mnemiopsis leidyi and Beroe ovata." Front Microbiol **6**: 1427.

Gelatinous zooplankton, such as ctenophores and jellyfish, are important components of marine and brackish ecosystems and play critical roles in aquatic biogeochemistry. As voracious predators of plankton, ctenophores have key positions in aquatic food webs and are often successful invaders when introduced to new areas. Gelatinous zooplankton have strong impacts on ecosystem services, particularly in coastal environments. However, little is known about the factors responsible for regulating population dynamics of gelatinous organisms, including biological interactions that may contribute to bloom demise. Ctenophores are known to contain specific bacterial communities and a variety of invertebrate parasites and symbionts; however, no previous studies have examined the presence of viruses in these organisms. Building upon recent studies demonstrating a diversity of single-stranded DNA viruses that encode a replication initiator protein (Rep) in aquatic invertebrates, this study explored the presence of circular, Rep-encoding single-stranded DNA (CRESS-DNA) viruses in the ctenophores Mnemiopsis leidyi and Beroe ovata collected from the Skidaway River Estuary and Savannah River in Georgia, USA. Using rolling circle amplification followed by restriction enzyme digestion, this study provides the first evidence of viruses in ctenophores. Investigation of four CRESS-DNA viruses over an 8-month period using PCR demonstrated temporal trends in viral prevalence and indicated that some of the viruses may persist in ctenophore populations throughout the year. Although future work needs to examine the ecological roles of these ctenophore-associated viruses, this study indicates that viral infection may play a role in population dynamics of gelatinous zooplankton.

Breitburg, D. L., et al. (2010). "Ecosystem engineers in the pelagic realm: alteration of habitat by species ranging from microbes to jellyfish." Integr Comp Biol **50**(2): 188-200.

Ecosystem engineers are species that alter the physical environment in ways that create new habitat or change the suitability of existing habitats for themselves or other organisms. In marine systems, much of the focus has been on species such as corals, oysters, and macrophytes that add physical structure to the environment, but organisms ranging from microbes to jellyfish and finfish that reside in the water column of oceans, estuaries, and coastal seas alter the chemical and physical environment both within the water column and on the benthos. By causing hypoxia, changing light regimes, and influencing physical mixing, these organisms may have as strong an effect as species that fall more clearly within the classical category of ecosystem engineer. In addition, planktonic species, such as jellyfish, may indirectly alter the physical environment through predator-mediated landscape structure. By creating spatial patterns of habitats that vary in their rates of mortality due to predation, planktonic predators may control spatial patterns and abundances of species that are the direct creators or modifiers of physical habitat.

Brejc, K., et al. (1997). "Structural basis for dual excitation and photoisomerization of the Aequorea victoria green fluorescent protein." Proc Natl Acad Sci U S A **94**(6): 2306-2311.

The 2.1-A resolution crystal structure of wild-type green fluorescent protein and comparison of it with the recently determined structure of the Ser-65 --> Thr (S65T) mutant explains the dual wavelength absorption and photoisomerization properties of the wild-type protein. The two absorption maxima are caused by a change in the ionization state of the chromophore. The equilibrium between these states appears to be governed by a hydrogen bond network that permits proton transfer between the chromophore and neighboring side chains. The predominant neutral form of the fluorophore maximally absorbs at 395 nm. It is maintained by the carboxylate of Glu-222 through electrostatic repulsion and hydrogen bonding via a bound water molecule and Ser-205. The ionized form of the fluorophore, absorbing at 475 nm, is present in a minor fraction of the native protein. Glu-222 donates its charge to the fluorophore by proton abstraction through a hydrogen bond network, involving Ser-205 and bound water. Further stabilization of the ionized state of the fluorophore occurs through a rearrangement of the side chains of Thr-203 and His-148. UV irradiation shifts the ratio of the two absorption maxima by pumping a proton relay from the neutral chromophore's excited state to Glu-222. Loss of the Ser-205-Glu-222 hydrogen bond and isomerization of neutral Glu-222 explains the slow return to the equilibrium dark-adapted state of the chromophore. In the S65T structure, steric hindrance by the extra methyl group stabilizes a hydrogen bonding network, which prevents ionization of Glu-222. Therefore the fluorophore is permanently ionized, causing only a 489-nm excitation peak. This new understanding of proton redistribution in green fluorescent protein should enable engineering of environmentally sensitive fluorescent indicators and UV-triggered fluorescent markers of protein diffusion and trafficking in living cells.

Brinkman, D. L. and J. N. Burnell (2009). "Biochemical and molecular characterisation of cubozoan protein toxins." Toxicon **54**(8): 1162-1173.

Class Cubozoa includes several species of box jellyfish that are harmful to humans. The venoms of box jellyfish are stored and discharged by nematocysts and contain a variety of bioactive proteins that are cytolytic, cytotoxic, inflammatory or lethal. Although cubozoan venoms generally share similar biological activities, the diverse range and severity of effects caused by different species indicate that their venoms vary in protein composition, activity and potency. To date, few individual venom proteins have been thoroughly characterised, however, accumulating evidence suggests that cubozoan jellyfish produce at least one group of homologous bioactive proteins that are labile, basic, haemolytic and similar in molecular mass (42-46 kDa). The novel box jellyfish toxins are also potentially lethal and the cause of cutaneous pain, inflammation and necrosis, similar to that observed in envenomed humans. Secondary structure analysis and remote protein homology predictions suggest that the box jellyfish toxins may act as alpha-pore-forming toxins. However, more research is required to elucidate their structures and investigate their mechanism (s) of action. The biological, biochemical and molecular characteristics of cubozoan venoms and their bioactive protein components are reviewed, with particular focus on cubozoan cytolysins and the newly emerging family of box jellyfish toxins.

Brinkman, D. L., et al. (2015). "Transcriptome and venom proteome of the box jellyfish Chironex fleckeri." BMC Genomics **16**: 407.

BACKGROUND: The box jellyfish, Chironex fleckeri, is the largest and most dangerous cubozoan jellyfish to humans. It produces potent and rapid-acting venom and its sting causes severe localized and systemic effects that are potentially life-threatening. In this study, a combined transcriptomic and proteomic approach was used to identify C. fleckeri proteins that elicit toxic effects in envenoming. RESULTS: More than 40,000,000 Illumina reads were used to de novo assemble approximately 34,000 contiguous cDNA sequences and approximately 20,000 proteins were predicted based on homology searches, protein motifs, gene ontology and biological pathway mapping. More than 170 potential toxin proteins were identified from the transcriptome on the basis of homology to known toxins in publicly available sequence databases. MS/MS analysis of C. fleckeri venom identified over 250 proteins, including a subset of the toxins predicted from analysis of the transcriptome. Potential toxins identified using MS/MS included metalloproteinases, an alpha-macroglobulin domain containing protein, two CRISP proteins and a turripeptide-like protease inhibitor. Nine novel examples of a taxonomically restricted family of potent cnidarian pore-forming toxins were also identified. Members of this toxin family are potently haemolytic and cause pain, inflammation, dermonecrosis, cardiovascular collapse and death in experimental animals, suggesting that these toxins are responsible for many of the symptoms of C. fleckeri envenomation. CONCLUSIONS: This study provides the first overview of a box jellyfish transcriptome which, coupled with venom proteomics data, enhances our current understanding of box jellyfish venom composition and the molecular structure and function of cnidarian toxins. The

generated data represent a useful resource to guide future comparative studies, novel protein/peptide discovery and the development of more effective treatments for jellyfish stings in humans. (Length: 300).

Brinkman, D. L., et al. (2014). "Chironex fleckeri (box jellyfish) venom proteins: expansion of a cnidarian toxin family that elicits variable cytolytic and cardiovascular effects." J Biol Chem **289**(8): 4798-4812.

The box jellyfish Chironex fleckeri produces extremely potent and rapid-acting venom that is harmful to humans and lethal to prey. Here, we describe the characterization of two C. fleckeri venom proteins, CfTX-A (approximately 40 kDa) and CfTX-B (approximately 42 kDa), which were isolated from C. fleckeri venom using size exclusion chromatography and cation exchange chromatography. Full-length cDNA sequences encoding CfTX-A and -B and a third putative toxin, CfTX-Bt, were subsequently retrieved from a C. fleckeri tentacle cDNA library. Bioinformatic analyses revealed that the new toxins belong to a small family of potent cnidarian pore-forming toxins that includes two other C. fleckeri toxins, CfTX-1 and CfTX-2. Phylogenetic inferences from amino acid sequences of the toxin family grouped CfTX-A, -B, and -Bt in a separate clade from CfTX-1 and -2, suggesting that the C. fleckeri toxins have diversified structurally and functionally during evolution. Comparative bioactivity assays revealed that CfTX-1/2 (25 mug kg (-1)) caused profound effects on the cardiovascular system of anesthetized rats, whereas CfTX-A/B elicited only minor effects at the same dose. Conversely, the hemolytic activity of CfTX-A/B (HU50 = 5 ng ml (-1)) was at least 30 times greater than that of CfTX-1/2. Structural homology between the cubozoan toxins and insecticidal three-domain Cry toxins (delta-endotoxins) suggests that the toxins have a similar pore-forming mechanism of action involving alpha-helices of the N-terminal domain, whereas structural diversification among toxin members may modulate target specificity. Expansion of the cnidarian toxin family therefore provides new insights into the evolutionary diversification of box jellyfish toxins from a structural and functional perspective.

Broadhurst, M. K., et al. (2008). "Mortality of discards from southeastern Australian beach seines and gillnets." Dis Aquat Organ **80**(1): 51-61.

Two experiments were done in an Australian estuary to quantify the mortalities and contributing factors for key species discarded during 8 and 9 deployments of commercial beach (or shore) seines and gillnets, respectively. In both experiments, bycatches (2347 individuals comprising 16 species) were handled according to conventional practices and assessed for immediate mortalities before live samples of selected species were discarded into replicate cages along with appropriate controls, and monitored for short-term mortalities (< or =10 d). All of the seined or gilled fish were alive prior to discarding. During the beach seine experiment, 20% of caged seined-and-discarded surf bream Acanthopagrus australis (n = 290) were dead after 5 d, with most mortalities occurring between the second and fifth day. In the gillnet experiment, 42 and 11% of gilled-and-discarded A. australis (n = 161) and lesser salmon catfish Neoarius graeffei (n = 67), respectively, died during a 10 d monitoring period, mostly within the first 5 d. There were no deaths in any controls for these fish. Mixed-effects logistic models revealed that the mortality of A. australis discarded from both gears was significantly ($p < 0.01$) and negatively correlated with their total length, while N. graeffei had a significantly ($p < 0.05$) greater (5-fold) probability of dying when jellyfish Catostylus sp. were present in the gillnet. Simple modifications to the operations of beach seines and gillnets and/or post-capture handling procedures, such as close regulation of size selectivity for the target species, careful removal of fish from meshes, and abstention from setting during high abundances of jellyfish will maximise the survival of discarded bycatch.

Brockes, J. (1994). "Cell differentiation. Muscle escapes from a jelly mould." Curr Biol **4**(11): 1030-1032.

Striated muscle cells from the medusa of the jellyfish Podocoryne show remarkable plasticity; vertebrate myotubes are less plastic, but can re-enter the cell cycle in the absence of the retinoblastoma protein.

Brolin, S. E. and A. Agren (1981). "Potentialities of bioluminescence analyses in research on the pancreatic islets." Ups J Med Sci **86**(2): 125-130.

Progress in bioluminescence assay permits not only determinations of nucleotide and substrate concentrations, but also estimation of concentration shifts. The analyses can be extended to comprise Ca2+ since the Aequorea system is sensitive enough for applications in islet research. By connecting the bioluminometer to a microprocessor with a suitable readout device, it is possible to collect and evaluate large amounts of data which may be required in studies of concentration shifts. Thus, blanks, samples and standards can be processed completely within short time periods so that the light-yielding solutions remain stable.

Brown, S. A., et al. (2013). "Management of envenomations during pregnancy." Clin Toxicol (Phila) **51**(1): 3-15.

CONTEXT: Envenomations during pregnancy pose all the problems of envenomation in the nonpregnant state with additional complexity related to maternal physiologic changes, medication use during pregnancy, and the well-being of the fetus. OBJECTIVE: We review the obstetric literature and management options available to prevent maternal morbidity and mortality while limiting adverse obstetric outcomes after envenomation in pregnancy. METHODS: In January 2012, we searched the U.S. National Library of Medicine Medline/PubMed, Toxline, Reprotox, Google Scholar and Micromedex databases, core surgery and internal medicine textbooks, and references of retrieved articles for the years 1966 through 2011. Search terms included "envenomation in pregnancy," "stings in pregnancy," "antivenom use in pregnancy," "anaphylaxis in pregnancy," and variants of these with known venomous animals. Reference lists generated further case reports and articles. We included English language articles and abstracts. Levels of Evidence (LOE) for the reports cited and Grades of Recommendations (GOR) based on LOE for our recommendations use the National Guidelines Clearinghouse metric of the US DHHS. RESULTS: Recommendations for the management of envenomation in pregnancy are guided primarily by studies on nonpregnant persons and case reports of pregnancy. Clinically significant envenomations in pregnancy are reported for snakes, spiders, scorpions, jellyfish, and hymenoptera (bees, wasps, hornets, and ants). Adverse obstetric outcomes including miscarriage, preterm birth, placental abruption, and stillbirth are associated with envenomation in pregnancy. The limited available literature suggests that adverse outcomes are primarily related to venom effects on the mother. Optimization of maternal health such as management of anaphylaxis and antivenom administration is likely the best approach to improve fetal outcomes despite potential risks to the fetus of medication administration during pregnancy. Obstetric evaluation and fetal monitoring are imperative in cases of severe envenomation. CONCLUSION: The medical literature regarding envenomation in pregnancy includes primarily retrospective reviews and case series. The limited available evidence suggests that optimal management includes a venom-specific approach, including supportive care, antivenom administration in appropriate cases, treatment of anaphylaxis if present, and fetal assessment. The current available evidence suggests that antivenom use is safe in pregnancy and that what is good for the mother is good for the fetus. Further research is needed to clarify the optimal management schema for envenomation in pregnancy.

Brown, T. P. (2005). "Diagnosis and management of injuries from dangerous marine life." MedGenMed **7**(3): 5.

Injuries from marine life encompass a wide spectrum, from mild stings to severe bites. Fortunately most of the injuries are mild, although some may be significant, resulting in death. Most of these injuries can be treated by family physicians with a knowledge of the cause of the pathology. Over the years, there have been many treatment options. Some have actually caused an increase in severity. An important rule in treating these injuries is to inactivate the venom, treat the local reaction or injury, and treat the systemic sequelae. Jellyfish stings are the most common type of marine injury. The tentacles possess nematocysts, which are stinging units that are inactivated by the application of vinegar. Sea urchin and stingray injuries require the removal of the imbedded spines after the wound is soaked in hot water. Coral, sea bathers eruption, and swimmer's itch require thorough scrubbing and irrigation. Sea snakes, cone shells, and venomous fish possess a neurotoxin that requires close monitoring in the event of cardiopulmonary collapse. All of these injuries require tetanus status monitoring and consideration of coverage for infectious sequelae.

Bruschetta, G., et al. (2014). "Pelagia noctiluca (Scyphozoa) crude venom injection elicits oxidative stress and inflammatory response in rats." Mar Drugs **12**(4): 2182-2204.

Cnidarian toxins represent a rich source of biologically active compounds. Since they may act via oxidative stress events, the aim of the present study was to verify whether crude venom, extracted from the jellyfish Pelagia noctiluca, elicits inflammation and oxidative stress processes, known to be mediated by Reactive Oxygen Species (ROS) production, in rats. In a first set of experiments, the animals were injected with crude venom (at three different doses 6, 30 and 60 microg/kg, suspended in saline solution, i.v.) to test the mortality and possible blood pressure changes. In a second set of experiments, to confirm that Pelagia noctiluca crude venom enhances ROS formation and may contribute to the pathophysiology of inflammation, crude venom-injected animals (30 microg/kg) were also treated with tempol, a powerful antioxidant (100 mg/kg i.p., 30 and 60 min after crude venom). Administration of tempol after crude venom challenge, caused a significant reduction of each parameter related to inflammation. The potential effect of Pelagia noctiluca crude venom in the systemic inflammation process has been here demonstrated, adding novel information about its biological activity.

Bryant, P. J. and T. E. Arehart (2019). "Diversity and life-cycle analysis of Pacific Ocean zooplankton by videomicroscopy and DNA barcoding: Hydrozoa." PLoS One **14**(10): e0218848.

Most, but not all cnidarian species in the class Hydrozoa have a life cycle in which a colonial, asexually reproducing hydroid phase alternates with a free-swimming, sexually reproducing medusa phase. They are not well known, in part because many of them are microscopic, at least in the medusa phase. Matching the two phases has previously required rearing of the organism from one phase to another, which has not often been possible. Here we show that DNA barcoding makes it possible to easily link life-cycle phases without the need for laboratory rearing. Hydrozoan medusae were collected by zooplankton tows in Newport Bay and the Pacific Ocean near Newport Beach, California, and hydroid colonies were collected from solid substrates in the same areas. Specimens were documented by videomicroscopy, preserved in ethanol, and sent to the Canadian Centre for DNA Barcoding at the University of Guelph, Ontario, Canada for sequencing of the COI DNA barcode. In the order Anthoathecata (athecate hydroids), DNA barcoding allowed for the discrimination between the medusae of eight putative species of Bougainvillia, and the hydroid stages were documented for two of these. The medusae of three putative species of Amphinema were identified, and the hydroid stages were identified for two of them. DNA barcodes were obtained from medusae of one species of Cladonema, one adult of the by-the wind Sailor, Velella velella, five putative species of Corymorpha with the matching hydroid phase for one; and Coryne eximia, Turritopsis dohrnii and Turritopsis nutricula with the corresponding hydroid phases. The actinula larvae and hydroid for the pink-hearted hydroid Ectopleura crocea were identified and linked by DNA barcoding. In the order Leptothecata (thecate hydroids) medusae were identified for Clytia elsaeoswaldae, Clytia gracilis and Clytia sp. 701 AC and matched with the hydroid phases for the latter two species. Medusae were matched with the hydroid phases for two species of Obelia (including O. dichotoma) and Eucheilota bakeri. Obelia geniculata was collected as a single hydroid. DNA barcodes were obtained for hydroids of Orthopyxis everta and three other species of Orthopyxis. One member of the family Solmarisidae, representing the order Narcomedusae, and one member (Liriope tetraphylla) of the order Trachymedusae were recognized as medusae. The results show the utility of DNA barcoding for matching life-cycle stages as well as for documenting the diversity of this class of organisms.

Bulina, M. E., et al. (2004). "New class of blue animal pigments based on Frizzled and Kringle protein domains." J Biol Chem **279**(42): 43367-43370.

The nature of coloration in many marine animals remains poorly investigated. Here we studied the blue pigment of a scyfoid jellyfish Rhizostoma pulmo and determined it to be a soluble extracellular 30-kDa chromoprotein with a complex absorption spectrum peaking at 420, 588, and 624 nm. Furthermore, we cloned the corresponding cDNA and confirmed its identity by immunoblotting and mass spectrometry experiments. The chromoprotein, named rpulFKz1, consists of two domains, a Frizzled cysteine-rich domain and a Kringle domain, inserted into one another. Generally, Frizzleds are members of a basic Wnt signal transduction pathway investigated intensely with regard to development and cancerogenesis. Kringles are autonomous structural domains found throughout the blood clotting and fibrinolytic proteins. Neither Frizzled and Kringle domains association with any type of coloration nor Kringle intrusion into Frizzled sequence was ever observed. Thus, rpulFKz1 represents a new class of animal pigments, whose chromogenic group remains undetermined. The striking homology between a chromoprotein and members of the signal transduction pathway provides a novel node in the evolution track of growth factor-mediated morphogenesis compounds.

Burakova, L. P., et al. (2016). "All Ca (2+)-binding loops of light-sensitive ctenophore photoprotein berovin bind magnesium ions: The spatial structure of Mg (2+)-loaded apo-berovin." J Photochem Photobiol B **154**: 57-66.

Light-sensitive photoprotein berovin accounts for a bright bioluminescence of ctenophore Beroe abyssicola. Berovin is functionally identical to the well-studied Ca (2+)-regulated photoproteins of jellyfish, however in contrast to those it is extremely sensitive to the visible light. Berovin contains three EF-hand Ca (2+)-binding sites and consequently belongs to a large family of the EF-hand Ca (2+)-binding proteins. Here we report the spatial structure of apo-berovin with bound Mg (2+) determined at 1.75A. The magnesium ion is found in each functional EF-hand loop of a photoprotein and coordinated by oxygen atoms donated by the side-chain groups of aspartate, carbonyl groups of the peptide backbone, or hydroxyl group of serine with characteristic oxygen-Mg (2+) distances. As oxygen supplied by the side-chain of the twelfth residue of all Ca (2+)-binding loops participates in the magnesium ion coordination, it was suggested that Ca (2+)-binding loops of berovin belong to the mixed Ca (2+)/Mg (2+) rather than Ca (2+)-specific type. In addition, we report an effect of physiological concentration of Mg (2+) on

bioluminescence of berovin (sensitivity to Ca (2+), rapid-mixed kinetics, light-sensitivity, thermostability, and apo-berovin conversion into active protein). The different impact of physiological concentration of Mg (2+) on berovin bioluminescence as compared to hydromedusan photoproteins was attributed to different affinities of the Ca (2+)-binding sites of these photoproteins to Mg (2+).

Cariello, L., et al. (1988). "Isolation and partial characterization of rhizolysin, a high molecular weight protein with hemolytic activity, from the jellyfish Rhizostoma pulmo." Toxicon **26**(11): 1057-1065.

A new cytolysin has been isolated from the nematocysts of the jellyfish, Rhizostoma pulmo, and named rhizolysin. The hemolysin has a mol. wt of approximately 260,000, a sedimentation coefficient of 10.3 S and is rod-shaped with a calculated axial ratio of about 1:5. It appears to be composed of three subunits with a pI value near 7.8. Rhizolysin shows no phospholipase A activity, nor an induction period for its hemolytic activity and is completely inhibited by sucrose. The optimum pH was 6.75. The mu value calculated from the Arrhenius plot is 5940 cal/mole. Rhizolysin was inhibited by cholesterol and less by sphingomyelin.

Carla, E. C., et al. (2003). "Morphological and ultrastructural analysis of Turritopsis nutricula during life cycle reversal." Tissue Cell **35**(3): 213-222.

The hydrozoa life cycle is characterized, in normal conditions, by the alternation of a post-larval benthic polyp and an adult pelagic medusa; however, some species of Hydrozoa react to environmental stress by reverting their life cycle: i.e. an adult medusa goes back to the juvenile stage of polyp. This very uncommon life cycle could be considered as some sort of inverted metamorphosis. A morphological study of different stages during the reverted life cycle of Turritopsis nutricula led to the characterization of four different stages: healthy medusa, unhealthy medusa, four-leaf clover and cyst. The ultrastructural study of the cellular modifications (during the life cycle reversion of T. nutricula) showed the presence of both degenerative and apoptotic processes. Degeneration was prevalent during the unhealthy medusa and four-leaf clover stages, while the apoptotic rate was higher during the healthy medusa and cyst stages. The significant presence of degenerative and apoptotic processes could be related to the occurrence of a sort of metamorphosis when an adult medusa transforms itself into a polyp.

Carlberg, M., et al. (1995). "Taurine-like Immunoreactivity in the Motor Nerve Net of the Jellyfish Cyanea capillata." Biol Bull **188**(1): 78-82.

Two antisera against the sulfonated amino acid taurine were applied to subumbrella tissue of the jellyfish Cyanea capillata. Taurine-immunoreactive nerve nets were found in both the ectoderm and endoderm. The ectoderm had two morphologically and immunocytochemically distinct populations of neurons, the motor nerve net (MNN), which was immunoreactive to the taurine-like molecule, and the diffuse nerve net (DNN), which was immunoreactive to the neuropeptide Phe-Met-Arg-Phe-NH2 (FMRFamide). In the endoderm, immunoreactivity was found in the endodermal DNN. This localization was confirmed by double-labeling experiments, which also revealed that the endodermal DNN neurons may contain both taurine and FMRFamide-related peptide. The presence of a taurine immunoreactivity in the MNN supports the hypothesis that taurine or some chemically related compound is the neurotransmitter at synapses within the MNN of Cyanea.

Carli, A., et al. (1996). "Toxicity of jellyfish and sea-anemone venoms on cultured V79 cells." Toxicon **34**(4): 496-500.

Cnidarian toxins exert an influence on human activities and public health. The cytotoxicity of crude toxins (nematocyst and surrounding tissue venom) of Aequorea aequorea, Rhizostoma pulmo and Anemonia sulcata was assessed on V79 cells. Rhizostoma pulmo and Anemonia sulcata crude venoms showed remarkable cytotoxicity and killed all treated cells at highest tested concentration within 2 and 3 hr, respectively. Aequorea aequorea crude venom greatly affected growth rate during long-term experiments. No genotoxic effect was observed.

Carman, M. R., et al. (2017). "Species-specific crab predation on the hydrozoan clinging jellyfish Gonionemus sp. (Cnidaria, Hydrozoa), subsequent crab mortality, and possible ecological consequences." PeerJ **5**: e3966.

Here we report a unique trophic interaction between the cryptogenic and sometimes highly toxic hydrozoan clinging jellyfish Gonionemus sp. and the spider crab Libinia dubia. We assessed species-specific predation on the Gonionemus medusae by crabs found in eelgrass meadows in Massachusetts, USA. The native spider crab species L. dubia consumed Gonionemus medusae, often enthusiastically, but the invasive green crab Carcinus maenus avoided consumption in all trials. One out of two blue crabs (Callinectes sapidus) also consumed Gonionemus, but this species was too rare in our study system to evaluate further. Libinia crabs could consume up to 30 jellyfish, which was the maximum jellyfish density treatment in our experiments, over a 24-hour period. Gonionemus consumption was

associated with Libinia mortality. Spider crab mortality increased with Gonionemus consumption, and 100% of spider crabs tested died within 24 h of consuming jellyfish in our maximum jellyfish density containers. As the numbers of Gonionemus medusae used in our experiments likely underestimate the number of medusae that could be encountered by spider crabs over a 24-hour period in the field, we expect that Gonionemus may be having a negative effect on natural Libinia populations. Furthermore, given that Libinia overlaps in habitat and resource use with Carcinus, which avoids Gonionemus consumption, Carcinus populations could be indirectly benefiting from this unusual crab-jellyfish trophic relationship.

Carneiro, R. F., et al. (2011). "The extract of the jellyfish Phyllorhiza punctata promotes neurotoxic effects." J Appl Toxicol **31**(8): 720-729.

Phyllorhiza punctata (P. punctata) is a jellyfish native to the southwestern Pacific. Herewith we present the biochemical and pharmacological characterization of an extract of the tentacles of P. punctata. The tentacles were subjected to three freeze-thaw cycles, homogenized, ultrafiltered, precipitated, centrifuged and lyophilized to obtain a crude extract (PHY-N). Paralytic shellfish poisoning compounds such as saxitoxin, gonyautoxin-4, tetrodotoxin and brevetoxin-2, as well as several secretory phospholipase A (2) were identified. PHY-N was tested on autonomic and somatic neuromuscular preparations. In mouse vas deferens, PHY-N induced phasic contractions that reached a peak of 234 +/- 34.7% of control twitch height, which were blocked with either 100 mu m of phentolamine or 1 m m of lidocaine. In mouse corpora cavernosa, PHY-N evoked a relaxation response, which was blocked with either L-N (G) -Nitroarginine methyl ester (0.5 m m) or 1 m m of lidocaine. PHY-N (1, 3 and 10 mug ml (-1)) induced an increase in tonus of the biventer-cervicis neuromuscular preparation that was blocked with pre-treatment of galamine (10 mu m). Administration of 6 mg kg (-1) PHY-N intramuscularly produced death in broilers by spastic paralysis. In conclusion, PHY-N induces nerve depolarization and nonspecifically increases neurotransmitter release.

Caron, A. G. M., et al. (2018). "Validation of an optimised protocol for quantification of microplastics in heterogenous samples: A case study using green turtle chyme." MethodsX **5**: 812-823.

Quantifying the extent of microplastic (<5mm) contamination in the marine environment is an emerging field of study. Reliable extraction of microplastics from the gastro-intestinal content of marine organisms is crucial to evaluate microplastic contamination in marine fauna. Extraction protocols and variations thereof have been reported, however, these have mostly focussed on relatively homogenous samples (i.e. water, sediment, etc.). Here, we present a microplastic extraction protocol for examining green turtle (Chelonia mydas) chyme (i.e. ingested material and digestive tract fluid), which is a heterogeneous composite of various organic dietary items (e.g. seagrass, jellyfish) and incidentally-ingested inorganic materials (sediment). Established extraction methods were modified and combined. This protocol consists of acid digestion of organic matter, emulsification of residual fat, density separation from sediment, and chemical identification by Fourier transform-infrared spectroscopy. This protocol enables the extraction of the most common microplastic contaminants>100mum: polyethylene, high-density polyethylene, (aminoethyl) polystyrene, polypropylene, and polyvinyl chloride, with 100% efficiency. This validated protocol will enable researchers worldwide to quantify microplastic contamination in turtles in a reliable and comparable way. *Optimization of microplastic extraction from multifarious tissues by applying established methods in a sequential manner.*Effective for heterogenous samples comprising organic and inorganic material.

Carrette, T. J., et al. (2002). "Temperature effects on box jellyfish venom: a possible treatment for envenomed patients?" Med J Aust **177**(11-12): 654-655.

OBJECTIVE: To determine the effect of temperature on lethality of venom from Chironex fleckeri (the potentially fatal box jellyfish). DESIGN: Venom extracted from nematocysts of mature Chironex fleckeri specimens was exposed to temperatures between 4 degrees C and 58 degrees C for periods of two, five or 20 minutes, and then injected into freshwater crayfish (Cherax quadricarinatus) to assess lethality. MAIN OUTCOME MEASURE: Venom lethality, assessed as time to cardiac standstill in crayfish after intramuscular injection. RESULTS: Venom lethality was significantly affected by both temperature ($F_{7,34} = 21915$; $P < 0.0001$) and time of exposure ($F_{2,34} = 9907$; $P < 0.0001$). No significant loss of lethality was seen after exposure to temperatures <or= 39 degrees C, even after 20 minutes' exposure. At temperatures >or= 43 degrees C, venom lost its lethality more rapidly the longer the exposure time. Venom was non-lethal after exposure to 48 degrees C for 20 minutes, 53 degrees C for five minutes, and 58 degrees C for two minutes. CONCLUSION: Exposure to heat dramatically reduces the lethality of extracted C. fleckeri venom. Although heat application may be of limited use in treating C. fleckeri envenoming because of the speed

of symptom onset, its use in other box-jellyfish envenomings, such as Irukandji syndrome, requires investigation.

Carrette, T. J. and J. J. Seymour (2013). "Long-term analysis of Irukandji stings in Far North Queensland." Diving Hyperb Med **43**(1): 9-15.

INTRODUCTION: We reviewed the occurrence, trends, definition and severity of the Irukandji syndrome for the Cairns region of North Queensland, Australia. METHODS: A retrospective analysis of patient files from two sources was conducted: historic accounts kept by Dr Jack Barnes for the period 1942 to 1967, and records from the Emergency Unit in Cairns Base Hospital for 1995 to 2007. RESULTS: There has been a significant increase in the length of the Irukandji season since it was first reliably recorded (15 days in 1961; 151 days in 2002); however, annual numbers of envenomations were highly variable. Traditionally, greater frequencies of Irukandji stings were reported at onshore as opposed to offshore locations. However, in recent years this trend has reversed, potentially because of increased safety protocols for beach regions. Mean Troponin I levels were higher in offshore reef envenomations compared to those from islands or coastal regions. In terms of morphine-equivalent doses, patients given fentanyl received significantly greater opioid doses compared to those given morphine or pethidine. Opioid dosage was indicative of syndrome severity and correlated with other physiological parameters measured. Five major symptoms were associated with Irukandji syndrome: pain, nausea/vomiting, diaphoresis, headache and shortness of breath. Pain was the overwhelming symptom, followed closely by nausea/vomiting. CONCLUSIONS: The duration of the Irukandji season appears to be increasing. Conversely the number of envenomings appears to be decreasing, possibly because of improved beach management in recent years. Offshore envenomings appear to have a higher potential for more severe envenomings with five associated major symptoms.

Cenamor, R., et al. (1999). "The budding yeast Cdc15 localizes to the spindle pole body in a cell-cycle-dependent manner." Mol Cell Biol Res Commun **2**(3): 178-184.

Exit from mitosis in the budding yeast Saccharomyces cerevisiae cell cycle is regulated by a regulatory network that involves, among other proteins, the small GTPase Tem1, the protein phosphatase Cdc14, and the protein kinases Dbf2 and Cdc15. Using a fusion to jellyfish green fluorescent protein (GFP), here we report that Cdc15 costains with the microtubular-organizing apparatus and that this localization is precluded in a mutant lacking the outer plaque of the spindle pole body (SPB). The appearance of Cdc15 in the SPB is asymmetric and cell-cycle-regulated, preferentially marking the daughter cell SPB at anaphase and eventually disappearing at cytokinesis. Overproduction of GFP-tagged Cdc15 led to an accumulation of the fusion protein in both mother and daughter cells SPBs and, transiently, in small budded cells and shmoos. The Cdc15 localization pattern was maintained in dbf2, cdc14 and anaphase-promoting complex (cdc16) mutants, suggesting that the function of these proteins is not related to the localization of Cdc15 to the SPB but rather, at least in the case of Cdc14, to its timely removal from this structure. Tem1-depleted cells kept alive by Cdc15-GFP overexpression still display a proper localization of Cdc15. The results presented here suggest that the transient cell-cycle-dependent localization of Cdc15 to the SPB plays a role in the regulation of the latest stages of the cell cycle.

Cerfolio, R. J. (2001). "Beware the malignant jellyfish." Ann Thorac Surg **72**(6): 2113-2115.

Small pleural effusions that cannot be assessed by thoracentesis prior to surgery may represent a diagnostic challenge in the patient with a resectable, non-small cell cancer of the lung. Even if the effusion is drained preoperatively and analyzed, the cytology may be falsely negative. We have found that careful inspection of pleural effusions using a single small 2-cm incision and video-assisted thoracoscopy may reveal a gelatinous piece of clotlike material that resembles a jellyfish. This cohesive particulate piece of material lies in the effusion. This material can be sent for frozen section (unlike cytologic exams in most hospitals), and an immediate answer can be obtained. Cytology results of the surrounding effusion that return 24 hours later confirm the frozen section findings. If malignant, this avoids thoracotomy and pulmonary resection in a patient with unsuspected T4, stage IIIB lung cancer. It also avoids closing a patient with an unsuspected effusion and having to wait 24 hours for the cytology results. We review our experience with this jellyfish-like material.

Chae, J., et al. (2018). "Comprehensive Analysis of the Jellyfish Chrysaora pacifica (Goette, 1886) (Semaeostomeae: Pelagiidae) with Description of the Complete rDNA Sequence." Zool Stud **57**: e51.

Jinho Chae, Yoseph Seo, Won Bae Yu, Won Duk Yoon, Hye Eun Lee, Soo-Jung Chang, and Jang-Seu Ki (2018) The Scyphomedusae genus Chrysaora consists of highly diversified jellyfishes. Although morphological systematics of the genus has been documented over the past century, characterization of molecular taxonomy has been attempted only recently. In the present study, we sequenced an 8,167 bp region,

encompassing a single ribosomal DNA (rDNA) repeat unit, from Chrysaora pacifica, and used it for phylogenetic analyses. The tandemly repeated rDNA units turned out to consist of both coding and noncoding regions, whose arrangement was found to be the same as that of a typical eukaryote. None of the 5S rRNA sequences were found among the repeat units. Comparative analyses of jellyfish rDNA sequences showed that the 28S locus is highly informative and divergent compared to the 18S locus. Phylogenetic analyses of the 18S and 28S loci revealed that the Semaeostomeae order of jellyfish is separated into taxonomic groups by families and genera, with a few exceptions. The family Pelagiidae was in a clade separate from other groups, thus forming a monophyletic lineage. All Chrysaora included here formed a strongly supported clade within the family Pelagiidae, and Pelagiidae manifested a sister relationship with Cyanea. Nonetheless, Chrysaora was found to be paraphyletic in both 18S and 28S phylogenies. Chrysaora pacifica was clearly distinct from close relatives C. melanaster and C. quinquecirrha. These results provide a special reference for the DNA taxonomy of Pelagiidae jellyfishes in terms of nuclear cistron rDNA sequences and improve our understanding of the molecular phylogenetic relationships among Semaeostomeae jellyfishes.

Chakrabarti, A. and S. Sengupta (2015). "Jellyfish Envenomation Presenting with Delayed Identical Cutaneous Lesions in a Mother and Child." Indian J Dermatol **60**(5): 488-490.

Jellyfish envenomation can present with local cutaneous lesions both immediate and delayed. While the immediate reaction is toxin mediated, an immune mechanism is responsible for the delayed eruptions. This is a report of a mother and child who developed identical papular lesions in a bizarre, linear distribution after coming in contact with jellyfish almost simultaneously while on holiday. Histology showed focal basal cell degeneration along with peri-vascular and peri-appendageal lympho-mononuclear infiltrate. Both patients responded well to topical tacrolimus.

Chalfie, M. (1995). "Green fluorescent protein." Photochem Photobiol **62**(4): 651-656.

Several bioluminescent coelenterates use a secondary fluorescent protein, the green fluorescent protein (GFP), in an energy transfer reaction to produce green light. The most studied of these proteins have been the GFPs from the jellyfish Aequorea victoria and the sea pansy Renilla reniformis. Although the proteins from these organisms are not identical, they are thought to have the same chromophore, which is derived from the primary amino acid sequence of GFP. The differences are thought to be due to changes in the protein environment of the chromophore. Recent interest in these molecules has arisen from the cloning of the Aequorea gfp cDNA and the demonstration that its expression in the absence of other Aequorea proteins results in a fluorescent product. This demonstration indicated that GFP could be used as a marker of gene expression and protein localization in living and fixed tissues. Bacterial, plant and animal (including mammalian) cells all express GFP. The heterologous expression of the gfp cDNA has also meant that it could be mutated to produce proteins with different fluorescent properties. Variants with more intense fluorescence or alterations in the excitation and emission spectra have been produced.

Chan, M. C., et al. (2006). "Structural characterization of a blue chromoprotein and its yellow mutant from the sea anemone Cnidopus japonicus." J Biol Chem **281**(49): 37813-37819.

Green fluorescent protein (GFP) and its relatives (GFP protein family) have been isolated from marine organisms such as jellyfish and corals that belong to the phylum Cnidaria (stinging aquatic invertebrates). They are intrinsically fluorescent proteins. In search of new members of the family of green fluorescent protein family, we identified a non-fluorescent chromoprotein from the Cnidopus japonicus species of sea anemone that possesses 45% sequence identity to dsRed (a red fluorescent protein). This newly identified blue color protein has an absorbance maximum of 610 nm and is hereafter referred to as cjBlue. Determination of the cjBlue 1.8 A crystal structure revealed a chromophore comprised of Gln (63)-Tyr (64)-Gly (65). The ring stacking between Tyr (64) and His (197) stabilized the cjBlue trans chromophore conformation along the Calpha2-Cbeta2 bond of 5-[(4-hydroxyphenyl)methylene]-imidazolinone, which closely resembled that of the "Kindling Fluorescent Protein" and Rtms5. Replacement of Tyr (64) with Leu in wild-type cjBlue produced a visible color change from blue to yellow with a new absorbance maximum of 417 nm. Interestingly, the crystal structure of the yellow mutant Y64L revealed two His (197) imidazole ring orientations, suggesting a flip-flop interconversion between the two conformations in solution. We conclude that the dynamics and structure of the chromophore are both essential for the optical appearance of these color proteins.

Chand, R. P. and K. Selliah (1984). "Reversible parasympathetic dysautonomia following stinging attributed to the box jelly fish (Chironex fleckeri)."

Aust N Z J Med **14**(5): 673-675.

Following a box jelly fish sting, a 52 year old Chinese fisherman developed acute abdominal distension, inability to pass urine and failure of erection. Examination revealed gaseous abdominal distension and a distended urinary bladder. Absence of lachrimation and absence of changes in the R-R interval in the ECG during breathing and carotid sinus massage gave further evidence of parasympathetic dysautonomia. The patient made a complete recovery. The case highlights the occurrence of reversible parasympathetic dysautonomia following box jelly fish sting.

Chang, E. S., et al. (2015). "Genomic insights into the evolutionary origin of Myxozoa within Cnidaria." Proc Natl Acad Sci U S A **112**(48): 14912-14917.

The Myxozoa comprise over 2,000 species of microscopic obligate parasites that use both invertebrate and vertebrate hosts as part of their life cycle. Although the evolutionary origin of myxozoans has been elusive, a close relationship with cnidarians, a group that includes corals, sea anemones, jellyfish, and hydroids, is supported by some phylogenetic studies and the observation that the distinctive myxozoan structure, the polar capsule, is remarkably similar to the stinging structures (nematocysts) in cnidarians. To gain insight into the extreme evolutionary transition from a free-living cnidarian to a microscopic endoparasite, we analyzed genomic and transcriptomic assemblies from two distantly related myxozoan species, Kudoa iwatai and Myxobolus cerebralis, and compared these to the transcriptome and genome of the less reduced cnidarian parasite, Polypodium hydriforme. A phylogenomic analysis, using for the first time to our knowledge, a taxonomic sampling that represents the breadth of myxozoan diversity, including four newly generated myxozoan assemblies, confirms that myxozoans are cnidarians and are a sister taxon to P. hydriforme. Estimations of genome size reveal that myxozoans have one of the smallest reported animal genomes. Gene enrichment analyses show depletion of expressed genes in categories related to development, cell differentiation, and cell-cell communication. In addition, a search for candidate genes indicates that myxozoans lack key elements of signaling pathways and transcriptional factors important for multicellular development. Our results suggest that the degeneration of the myxozoan body plan from a free-living cnidarian to a microscopic parasitic cnidarian was accompanied by extreme reduction in genome size and gene content.

Chaousis, S., et al. (2014). "Rapid short term and gradual permanent cardiotoxic effects of vertebrate toxins from Chironex fleckeri (Australian box jellyfish) venom." Toxicon **80**: 17-26.

The vertebrate cardiotoxic components of the venom produced by the Australian box jellyfish, Chironex fleckeri, have not previously been isolated. We have uncovered for the first time, three distinct cytotoxic crude fractions from within the vertebrate cardiotoxic peak of C. fleckeri venom by monitoring viability of human muscle cells with an impedance based assay (ACEA xCELLigence system) measuring cell detachment as cytotoxicity which was correlated with a reduction in cell metabolism using a cell proliferation (MTS) assay. When the effects of the venom components on human cardiomyocytes and human skeletal muscle cells were compared, two fractions were found to specifically affect cardiomyocytes with distinct temporal profiles (labelled Crude Toxic Fractions (CTF), alpha and beta). A third fraction (CTF-gamma) was toxic to both muscle cell types and therefore not cardio specific. The vertebrate, cardio specific CTF-alpha and CTF-beta, presented distinct activities; CTF-alpha caused rapid but short term cell detachment and reduction in cell metabolism with enhanced activity at lower concentrations than CTF-beta. This activity was not permanent, with cell reattachment and subsequent increased metabolism of heart muscle cells observed when exposed to all but the highest concentrations of CTF-alpha tested. The cytotoxic effect of CTF-beta took twice as long to act on the cells compared to CTF-alpha, however, the activity was permanent. Furthermore, we showed that the two fractions combined have a synergistic effect causing a much stronger and faster cell detachment (death) when combined than the sum of the individual effects of each toxin. These data presented here improves the current understanding of the toxic mechanisms of the Australian box jellyfish, C. fleckeri, and provides a basis for in vivo research of these newly isolated toxic fractions.

Chattoraj, M., et al. (1996). "Ultra-fast excited state dynamics in green fluorescent protein: multiple states and proton transfer." Proc Natl Acad Sci U S A **93**(16): 8362-8367.

The green fluorescent protein (GFP) of the jellyfish Aequorea Victoria has attracted widespread interest since the discovery that its chromophore is generated by the autocatalytic, posttranslational cyclization and oxidation of a hexapeptide unit. This permits fusion of the DNA sequence of GFP with that of any protein whose expression or transport can then be readily monitored by sensitive fluorescence methods without the need to add exogenous fluorescent dyes. The excited state dynamics of GFP were studied following photo-excitation of each of its

two strong absorption bands in the visible using fluorescence upconversion spectroscopy (about 100 fs time resolution). It is shown that excitation of the higher energy feature leads very rapidly to a form of the lower energy species, and that the excited state interconversion rate can be markedly slowed by replacing exchangeable protons with deuterons. This observation and others lead to a model in which the two visible absorption bands correspond to GFP in two ground-state conformations. These conformations can be slowly interconverted in the ground state, but the process is much faster in the excited state. The observed isotope effect suggests that the initial excited state process involves a proton transfer reaction that is followed by additional structural changes. These observations may help to rationalize and motivate mutations that alter the absorption properties and improve the photo stability of GFP.

Chelsky, A., et al. (2016). "Decomposition of jellyfish carrion in situ: Short-term impacts on infauna, benthic nutrient fluxes and sediment redox conditions." Sci Total Environ **566-567**: 929-937.

Jellyfish often form blooms that persist for weeks to months before they collapse en masse, resulting in the sudden release of large amounts of organic matter to the environment. This study investigated the biogeochemical and ecological effects of the decomposition of jellyfish in a shallow coastal lagoon in New South Wales, Australia. Catostylus mosaicus carrion was added to the surface of shallow sub-tidal sediments and biogeochemical parameters and macrofaunal abundance immediately below the jellyfish carrion were measured over three days. Sediment plots without jellyfish served as controls. Sediment oxygen demand and carbon and nitrogen efflux increased by up to 60-fold in the jellyfish plots, compared to control plots, and dissolved organic nutrient fluxes were more sustained than in previous studies due to the use of fresh rather than frozen biomass. The decomposing jellyfish progressively altered sediment redox conditions, indicated by an increase in porewater iron (II) and sulfide concentrations measured by high-resolution in situ diffusive samplers. Abundance of some macrofaunal taxa in the jellyfish plots decreased relative to controls, however, the abundance of a carnivorous gastropod, which was presumably feeding on the carrion, increased in the jellyfish plots. While jellyfish carrion may be a food source for some macrofauna, low oxygen conditions coupled with the accumulation of toxic dissolved sulfides in the near-surface sediments may explain the overall change in the macroinfaunal community.

Chen, C. C., et al. (2007). "Effectiveness and stability of heterologous proteins expressed in plants by Turnip mosaic virus vector at five different insertion sites." Virus Res **130**(1-2): 210-227.

The N-terminal (NT) regions of particular protein-coding sequences are generally used for in-frame insertion of heterologous open reading frames (ORFs) in potyviral vectors for protein expression in plants. An infectious cDNA clone of Turnip mosaic virus (TuMV) isolate YC5 was engineered at the generally used NT regions of HC-Pro and CP, and other possibly permissive sites to investigate their effectiveness to express the GFP (jellyfish green fluorescent protein) and Der p 5 (allergen from the dust mite, Dermatophagoides pteronyssinus) ORFs. The results demonstrated the permissiveness of the NT regions of P3, CIP and NIb to carry the ORFs and express the translates as part of the viral polyprotein, the processing of which released free-form proteins in the host cell milieu. However, these sites varied in their permissiveness to retain the ORFs intact and hence affect the heterologous protein expression. Moreover, strong influence of the inserted ORF and host plants in determining the permissiveness of a viral genomic context to stably carry the alien ORFs and hence to support their prolonged expression was also noticed. In general, the engineered sites were relatively more permissive to the GFP ORF than to the Der p 5 ORF. Among the hosts, the local lesion host, Chenopodium quinoa Willd. showed the highest extent of support to TuMV to stably carry the heterologous ORFs at the engineered sites and the protein expression therefrom. Among the systemic hosts, Nicotiana benthamiana Domin proved more supportive to TuMV to carry and express the heterologous ORFs than the Brassica hosts, whereas the protein expression levels were significantly higher and more stable in the plants of Brassica campestris L. var. chinensis and B. campestris L. var. ching-geeng than those in the plants of B. juncea L. and B. campestris L. var. pekinensis.

Chen, H., et al. (2019). "Near-Infrared Light-Driven Controllable Motions of Gold-Hollow-Microcone Array." ACS Appl Mater Interfaces **11**(17): 15927-15935.

Micro/nanomotors can effectively convert other forms of energy into mechanical energy, which have been widely used in microscopic fields. However, it is still challenging to integrate the micro/nanomotors to perform complex tasks for broad applications. Herein, a new mode for driving the collective motion behaviors of integrated micro/nanomotors in a liquid by plasmonic heating is reported. The integrated micro/nanomotors, constituted by gold hollow microcone array (AuHMA), are fabricated via colloidal lithography. Owing to the excellent plasmonic-heating property of the AuHMA, the

integrated micro/nanomotors can generate vapor bubbles in the liquid as exposure to near-infrared (NIR) irradiation, therefore inducing versatile motions via on/off NIR irradiation. The floating-diving motions are reversible for at least 60 cycles without fatigue. In addition, precise manipulation of the coordinated motion behaviors, including bending, convex, and jellyfish-like floating motions, can be realized by adjusting the irradiated positions of incident NIR light together with the sizes and shapes of AuHMA films. Moreover, the AuHMA film can act as a robust motor to drive a foam craft over 57-folds of its own weight as exposure to NIR irradiation. Our investigation into the NIR-driven AuHMA film provides a facile approach for obtaining integrated micro/nanomotors with controllable collective motions, which holds promise in remotely controlled smart devices and soft robotics in liquids.

Chen, K., et al. (2014). "Reconstructing source-sink dynamics in a population with a pelagic dispersal phase." PLoS One **9**(5): e95316.

For many organisms, the reconstruction of source-sink dynamics is hampered by limited knowledge of the spatial assemblage of either the source or sink components or lack of information on the strength of the linkage for any source-sink pair. In the case of marine species with a pelagic dispersal phase, these problems may be mitigated through the use of particle drift simulations based on an ocean circulation model. However, when simulated particle trajectories do not intersect sampling sites, the corroboration of model drift simulations with field data is hampered. Here, we apply a new statistical approach for reconstructing source-sink dynamics that overcomes the aforementioned problems. Our research is motivated by the need for understanding observed changes in jellyfish distributions in the eastern Bering Sea since 1990. By contrasting the source-sink dynamics reconstructed with data from the pre-1990 period with that from the post-1990 period, it appears that changes in jellyfish distribution resulted from the combined effects of higher jellyfish productivity and longer dispersal of jellyfish resulting from a shift in the ocean circulation starting in 1991. A sensitivity analysis suggests that the source-sink reconstruction is robust to typical systematic and random errors in the ocean circulation model driving the particle drift simulations. The jellyfish analysis illustrates that new insights can be gained by studying structural changes in source-sink dynamics. The proposed approach is applicable for the spatial source-sink reconstruction of other species and even abiotic processes, such as sediment transport.

Chen, N., et al. (2014). "Bioinspired affinity DNA polymers on nanoparticles for drug sequestration and detoxification." Biomaterials **35**(36): 9709-9718.

Nanomaterials with the ability of sequestering target molecules hold great potential for a variety of applications. To ensure the stable sequestration, most of these nanomaterials have been traditionally designed with a clear boundary or compact structures and behave as closed systems. While this feature is beneficial to applications such as drug delivery, it may pose a challenge to applications where fast molecular transport from the environment to nanomaterials is critical. Thus, this study was aimed at exploring a nanomaterial with affinity DNA polymers and nanoparticles as an open system with function similar to jellyfish tentacles in sequestering target molecules from surroundings. The results show that this nanomaterial can effectively and rapidly sequester both small molecule drugs and large molecule biologics and resultantly mitigate their biological effects. Thus, this nanomaterial holds potential as a universal nanoscale antidote for drug removal and detoxification. While this nanomaterial was evaluated by using drug removal and detoxification as a model, the synthesis of periodically oriented affinity polymers on a nanoparticle with the capability of sequestering target molecules may be tuned for broad applications such as separation, sensing, imaging and drug delivery.

Chen, S. F., et al. (2013). "QM/MM study on the light emitters of aequorin chemiluminescence, bioluminescence, and fluorescence: a general understanding of the bioluminescence of several marine organisms." Chemistry **19**(26): 8466-8472.

Aequorea victoria is a type of jellyfish that is known by its famous protein, green fluorescent protein (GFP), which has been widely used as a probe in many fields. Aequorea has another important protein, aequorin, which is one of the members of the EF-hand calcium-binding protein family. Aequorin has been used for intracellular calcium measurements for three decades, but its bioluminescence mechanism remains largely unknown. One of the important reasons is the lack of clear and reliable knowledge about the light emitters, which are complex. Several neutral and anionic forms exist in chemiexcited, bioluminescent, and fluorescent states and are connected with the H-bond network of the binding cavity in the protein. We first theoretically investigated aequorin chemiluminescence, bioluminescence, and fluorescence in real proteins by performing hybrid quantum mechanics and molecular mechanics methods combined with a molecular dynamics method. For the first time, this study reported the origin and clear differences in the chemiluminescence, bioluminescence and fluorescence of aequorin, which is important for understanding the bioluminescence

not only of jellyfish, but also of many other marine organisms (that have the same coelenterazine caved in different coelenterazine-type luciferases).

Cheng, X., et al. (2017). "Isolation, Characterization and Evaluation of Collagen from Jellyfish Rhopilema esculentum Kishinouye for Use in Hemostatic Applications." PLoS One **12**(1): e0169731.

Hemostat has been a crucial focus since human body is unable to control massive blood loss, and collagen proves to be an effective hemostat in previous studies. In this study, collagen was isolated from the mesoglea of jellyfish Rhopilema esculentum Kishinouye and its hemostatic property was studied. The yields of acid-soluble collagen (ASC) and pepsin-soluble (PSC) were 0.12% and 0.28% respectively. The SDS-PAGE patterns indicated that the collagen extracted from jellyfish mesoglea was type I collagen. The lyophilized jellyfish collagen sponges were cross-linked with EDC and interconnected networks in the sponges were revealed by scanning electron microscope (SEM). Collagen sponges exhibited higher water absorption rates than medical gauze and EDC/NHS cross-linking method could improve the stability of the collagen sponges. Compared with medical gauze groups, the blood clotting indexes (BCIs) of collagen sponges were significantly decreased ($P < 0.05$) and the concentration of collagen also had an influence on the hemostatic property ($P < 0.05$). Collagen sponges had an improved hemostatic ability compared to the gauze control in tail amputation rat models. Hemostatic mechanism studies showed that hemocytes and platelets could adhere and aggregate on the surface of collagen sponge. All properties make jellyfish collagen sponge to be a suitable candidate used as hemostatic material and for wound healing applications.

Chernyak, S. A., et al. (2018). "Kinetics of the defunctionalization of oxidized few-layer graphene nanoflakes." Phys Chem Chem Phys **20**(37): 24117-24122.

Thermal defunctionalization of oxidized jellyfish-like few-layer graphene nanoflakes was studied under non-isothermal conditions by simultaneous thermal analysis. Activation energies for thermal decomposition of different oxygen functional groups were calculated by the Kissinger method and compared with those for oxidized carbon nanotubes. Oxygen content in graphene nanoflakes was found to significantly affect the decomposition activation energies of carboxylic and keto/hydroxy acids because of their acceptor properties and strong distortion of the graphene layers at the edges of the nanoflakes. The structure of the carbon material and the oxygen chemical state significantly influence the decomposition kinetics of thermally stable oxygen-containing groups. The activation energy for thermal decomposition of phenol groups (110-150 kJ mol (-1)) is close to that for graphene oxide reduction.

Chernyshev, A. V., et al. (2001). "[Comparative analysis of topological organization in Metazoa]." Zh Obshch Biol **62**(1): 49-56.

Topological patterns in Metazoa, using previously elaborated methodology with employment of the genus of the surface (p) as topological invariant are considered. The term "density of the genus of the surface" is introduced. In sponges and in a lesser degree among Cnidaria and, Ctenophoria an increase of genus p up to indefinite high values and the shaping of topologically complicated quasifractal systems (irrigation system in sponges and gastro-vascular system in Radiata) are evident. In most Bilateria a stable topological pattern with open digestive tube is formed and subsequent topological complications of other systems may occur. Complicated topological patterns increasing the genus of the surface are evolved on the base of quasifractal systems: gut pockets in turbellaria, tracheal system in arthropods, bronchial system in birds, gills in bivalve mollusks, etc. Peculiarities of ordered and disordered topological patterns as well as topological origin of the increase of the genus of the surface are considered.

Chi, X., et al. (2019). "Food quality matters: Interplay among food quality, food quantity and temperature affecting life history traits of Aurelia aurita (Cnidaria: Scyphozoa) polyps." Sci Total Environ **656**: 1280-1288.

Understanding the interaction between organisms' life history traits and environmental factors is an essential task in ecology. In spite of the increasing appreciation of jellyfish as an important component in marine ecosystem, there are still considerable gaps in understanding how the phase transition from the benthic polyp to the pelagic medusa stage is influenced by multiple environmental factors, including nutrition. To investigate survival, growth, and phase transition of Aurelia aurita polyps, we designed a factorial experiment manipulating food quantity (20mug C, 5mug C and 1.5mug C polyp (-1) every other day), food quality (Artemia salina and two dietary manipulated Acartia tonsa), and temperature (13 degrees C, 20 degrees C, and 27 degrees C). Temperature was the key factor determining phase transition of polyps and negatively affecting their survival rate and growth at 27 degrees C, which reflected a summer heatwave scenario. Furthermore, at polyps' optimum tolerance temperature (20 degrees C) in our study, budding reproduction benefits from high food concentrations. Interestingly, polyps fed with

food containing high level highly unsaturated fatty acid (HUFA) were able to compensate for physiological stress caused by the extreme temperature, and could enhance budding reproduction at optimum temperature. Moreover, benthic-pelagic coupling (strobilation) was determined by temperature but affected significantly by food conditions. Mild temperature together with optimum food conditions contributes to inducing more polyps, which may potentially bring about great ephyrae recruitments during overwintering. In contrast, heatwave events can potentially regulate plankton community structure accompanied by changes of nutritional conditions of primary and secondary producers and thus, negatively affect the population dynamics of polyps. We suggest a novel polyp tolerance curve, which can help to understand jellyfish population dynamics in different seasons and ecosystems. This sets up a baseline for understanding how anticipated global warming and food conditions may affect the population size of benthic polyps and consequently pelagic medusae.

Chia, F. S., et al. (1984). "Ultrastructure of the neuromuscular system of the polyp of Aurelia aurita L., 1758 (Cnidaria, scyphozoa)." J Morphol **180**(1): 69-79.

Fine structural study indicates that the neuromuscular system of stage I polyps of Aurelia aurita is exclusively ectodermal. The three major muscle fields are the radial muscles of the oral disc, the longitudinal muscles of the tentacles, and the muscle cords of the septae and the column; the muscle fields are in physical continuity at the peristomial pits and share a common innervation and type of myofibril. The myofibril is striated in the tentacle base, in the outer oral disc, and in the upper part of the muscle cord; it grades into a smooth muscle toward the tentacle tip, the mouth, and the lower part of the cord. There is a fourth field of longitudinal smooth muscle in the pharynx. The nervous system consists of an epithelial sensory cell in the tentacle and a single type of neuron found in the subepithelial layer of the tentacle, oral disc, and muscle cord. The lack of gap junctions suggests that there is no nonnervous conduction system. The subepithelial layer also contains three types of fibers and a type of soma which cannot be characterized as neuronal. The soma is identified as the "neurosecretory cell" described in Chrysaora. The absence of neuromuscular elements in the column and stolon distinguishes the Aurelia aurita collected from Washington, USA, from English polyps previously described.

Chiaverano, L. M., et al. (2013). "Long-term fluctuations in circalunar Beach aggregations of the box jellyfish Alatina moseri in Hawaii, with links to environmental variability." PLoS One **8**(10): e77039.

The box jellyfish Alatina moseri forms monthly aggregations at Waikiki Beach 8-12 days after each full moon, posing a recurrent hazard to swimmers due to painful stings. We present an analysis of long-term (14 years: Jan 1998- Dec 2011) changes in box jellyfish abundance at Waikiki Beach. We tested the relationship of beach counts to climate and biogeochemical variables over time in the North Pacific Sub-tropical Gyre (NPSG). Generalized Additive Models (GAM), Change-Point Analysis (CPA), and General Regression Models (GRM) were used to characterize patterns in box jellyfish arrival at Waikiki Beach 8-12 days following 173 consecutive full moons. Variation in box jellyfish abundance lacked seasonality, but exhibited dramatic differences among months and among years, and followed an oscillating pattern with significant periods of increase (1998-2001; 2006-2011) and decrease (2001-2006). Of three climatic and 12 biogeochemical variables examined, box jellyfish showed a strong, positive relationship with primary production, >2 mm zooplankton biomass, and the North Pacific Gyre Oscillation (NPGO) index. It is clear that that the moon cycle plays a key role in synchronizing timing of the arrival of Alatina moseri medusae to shore. We propose that bottom-up processes, likely initiated by inter-annual regional climatic fluctuations influence primary production, secondary production, and ultimately regulate food availability, and are therefore important in controlling the inter-annual changes in box jellyfish abundance observed at Waikiki Beach.

Chopra, S. S., et al. (2007). "Molecular cloning and analysis of zebrafish voltage-gated sodium channel beta subunit genes: implications for the evolution of electrical signaling in vertebrates." BMC Evol Biol **7**: 113.

BACKGROUND: Action potential generation in excitable cells such as myocytes and neurons critically depends on voltage-gated sodium channels. In mammals, sodium channels exist as macromolecular complexes that include a pore-forming alpha subunit and 1 or more modulatory beta subunits. Although alpha subunit genes have been cloned from diverse metazoans including flies, jellyfish, and humans, beta subunits have not previously been identified in any non-mammalian species. To gain further insight into the evolution of electrical signaling in vertebrates, we investigated beta subunit genes in the teleost Danio rerio (zebrafish). RESULTS: We identified and cloned single zebrafish gene homologs for beta1-beta3 (zbeta1-zbeta3) and duplicate genes for beta4 (zbeta4.1, zbeta4.2). Sodium channel beta subunit loci are similarly organized in fish and mammalian genomes. Unlike their mammalian counterparts, zbeta1 and zbeta2 subunit genes display extensive

alternative splicing. Zebrafish beta subunit genes and their splice variants are differentially-expressed in excitable tissues, indicating tissue-specific regulation of zbeta1-4 expression and splicing. Co-expression of the genes encoding zbeta1 and the zebrafish sodium channel alpha subunit Nav1.5 in Chinese Hamster Ovary cells increased sodium current and altered channel gating, demonstrating functional interactions between zebrafish alpha and beta subunits. Analysis of the synteny and phylogeny of mammalian, teleost, amphibian, and avian beta subunit and related genes indicated that all extant vertebrate beta subunits are orthologous, that beta2/beta4 and beta1/beta3 share common ancestry, and that beta subunits are closely related to other proteins sharing the V-type immunoglobulin domain structure. Vertebrate sodium channel beta subunit genes were not identified in the genomes of invertebrate chordates and are unrelated to known subunits of the para sodium channel in Drosophila. CONCLUSION: The identification of conserved orthologs to all 4 voltage-gated sodium channel beta subunit genes in zebrafish and the lack of evidence for beta subunit genes in invertebrate chordates together indicate that this gene family emerged early in vertebrate evolution, prior to the divergence of teleosts and tetrapods. The evolutionary history of sodium channel beta subunits suggests that these genes may have played a key role in the diversification and specialization of electrical signaling in early vertebrates.

Choudhary, I., et al. (2019). "Proteomic Analysis of Novel Components of Nemopilema nomurai Jellyfish Venom: Deciphering the Mode of Action." Toxins (Basel) **11**(3).

Nowadays, proliferation of jellyfish has become a severe matter in many coastal areas around the world. Jellyfish Nemopilema nomurai is one of the most perilous organisms and leads to significant deleterious outcomes such as harm to the fishery, damage the coastal equipment, and moreover, its envenomation can be hazardous to the victims. Till now, the components of Nemopilema nomurai venom (NnV) are unknown owing to scant transcriptomics and genomic data. In the current research, we have explored a proteomic approach to identify NnV components and their interrelation with pathological effects caused by the jellyfish sting. Altogether, 150 proteins were identified, comprising toxins and other distinct proteins that are substantial in nematocyst genesis and nematocyte growth by employing two-dimensional gel electrophoresis and matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI/TOF/MS). The identified toxins are phospholipase A2, phospholipase D Li Sic Tox beta IDI, a serine protease, putative Kunitz-type serine protease inhibitor, disintegrin and metalloproteinase, hemolysin, leukotoxin, three finger toxin MALT0044C, allergens, venom prothrombin activator trocarin D, tripeptide Gsp 9.1, and along with other toxin proteins. These toxins are relatively well characterized in the venoms of other poisonous species to induce pathogenesis, hemolysis, inflammation, proteolysis, blood coagulation, cytolysis, hemorrhagic activity, and type 1 hypersensitivity, suggesting that these toxins in NnV can also cause similar deleterious consequences. Our proteomic works indicate that NnV protein profile represents valuable source which leads to better understanding the clinical features of the jellyfish stings. As one of the largest jellyfish in the world, Nemopilema nomurai sting is considered to be harmful to humans due to its potent toxicity. The identification and functional characterization of its venom components have been poorly described and are beyond our knowledge. Here is the first report demonstrating the methodical overview of NnV proteomics research, providing significant information to understand the mechanism of NnV envenomation. Our proteomics findings can provide a platform for novel protein discovery and development of practical ways to deal with jellyfish stings on human beings.

Choudhary, I., et al. (2015). "Nemopilema nomurai Jellyfish venom treatment leads to alterations in rat cardiomyocytes proteome." Data Brief **5**: 884-887.

This data article restrains data associated to the Choudhary et al. [1]. Nemopilema nomurai Jellyfish venom (NnV) can lead to cardiac toxicity. Here we analyzed the effect of NnV on rat cardiomyocytes cell line H9c2 at the proteome level using two-dimensional gel electrophoresis and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF/MS). This analysis resulted in 34 proteins with differential expression. Here we provide the dataset for the proteins with amplified or reduced level as compare to control.

Choudhary, I., et al. (2015). "Proteomics approach to examine the cardiotoxic effects of Nemopilema nomurai Jellyfish venom." J Proteomics **128**: 123-131.

UNLABELLED: Nemopilema nomurai is one of the largest species of jellyfish in the world. It blooms mainly offshore of Korea, China, and Japan. Increasing population numbers of N. nomurai is increasing the risk of sea bathers to the jellyfish stings and accompanying envenomations. Cardiovascular effects, and cytotoxicity and hemolytic activities have been previously reported in rodent models. To understand the mechanism of cardiac toxicity, we examined the effect of N. nomurai jellyfish venom

(NnV) at the proteome level on rat cardiomyocytes cell line H9c2 using two-dimensional gel electrophoresis and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF/MS). Cells treated with NnV displayed dose-dependent inhibition of viability. Cellular changes at proteome level were investigated after 6h and 12h of venom treatment. Electrophoretic examination revealed 72 protein spots displaying significant quantitative changes. These proteins were analyzed by MALDI-TOF/MS. Thirty four differentially expressed proteins were successfully identified; 24 proteins increased in quantity and 10 proteins decreased, compared to the respective controls. Proteins altered in content in Western blot analyses included myosin VII, annexin A2, aldose reductase, suppressor of cytokine signaling 1 (SOCS1), and calumenin, which are well-known marker proteins of cardiac dysfunctions. BIOLOGICAL SIGNIFICANCE: This is the first report revealing the cardiac toxicity of NnV at the proteome level. NnV directly targeted proteins involved in cardiac dysfunction or maintenance. Suppressor of cytokine signaling 1 (SOCS1), which inhibits the Janus kinase/signal transducers and activators of transcription (JAK/STAT) pathway, was upregulated by NnV. Other proteins related to cardiac arrest that were over-expressed included aldose reductase and calumenin. These results clarify the underlying mechanism of cardiomyocyte damage caused by NnV. By inhibiting these particular targets and more precisely identifying the components of NnV-mediated cardiac toxicity, jellyfish venom-associated poisoning could be reduced or prevented.

Choudhary, I., et al. (2018). "Proteomic Investigation to Identify Anticancer Targets of Nemopilema nomurai Jellyfish Venom in Human Hepatocarcinoma HepG2 Cells." Toxins (Basel) **10**(5).

Nemopilema nomurai is a giant jellyfish that blooms in East Asian seas. Recently, N. nomurai venom (NnV) was characterized from a toxicological and pharmacological point of view. A mild dose of NnV inhibits the growth of various kinds of cancer cells, mainly hepatic cancer cells. The present study aims to identify the potential therapeutic targets and mechanism of NnV in the growth inhibition of cancer cells. Human hepatocellular carcinoma (HepG2) cells were treated with NnV, and its proteome was analyzed using two-dimensional gel electrophoresis, followed by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI/TOF/MS). The quantity of twenty four proteins in NnV-treated HepG2 cells varied compared to non-treated control cells. Among them, the amounts of fourteen proteins decreased and ten proteins showed elevated levels. We also found that the amounts of several cancer biomarkers and oncoproteins, which usually increase in various types of cancer cells, decreased after NnV treatment. The representative proteins included proliferating cell nuclear antigen (PCNA), glucose-regulated protein 78 (GRP78), glucose-6-phosphate dehydrogenase (G6PD), elongation factor 1 & gamma; (EF1 & gamma;), nucleolar and spindle-associated protein (NuSAP), and activator of 90 kDa heat shock protein ATPase homolog 1 (AHSA1). Western blotting also confirmed altered levels of PCNA, GRP78, and G6PD in NnV-treated HepG2 cells. In summary, the proteomic approach explains the mode of action of NnV as an anticancer agent. Further characterization of NnV may help to unveil novel therapeutic agents in cancer treatment.

Chow, S., et al. (2019). "Molecular diet analysis of Anguilliformes leptocephalus larvae collected in the western North Pacific." PLoS One **14**(11): e0225610.

Natural diets of leptocephalus larvae have been enigmatic. In this study, we collected DNA samples from the gut contents and body surface of leptocephali belonging to the five Anguilliform families (Anguillidae, Chlopsidae, Congridae, Muraenidae, and Serrivomeridae) from the northwest Pacific and performed next-generation 18S rDNA sequencing. Wide variety of eukaryotes was detected in both samples, from which eight eukaryotic groups (jellyfish, conoid parasite, tunicate, copepod, krill, segmented worm, fungi, and dinoflagellate) were selected on the basis of abundance. All groups except conoid parasites were common in both the samples. Cnidarian 18S rDNA reads were the most abundant in both the samples; however, the number of samples having cnidarian reads and the read counts were significantly higher in the body surface scraping samples than in the gut content samples, regardless of careful rinsing of the body surface. These results indicate that the cnidarian DNAs are most likely found because of cross contamination from the body surface and/or environment. 18S rDNA read counts of copepod and tunicate in the gut contents were greater than or comparable with those in the body surface scraping samples, which may correspond to the previous observations of fecal pellets and larvacean houses in the leptocephali gut. Thus, the present study supports previous implications that leptocephali utilize detritus materials, so called marine snow.

Christensen, B. B., et al. (1996). "Bacterial plasmid conjugation on semi-solid surfaces monitored with the green fluorescent protein (GFP) from Aequorea victoria as a marker." Gene **173**(1 Spec No): 59-65.

Horizontal transfer of the TOL plasmid was

examined in Pseudomonas putida (Pp) KT2442 micro-colonies on semi-solid agar surfaces. Horizontal gene transfer is usually studied in large populations where all information is based on average estimates of the transfer events in the entire population. We have used the green fluorescent protein (GFP) from the jellyfish Aequorea victoria as a plasmid marker, in combination with single-cell observations. This provided hitherto unknown details on the distribution of cells active in conjugation. In the present study, donor cells containing the gfp gene expressed from the bacteriophage T7 phi 10 promoter on the TOL plasmid, and recipient cells expressing the corresponding phage RNA polymerase allowed us to monitor the occurrence of ex-conjugants as green fluorescent cells upon illumination with blue light (470-490 nm). Further, the recipients were labeled with the luxAB genes to distinguish micro-colonies of donor cells from recipient cells. We conclude that conjugal plasmid transfer in Pp KT2442 cells on semi-solid surfaces occurs mainly during a short period of time after the initial contact of donors and recipients, indicating that spread of the TOL plasmid is limited in static, but viable cultures.

Christophe-Hobertus, C., et al. (1999). "Critical residues of the homeodomain involved in contacting DNA bases also specify the nuclear accumulation of thyroid transcription factor-1." Eur J Biochem **265**(1): 491-497.

The N-terminal end of thyroid transcription factor-1 (TTF-1) homeodomain is composed of a stretch of five basic amino-acids that is conserved in both POU- and NK2-class homeodomains and constitutes a functional nuclear localization signal. By analyzing the cellular distribution of fusion proteins, composed of a jellyfish green fluorescent variant and different parts of TTF-1, we show here that the presence of this basic sequence is not sufficient by itself to confer complete nuclear accumulation. By mutagenesis, we identified a second region located in the center of the DNA recognition helix of the homeodomain that is also able to specify a predominantly nuclear localization of the chimeric proteins, independently of the presence of the basic NLS. The destruction, by mutagenesis, of both the basic stretch and the motif in the DNA recognition helix led to the total loss of nuclear accumulation, indicating that complete nuclear accumulation of TTF-1 results from the concerted action of these two proteic signals. Both of the regions of the homeodomain that are involved in nuclear targeting also encompass critical amino-acids responsible for DNA binding site recognition, as evidenced by the loss of DNA binding activity in vitro upon mutagenesis. Specifically, residues in the central part of the DNA recognition helix are involved in contacting bases in the major groove of DNA and are the most conserved in homeodomain proteins, suggesting that this part of the homeodomain could play a general role in the nuclear localization of members of this family of proteins.

Chuard, P. J. C., et al. (2019). "Ocean acidification causes mortality in the medusa stage of the cubozoan Carybdea xaymacana." Sci Rep **9**(1): 5622.

Ocean pH is decreasing due to anthropogenic activities, and the consequences of this acidification on marine fauna and ecosystems are the subject of an increasing number of studies. Yet, the impact of ocean acidification (OA) on several abundant and ecologically important taxa, such as medusozoans, is poorly documented. To date there have been no studies on the effect of post-2050 OA projections on the medusa stage of jellyfish. As medusae represent the reproductive stage of cnidarians, negative impacts on adult jellyfish could severely impact the long-term survival of this group. Using a laboratory experiment, we investigated the effect of 2300 OA projections (i.e. pH of 7.5) on the mortality rate of the medusa-stage of the cubozoan species Carybdea xaymacana, compared to ambient seawater pH conditions (i.e. pH of 8.1). After a 12-h exposure to OA, C. xaymacana medusae suffered higher mortality rates compared to ambient conditions. This study represents the first evidence of the potential lethal effects of post-2050 OA projections on jellyfish. The higher metabolic rates of cubozoans compared to other cnidarians might make box jellyfish more vulnerable to OA. A decrease in the density of cnidarians could lead to harmful ecological events, such as algal blooms.

Colin, S. P., et al. (2012). "Biomimetic and live medusae reveal the mechanistic advantages of a flexible bell margin." PLoS One **7**(11): e48909.

Flexible bell margins are characteristic components of rowing medusan morphologies and are expected to contribute towards their high propulsive efficiency. However, the mechanistic basis of thrust augmentation by flexible propulsors remained unresolved, so the impact of bell margin flexibility on medusan swimming has also remained unresolved. We used biomimetic robotic jellyfish vehicles to elucidate that propulsive thrust enhancement by flexible medusan bell margins relies upon fluid dynamic interactions between entrained flows at the inflexion point of the exumbrella and flows expelled from under the bell. Coalescence of flows from these two regions resulted in enhanced fluid circulation and, therefore, thrust augmentation for flexible margins of both medusan vehicles and living medusae. Using particle image velocimetry (PIV) data we estimated pressure

fields to demonstrate a mechanistic basis of enhanced flows associated with the flexible bell margin. Performance of vehicles with flexible margins was further enhanced by vortex interactions that occur during bell expansion. Hydrodynamic and performance similarities between robotic vehicles and live animals demonstrated that the propulsive advantages of flexible margins found in nature can be emulated by human-engineered propulsors. Although medusae are simple animal models for description of this process, these results may contribute towards understanding the performance of flexible margins among other animal lineages.

Coll, M., et al. (2014). "Assessing fishing and marine biodiversity changes using fishers' perceptions: the Spanish Mediterranean and Gulf of Cadiz case study." PLoS One **9**(1): e85670.

BACKGROUND: The expansion of fishing activities has intensively transformed marine ecosystems worldwide. However, available time series do not frequently cover historical periods. METHODOLOGY: Fishers' perceptions were used to complement data and characterise changes in fishing activity and exploited ecosystems in the Spanish Mediterranean Sea and Gulf of Cadiz. Fishers' interviews were conducted in 27 fishing harbours of the area, and included 64 fishers from ages between 20 to >70 years old to capture the experiences and memories of various generations. Results are discussed in comparison with available independent information using stock assessments and international convention lists. PRINCIPAL FINDINGS: According to fishers, fishing activity substantially evolved in the area with time, expanding towards deeper grounds and towards areas more distant from the coast. The maximum amount of catch ever caught and the weight of the largest species ever captured inversely declined with time. Fishers (70%) cited specific fishing grounds where depletion occurred. They documented ecological changes of marine biodiversity during the last half of the century: 94% reported the decline of commercially important fish and invertebrates and 61% listed species that could have been extirpated, with frequent mentions to cartilaginous fish. Declines and extirpations were in line with available quantitative evaluations from stock assessments and international conventions, and were likely linked to fishing impacts. Conversely, half of interviewed fishers claimed that several species had proliferated, such as cephalopods, jellyfish, and small-sized fish. These changes were likely related to trophic cascades due to fishing and due to climate change effects. The species composition of depletions, local extinctions and proliferations showed differences by region suggesting that regional dynamics are important when analysing biodiversity changes. CONCLUSIONS/SIGNIFICANCE: Using fishers' perceptions, fishing and ecological changes in the study area were documented. The recovery of local ecological knowledge provides valuable information complementing quantitative monitoring and evaluation surveys.

Colley, N. J. and R. K. Trench (1983). "Selectivity in phagocytosis and persistence of symbiotic algae in the scyphistoma stage of the jellyfish Cassiopeia xamachana." Proc R Soc Lond B Biol Sci **219**(1214): 61-82.

We have investigated whether interactions between cell-surface macromolecules play a role in cellular recognition leading to specificity in the establishment of intracellular symbiosis between dinoflagellates and the polyp (scyphistoma) stage of the jellyfish Cassiopeia xamachana. All strains of the symbiotic dinoflagellate Symbiodinium microadriaticum were phagocytosed by the endodermal cells of the scyphistomae when presented to them as cells freshly isolated from their respective hosts. The rates of phagocytosis of such cells were high, and were directly correlated with the presence of a membrane, thought to be the host cell vacuolar membrane that surrounds the freshly isolated algae. Cultured algae lack this membrane. All cultured algae, even those that proliferate in host tissues, were phagocytosed at very low or undetectable rates. Freshly isolated algae treated with reagents that removed the host membrane were phagocytosed at low rates. The endodermal cells of the scyphistomae of the non-symbiotic medusa Aurelia aurita also phagocytosed freshly isolated algae, but did not phagocytose cultured algae. Phagocytosis of algae and carmine particles was found to be a competitive process in scyphistomae of C. xamachana. No correlation was observed between the surface electrical charge on algae and their phagocytosis by host endodermal cells. Neither was there any correlation between phagocytosis and persistence. We conclude that the specificity in symbioses between marine invertebrates and dinoflagellates appears to be regulated by processes that occur after potential algal symbionts are phagocytosed.

Colley, N. J. and R. K. Trench (1985). "Cellular events in the reestablishment of a symbiosis between a marine dinoflagellate and a coelenterate." Cell Tissue Res **239**(1): 93-103.

Summary. Within 24 h after the initial phagocytotic uptake of freshly isolated (from host tissue) symbiotic algae (Symbiodinium mieroadriaticum) by the endodermal cells of the polyp (scyphistoma) stage of the jellyfish Cassiopeia xamachana,the algal population was observed to

decline despite evidence of algal cell division. Analyses of the frequency of phago-lysosome fusion as an indicator of possible attempts of the host to digest the algae indicated that, althoughphago-lysosome fusion did occur, the low frequency of occurrence is inconsistent with the interpretation that the animals digested the algae. Animal cell lysosomes were located predominantly at the apices of the endodermal cells,and the symbiotic algae were transported toward the bases of the endodermal cells.Within 3 days after initial infection, most endodermal cells with algae ceased to be phagocytotically active (with respect to the uptake of carmine particles). Many of these endodermal cells soon migrated into the mesoglea to become what are traditionally referred to as "amoebocytes".Within amoebocytes the algae proliferated. The onset of strobilation by the scyphistomae was directly correlated with the increase in the algal population within these amoebocytes.

Collins, A. G., et al. (2006). "Medusozoan phylogeny and character evolution clarified by new large and small subunit rDNA data and an assessment of the utility of phylogenetic mixture models." Syst Biol **55**(1): 97-115.

A newly compiled data set of nearly complete sequences of the large subunit of the nuclear ribosome (LSU or 28S) sampled from 31 diverse medusozoans greatly clarifies the phylogenetic history of Cnidaria. These data have substantial power to discern among many of the competing hypotheses of relationship derived from prior work. Moreover, LSU data provide strong support at key nodes that were equivocal based on other molecular markers. Combining LSU sequences with those of the small subunit of the nuclear ribosome (SSU or 18S), we present a detailed working hypothesis of medusozoan relationships and discuss character evolution within this diverse clade. Stauromedusae, comprising the benthic, so-called stalked jellyfish, appears to be the sister group of all other medusozoans, implying that the free-swimming medusa stage, the motor nerve net, and statocysts of ecto-endodermal origin are features derived within Medusozoa. Cubozoans, which have had uncertain phylogenetic affinities since the elucidation of their life cycles, form a clade-named Acraspeda-with the scyphozoan groups Coronatae, Rhizostomeae, and Semaeostomeae. The polyps of both cubozoans and hydrozoans appear to be secondarily simplified. Hydrozoa is comprised by two well-supported clades, Trachylina and Hydroidolina. The position of Limnomedusae within Trachylina indicates that the ancestral hydrozoan had a biphasic life cycle and that the medusa was formed via an entocodon. Recently hypothesized homologies between the entocodon and bilaterian mesoderm are therefore suspect. Laingiomedusae, which has often been viewed as a close ally of the trachyline group Narcomedusae, is instead shown to be unambiguously a member of Hydroidolina. The important model organisms of the Hydra species complex are part of a clade, Aplanulata, with other hydrozoans possessing direct development not involving a ciliated planula stage. Finally, applying phylogenetic mixture models to our data proved to be of little additional value over a more traditional phylogenetic approach involving explicit hypothesis testing and bootstrap analyses under multiple optimality criteria. [18S; 28S; Cubozoa; Hydrozoa; medusa; molecular systematics; polyp; Scyphozoa; Staurozoa.].

Collins, G. A., et al. (1979). "Prostaglandins have limited actions on abnormalities of beating induced in cultured heart cells." Prostaglandins **18**(4): 591-603.

Prostaglandins are antiarrhythmic in a variety of situations including ischaemic arrhythmias, but the mechanisms involved are not known. In view of this, the protective actions of prostaglandins A2, E2, F1 alpha, F2 beta, and I2 against abnormalities of beating induced in cultured heart cells were investigated. Abnormalities of beating were induced in single cells by variety of agents including ouabain Ca++, K+, dinitrophenol (DNP), and toxic material from the jellyfish Cyanea. Abnormalities were assessed in terms of rate, rate range, subjective arrhythmic behaviour and percent cells beating. The prostaglandins (at 10(-7)-10(-5) M) were added with the arrhythmogenic agent to test for their ability to modify agent-induced beating abnormalities and were compared with lidocaine and quinidine. Prostaglandins alone had minimal direct effects on the cells and only minimally reduced responses to arrhythmogenic agents. The most protective prostaglandins, PGE2 and PGF1 alpha, tended to normalise beating behaviour most noticeably in DNP-treated cells, unlike lidocaine and quinidine which were effective against Ca++-induced changes while worsening those of K+. Thus, a general ability to protect disturbed cardiac cells is not seen with high concentrations of prostaglandins.

Collins, L. A., et al. (1998). "Green fluorescent protein reporter microplate assay for high-throughput screening of compounds against Mycobacterium tuberculosis." Antimicrob Agents Chemother **42**(2): 344-347.

An optimal assay for high-throughput screening for new antituberculosis agents would combine the microplate format and low cost of firefly luciferase reporter assays and redox dyes with the ease of kinetic monitoring inherent in the BACTEC system. The green fluorescent protein (GFP) of the jellyfish

Aequorea victoria is a useful reporter molecule which requires neither substrates nor cofactors due to the intrinsically fluorescent nature of the protein. The gene encoding a red-shifted, higher-intensity GFP variant was introduced by electroporation into Mycobacterium tuberculosis H37Ra and M. tuberculosis H37Rv on expression vector pFPV2. A microplate-based fluorescence assay (GFP microplate assay [GFPMA]) was developed and evaluated by determining the MICs of existing antimycobacterial agents. The MICs of isoniazid, rifampin, ethambutol, streptomycin, amikacin, ofloxacin, ethionamide, thiacetazone, and capreomycin, but not cycloserine, determined by GFPMA were within 1 log2 dilution of those determined with the BACTEC 460 system and were available in 7 days. Equivalent MICs of antituberculosis agents in the BACTEC 460 system for both the reporter and parent strains suggested that introduction of pFPV2 did not influence drug susceptibility, in general. GFPMA provides a unique tool with which the dynamic response of M. tuberculosis to the existing and potential antituberculosis agents can easily, rapidly, and inexpensively be monitored.

Collins, S. P., et al. (1993). "Monoclonal antibodies neutralizing the haemolytic activity of box jellyfish (Chironex fleckeri) tentacle extracts." Comp Biochem Physiol B **106**(1): 67-70.

1. Three monoclonal antibodies have been produced which neutralize in vitro the haemolytic activity present in tentacle extracts of the box jellyfish (Chironex fleckeri). 2. Two of these monoclonal antibodies bound specifically to a component of relative molecular mass 50,000 in tentacle extract on Western blots. 3. This binding only occurred when the extracts were electrophoresed under non-reducing conditions. 4. The third monoclonal antibody did not display binding to Western blots of tentacle extract under any of our experimental conditions.

Colussi, P. A., et al. (1998). "Prodomain-dependent nuclear localization of the caspase-2 (Nedd2) precursor. A novel function for a caspase prodomain." J Biol Chem **273**(38): 24535-24542.

Caspases are cysteine proteases that play an essential role in apoptosis by cleaving several key cellular proteins. Despite their function in apoptosis, little is known about where in the cell they are localized and whether they are translocated to specific cellular compartments upon activation. In the present paper, using Aequorea victoria green fluorescent protein fusion constructs, we have determined the localization of Nedd2 (mouse caspase-2) and show that both precursor and processed caspase-2 localize to the cytoplasmic and the nuclear compartments. We demonstrate that the nuclear localization of caspase-2 is strictly dependent on the presence of the prodomain. A caspase-2 prodomain-green fluorescent protein localized to dot- and fiber-like structures mostly in the nucleus, whereas a protein lacking the prodomain was largely concentrated in the cytoplasm. We also show that an amino-terminal fusion of the prodomain of caspase-2 to caspase-3 mediates nuclear transport of caspase-3, which is normally localized in the cytoplasm. These results suggest that, in addition to roles in dimerization and recruitment through adaptors, the caspase-2 prodomain has a novel function in nuclear transport.

Comis, A., et al. (1989). "Stabilization of lethal and hemolytic activities of box jellyfish (Chironex fleckeri) venom." Toxicon **27**(4): 439-447.

The stability of both the lethal and hemolytic activities of box jellyfish (Chironex fleckeri) tentacle extract was assessed after various extraction procedures. Both activities were higher when no buffers or water were used during the initial extraction. Also, when the extract was first filtered through a Sep-pak C18 cartridge, the residual lethal titre, after incubation for 24 hr at room temperature, was increased 16-fold and hemolysis was increased 2.6-fold. Evidence for proteolytic activity in the extract was also obtained and monitored by size exclusion HPLC.

Condon, R. H., et al. (2013). "Recurrent jellyfish blooms are a consequence of global oscillations." Proc Natl Acad Sci U S A **110**(3): 1000-1005.

A perceived recent increase in global jellyfish abundance has been portrayed as a symptom of degraded oceans. This perception is based primarily on a few case studies and anecdotal evidence, but a formal analysis of global temporal trends in jellyfish populations has been missing. Here, we analyze all available long-term datasets on changes in jellyfish abundance across multiple coastal stations, using linear and logistic mixed models and effect-size analysis to show that there is no robust evidence for a global increase in jellyfish. Although there has been a small linear increase in jellyfish since the 1970s, this trend was unsubstantiated by effect-size analysis that showed no difference in the proportion of increasing vs. decreasing jellyfish populations over all time periods examined. Rather, the strongest nonrandom trend indicated jellyfish populations undergo larger, worldwide oscillations with an approximate 20-y periodicity, including a rising phase during the 1990s that contributed to the perception of a global increase in jellyfish abundance. Sustained monitoring is required over the next decade to elucidate with statistical confidence whether the weak increasing

linear trend in jellyfish after 1970 is an actual shift in the baseline or part of an oscillation. Irrespective of the nature of increase, given the potential damage posed by jellyfish blooms to fisheries, tourism, and other human industries, our findings foretell recurrent phases of rise and fall in jellyfish populations that society should be prepared to face.

Condon, R. H., et al. (2011). "Jellyfish blooms result in a major microbial respiratory sink of carbon in marine systems." Proc Natl Acad Sci U S A **108**(25): 10225-10230.

Jellyfish blooms occur in many estuarine and coastal regions and may be increasing in their magnitude and extent worldwide. Voracious jellyfish predation impacts food webs by converting large quantities of carbon (C), fixed by primary producers and consumed by secondary producers, into gelatinous biomass, which restricts C transfer to higher trophic levels because jellyfish are not readily consumed by other predators. In addition, jellyfish release colloidal and dissolved organic matter (jelly-DOM), and could further influence the functioning of coastal systems by altering microbial nutrient and DOM pathways, yet the links between jellyfish and bacterioplankton metabolism and community structure are unknown. Here we report that jellyfish released substantial quantities of extremely labile C-rich DOM, relative to nitrogen (25.6 +/- 31.6 C:1N), which was quickly metabolized by bacterioplankton at uptake rates two to six times that of bulk DOM pools. When jelly-DOM was consumed it was shunted toward bacterial respiration rather than production, significantly reducing bacterial growth efficiencies by 10% to 15%. Jelly-DOM also favored the rapid growth and dominance of specific bacterial phylogenetic groups (primarily gamma-proteobacteria) that were rare in ambient waters, implying that jelly-DOM was channeled through a small component of the in situ microbial assemblage and thus induced large changes in community composition. Our findings suggest major shifts in microbial structure and function associated with jellyfish blooms, and a large detour of C toward bacterial CO (2) production and away from higher trophic levels. These results further suggest fundamental transformations in the biogeochemical functioning and biological structure of food webs associated with jellyfish blooms.

Constantino, M. A. and M. Salmon (2003). "Role of chemical and visual cues in food recognition by leatherback posthatchlings (Dermochelys coriacea L)." Zoology (Jena) **106**(3): 173-181.

We raised leatherback posthatchlings in the laboratory for up to 7 weeks to study the role of visual and chemical cues in food recognition and food-seeking behavior. Turtles were reared on a formulated (artificial gelatinous) diet and had no contact with test materials until experiments began. Subjects were presented with visual cues (a plastic jellyfish; white plastic shapes [circle, square, diamond] similar in surface area to the plastic model), chemical cues (homogenates of lion's mane jellyfish, Cyanea capillata; moon jellyfish, Aurelia aurita; and a ctenophore, Ocyropsis sp., introduced through a water filter outflow), and visual and chemical cues presented simultaneously. Visual stimuli evoked an increase in swimming activity, biting, diving, and orientation toward the object. Chemical cues elicited an increase in biting, and orientation into water currents (rheotaxis). When chemical and visual stimuli were combined, turtles ignored currents and oriented toward the visual stimuli. We conclude that both cues are used to search for, and locate, food but that visual cues may be of primary importance. We hypothesize that under natural conditions turtles locate food visually, then, as a consequence of feeding, associate chemical with visual cues. Chemical cues then may function alone as a feeding attractant.

Cortes-Lara, S., et al. (2015). "Prokaryotic microbiota in the digestive cavity of the jellyfish Cotylorhiza tuberculata." Syst Appl Microbiol **38**(7): 494-500.

The microbiota associated to the gastric cavity of four exemplars of the jellyfish Cotylorhiza tuberculata has been studied by means of cultured-dependent and -independent methods. The pyrosequencing approach rendered a very reduced diversity of Bacteria with four major groups shared by the four exemplars that made up to 95% of the total diversity. The culturing approach recovered low abundant organisms and some of them also detected by the pyrosequencing approach. The major key organisms were related to the genera Spiroplasma, Thalassospira, Tenacibaculum (from the pyrosequencing data), and Vibrio (from the cultivable fraction). Altogether the results indicate that C. tuberculata harbors an associated microbiota of very reduced diversity. On the other hand, some of the major key players may be potential pathogens and the host may serve as dispersal mechanism.

Costa, E., et al. (2020). "Microplastics ingestion in the ephyra stage of Aurelia sp. triggers acute and behavioral responses." Ecotoxicol Environ Saf **189**: 109983.

For the first time, we report a correspondence between microplastics (MP) ingestion and ecotoxicological effects in gelatinous zooplankton (Cnidarian jellyfish). The ephyra stage of the jellyfish Aurelia sp. was exposed to both environmental and high concentrations of fluorescent 1-4 mum

polyethylene MP (0.01-10 mg/L). After 24 and 48 h, MP accumulation, acute (Immobility) and behavioral (Frequency pulsation) endpoints were investigated. MP were detected by confocal and tomographic investigations on gelatinous body and mouth, either attached on the surface or ingested. This interaction was responsible for impairing ephyrae survival and behavior at all tested concentrations after 24 h. Acute and behavioral effects were also related to mechanical disturbance, caused by MP, triggering a loss of radial symmetry. Contaminated ephyrae exposed to clean seawater showed full recovery after 72 h highlighting the organisms without the microspheres, attached on body jellyfish surface around the mouth and lappets. In conclusion, short-term exposure to MP affects ephyrae jellyfish health, impairing both their survival and behavior. Polyethylene MP temporarily affect both Immobility and Frequency of pulsation of Aurelia sp. jellyfish. This study provides a first step towards understanding and clarifying the potential impacts of MP contamination in gelatinous zooplankton.

Costa, M. A., et al. (2001). "Genetic and cytological characterization of a developmental mutant of Aspergillus nidulans induced by 5-azacytidine." Biol Res **34**(2): 91-98.

An analysis of a new medusa mutant of Aspergillus nidulans obtained by 5-azacytidine-treatment and named B116 is provided. The B116 mutant was phenotypically characterized by the production of conidiophores with reduced pigmentation and vesicles bearing multiple tiers of sterigmata. A single nuclear gene located on chromosome I is responsible for phenotypical changes in the mutant. The 5-azacytidine-altered locus, designated medA102, is recessive in heterozygous diploid and the medusa mutant is a Dp (II,I) duplication bearer that renders the strain mitotically unstable.

Costa, R., et al. (2019). "A Multi-screening Evaluation of the Nutritional and Nutraceutical Potential of the Mediterranean Jellyfish Pelagia noctiluca." Mar Drugs **17**(3).

The phylum Cnidaria is one of the most important contributors in providing abundance of bio- and chemodiversity. In this study, a comprehensive chemical investigation on the nutritional and nutraceutical properties of Mediterranean jellyfish Pelagia noctiluca was carried out. Also, compositional differences between male and female organisms, as well as between their main anatomical parts, namely bell and oral arms, were explored in an attempt to select the best potential sources of nutrients and/or nutraceuticals from jellyfish. With the exception of higher energy densities and total phenolic contents observed in females than males, no statistically significant differences related to the specimen's sex were highlighted for the other compound classes. Rather, the distribution of the investigated chemical classes varied depending on the jellyfish's body parts. In fact, crude proteins were more abundant in oral arms than bells; saturated fatty acids were more concentrated in bells than oral arms, whereas polyunsaturated fatty acids were distributed in the exact opposite way. On the other hand, major elements and trace elements demonstrated an opposite behavior, being the latter most accumulated in oral arms than bells. Additionally, important nutraceuticals, such as eicosapentaenoic and docosahexaenoic acids, and antioxidant minerals, were determined. Overall, obtained data suggest the potential employment of the Mediterranean P. noctiluca for the development of natural aquafeed and food supplements.

Dabiri, J. O. and M. Gharib (2003). "Sensitivity analysis of kinematic approximations in dynamic medusan swimming models." J Exp Biol **206**(Pt 20): 3675-3680.

Models of medusan swimming typically rely on kinematic approximations to observed animal morphology to make such investigations tractable. The effect of these simplifications on the accuracy of predicted dynamics has not been examined in detail. We conduct a case study of the scyphozoan jellyfish Chrysaora fuscescens to isolate and quantify the sensitivity of dynamic models to common kinematic approximations. It is found that dynamic models exhibit strong dependence on the nature of some approximations and the context in which they are implemented. Therefore it is incorrect and potentially misleading to assume that achieving kinematic similarity in models of measured animal locomotion will necessarily provide dynamically correct models.

Daguzan, C., et al. (1995). "Expression of membrane targeted aequorin in Xenopus laevis oocytes." Int J Dev Biol **39**(4): 653-657.

We described here a system for high level of expression of the calcium activated photoprotein aequorin. This protein has been targeted to the plasma membrane of Xenopus oocyte by nuclear microinjection of a plasmid containing a construction of a chimeric cDNA encoding a fusion protein composed of the photoprotein aequorin and the 5-HT1A receptor. The expression of this fusion protein is placed under the control of RSV promoter. Functional photoprotein was reconstituted in the oocyte by incubation with coelenterazine. The amount of photoprotein 24 h after nuclear microinjection of the plasmid was sufficient to trigger a detectable light emission following calcium entry. The efficiency of

the expression is correlated with the dose of plasmid injected. Intracytoplasmic injection of the plasmid always failed in photoprotein expression. Targeting of the apoprotein was demonstrated by immunolocalization under confocal microscopy. In our experimental conditions, the apoprotein was always localized at the animal pole above the nucleus. We never observed expression and targeting to the plasma membrane of the vegetal pole. WE suggest that such expression might be of great interest for the study of numerous problems of developmental biology, in which calcium-dependent pathways are involved.

Dahlgren, T. G., et al. (2016). "Abyssal fauna of the UK-1 polymetallic nodule exploration area, Clarion-Clipperton Zone, central Pacific Ocean: Cnidaria." Biodivers Data J (4): e9277.

BACKGROUND: We present data from a DNA taxonomy register of the abyssal Cnidaria collected as part of the Abyssal Baseline (ABYSSLINE) environmental survey cruise 'AB01' to the UK Seabed Resources Ltd (UKSRL) polymetallic-nodule exploration area 'UK-1' in the eastern Clarion-Clipperton Zone (CCZ), central Pacific Ocean abyssal plain. This is the second paper in a series to provide regional taxonomic data for a region that is undergoing intense deep-sea mineral exploration for high-grade polymetallic nodules. Data were collected from the UK-1 exploration area following the methods described in Glover et al. (2015b). NEW INFORMATION: Morphological and genetic data are presented for 10 species and 18 records identified by a combination of morphological and genetic data, including molecular phylogenetic analyses. These included 2 primnoid octocorals, 2 isidid octocorals, 1 anemone, 4 hydroids (including 2 pelagic siphonophores accidentally caught) and a scyphozoan jellyfish (in the benthic stage of the life cycle). Two taxa matched previously published genetic sequences (pelagic siphonophores), two taxa matched published morphological descriptions (abyssal primnoids described from the same locality in 2015) and the remaining 6 taxa are potentially new species, for which we make the raw data, imagery and vouchers available for future taxonomic study. We have used a precautionary approach in taxon assignments to avoid over-estimating species ranges. The Clarion-Clipperton Zone is a region undergoing intense exploration for potential deep-sea mineral extraction. We present these data to facilitate future taxonomic and environmental impact study by making both data and voucher materials available through curated and accessible biological collections. For some of the specimens we also provide image data collected at the seabed by ROV, wich may facilitate more accurate taxon designation in coming ROV or AUV surveys.

Dalle, B., et al. (2005). "eGFP reporter genes silence LCRbeta-globin transgene expression via CpG dinucleotides." Mol Ther **11**(4): 591-599.

beta-Globin transgenes regulated by the locus control region (LCR) are dominantly silenced by linked bacterial reporter genes in transgenic mice. Enhanced green fluorescent protein (eGFP) from jellyfish is an alternative reporter used in retrovirus vectors to transfer LCRbeta-globin genes into bone marrow. We show here that the eGFP coding sequence silences LCRbeta-globin in transgenic mice, but the PGK promoter did not provoke such silencing. As eGFP contains 60 CpG dinucleotides, which are targets of DNA methylation, we synthesized a novel CpG-free variant called dmGFP. Its utility was demonstrated in MSCV retrovirus vectors transcriptionally controlled by the viral 5'LTR or internal PGK or EF1alpha promoter. Specific fluorescence was detected from eGFP, and at lower levels from dmGFP, in transduced mouse CFU-S and embryonic stem cells. While eGFP was rarely silenced in CFU-S, dmGFP was not silenced in these progenitors. Moreover, the dmGFP coding sequence did not silence LCRbeta-globin in transgenic mice, showing that the eGFP silencing mechanism acts primarily via CpG dinucleotides. However, LCRbeta-globin expression remained suboptimal, indicating that other silencing pathways recognize dmGFP in the absence of CpG dinucleotides. We conclude that dmGFP ameliorates silencing, but optimal LCRbeta-globin expression is obtained in the absence of nonmammalian reporters.

Davies, E., et al. (1999). "Gravity, stress, calcium and gene expression." J Gravit Physiol **6**(1): P21-22.

Cytoplasmic calcium is a major regulator of plant metabolism and its levels are under strict control, but it increases rapidly and transiently after stress treatments such as cold and touch (Trewavas 1999). Gravity is also thought to affect Ca2+ levels, although one report, using fluorescence microscopy of Ca (2+)-binding dyes, showed no changes (Legue et al. 1997). However, in these studies Ca2+ could not be visualized for at least 1 min after gravistimulation and thus changes could have occurred more rapidly. In order to circumvent problems associated with the delay in taking readings imposed by the fluorescence microscopy techniques, we chose a different method using plants transgenic for the Ca (2+)-binding, light-emitting jellyfish protein aequorin (Knight & Knight 1995). We subjected Arabidopsis and tomato plants to heat-wounding, vibration and gravity stimulation and measured cytoplasmic Ca2+ levels. We also measured the levels of several transcripts after heat-wound and gravity stimulation to determine whether both

treatments evoked the same changes.

Davis, I., et al. (1995). "A nuclear GFP that marks nuclei in living Drosophila embryos; maternal supply overcomes a delay in the appearance of zygotic fluorescence." Dev Biol **170**(2): 726-729.

The central role of gene expression in regulating development has largely been studied by in situ hybridization and antibody staining techniques in fixed material. However, rapid temporal and spatial changes in gene expression are often difficult to correlate with complex morphogenetic movements. A green fluorescent protein (GFP) from the jellyfish, Aequorea victoria, can be used as a real-time reporter for gene expression and could aid analysis of dynamic events during embryogenesis. Here, we describe a transgenic Drosophila line ubiquitously expressing a nuclear GFP fusion protein that highlights morphogenesis, cell movement, and mitosis in living embryos. The fusion protein is highly fluorescent when maternally supplied, but there is a long delay between its zygotic expression and the appearance of fluorescence. GFP is thus an excellent marker for the expression of stable gene products, but a poor reporter for dynamic zygotic gene expression in early Drosophila embryos.

Dawson, M. N., et al. (1998). "Field preservation of marine invertebrate tissue for DNA analyses." Mol Mar Biol Biotechnol **7**(2): 145-152.

Successful preservation of tissue samples is a prerequisite for long field studies in remote areas. However, there is little published information concerning field preservation of marine invertebrate tissues for DNA analyses. This omission is significant because marine biodiversity is centered in the Indo-Pacific, where immediate DNA analysis is often impossible. Consequently, we used an assay based on polymerase chain reaction (PCR) to examine the effect of five storage solutions and three temperature regimens on the degradation of DNA from four common classes of marine invertebrates (Anthozoa, Gastropoda, Polychaeta, and Scyphozoa). Control samples were cryopreserved. Storage solution and the type of tissue preserved were the best predictors of preservation success. The length of time in storage and the storage temperature also affected the preservation of DNA. A field test demonstrates that a solution of dimethylsulfoxide and sodium chloride (DMSO-NaCl) preserves a wide range of tissues for DNA analyses and is very simple to use in remote field locations.

Dawson, M. N., et al. (2005). "Coupled biophysical global ocean model and molecular genetic analyses identify multiple introductions of cryptogenic species." Proc Natl Acad Sci U S A **102**(34): 11968-11973.

The anthropogenic introduction of exotic species is one of the greatest modern threats to marine biodiversity. Yet exotic species introductions remain difficult to predict and are easily misunderstood because knowledge of natural dispersal patterns, species diversity, and biogeography is often insufficient to distinguish between a broadly dispersed natural population and an exotic one. Here we compare a global molecular phylogeny of a representative marine meroplanktonic taxon, the moon-jellyfish Aurelia, with natural dispersion patterns predicted by a global biophysical ocean model. Despite assumed high dispersal ability, the phylogeny reveals many cryptic species and predominantly regional structure with one notable exception: the globally distributed Aurelia sp.1, which, molecular data suggest, may occasionally traverse the Pacific unaided. This possibility is refuted by the ocean model, which shows much more limited dispersion and patterns of distribution broadly consistent with modern biogeographic zones, thus identifying multiple introductions worldwide of this cryptogenic species. This approach also supports existing evidence that (i) the occurrence in Hawaii of Aurelia sp. 4 and other native Indo-West Pacific species with similar life histories is most likely due to anthropogenic translocation, and (ii) there may be a route for rare natural colonization of northeast North America by the European marine snail Littorina littorea, whose status as endemic or exotic is unclear.

Day, R. N. (1998). "Visualization of Pit-1 transcription factor interactions in the living cell nucleus by fluorescence resonance energy transfer microscopy." Mol Endocrinol **12**(9): 1410-1419.

The pituitary-specific transcription factor Pit-1 forms dimers when interacting with specific DNA elements and has been shown to associate with several other nuclear proteins. Recently, techniques have become available that allow visualization of protein-protein interactions as they occur in single living cells. In this study, the technique of fluorescence resonance energy transfer (FRET) microscopy was used to visualize the physical interactions of Pit-1 proteins fused to spectral variants of the jellyfish green fluorescent protein (GFP) that emit green or blue light [blue fluorescent protein (BFP)]. An optimized imaging system was used to discriminate fluorescence signals from single cells coexpressing the BFP- and GFP-fusion proteins, and the contribution of spectral overlap to background fluorescence detected in the FRET images was established. Energy transfer signals from living cells expressing a fusion protein in which GFP was tethered to BFP by short protein linker was used to demonstrate acquisition of FRET signals. Genetic vectors encoding GFP- and BFP-Pit-1 proteins

were prepared, and biological function of the fusion proteins was confirmed. FRET microscopy of HeLa cells coexpressing the GFP- and BFP-Pit-1 demonstrated energy transfer, which required the two fluorophores to be separated by less than 100 A. Biochemical studies previously demonstrated that Pit-1 physically interacts with both c-Ets-1 and the estrogen receptor. FRET imaging of cells coexpressing BFP-Pit-1 and GFP-Ets-1 demonstrated energy transfer between these fusion proteins, a result consistent with their association in the nucleus of these living cells. In contrast, there was no evidence for energy transfer between the BFP-Pit-1 and an estrogen receptor-GFP fusion proteins. It is likely that the FRET imaging approach described here can be applied to many different protein-partner pairs in a variety of cellular contexts.

Day, R. N., et al. (1998). "Dual-function reporter protein for analysis of gene expression in living cells." Biotechniques **25**(5): 848-850, 852-844, 856.

The firefly luciferase (Luc) protein and the jellyfish green fluorescent protein (GFP) are two commonly used molecular reporters that can be detected noninvasively in living cells. The properties that make GFP or Luc useful for a particular experimental application are quite distinct. A recombinant protein with both fluorescent and bioluminescent characteristics might take advantage of the strengths of both reporters. An expression vector encoding a chimeric protein in which GFP was tethered to Luc through a 19-amino acid linker was prepared and characterized. Western blotting with antibodies specific for either GFP or Luc showed that a protein of appropriate size was expressed in transfected cells. Fluorescence microscopy revealed bright green fluorescence from transfected cells, indicating proper formation of the GFP chromophore. Luc enzymatic activity in protein extracts from transfected cells showed that Luc was fully functional. The treatment of living cell cultures stably expressing the GFP-Luc fusion protein with the protein translation-inhibitor cycloheximide (Chx) was used to show that the half-life for Luc protein activity was approximately 2 h at 37 degrees C. The utility of this dual-function reporter protein was shown by the identification of single living cells expressing the chimeric protein within a population by fluorescence microscopy, followed by quantification of Luc activity from the same living cells.

Day, R. N., et al. (2001). "Fluorescence resonance energy transfer microscopy of localized protein interactions in the living cell nucleus." Methods **25**(1): 4-18.

Cells respond to environmental cues by modifying protein complexes in the nucleus to produce a change in the pattern of gene expression. In this article, we review techniques that allow us to visualize these protein interactions as they occur in living cells. The cloning of genes from marine organisms that encode fluorescent proteins provides a way to tag and monitor the intracellular behavior of expressed fusion proteins. The genetic engineering of jellyfish green fluorescent protein (GFP) and the recent cloning of a sea anemone red fluorescent protein (RFP) have provided fluorescent tags that emit light at wavelengths ranging from the blue to the red spectrum. Several of these color variants can be readily distinguished by fluorescence microscopy, allowing them to be used in combination to monitor the behavior of two or more independent proteins in the same living cell. We describe the use of this approach to examine where transcription factors are assembled in the nucleus. To demonstrate that these labeled nuclear proteins are interacting, however, requires spatial resolution that exceeds the optical limit of the light microscope. This degree of spatial resolution can be achieved with the conventional light microscope using the technique of fluorescence resonance energy transfer (FRET). The application of FRET microscopy to detect the interactions between proteins labeled with the color variants of GFP and the limitations of the FRET approach are discussed. The use of different-color fluorescent proteins in combination with FRET offers the opportunity to study the complex behavior of key regulatory proteins in their natural environment within the living cell.

DeClerck, M. P., et al. (2016). "Efficacy of Topical Treatments for Chrysaora chinensis Species: A Human Model in Comparison with an In Vitro Model." Wilderness Environ Med **27**(1): 25-38.

OBJECTIVES: This study sought to create a model for testing topical treatment of jellyfish stings. It sought to determine which treatments 1) stimulate/inhibit nematocyst discharge; 2) decrease pain; and 3) decrease skin inflammation; it also sought to discover whether there is a clinical correlation between stimulated nematocyst discharge observed in vitro to the pain and erythema experienced by humans stung by a particular species of jellyfish, C chinensis. METHODS: Chrysaora chinensis stung 96 human subjects, who were then treated with isopropyl alcohol, hot water, acetic acid, papain meat tenderizer, lidocaine, or sodium bicarbonate. Pain and erythema were measured. In a separate experiment, nematocysts were examined microscopically after exposure to the same topical treatments used in the human experiment. RESULTS: Forearms treated with papain showed decreased mean pain over the first 30 minutes after being stung, relative to placebo, although only by a

small amount. The other topical treatments tested did not reach statistical significance. Sodium bicarbonate may reduce erythema after 30 minutes of treatment; sodium bicarbonate and papain may reduce erythema at 60 minutes. The other topical treatments tested did not reach statistical significance. Nematocyst discharge in vitro occurred when tentacles of C chinensis were exposed to acetic acid or isopropyl alcohol. Sodium bicarbonate, papain, heated water, and lidocaine did not induce nematocyst discharge. CONCLUSIONS: Papain-containing meat tenderizer used as a topical treatment for C chinensis stings may decrease pain. Although there is published experimental support for the concept that in vitro nematocyst discharge correlates with in vivo human pain perception, no definitive randomized controlled trial, including ours, has yet provided incontrovertible evidence of this assertion. Despite this study's limitations, it presents a viable basis for future human studies looking at the efficacy of topical treatments for jellyfish stings.

Del Pozo, L. J., et al. (2016). "Dermoscopic Findings of Jellyfish Stings Caused by Pelagia noctiluca." Actas Dermosifiliogr **107**(6): 509-515.

BACKGROUND AND OBJECTIVES: Jellyfish are free-living members of the phylum Cnidaria who share a specialized stinging cell, the cnidocyte. Pelagia noctiluca is the most frequent and toxic jellyfish species found in the Balearic beaches and cnidocytes are arranged in pigmented clusters called "warts". Dermoscopy continues to expand its use much beyond the pigmentary lesions and to date, there is no data regarding dermoscopic findings in jellyfish stings. The aim of the present work was to study the dermoscopic findings of jellyfish stings in the island of Mallorca. PATIENTS AND METHODS: We retrospectively reviewed the clinical and dermoscopic images of 25 episodes of jellyfish stings caused by P. noctiluca that occurred between 2009 and 2015. RESULTS: Overall, the following dermoscopic features were found: brown dots (84%), pinkish hue (56%), pinpoint brown crusts (44%), scale-crust (40%), brown "Chinese characters pattern" (32%), "serpentine" ulceration (28%), linear purpura (20%), and whitish-yellow crusts (15%). Vessels were mainly dotted (36%) or reticular (16%). Scale-crust, serpentine ulceration and pinkish hue were significantly more frequent in lesions older than 2 days. CONCLUSIONS AND LIMITATIONS: Our study identifies 4 dermoscopic features that may represent the contact with P. noctiluca cnidocytes: brown dots, brown "Chinese characters pattern", pinpoint brown crusts and whitish-yellow crusts. A peculiar finding of "serpentine ulceration" with brown dots would be very suggestive of P. noctiluca sting. We believe dermoscopy is a valuable tool in the diagnosis of jellyfish stings when a clear history of contact is lacking. Further studies are needed to validate our findings in other jellyfish species.

Delagrave, S., et al. (1995). "Red-shifted excitation mutants of the green fluorescent protein." Biotechnology (N Y) **13**(2): 151-154.

Using optimized combinatorial mutagenesis techniques and Digital Imaging Spectroscopy (DIS), we have isolated mutants of the cloned Aequorea victoria green fluorescent protein (GFP) that show red-shifted excitation spectra similar to that of Renilla reniformis GFP. Selective excitation of wild-type versus Red-Shifted GFP (RSGFP) enables spectral separation of these proteins. Six contiguous codons spanning the tyrosine chromophore region were randomized and sequence analysis of the mutants revealed a tyrosineglycine consensus. These mutants will enable the simultaneous analysis of two promoters or proteins per cell or organism. In consideration of the multitude of applications which are developing for GFP alone, we envisage that spectrally shifted fluorescent proteins will be of value to a diversity of research programs, including developmental and cell biology, drug-screening, and diagnostic assays.

Delpy, F., et al. (2012). "Man-induced hydrological changes, metazooplankton communities and invasive species in the Berre Lagoon (Mediterranean Sea, France)." Mar Pollut Bull **64**(9): 1921-1932.

The Berre Lagoon has been under strong anthropogenic pressure since the early 1950s. The opening of the hydroelectric EDF power plant in 1966 led to large salinity drops. The zooplankton community was mainly composed of two common brackish species: Acartia tonsa and Brachionus plicatilis. Since 2006, European litigation has strongly constrained the input of freshwater, maintaining the salinity above 15. A study was performed between 2008 and 2010 to evaluate how these modifications have impacted the zooplankton community. Our results show that the community is more diverse and contains several coastal marine species (i.e., Centropages typicus, Paracalanus parvus and Acartia clausi). A. tonsa is still present but is less abundant, whereas B. plicatilis has completely disappeared. Strong predatory marine species, such as chaetognaths, the large conspicuous autochtonous jellyfish Aurelia aurita and the invasive ctenophore Mnemiopsis leidyi, are now very common as either seasonal or permanent features of the lagoon.

DeMella, K. C. and S. R. Raghavan (2019). "Catalyst-Loaded Capsules that Spontaneously Inflate and Violently Eject their Core." Langmuir **35**(42):

13718-13726.

We present a design for polymer capsules that exhibit a range of unusual autonomous behaviors when exposed to a chemical fuel. The capsules have a physically gelled core (alginate-Ca (2+)) loaded with catalytic (silver) particles and a shell composed of a chemically cross-linked gel. In the presence of the fuel (H2O2), a catalytic reaction occurs, which generates oxygen (O2) gas. The gas collects in a zone between the core and the shell, and the resulting gas pressure causes the elastic shell to stretch. This makes the capsule inflate in a process reminiscent of a swelling pufferfish. As the capsule inflates, the polymer chains in the shell continue to stretch until a breaking point is reached, whereupon the shell ruptures. Three rupture modes are documented: gentle, moderate, and violent. The latter involves the gelled core being forcefully ejected out of the shell in a manner similar to the ejection of needles out of nematocysts on jellyfish. The extent and duration of inflation can be tuned by altering the core and shell composition; for example, shells that are more densely cross-linked swell less and rupture faster. Also, instead of a catalytic reaction, capsule inflation can be achieved by combining reactants, one in the capsule and the other in the external solution, that together generate a different gas (e.g., CO2).

Deng, Y., et al. (2016). "Proton mediated control of biochemical reactions with bioelectronic pH modulation." Sci Rep **6**: 24080.

In Nature, protons (H (+)) can mediate metabolic process through enzymatic reactions. Examples include glucose oxidation with glucose dehydrogenase to regulate blood glucose level, alcohol dissolution into carboxylic acid through alcohol dehydrogenase, and voltage-regulated H (+) channels activating bioluminescence in firefly and jellyfish. Artificial devices that control H (+) currents and H (+) concentration (pH) are able to actively influence biochemical processes. Here, we demonstrate a biotransducer that monitors and actively regulates pH-responsive enzymatic reactions by monitoring and controlling the flow of H (+) between PdHx contacts and solution. The present transducer records bistable pH modulation from an "enzymatic flip-flop" circuit that comprises glucose dehydrogenase and alcohol dehydrogenase. The transducer also controls bioluminescence from firefly luciferase by affecting solution pH.

Deo, S. K. and S. Daunert (2001). "Luminescent proteins from Aequorea victoria: applications in drug discovery and in high throughput analysis." Fresenius J Anal Chem **369**(3-4): 258-266.

Recent progress in generating a vast number of drug targets through genomics and large compound libraries through combinatorial chemistry have stimulated advancements in drug discovery through the development of new high throughput screening (HTS) methods. Automation and HTS techniques are also highly desired in fields such as clinical diagnostics. Luminescence-based assays have emerged as an alternative to radiolabel-based assays in HTS as they approach the sensitivity of radioactive detection along with ease of operation, which makes them amenable to miniaturization. Luminescent proteins provide the advantage of reduced reagent and operating costs because they can be produced in unlimited amounts through the use of genetic engineering tools. In that regard, the use of two naturally occurring and recombinantly produced luminescent proteins from the jellyfish Aequorea victoria, namely, aequorin and the green fluorescent protein (GFP), has attracted attention in a number of analytical applications in diverse research areas. Aequorin is naturally bioluminescent and has therefore, virtually no associated background signal, which allows its detection down to attomole levels. GFP has become the reporter of choice in a variety of applications given that it is an autofluorescent protein that does not require addition of any co-factors for fluorescence emission. Furthermore, the generation of various mutants of GFP with differing luminescent and spectral properties has spurred additional interest in this protein. In this review, we focus on the use of aequorin and GFP in the development of highly sensitive assays that find applications in drug discovery and in high throughput analysis.

Deo, S. K., et al. (2005). "Bioluminescence resonance energy transfer from aequorin to a fluorophore: an artificial jellyfish for applications in multianalyte detection." Anal Bioanal Chem **381**(7): 1387-1394.

In nature, the green light emission observed in the jellyfish Aequorea victoria is a result of a non-radiative energy transfer from the excited-state aequorin to the green fluorescent protein. In this work, we have modified the photoprotein aequorin by attaching selected fluorophores at a unique site on the protein. This will allow for in vitro transfer of bioluminescent energy from aequorin to the fluorophore thus creating an "artificial jellyfish". The fluorophores are selected such that the excitation spectrum of the fluorophore overlaps with the emission spectrum of aequorin. By modifying aequorin with different fluorophores, bioluminescent labels with different emission maxima are produced, which will allow for the simultaneous detection of multiple analytes. By examining the X-ray crystal structure of the protein, four different sites for

introduction of the unique cysteine residue were evaluated. Two fluorophores with differing emission maxima were attached individually to the mutants through the sulfhydryl group of the cysteine molecule. Two of the fluorophore-labeled mutants showed a peak corresponding to fluorophore emission thus indicating resonance energy transfer from aequorin to the fluorophore.

Deorowicz, S., et al. (2015). "KMC 2: fast and resource-frugal k-mer counting." Bioinformatics **31**(10): 1569-1576.

MOTIVATION: Building the histogram of occurrences of every k-symbol long substring of nucleotide data is a standard step in many bioinformatics applications, known under the name of k-mer counting. Its applications include developing de Bruijn graph genome assemblers, fast multiple sequence alignment and repeat detection. The tremendous amounts of NGS data require fast algorithms for k-mer counting, preferably using moderate amounts of memory. RESULTS: We present a novel method for k-mer counting, on large datasets about twice faster than the strongest competitors (Jellyfish 2, KMC 1), using about 12 GB (or less) of RAM. Our disk-based method bears some resemblance to MSPKmerCounter, yet replacing the original minimizers with signatures (a carefully selected subset of all minimizers) and using (k, x)-mers allows to significantly reduce the I/O and a highly parallel overall architecture allows to achieve unprecedented processing speeds. For example, KMC 2 counts the 28-mers of a human reads collection with 44-fold coverage (106 GB of compressed size) in about 20 min, on a 6-core Intel i7 PC with an solid-state disk.

Derkus, B., et al. (2016). "Enhancement of aptamer immobilization using egg shell-derived nano-sized spherical hydroxyapatite for thrombin detection in neuroclinic." Talanta **158**: 100-109.

In the present study, we describe the sonochemical isolation of nano-sized spherical hydroxyapatite (nHA) from egg shell and application towards thrombin aptasensing. In addition to the sonochemical method, two conventional methods present in literature were carried out to perform a comparative study. Various analysis methods including Transmission Electron Microscopy (TEM), Scanning Electron Microscopy (SEM), Fourier Transform Infrared Spectroscopy (FTIR), X-Ray Diffraction (XRD), Energy-Dispersive Analysis of X-Rays (EDAX), and Thermal Gravimetric Analysis (TGA) have been applied for the characterization of nHA and its nanocomposite with marine-derived collagen isolated from Rhizostoma pulmo jellyfish. TEM micrographs revealed the sonochemically synthesized nHA nanoparticles to have a unique porous spherical shape with a diameter of approximately 60-80nm when compared to hydroxyapatite nanoparticles synthesized using the other two methods which had a typical needle shaped morphology. EDAX, XRD and FTIR results demonstrated that the obtained patterns belonged to hydroxyapatite. Electrochemical impedance spectroscopy (EIS) is the main analyzing technique of the developed thrombin aptasensor. The proposed aptasensor has a detection limit of 0.25nM thrombin. For clinical application of the developed aptasensor, thrombin levels in blood and cerebrospinal fluid (CSF) samples obtained from patients with Multiple Sclerosis, Myastenia Gravis, Epilepsy, Parkinson, polyneuropathy and healthy donors were analyzed using both the aptasensor and commercial ELISA kit. The results showed that the proposed system is a promising candidate for clinical analysis of thrombin.

Desai, P. and S. Person (1998). "Incorporation of the green fluorescent protein into the herpes simplex virus type 1 capsid." J Virol **72**(9): 7563-7568.

The herpes simplex virus type 1 (HSV-1) UL35 open reading frame (ORF) encodes a 12-kDa capsid protein designated VP26. VP26 is located on the outer surface of the capsid specifically on the tips of the hexons that constitute the capsid shell. The bioluminescent jellyfish (Aequorea victoria) green fluorescent protein (GFP) was fused in frame with the UL35 ORF to generate a VP26-GFP fusion protein. This fusion protein was fluorescent and localized to distinct regions within the nuclei of transfected cells following infection with wild-type virus. The VP26-GFP marker was introduced into the HSV-1 (KOS) genome resulting in recombinant plaques that were fluorescent. A virus, designated K26GFP, was isolated and purified and was shown to grow as well as the wild-type virus in cell culture. An analysis of the intranuclear capsids formed in K26GFP-infected cells revealed that the fusion protein was incorporated into A, B, and C capsids. Furthermore, the fusion protein incorporated into the virion particle was fluorescent as judged by fluorescence-activated cell sorter (FACS) analysis of infected cells in the absence of de novo protein synthesis. Cells infected with K26GFP exhibited a punctate nuclear fluorescence at early times in the replication cycle. At later times during infection a generalized cytoplasmic and nuclear fluorescence, including fluorescence at the cell membranes, was observed, confirming visually that the fusion protein was incorporated into intranuclear capsids and mature virions.

DeSalle, R. and B. Schierwater (2008). "An even "newer" animal phylogeny." Bioessays **30**(11-12):

1043-1047.

Metazoa are one of the great monophyletic groups of organisms. They comprise several major groups of organisms readily recognizable based on their anatomy. These major groups include the Bilateria (animals with bilateral symmetry), Cnidaria (jellyfish, corals and other closely related animals), Porifera (sponges), Ctenophores (comb jellies) and a phylum currently made up of a single species, the Placozoa. Attempts to systematize the relationships of these major groups as well as to determine relationships within the groups have been made for nearly two centuries. Many of the attempts have led to frustration, because of a lack of resolution between and within groups. Other attempts have led to "a new animal phylogeny". Now, a study by Dunn et al., using the expresssed sequence tag (EST) approach to obtaining high-throughput large phylogenetic matrices, presents an "even newer" animal phylogeny. There are two major aspects of this study that should be of interest to the general biological community. First, the methods used by the authors to generate their phylogenetic hypotheses call for close examination. Second, the relationships of animal taxa in their resultant trees also prompt further discussion.

Desax-Willer, D., et al. (2018). "Delayed deep dermal necrosis after jellyfish sting in a 4-year-old female infant." Case Reports Plast Surg Hand Surg **5**(1): 75-79.

We report the case of a 4-year-old female infant who developed ongoing deep dermal necrosis of the bilateral legs after jellyfish contact in Thailand. Stepwise radical debridement and vacuum assisted wound therapy seemed to be an effective strategy to prevent progressive soft tissue loss.

Deschamps, J. R., et al. (1995). "Rapid purification of recombinant green fluorescent protein using the hydrophobic properties of an HPLC size-exclusion column." Protein Expr Purif **6**(4): 555-558.

The green fluorescent protein (GFP) of the jelly fish Aequoria victoria was cloned into an Escherichia coli cell line that is a methionine auxotroph. The recombinant GFP (rGFP) was isolated from the cells and purified using a simple procedure consisting of only two chromatographic steps: size-exclusion chromatography and ion-exchange HPLC. Due to the hydrophobic nature of the protein, the surface characteristics of the HPLC size column, and the high initial salt concentration, the rGFP sticks to the size column and is eluted by reducing the salt concentration. Due to this unique behavior the purification procedure can readily be scaled to handle larger quantities of rGFP.

Detert, J. A., et al. (2013). "Pretreatment with apoaequorin protects hippocampal CA1 neurons from oxygen-glucose deprivation." PLoS One **8**(11): e79002.

Ischemic stroke affects approximately 795,000 people each year in the U.S., which results in an estimated annual cost of $73.7 billion. Calcium is pivotal in a variety of neuronal signaling cascades, however, during ischemia, excess calcium influx can trigger excitotoxic cell death. Calcium binding proteins help neurons regulate/buffer intracellular calcium levels during ischemia. Aequorin is a calcium binding protein isolated from the jellyfish Aequorea victoria, and has been used for years as a calcium indicator, but little is known about its neuroprotective properties. The present study used an in vitro rat brain slice preparation to test the hypothesis that an intra-hippocampal infusion of apoaequorin (the calcium binding component of aequorin) protects neurons from ischemic cell death. Bilaterally cannulated rats received an apoaequorin infusion in one hemisphere and vehicle control in the other. Hippocampal slices were then prepared and subjected to 5 minutes of oxygen-glucose deprivation (OGD), and cell death was assayed by trypan blue exclusion. Apoaequorin dose-dependently protected neurons from OGD--doses of 1% and 4% (but not 0.4%) significantly decreased the number of trypan blue-labeled neurons. This effect was also time dependent, lasting up to 48 hours. This time dependent effect was paralleled by changes in cytokine and chemokine expression, indicating that apoaequorin may protect neurons via a neuroimmunomodulatory mechanism. These data support the hypothesis that pretreatment with apoaequorin protects neurons against ischemic cell death, and may be an effective neurotherapeutic.

Devarapalli, P., et al. (2014). "The conserved mitochondrial gene distribution in relatives of Turritopsis nutricula, an immortal jellyfish." Bioinformation **10**(9): 586-591.

Turritopsis nutricula (T. nutricula) is the one of the known reported organisms that can revert its life cycle to the polyp stage even after becoming sexually mature, defining itself as the only immortal organism in the animal kingdom. Therefore, the animal is having prime importance in basic biological, aging, and biomedical researches. However, till date, the genome of this organism has not been sequenced and even there is no molecular phylogenetic study to reveal its close relatives. Here, using phylogenetic analysis based on available 16s rRNA gene and protein sequences of Cytochrome oxidase subunit-I (COI or COX1) of T. nutricula, we have predicted the closest relatives of the organism. While we found Nemopsis bachei could be closest organism based on COX1 gene sequence; T. dohrnii may be designated as the closest

taxon to T. nutricula based on rRNA. Moreover, we have figured out four species that showed similar root distance based on COX1 protein sequence.

Devere, R. (2011). "Guillain-Barre syndrome after a jellyfish sting." J Clin Neuromuscul Dis **12**(4): 227-230.

This is the case of a jellyfish sting associated with the rare development of Guillain-Barre syndrome. The patient, a 66-year-old woman, was stung by a jellyfish on the right thigh while swimming in the Atlantic Ocean, off Charleston, SC. Ten days later, she developed low back and right thigh pain followed by progressive numbness and weakness in all extremities. These symptoms reached their peak in 30 days and slowly began to improve. Initial neurologic examination showed areflexia, weakness, absent vibration and position sense, and hyperesthesia to pin and light touch in the mid to distal region of all four extremities. Serial electromyography and nerve conductions were consistent with an improving predominantly demyelinating polyneuropathy. Spinal fluid analysis showed no cells, elevated protein (108), gammaglobulin 6 (normal less than 5.4), and immunoglobulin G 8.2 (normal less than 6). The only treatment was gabapentin for neuropathy pain. The patient made an excellent recovery in less than 1 year with minimal residual numbness in both thumbs, index fingers, and middle toes.

Dhandayuthapani, S., et al. (1995). "Green fluorescent protein as a marker for gene expression and cell biology of mycobacterial interactions with macrophages." Mol Microbiol **17**(5): 901-912.

The green fluorescent protein (GFP) of the jellyfish Aequorea victoria offers certain advantages over other bioluminescence systems because no exogenously added substrate or co-factors are necessary, and fluorescence can be elicited by irradiation with blue light without exposing the cells producing GFP to invasive treatments. A mycobacterial shuttle-plasmid vector carrying gfp cDNA was constructed and used to generate transcriptional fusions with promoters of interest and to examine their expression in Mycobacterium smegmatis and Mycobacterium bovis BCG grown in macrophages or on laboratory media. The promoters studied were: (i) ahpC from Mycoosis and Mycobacterium leprae, a gene encoding alkyl hydroperoxide reductase which, along with the divergently transcribed regulator oxyR, are homologues of corresponding stress-response systems in enteric bacteria and play a role in isoniazid sensitivity; (ii) mtrA, an M. tuberculosis response regulator belonging to the superfamily of bacterial two-component signal-transduction systems; (iii) hsp60, a previously characterized heat-shock gene from M. bovis; and (iv) tbprc3, a newly isolated promoter from M. tuberculosis. Expression of these promoters in mycobacteria was analysed using epifluorescence microscopy, laser scanning confocal microscopy, fluorescence spectroscopy, and flow cytometry. These approaches permitted assessment of fluorescence prior to and after macrophage infection, and analyses of promoter expression in individual mycobacteria and its distribution within populations of bacterial cells. Bacteria expressing GFP from a strong promoter could be separated by fluorescence-activated cell sorting from cells harbouring the vector used to construct the fusion. In addition, the stable expression of mtrA-gfp fusion in M. bovis BCG facilitated localization and isolation of phagocytic vesicles containing mycobacteria. The experiments presented here suggest that GFP will be a useful tool for analysis of mycobacterial gene expression and a convenient cell biology marker to study mycobacterial interactions with macrophages.

Di Costanzo, L., et al. (2009). "Successful management of a delayed and persistent cutaneous reaction to jellyfish with pimecrolimus." J Dermatolog Treat **20**(3): 179-180.

The contact with a jellyfish is usually followed by acute inflammatory lesions, characterized by erythema, swelling, vesicles, and bullae, accompanied by burning and pain sensation. The pathogenesis is due to the direct toxic effect of the fluid contained in jellyfish tentacles. Sometimes, jellyfish may induce delayed cutaneous lesions. Delayed cutaneous reaction to jellyfish represents a clinical entity where eczematous lesions develop after days or months after contact with the invertebrate. We report the case of a patient with a delayed and persistent skin reaction due to jellyfish envenomation successfully treated with pimecrolimus.

Dickson, R. M., et al. (1997). "On/off blinking and switching behaviour of single molecules of green fluorescent protein." Nature **388**(6640): 355-358.

Optical studies of individual molecules at low and room temperature can provide information about the dynamics of local environments in solids, liquids and biological systems unobscured by ensemble averaging. Here we present a study of the photophysical behaviour of single molecules of the green fluorescent protein (GFP) derived from the jellyfish Aequorea victoria. Wild-type GFP and its mutant have attracted interest as fluorescent biological labels because the fluorophore may be formed in vivo. GFP mutants immobilized in aereated aqueous polymer gels and excited by 488-nm light undergo repeated cycles of fluorescent emission ('blinking') on

a timescale of several seconds-behaviour that would be unobservable in bulk studies. Eventually the individual GFP molecules reach a long-lasting dark state, from which they can be switched back to the original emissive state by irradiation at 405 nm. This suggests the possibility of using these GFPs as fluorescent markers for time-dependent cell processes, and as molecular photonic switches or optical storage elements, addressable on the single-molecule level.

Dinasquet, J., et al. (2012). "Stimulated bacterioplankton growth and selection for certain bacterial taxa in the vicinity of the ctenophore Mnemiopsis leidyi." Front Microbiol **3**: 302.

Episodic blooms of voracious gelatinous zooplankton, such as the ctenophore Mnemiopsis leidyi, affect pools of inorganic nutrients and dissolved organic carbon by intensive grazing activities and mucus release. This will potentially influence bacterioplankton activity and community composition, at least at local scales; however, available studies on this are scarce. In the present study we examined effects of M. leidyi on bacterioplankton growth and composition in incubation experiments. Moreover, we examined community composition of bacteria associated with the surface and gut of M. leidyi. High release of ammonium and high bacterial growth was observed in the treatments with M. leidyi relative to controls. Deep 454 pyrosequencing of 16 S rRNA genes showed specific bacterial communities in treatments with M. leidyi as well as specific communities associated with M. leidyi tissue and gut. In particular, members of Flavobacteriaceae were associated with M. leidyi. Our study shows that M. leidyi influences bacterioplankton activity and community composition in the vicinity of the jellyfish. In particular during temporary aggregations of jellyfish, these local zones of high bacterial growth may contribute significantly to the spatial heterogeneity of bacterioplankton activity and community composition in the sea.

Ding, D. Q., et al. (1998). "Oscillatory nuclear movement in fission yeast meiotic prophase is driven by astral microtubules, as revealed by continuous observation of chromosomes and microtubules in living cells." J Cell Sci **111 (Pt 6)**: 701-712.

Using a computerized fluorescence microscope system to observe fluorescently stained cellular structures in vivo, we have examined the dynamics of chromosomes and microtubules during the process of meiosis in the fission yeast Schizosaccharomyces pombe. Fission yeast meiotic prophase is characterized by a distinctive type of nuclear movement that is led by telomeres clustered at the spindle-pole body (the centrosome-equivalent structure in fungi): the nucleus oscillates back and forth along the cell axis, moving continuously between the two ends of the cell for some hours prior to the meiotic divisions. To obtain a dynamic view of this oscillatory nuclear movement in meiotic prophase, we visualized microtubules and chromosomes in living cells using jellyfish green fluorescent protein fused with alpha-tubulin and a DNA-specific fluorescent dye, Hoechst 33342, respectively. Continuous observation of chromosomes and microtubules in these cells demonstrated that the oscillatory nuclear movement is mediated by dynamic reorganization of astral microtubules originating from the spindle-pole body. During each half-oscillatory period, the microtubules extending rearward from the leading edge of the nucleus elongate to drive the nucleus to one end of the cell. When the nucleus reversed direction, its motion during the second half of the oscillation was not driven by the same microtubules that drove its motion during the first half, but rather by newly assembled microtubules. Reversible inhibition of nuclear movement by an inhibitor of microtubule polymerization, thiabendazole, confirmed the involvement of astral microtubules in oscillatory nuclear movement. The speed of the movement fluctuated within a range 0 to 15 micron/minute, with an average of about 5 microm/minute. We propose a model in which the oscillatory nuclear movement is mediated by dynamic instability and selective stabilization of astral microtubules.

Djalal, F. M., et al. (2019). "Is jellyfish more of a fish in English than in Dutch? The effect of informative labels." Q J Exp Psychol (Hove) **72**(4): 792-797.

Some words are lexically suggestive about the taxonomic position of their referent (e.g., jellyfish in English), and this information can vary across languages (e.g., in Dutch the equivalent of jellyfish holds no taxonomic information: kwal). To evaluate the role of such lexical suggestions, we conducted a cross-linguistic study in which similarity judgements from two language groups (Dutch and English speakers) were compared. We paired asymmetrically informative items with items that are considered to be typical members of the referenced category (e.g., jellyfish-salmon). Our analyses revealed that items were deemed more similar by speakers of a language in which the lexical information was present (e.g., English speakers tended to give relatively higher ratings for jellyfish-salmon than Dutch participants did for the non-informative equivalent kwal-zalm). Results are discussed in light of theories of concept representation and compound processing.

Doerr, M. and M. K. Stoskopf (2019).

"Evaluation of Euthanasia of Moon Jellyfish (Aurelia Aurita) Using Simple Salt Solutions." J Zoo Wildl Med **50**(1): 123-126.

Immersion euthanasia methods reported over the most recent decades for aquatic invertebrates use organic alcohols or halogenated hydrocarbons that can interfere with nuclear magnetic resonance (NMR) analysis. A rolling study design evaluated potassium chloride (KCl), magnesium chloride (MgCl2), and magnesium sulfate (MgSO4) as potential ion-based euthanasia methods for moon jellyfish (Aurelia aurita) destined for metabolomic analysis by NMR spectroscopy. Death was defined as the cessation of autonomous bell pulsing and response to external stimulus. MgCl2 applied at a dose of 142 g/L provided euthanasia within 32 sec of applications without the untoward effects observed with the other two salts. Euthanasia with KCl at the doses tested was associated with abnormal behavior and tissue degradation during dissection. MgSO4 at the doses tested resulted in abnormal behavior and failed to provide rapid euthanasia.

Domenici, P., et al. (2007). "Hypoxia and the antipredator behaviours of fishes." Philos Trans R Soc Lond B Biol Sci **362**(1487): 2105-2121.

Hypoxia is a phenomenon occurring in marine coastal areas with increasing frequency. While hypoxia has been documented to affect fish activity and metabolism, recent evidence shows that hypoxia can also have a detrimental effect on various antipredator behaviours. Here, we review such evidence with a focus on the effect of hypoxia on fish escape responses, its modulation by aquatic surface respiration (ASR) and schooling behaviour. The main effect of hypoxia on escape behaviour was found in responsiveness and directionality. Locomotor performance in escapes was expected to be relatively independent of hypoxia, since escape responses are fuelled anaerobically. However, hypoxia decreased locomotor performance in some species (Mugilidae) although only in the absence of ASR in severe hypoxia. ASR allows fish to show higher escape performance than fish staying in the water column where hypoxia occurs. This situation provides a trade-off whereby fish may perform ASR in order to avoid the detrimental effects of hypoxia, although they would be subjected to higher exposure to aerial predation. As a result of this trade-off, fishes appear to minimize surfacing behaviour in the presence of aerial predators and to surface near shelters, where possible. For many fish species, schooling can be an effective antipredator behaviour. Severe hypoxia may lead to the disruption of the school unit. At moderate levels, hypoxia can increase school volume and can change the shuffling behaviour of individuals. By altering school structure and dynamics, hypoxia may affect the well functioning of schooling in terms of synchronization and execution of antipredator manoeuvres. School structure and volume appear to be the results of numerous trade-offs, where school shape may be dictated by the presence of predators, the need for energy saving via hydrodynamic advantages and oxygen level. The effects of hypoxia on aquatic organisms can be taxon specific. While hypoxia may not necessarily increase the vulnerability of fish subject to predation by other fish (since feeding in fish also decreases in hypoxia), predators from other taxa such as birds, jellyfish or aquatic mammals may take advantage of the detrimental effects of hypoxia on fish escape ability. Therefore, the effect of hypoxia on fish antipredator behaviours may have major consequences for the composition of aquatic communities.

Dunlop, K. M., et al. (2017). "Direct evidence of an efficient energy transfer pathway from jellyfish carcasses to a commercially important deep-water species." Sci Rep **7**(1): 17455.

Here we provide empirical evidence of the presence of an energetic pathway between jellyfish and a commercially important invertebrate species. Evidence of scavenging on jellyfish carcasses by the Norway lobster (Nephrops norvegicus) was captured during two deployments of an underwater camera system to 250-287 m depth in Sognefjorden, western Norway. The camera system was baited with two Periphylla periphylla (Scyphozoa) carcasses to simulate the transport of jellyfish detritus to the seafloor, hereby known as jelly-falls. N. norveigus rapidly located and consumed a large proportion (>50%) of the bait. We estimate that the energy input from jelly-falls may represent a significant contribution to N. norvegicus energy demand (0.21 to 10.7 times the energy required for the population of N. norvegicus in Sognefjorden). This potentially high energetic contribution from jelly-falls highlights a possible role of gelatinous material in the support of commercial fisheries. Such an energetic pathway between jelly-falls and N. norvegicus could become more important with increases in jellyfish blooms in some regions.

Dunn, D. F. and M. H. Liberman (1983). "Chitin in sea anemone shells." Science **221**(4606): 157-159.

Chitin, which is widely distributed among life forms, is well documented in the coelenterate class Hydrozoa and is contained in one member of class Scyphozoa. In class Anthozoa, hard corals synthesize it but soft corals do not. Chitin was identified by infrared spectrophotometry in the trochoid shell of the actinian Stylobates. It constitutes 1.7 percent of the shell by weight, the rest probably being protein. The

ability of sea anemones to synthesize chitin is there by confirmed.

Dupont, N. and D. L. Aksnes (2010). "Simulation of optically conditioned retention and mass occurrences of Periphylla periphylla." J Plankton Res **32**(6): 773-783.

Jellyfish blooms are of increasing concern in many parts of the world, and in Norwegian fjords an apparent increase in mass occurrences of the deep water jellyfish Periphylla periphylla has attracted attention. Here we investigate the hypothesis that changes in the water column light attenuation might cause local retention and thereby facilitate mass occurrences. We use a previously tested individual-based model of light-mediated vertical migration in P. periphylla to simulate how retention is affected by changes in light attenuation. Our results suggest that light attenuation, in combination with advection, has a two-sided effect on retention and that three fjord categories can be defined. In category 1, increased light attenuation turns fjords into dark "deep-sea" environments which increase the habitat and retention of P. periphylla. In category 2, an optimal light attenuation facilitates the maximum retention and likelihood for mass occurrences. In category 3, further increase in light attenuation, however, shoals the habitat so that individuals are increasingly exposed to advection and this results in loss of individuals and decreased retention. This classification requires accurate determinations of the organism's light preference, the water column light attenuation and topographical characteristics affecting advection.

Dupriez, V. J., et al. (2002). "Aequorin-based functional assays for G-protein-coupled receptors, ion channels, and tyrosine kinase receptors." Receptors Channels **8**(5-6): 319-330.

Aequorin is a photoprotein originating from jellyfish, whose luminescent activity is dependent on the concentration of calcium ions. Due to the high sensitivity and low background linked to luminescent assays, as well as to its absence of toxicity and its large linear dynamic range, aequorin has been used as an intracellular calcium indicator since its discovery in the early 1960s. The first applications of aequorin involved its microinjection in cells. The cloning of its gene in 1985 opened the way to the stable expression of aequorin in cell lines or even entire organisms. Here we present the validation of aequorin as a functional assay for the screening of G-protein-coupled receptors, ion channels, and tyrosine kinase receptors, as well as for their pharmacological characterization in agonist and antagonist detection assays. We optimized our cell suspension-based assay and determined that the most sensitive assay was performed at room temperature, with mitochondrially expressed aequorin and using coelenterazine derivative h for reconstitution of aequorin. The robustness of the assay and the current availability of luminometers with integrated injectors allow aequorin to fit perfectly with high throughput functional assays requirements.

Dutto, M. S., et al. (2019). "Macroscale abundance patterns of hydromedusae in the temperate Southwestern Atlantic (27 degrees -56 degrees S)." PLoS One **14**(6): e0217628.

Gelatinous organisms are crucial components of marine ecosystems and some species imply social and economic consequences. However, certain geographic areas, such as the temperate Southwestern Atlantic (SWA, 27 degrees - 56 degrees S), remain understudied in terms of jellyfish ecological data. We analyzed 3,727 plankton samples collected along ~6.7 million km2 over a 31-year period (1983-2014) to determine the occurrence, abundance, and diversity patterns of hydromedusae in the SWA. Analyses were made at both community and species levels. Two abundance hot spots of hydromedusae were identified, where values up to 2,480 ind. m-3 were recorded between 2003 and 2014. Liriope tetraphylla and Obelia spp. were the main responsible for recurrent peaks. Diversity indexes were in the range of those published for temperate areas worldwide, and some coastal zones showed values that can be considered moderate to high for a temperate neritic region. The community analysis yielded 10 groups following previously determined biogeographic schemes throughout the study area. This work enhances the knowledge of hydromedusae in the SWA and provides essential information about the current global warming context and the gelatinous zooplankton data necessity.

Eales, J. G. (1997). "Iodine metabolism and thyroid-related functions in organisms lacking thyroid follicles: are thyroid hormones also vitamins?" Proc Soc Exp Biol Med **214**(4): 302-317.

Thyroid-related functions in organisms devoid of follicular thyroid tissue have been reviewed. In the lamprey, a primitive vertebrate, the larva concentrates iodide and synthesizes thyroid hormones (TH) by iodoperoxidase (IP)-mediated iodination of a thyroglobulin (TG)-like molecule in a subpharyngeal afollicular endostyle. The endostyle is the thyroid homolog, and it reorganizes into a follicular thyroid at metamorphosis to the adult. Ascidians and amphloxus, invertebrate protochordate relatives of vertebrates, also concentrate iodide and synthesize TH in a subpharyngeal afollicular endostyle, but the endostyle never transforms to follicles. Ascidian plasma contains L-thyroxine and its more biologically active derivative 3,5,3'-triiodo-L-thyronine, and TH receptors exist, but

TH effects are poorly understood. No other invertebrates possess an endostyle. Several invertebrates concentrate iodide at other sites and form protein-incorporated iodohistidines and iodotyrosines; however, de novo iodothyronine biosynthesis through IP-mediated TG iodination has not been established. Nevertheless, TH occur in invertebrates, and exogenous iodothyrosines or iodothyronines have effects on jellyfish, insects, and sea urchins. Furthermore, gut bacteria metabolize TH, and plants may synthesize TH by nonenzymatic oxidative iodination. Thus, TH occur in many organisms and, after ingestion and enteric absorption, can enter the food chain. Indeed, sea urchin larvae obtain TH required to induce metamorphosis from plant diatoms. Thyroid hormones can therefore have vitamin-like effects and, in conjunction with vitamin D, and possibly with other steroids, may be more aptly termed vitamones. Availability of exogenous TH has implications for models of invertebrate and vertebrate TH metabolism and iodine salvaging, and it may explain the prominent and probable ancestral role of peripheral mechanisms in regulating thyroidal status.

Eberhard, D. and H. Jockusch (2005). "Patterns of myocardial histogenesis as revealed by mouse chimeras." Dev Biol **278**(2): 336-346.

In order to study the pattern of clonal myocyte distribution during mammalian heart development, we have exploited embryo aggregation chimeras using, as cellular markers, an enhanced jellyfish green fluorescent protein (eGFP) transgene and a desmin-promoter-driven, nuclear-localized beta-galactosidase (nlacZ) knock-in. In neonatal, weanling, and adult chimeric atria and ventricles, irregularly formed patches of various sizes rather than highly dispersed cardiomyocytes were observed. Most of the smaller patches and single cardiomyocytes were found in spatial neighborhood of large patches. This indicated largely coherent clonal growth during myocardial histogenesis combined with tangential displacement or active migration of myocytes. The patterns of ventricular walls were simpler than those of the septum and the atria. In the adult heart, large myocardial volumes devoid of eGFP-positive cardiomyocytes indicated a lack of secondary immigration of blood-borne stem cells into the myocardium. The patterns of oligoclonal expansions revealed in this work might be helpful in detecting and analyzing cell-lineage-based pathological processes in the heart.

Ebert, M., et al. (2015). "Fauna and predator-prey relationships of Ettling, an actinopterygian fish-dominated Konservat-Lagerstatte from the Late Jurassic of southern Germany." PLoS One **10**(1): e0116140.

The newly recognized Konservat-Lagerstatte of Ettling (Bavaria), field site of the Jura-Museum Eichstatt (JME), is unique among Late Jurassic plattenkalk basins (Solnhofen region) in its abundant, extremely well preserved fossil vertebrates, almost exclusively fishes. We report actinopterygians (ginglymodins, pycnodontiforms, halecomorphs, aspidorynchiforms, "pholidophoriforms," teleosts); turtles; and non-vertebrates (echinoderms, arthropods, brachiopods, mollusks, jellyfish, sponges, biomats, plants) in a current faunal list. Ettling has yielded several new fish species (Bavarichthys incognitus; Orthogonikleithrus hoelli; Aspidorhynchus sanzenbacheri; Macrosemimimus fegerti). Upper and lower Ettling strata differ in faunal content, with the lower dominated by the small teleost Orthogonikleithrus hoelli (absent from the upper layers, where other prey fishes, Leptolepides sp. and Tharsis sp., occur instead). Pharyngeal and stomach contents of Ettling fishes provide direct evidence that Orthogonikleithrus hoelli was a primary food source during early Ettling times. Scarcity of ammonites and absence of vampyromorph coleoids at Ettling differ markedly from the situation at other nearby localities in the region (e.g., Eichstatt, Painten, Schamhaupten, the Mornsheim beds), where they are more common. Although the exact biochronological age of Ettling remains uncertain (lack of suitable index fossils), many Ettling fishes occur in other plattenkalk basins of Germany (e.g., Kelheim) and France (Cerin) dated as Late Kimmeridgian to Early Tithonian (eigeltingense horizon), suggesting a comparable geologic age. The Ettling deposits represent an independent basin within the larger Upper Jurassic "Solnhofen Archipelago", a shallow subtropical sea containing scattered islands, sponge-microbial and coral reefs, sandbars, and deeper basins on a vast carbonate platform along the northern margin of the Tethys Ocean.

Ebisawa, T., et al. (2009). "Crystallization and preliminary X-ray analysis of a monomeric mutant of Azami-Green (mAG), an Aequorea victoria green fluorescent protein-like green-emitting fluorescent protein from the stony coral Galaxea fascicularis." Acta Crystallogr Sect F Struct Biol Cryst Commun **65**(Pt 12): 1292-1295.

Monomeric Azami-Green (mAG) from the stony coral Galaxea fascicularis is the first monomeric green-emitting fluorescent protein that is not a derivative of Aequorea victoria green fluorescent protein (avGFP). mAG and avGFP are 27% identical in amino-acid sequence. Diffraction-quality crystals of recombinant mAG were obtained by the sitting-drop vapour-diffusion method using PEG 3350 as the

precipitant. The mAG crystal diffracted X-rays to 2.20 A resolution on beamline AR-NW12A at the Photon Factory (Tsukuba, Japan). The crystal belonged to space group P1, with unit-cell parameters a = 41.78, b = 51.72, c = 52.89 A, alpha = 90.96, beta = 103.41, gamma = 101.79 degrees. The Matthews coefficient (V (M) = 2.10 A (3) Da (-1)) indicated that the crystal contained two mAG molecules per asymmetric unit.

Echols, B. S., et al. (2016). "The use of ephyrae of a scyphozoan jellyfish, Aurelia aurita, in the aquatic toxicological assessment of Macondo oils from the Deepwater Horizon incident." Chemosphere **144**: 1893-1900.

Ephyrae of the scyphozoan jellyfish, Aurelia aurita, were evaluated in 96-hr acute toxicity tests for lethal response to Macondo crude oils from the Deepwater Horizon (DWH) incident in the Gulf of Mexico (GOM), Corexit 9500, and oil-dispersant mixtures. Water accommodated fractions (WAFs) of weathered and unweathered Macondo crude oils were not acutely toxic to ephyrae (LC50s > 100% WAF). The total PAHs (TPAHs), measured as the sum of 46 PAHs, averaged 21.1and 152 microg TPAH/L for WAFs of weathered and unweathered oil, respectively. Mortality was significantly (p = <0.0001) higher in the three highest exposure concentrations (184-736 microg TPAH/L) of chemically dispersed WAFs (CEWAF) compared to controls. Dispersant only tests resulted in a mean LC50 of 32.3 microL/L, which is in the range of previously published LC50s for marine zooplankton. Changes in appearance and muscle contractions were observed in organisms exposed to CEWAF dilutions of 12.5 and 25%, as early as 24 h post-exposure. Based on the results of these tests, crude oil alone did not cause significant acute toxicity; however, the presence of chemical dispersant resulted in substantial mortality and physical and behavioral abnormalities either due to an increase in hydrocarbons or droplet exposure.

Echols, B. S., et al. (2015). "Factors affecting toxicity test endpoints in sensitive life stages of native Gulf of Mexico species." Arch Environ Contam Toxicol **68**(4): 655-662.

Indigenous species are less commonly used in laboratory aquatic toxicity tests compared with standard test species due to (1) limited availability lack of requisite information necessary for their acclimation and maintenance under laboratory conditions and (2) lack of information on their sensitivity and the reproducibility of toxicity test results. As part of the Natural Resource Damage Assessment aquatic toxicity program in response to the Deepwater Horizon Oil incident (2010), sensitive life stages of native Gulf of Mexico species were evaluated in laboratory toxicity tests to determine the potential effects of the spill. Fish (n = 5) and invertebrates (n = 2) selected for this program include the following: the Florida pompano (Trachinotus carolinus), red drum (Sciaenops ocellatus), spotted sea trout (Cynoscion nebulosus), cobia (Rachycentron canadum), red porgy (Pagrus pagrus), blue crab (Callinectes sapidus), and the common moon jellyfish (Aurelia aurita). Initially in the program, to establish part of the background information, acute tests with reference toxicants (CdCl2, KCl, CuSO4) were performed with each species to establish data on intraspecies variability and test precision as well as identify other factors that may affect toxicity results. Median lethal concentration (LC50) values were calculated for each acute toxicity test with average LC50 values ranging from 248 to 862 mg/L for fish exposures to potassium chloride. Variability between test results was determined for each species by calculating the coefficient of variation (%CV) based on LC50 values. CVs ranged from 11.2 % for pompano (96-h LC50 value) to 74.8 % for red porgy 24-h tests. Cadmium chloride acute toxicity tests with the jellyfish A. aurita had the lowest overall CV of 3.6 %. By understanding acute toxicity to these native organisms from a compound with known toxicity ranges and the variability in test results, acute tests with nonstandard species can be better interpreted and used appropriately when determining risk.

Eckelbarger, K. J. and R. J. Larson (1993). "Ultrastructural study of the ovary of the sessile scyphozoan, Haliclystus octoradiatus (Cnidaria: Stauromedusae)." J Morphol **218**(2): 225-236.

An ultrastructural study of the ovary of the sessible jellyfish, Haliclystus octoradiatus, indicates that it is fundamentally different from that of other scyphozoans and is the most structurally complex within the class. Oocytes develop within a series of spherical, sac-like ovarian follicles consisting of an enlarged intercellular space between two layers of subumbrellar gastrodermis. Developing oocytes are largely restricted to a thin germinal epithelium at the periphery of each follicle and gradually migrate toward the lumen as they mature. Individual oocytes are surrounded by early germ cells and follicle-like accessory cells of presumed somatic origin. Similar folliclelike cells have not been described in the Cnidaria previously. Vitellogenesis appears to involve the combined activity of the Golgi complex and associated rough endoplasmic reticulum. Ovarian morphology may be helpful in deciphering phylogeneitc relationships within the Cnidaria. (c) 1993 Wiley-Liss, Inc.

Ehara, H., et al. (2015). "Crystal Structure of Okadaic Acid Binding Protein 2.1: A Sponge Protein Implicated in Cytotoxin Accumulation."

Chembiochem **16**(10): 1435-1439.

Okadaic acid (OA) is a marine polyether cytotoxin that was first isolated from the marine sponge Halichondria okadai. OA is a potent inhibitor of protein serine/threonine phosphatases (PP) 1 and 2A, and the structural basis of phosphatase inhibition has been well investigated. However, the role and mechanism of OA retention in the marine sponge have remained elusive. We have solved the crystal structure of okadaic acid binding protein 2.1 (OABP2.1) isolated from H. okadai; it has strong affinity for OA and limited sequence homology to other proteins. The structure revealed that OABP2.1 consists of two alpha-helical domains, with the OA molecule deeply buried inside the protein. In addition, the global fold of OABP2.1 was unexpectedly similar to that of aequorin, a jellyfish photoprotein. The presence of structural homologues suggested that, by using similar protein scaffolds, marine invertebrates have developed diverse survival systems adapted to their living environments.

Eichinger, J. M. and R. A. Satterlie (2014). "Organization of the ectodermal nervous structures in medusae: cubomedusae." Biol Bull **226**(1): 41-55.

At least two conducting systems are well documented in cubomedusae. A variably diffuse network of large neurons innervates the swim musculature and can be visualized immunohistochemically using antibodies against alpha- or beta-tubulin. Despite the non-specificity of these antibodies, multiple lines of evidence suggest that staining highlights the primary motor networks. These networks exhibit unique neurite distributions among the muscle sheets in that network density is greatest in the perradial frenula, where neurites are oriented in parallel with radial muscle fibers. This highly innervated, buttress-like muscle sheet may serve a critical role in the cubomedusan mechanism of turning. In scyphomedusae, a second subumbrellar network immunoreactive to antibodies against the neuropeptide FMRFamide innervates the swim musculature, but it is absent in cubomedusae. Immunoreactivity to FMRFamide in cubomedusae is mostly limited to a small network of neurons in the pacemaker region of the rhopalia, the pedalial apex at the nerve ring junction, and a few neuron tracts in the nerve ring. However, FMRFamide-immunoreactive networks, as well as tubulin-immunoreactive networks, are nearly ubiquitous outside of the swim muscle sheets in the perradial smooth muscle bands, manubrium, pedalia, and tentacles. Here we describe in detail the peripheral nerve nets of box jellyfish on the basis of immunoreactivity to the antibodies above. Our results offer insight into how the peripheral nerve nets are organized to produce the complex swimming, feeding, and defensive behaviors observed in cubomedusae.

Ekstrom, P., et al. (2008). "Immunohistochemical evidence for multiple photosystems in box jellyfish." Cell Tissue Res **333**(1): 115-124.

Cubomedusae (box jellyfish) possess a remarkable visual system with 24 eyes distributed in four sensory structures termed rhopalia. Each rhopalium is equipped with six eyes: two pairs of pigment cup eyes and two unpaired lens eyes. Each eye type probably captures specific features of the visual environment. To investigate whether multiple types of photoreceptor cells are present in the rhopalium, and whether the different eye types possess different types of photoreceptors, we have used immunohistochemistry with a range of vertebrate opsin antibodies to label the photoreceptors, and electroretinograms (ERG) to determine their spectral sensitivity. All photoreceptor cells of the two lens eyes of the box jellyfish Tripedalia cystophora and Carybdea marsupialis displayed immunoreactivity for an antibody directed against the zebrafish ultraviolet (UV) opsin, but not against any of eight other rhodopsin or cone opsin antibodies tested. In neither of the two species were the pigment cup eyes immunoreactive for any of the opsin antibodies. ERG analysis of the Carybdea lower lens eyes demonstrated a single spectral sensitivity maximum at 485 nm suggesting the presence of a single opsin type. Our data demonstrate that the lens eyes of box jellyfish utilize a single opsin and are thus color-blind, and that there is probably a different photopigment in the pigment cup eyes. The results support our hypothesis that the lens eyes and the pigment cup eyes of box jellyfish are involved in different and specific visual tasks.

El-Shemy, H. A., et al. (2009). "The role of green fluorescent protein (GFP) in transgenic plants to reduce gene silencing phenomena." Curr Issues Mol Biol **11 Suppl 1**: i21-28.

The green fluorescent protein (GFP) of jellyfish (Aequorea victoria) has significant advantages over other reporter genes, because expression can be detected in living cells without any substrates. Recently, epigenetic phenomena are important to consider in plant biotechnology experiments for elucidate unknown mechanism. Therefore, soybean immature cotyledons were generated embryogenesis cells and engineered with two different gene constructs (pHV and pHVS) using gene gun method. Both constructs contain a gene conferring resistance to hygromycin (hpt) as a selective marker and a modified glycinin (11S globulin) gene (V3-1) as a target. However, sGFP (S65T) as a reporter gene was used only in pHVS as a reporter gene for study the relation

between using sGFP (S65T) and gene silencing phenomena. Fluorescence microscopic was used for screening after the selection of hygromycin, identified clearly the expression of sGFP (S65T) in the transformed soybean embryos bombarded with the pHVS construct. Protein analysis was used to detect gene expression overall seeds using SDS-PAGE. Percentage of gene down regulation was highly in pHV construct compared with pHVS. Thus, sGFP (S65T) as a reporter gene in vector system may be play useful role for transgenic evaluation and avoid gene silencing in plants for the benefit of plant transformation system.

Elsliger, M. A., et al. (1999). "Structural and spectral response of green fluorescent protein variants to changes in pH." Biochemistry **38**(17): 5296-5301.

The green fluorescent protein (GFP) from the jellyfish Aequorea victoria has become a useful tool in molecular and cell biology. Recently, it has been found that the fluorescence spectra of most mutants of GFP respond rapidly and reversibly to pH variations, making them useful as probes of intracellular pH. To explore the structural basis for the titration behavior of the popular GFP S65T variant, we determined high-resolution crystal structures at pH 8.0 and 4.6. The structures revealed changes in the hydrogen bond pattern with the chromophore, suggesting that the pH sensitivity derives from protonation of the chromophore phenolate. Mutations were designed in yellow fluorescent protein (S65G/V68L/S72A/T203Y) to change the solvent accessibility (H148G) and to modify polar groups (H148Q, E222Q) near the chromophore. pH titrations of these variants indicate that the chromophore pKa can be modulated over a broad range from 6 to 8, allowing for pH determination from pH 5 to pH 9. Finally, mutagenesis was used to raise the pKa from 6.0 (S65T) to 7.8 (S65T/H148D). Unlike other variants, S65T/H148D exhibits two pH-dependent excitation peaks for green fluorescence with a clean isosbestic point. This raises the interesting possibility of using fluorescence at this isosbestic point as an internal reference. Practical real time in vivo applications in cell and developmental biology are proposed.

Endean, R. (1987). "Separation of two myotoxins from nematocysts of the box jellyfish (Chironex fleckeri)." Toxicon **25**(5): 483-492.

Two myotoxins, both lethal to mice by i.v. injection, were obtained by chromatography on Sephadex G-200 of material released from isolated microbasic mastigophores of C. fleckeri. Both toxins elicit contractures of skeletal (diaphragm) musculature of the rat and of smooth (ileum and vas deferens) and atrial musculature of the guinea-pig, although consistent differences in the parameters of the contractures of each muscle type elicited by the two toxins are shown. Moreover, one toxin, with a molecular weight of approximately 150,000, also elicits activity on crustacean (barnacle) musculature, whilst the other toxin, with a molecular weight of approximately 600,000, elicits no activity in barnacle musculature at the concentrations tested. The toxins are labile when released from nematocysts and they lose all myotoxic activity within 3 days at 5 degrees C. They can also be isolated chromatographically from crude extracts of the contents of mixed nematocysts of C. fleckeri. They are considered to be the principal toxins injected by C. fleckeri during nematocyst discharge and appear to be different from the C. fleckeri toxins described by other workers.

Endean, R., et al. (1993). "Toxins from the box-jellyfish Chironex fleckeri." Toxicon **31**(4): 397-410.

Two myotoxins (T1 and T2) with mol. wts of approximately 600,000 and 150,000, respectively, and a haemolysin (T3) with a mol. wt of approximately 70,000 were isolated from the crude nematocyst venom of C. fleckeri by the use of Sephadex G-200 chromatography. A neurotoxic fraction (T4) and a haemolytic fraction (T5) containing proteins with apparent mol. wts of approximately 150,000 and 70,000, respectively, were also isolated by Sephadex chromatography from crude extracts of tentacular material from which nematocysts had been removed. The three nematocyst toxins and the two toxic fractions from tentacle extracts were lethal to mice on i.v. injection. After SDS-PAGE the myotoxins T1 and T2 yielded similar major bands corresponding with mol. wts different from those yielded by T3 and the toxic tentacle fractions. T1 and T2 appeared to be comprised of aggregations of subunits with mol. wts of approximately 18,000. On HPLC, crude nematocyst venom and the nematocyst toxins T1 and T2 lost their myotoxic properties. The need for thorough removal of extraneous tentacular material from isolated nematocysts, the need for effective rupture of nematocysts, the need to counter the lability of the nematocyst venom and the need to use myotoxicity as a criterion of venom activity if the active components of the venom are to be purified and characterized are emphasized.

Endean, R. and D. J. Sizemore (1988). "The effectiveness of antivenom in countering the actions of box-jellyfish (Chironex fleckeri) nematocyst toxins in mice." Toxicon **26**(5): 425-431.

The neutralizing ability of commercially available antivenom prepared against 'milked' box-jellyfish (Chironex fleckeri) venom was tested intravenously in mice against crude nematocyst venom

obtained by crushing isolated nematocysts and against each of two lethal toxins (T1 and T2) present in this venom. The in vitro neutralizing ability of the antivenom against crude venom was reduced markedly compared with its reported neutralizing ability against 'milked' venom whilst the in vivo neutralizing ability of the antivenom tested in both prophylactic and rescue experiments involving crude nematocyst venom was reduced approximately threefold. When tested in vitro and prophylactically in vivo the neutralizing ability of the antivenom was much more pronounced against T2 than against T1. This finding was in accord with the view that T1 was absent from the 'milked' venom against which the antivenom was prepared. Doses of crude venom in excess of twice the lethal dose killed mice within 2-3 min emphasizing the need for speed in the administration of antivenom.

Ender, A. and B. Schierwater (2003). "Placozoa are not derived cnidarians: evidence from molecular morphology." Mol Biol Evol **20**(1): 130-134.

The phylum Placozoa is represented by a single known species, Trichoplax adhaerens, a tiny marine organism that represents the most simple metazoan bauplan. Because of the latter, placozoans were originally considered the most basal metazoan phylum. A misinterpretation of the life cycle at the turn of the century and some more recent molecular phylogenetic analyses have placed Trichoplax as a derived species within the Cnidaria. The latter hypothesis assumes that the primitive organization of the Placozoa is the result of secondary reduction. Here we compare the molecular morphology of the predicted 16S rDNA structure and the mitochondrial genome between Trichoplax and representatives of all four cnidarian classes. Trichoplax shares a circular mtDNA molecule as a plesiomorphy with all other metazoans except for the derived cnidarian classes Hydrozoa, Scyphozoa, and Cubozoa. The predicted secondary structure of the 16S rRNA molecule differs substantially between Trichoplax and cnidarians, particularly with respect to the number and length of stem and loop regions. The new molecular morphological characters provide compelling evidence that Trichoplax is not a derived (medusozoan) cnidarian. Furthermore, it was found that the mitochondrial genome in Cubozoa consists of four linear molecules instead of a single circular molecule or two linear molecules, suggesting that the cubozoans may represent the most derived cnidarian group.

Endres, C. S. and K. J. Lohmann (2012). "Perception of dimethyl sulfide (DMS) by loggerhead sea turtles: a possible mechanism for locating high-productivity oceanic regions for foraging." J Exp Biol **215**(Pt 20): 3535-3538.

During their long-distance migrations, sea turtles of several species feed on jellyfish and other invertebrates that are particularly abundant in ocean regions characterized by high productivity. An ability to distinguish productive oceanic regions from other areas, and to concentrate foraging activities in locations where prey density is highest, might therefore be adaptive. The volatile compound dimethyl sulfide (DMS) accumulates in the air above productive ocean areas such as upwelling and frontal zones. In principle, DMS might therefore serve as an indicator of high prey density for turtles. To determine whether turtles perceive DMS, juvenile loggerhead sea turtles (Caretta caretta) were placed into a water-filled arena in which DMS and other odorants could be introduced to the air above the water surface. Turtles exposed to air that had passed over a cup containing 10 nmol l (-1) DMS spent more time at the surface with their noses out of the water than control turtles, which were exposed to air that had passed over a cup containing distilled water. Odors that do not occur in the sea (cinnamon, jasmine and lemon) did not elicit increased surface time, implying that the response to DMS is unlikely to reflect a generalized response to any novel odor. The results demonstrate for the first time that sea turtles can detect DMS, an ability that might enable the identification of favorable foraging areas.

Engel, U., et al. (2002). "Nowa, a novel protein with minicollagen Cys-rich domains, is involved in nematocyst formation in Hydra." J Cell Sci **115**(Pt 20): 3923-3934.

The novel protein Nowa was identified in nematocysts, explosive organelles of Hydra, jellyfish, corals and other CNIDARIA: Biogenesis of these organelles is complex and involves assembly of proteins inside a post-Golgi vesicle to form a double-layered capsule with a long tubule. Nowa is the major component of the outer wall, which is formed very early in morphogenesis. The high molecular weight glycoprotein has a modular structure with an N-terminal sperm coating glycoprotein domain, a central C-type lectin-like domain, and an eightfold repeated cysteine-rich domain at the C-terminus. Interestingly, the cysteine-rich domains are homologous to the cysteine-rich domains of minicollagens. We have previously shown that the cysteines of these minicollagen cysteine-rich domains undergo an isomerization process from intra- to intermolecular disulfide bonds, which mediates the crosslinking of minicollagens to networks in the inner wall of the capsule. The minicollagen cysteine-rich domains present in both proteins provide a potential link between Nowa in the outer wall and minicollagens in the inner wall. We propose a model for nematocyst formation that integrates cytoskeleton rearrangements

around the post-Golgi vesicle and protein assembly inside the vesicle to generate a complex structure that is stabilized by intermolecular disulfide bonds.

Engel, U., et al. (2001). "A switch in disulfide linkage during minicollagen assembly in Hydra nematocysts." EMBO J **20**(12): 3063-3073.

The smallest known collagens with only 14 Gly-X-Y repeats referred to as minicollagens are the main constituents of the capsule wall of nematocysts. These are explosive organelles found in Hydra, jellyfish, corals and other Cnidaria. Minicollagen-1 of Hydra recombinantly expressed in mammalian 293 cells contains disulfide bonds within its N- and C-terminal Cys-rich domains but no interchain cross-links. It is soluble and self-associates through non-covalent interactions to form 25-nm-long trimeric helical rod-like molecules. We have used a polyclonal antibody prepared against the recombinant protein to follow the maturation of minicollagens from soluble precursors present in the endoplasmic reticulum and post-Golgi vacuoles to the disulfide-linked insoluble assembly form of the wall. The switch from intra- to intermolecular disulfide bonds is associated with 'hardening' of the capsule wall and provides an explanation for its high tensile strength and elasticity. The process is comparable to disulfide reshuffling between the NC1 domains of collagen IV in mammalian basement membranes.

Enoki, S., et al. (2004). "Acid denaturation and refolding of green fluorescent protein." Biochemistry **43**(44): 14238-14248.

Green fluorescent protein from the jellyfish Aequorea victoria can serve as a good model protein to understand protein folding in a complex environment with molecular chaperones and other macromolecules such as those in biological cells, but little is known about the detailed mechanisms of the in vitro folding of green fluorescent protein itself. We therefore investigated the kinetic refolding of a mutant (F99S/M153T/V163A) of green fluorescent protein, which is known to mature more efficiently than the wild-type protein, from the acid-denatured state; refolding was observed by chromophore fluorescence, tryptophan fluorescence, and far-UV CD, using a stopped-flow technique. In this study, we demonstrated that the kinetics of the refolding of the mutant have at least five kinetic phases and involve nonspecific collapse within the dead time of a stopped-flow apparatus and the subsequent formation of an on-pathway intermediate with the characteristics of the molten globule state. We also demonstrated that the slowest phase and a major portion of the second slowest phase were rate-limited by slow prolyl isomerization in the intermediate state, and this rate limitation accounts for a major portion of the observed kinetics in the folding of green fluorescent protein.

Enterina, J. R., et al. (2015). "Emerging fluorescent protein technologies." Curr Opin Chem Biol **27**: 10-17.

Fluorescent proteins (FPs), such as the Aequorea jellyfish green FP (GFP), are firmly established as fundamental tools that enable a wide variety of biological studies. Specifically, FPs can serve as versatile genetically encoded markers for tracking proteins, organelles, or whole cells, and as the basis for construction of biosensors that can be used to visualize a growing array of biochemical events in cells and tissues. In this review we will focus on emerging applications of FPs that represent unprecedented new directions for the field. These emerging applications include new strategies for using FPs in biosensing applications, and innovative ways of using FPs to manipulate protein function or gene expression.

Entzminger, K. C., et al. (2012). "The Skp chaperone helps fold soluble proteins in vitro by inhibiting aggregation." Biochemistry **51**(24): 4822-4834.

The periplasmic seventeen kilodalton protein (Skp) chaperone has been characterized primarily for its role in outer membrane protein (OMP) biogenesis, during which the jellyfish-like trimeric protein encapsulates partially folded OMPs, protecting them from the aqueous environment until delivery to the BAM outer membrane protein insertion complex. However, Skp is increasingly recognized as a chaperone that also assists in folding soluble proteins in the bacterial periplasm. In this capacity, Skp coexpression increases the active yields of many recombinant proteins and bacterial virulence factors. Using a panel of single-chain antibodies and a single-chain T-cell receptor (collectively termed scFvs) possessing varying stabilities and biophysical characteristics, we performed in vivo expression and in vitro folding and aggregation assays in the presence or absence of Skp. For Skp-sensitive scFvs, the presence of Skp during in vitro refolding assays reduced aggregation but did not alter the observed folding rates, resulting in a higher overall yield of active protein. Of the proteins analyzed, Skp sensitivity in all assays correlated with the presence of folding intermediates, as observed with urea denaturation studies. These results are consistent with Skp acting as a holdase, sequestering partially folded intermediates and thereby preventing aggregation. Because not all soluble proteins are sensitive to Skp coexpression, we hypothesize that the presence of a long-lived protein folding intermediate renders a

protein sensitive to Skp. Improved understanding of the bacterial periplasmic protein folding machinery may assist in high-level recombinant protein expression and may help identify novel approaches to block bacterial virulence.

Eom, S. H., et al. (2016). "Synthesis of Phthalimide Derivatives as Potential PPAR-gamma Ligands." Mar Drugs **14**(6).

Paecilocin A, a phthalide derivative isolated from the jellyfish-derived fungus Paecilomyces variotii, activates PPAR-gamma (Peroxisome proliferator-activated receptor gamma) in rat liver Ac2F cells. Based on a SAR (Structure-activity relationships) study and in silico analysis of paecilocin A-mimetic derivatives, additional N-substituted phthalimide derivatives were synthesized and evaluated for PPAR-gamma agonistic activity in both murine liver Ac2F cells and in human liver HepG2 cells by luciferase assay, and for adipogenic activity in 3T3-L1 cells. Docking simulation indicated PD6 was likely to bind most strongly to the ligand binding domain of PPAR-gamma by establishing crucial H-bonds with key amino acid residues. However, in in vitro assays, PD1 and PD2 consistently displayed significant PPAR-gamma activation in Ac2F and HepG2 cells, and adipogenic activity in 3T3-L1 preadipocytes.

Epel, B. L., et al. (1996). "Plant virus movement protein dynamics probed with a GFP-protein fusion." Gene **173**(1 Spec No): 75-79.

A genetic fusion between the gene encoding green fluorescent protein (GFP) from the jellyfish Aequorea victoria, with that of the Ob-tobamovirus movement protein (MP) resulted in the expression of a fluorescent fusion protein (MP::GFP) that was fully biologically active in mediating the cell-to-cell spread of the Ob-virus. The MP::GFP fusion was used to follow in planta the subcellular trafficking of MP. GFP-tagged MP was transiently expressed and found to be associated with several subcellular compartments and structures including trans-wall structures, presumably plasmodesmata, and filament structures. The MP::GFP fusion can be used to monitor MP association with host proteins and structures, and for the isolation of interacting host components.

Epstein, H. E., et al. (2016). "Fine-scale detection of pollutants by a benthic marine jellyfish." Mar Pollut Bull **107**(1): 340-346.

Local sources of pollution can vary immensely on small geographic scales and short time frames due to differences in runoff and adjacent land use. This study examined the rate of uptake and retention of trace metals in Cassiopea maremetens, a benthic marine jellyfish, over a short time frame and in the presence of multiple pollutants. This study also validated the ability of C. maremetens to uptake metals in the field. Experimental manipulation demonstrated that metal accumulation in jellyfish tissue began within 24h of exposure to treated water and trended for higher accumulation in the presence of multiple pollutants. C. maremetens was found to uptake trace metals in the field and provide unique signatures among locations. This fine-scale detection and rapid accumulation of metals in jellyfish tissue can have major implications for both biomonitoring and the trophic transfer of pollutants through local ecosystems.

Eremeeva, E. V., et al. (2016). "Transient-state kinetic analysis of complex formation between photoprotein clytin and GFP from jellyfish Clytia gregaria." FEBS Lett **590**(3): 307-316.

Luminous organisms use different protein-mediated strategies to modulate light emission color. Here, we report the transient-state kinetic studies of the interaction between photoprotein clytin from Clytia gregaria and its antenna protein, cgreGFP. We propose that cgreGFP forms a transient complex with Ca (2+)-bound clytin before the excited singlet state of the coelenteramide product is formed. From the spectral distribution and donor-acceptor separation distance, we infer that clytin reaction intermediates may interact only with the middle side part of cgreGFP.

Eric Wu, L., et al. (2018). "In-Vitro Evaluation of Cardiac Energetics and Coronary Flow with Volume Displacement and Rotary Blood Pumps." Conf Proc IEEE Eng Med Biol Soc **2018**: 5277-5281.

Bridge to recovery with left ventricular assist device (LVAD) support has been more prominent with volume displacement pumps (VDPs) than with rotary blood pumps (RBPs), which may be due to VDPs providing greater ventricular unloading and coronary artery flow. To compare ventricular unloading and coronary flow of VDPs and RBPs in a repeatable environment, a physiologic coronary circulation was added to a pre-existing mock circulatory loop. In this study, a physiologic coronary circulation, mimicking a healthy or diseased auto-regulatory response was implemented in a mock circulatory loop. Using the mock circulation loop, a VDP with original (Bjork-Shiley) and then replacement (jellyfish) valves was operated in clinically recommended modes and compared to full and partial assist RBP operating at constant speed and rapid speed modulated modes. The Bjork-Shiley VDP resulted in increased pressure-volume area, which resulted in greater coronary artery flow when compared to the improved jellyfish valves. Full assist RBP support reduced left ventricular stroke work, pressure-volume area and coronary flow compared to partial assist, whilst the effect of speed

modulation modes was not as significant. Of all LVAD operating modes, the counter-pulsed VDP with jellyfish valves demonstrated the greatest reduction in pressure-volume area and improved coronary flow. This study provides a basis for further investigation into RBP speed modulation profiles to match the improved haemodynamic performance of VDPs.

Eriksen, E., et al. (2012). "Biomass of scyphozoan jellyfish, and its spatial association with 0-group fish in the Barents Sea." PLoS One **7**(3): e33050.

An 0-group fish survey is conducted annually in the Barents Sea in order to estimate fish population abundance. Data on jellyfish by-catch have been recorded since 1980, although this dataset has never been analysed. In recent years, however, the ecological importance of jellyfish medusae has become widely recognized. In this paper the biomass of jellyfish (medusae) in 0-60 m depths is calculated for the period 1980-2010. During this period the climate changed from cold to warm, and changes in zooplankton and fish distribution and abundance were observed. This paper discusses the less well known ecosystem component; jellyfish medusae within the Phylum Cnidaria, and their spatial and temporal variation. The long term average was ca. 9x10(8) kg, with some years showing biomasses in excess of 5x10(9) kg. The biomasses were low during 1980s, increased during 1990s, and were highest in early 2000s with a subsequent decline. The bulk of the jellyfish were observed in the central parts of the Barents Sea, which is a core area for most 0-group fishes. Jellyfish were associated with haddock in the western area, with haddock and herring in the central and coastal area, and with capelin in the northern area of the Barents Sea. The jellyfish were present in the temperature interval 1 degrees C<T<10 degrees C, with peak densities at ca. 5.5 degrees C, and the greatest proportion of the jellyfish occurring between 4.0-7.0 degrees C. It seems that the ongoing warming trend may be favourable for Barents Sea jellyfish medusae; however their biomass has showed a recent moderate decline during years with record high temperatures in the Barents Sea. Jellyfish are undoubtedly an important component of the Barents Sea ecosystem, and the data presented here represent the best summary of jellyfish biomass and distribution yet published for the region.

Eriksson, S., et al. (1996). "Green fluorescent protein as a tool for screening recombinant baculoviruses." J Virol Methods **59**(1-2): 127-133.

The gene encoding the green fluorescent protein (GFP) from the jellyfish Aequorea victoria, ligated to the honeybee melittin signal peptide-encoding sequence, was inserted under transcriptional control of the polyhedrin promoter of the Autographa californica nuclear polyhedrosis virus and expressed in the Spodoptera frugiperda insect cell line Sf9 during viral infection. The recombinant green fluorescent protein was identified by SDS-PAGE gel electrophoresis followed by Coomassie blue staining of lysates from the recombinant baculovirus infected insect cells. Emission and excitation scanning of the recombinant baculovirus infected insect cells gave an emission maximum of 509 nm and excitation maximum of 398 nm. The GFP protein expressed was also detected in infected insect cells by a flow cytometer analysis.

Escriou, V., et al. (1998). "Cationic lipid-mediated gene transfer: analysis of cellular uptake and nuclear import of plasmid DNA." Cell Biol Toxicol **14**(2): 95-104.

Cationic lipids are widely used for gene transfer in vitro and show promise as vectors for in vivo gene therapy applications. However, there is limited understanding of the cellular mechanisms involved in nonviral gene transfer. We investigated two major steps that could be limiting barriers to cationic lipid-mediated gene transfer in vitro. We used a fluorescent plasmid to study the cellular uptake and the intracellular fate of lipoplexes during in vitro transfection of fibroblast cells and found that 100% of the cells take up lipoplexes. The intracellular staining observed with lipoplexes was clearly different from that obtained with endocytosed fluorescent dextran. This suggests that cells readily take up lipoplexes by a mechanism that could be different from endocytosis in our conditions. However, the escape of DNA from intracellular vesicles could be a major limiting barrier to gene transfer. Direct injection of plasmid DNA into the nucleus and cytoplasm of cells indicated that DNA traffic from the cytoplasm to the nucleus might be also an important limiting step.

Estes, A. M., et al. (2003). "Localization and quantification of carbonic anhydrase activity in the symbiotic Scyphozoan Cassiopea xamachana." Biol Bull **204**(3): 278-289.

The relationship between density and location of zooxanthellae and levels of carbonic anhydrase (CA) activity was examined in Cassiopea xamachana. In freshly collected symbiotic animals, high densities of zooxanthellae corresponded with high levels of CA activity in host bell and oral arm tissues. Bleaching resulted in a significant loss of zooxanthellae and CA activity. Recolonization resulted in full restoration of zooxanthellar densities but only partial restoration of CA activity. High levels of CA activity were also seen in structures with inherently higher zooxanthellar densities, such as oral arm tissues. Similarly, the oral epidermal layer of bell tissue had significantly higher

zooxanthellar densities and levels of CA activity than did aboral bell tissues. Fluorescent labeling, using 5-dimethylaminonapthalene-1-sulfonamide (DNSA) also reflected this tight-knit relationship between the presence and density of zooxanthellae, as DNSA-CA fluorescence intensity was greatest in host oral epithelial cells directly overlying zooxanthellae. However, the presence and density of zooxanthellae did not always correspond with enzyme activity levels. A transect of bell tissue from the margin to the manubrium revealed a gradient of CA activity, with the highest values at the bell margin and the lowest at the manubrium, despite an even distribution of zooxanthellae. Thus, abiotic factors may also influence the distribution of CA and the levels of CA activity.

Estes, P. S., et al. (2000). "Synaptic localization and restricted diffusion of a Drosophila neuronal synaptobrevin--green fluorescent protein chimera in vivo." J Neurogenet **13**(4): 233-255.

Fluorescent markers for subcellular compartments in Drosophila neurons should allow one to combine genetic mutant analysis with visualization of subcellular structures in vivo. Here we describe an analysis of two markers which may be used to observe different compartments of live Drosophila synapses. Soluble jellyfish green fluorescent protein (GFP) expressed at high levels in neurons diffuses freely in the neuronal cytosol as evidenced by confocal microscopy and fluorescence recovery from photobleaching experiments. Thus, the distribution pattern of soluble GFP in motor axons and larval motor terminals indicates the expected distribution for diffusible presynaptic molecules. In contrast to GFP, a neurally expressed neuronal synaptobrevin-GFP chimera (n-syb GFP) is transported down axons and specifically localized to nerve terminals. We demonstrate that n-syb GFP labels synaptic-vesicle membrane at larval motor terminals by documenting its restriction to presynaptic varicosities, its colocalization with synaptic vesicle antigens, and its redistribution in Drosophila shits1 mutant nerve terminals transiently depleted of synaptic vesicles. Surprisingly, n-syb GFP expressed in muscle is concentrated at the subsynaptic reticulum (SSR), postsynaptic infoldings of muscle plasma membrane. We suggest, using different membrane markers, that this apparent postsynaptic enrichment simply reflects a concentration of plasma membrane in the SSR, rather than a selective targeting of n-syb GFP to postsynaptic sites. Utilities and implications of these studies are demonstrated or discussed.

Exton, D. R., et al. (1989). "Cold packs: effective topical analgesia in the treatment of painful stings by Physalia and other jellyfish." Med J Aust **151**(11-12): 625-626.

A study has shown that, when applied to Physalia ("bluebottle") jellyfish stings, cold packs are effective as topical analgesia in the relief of mild-to-moderate skin pain. The application of ice also has been shown to be effective for topical analgesia in a number of other jellyfish stings, including by Cyanea ("hair jellyfish"), Tamoya sp. ("Moreton Bay stinger" or "fire jelly") and Carybdea rastoni ("jimble") as well as by Physalia. In the current state of knowledge, cold packs or ice are recommended as the first-aid treatment for jellyfish stings with local skin pain.

Fabregat, M. E., et al. (1998). "Site-directed mutations of the FAD-linked glycerophosphate dehydrogenase gene impairs the mitochondrial anchoring of the enzyme in transfected COS-7 cells." Biochem Biophys Res Commun **252**(1): 173-177.

COS-7 cells were transfected with the green fluorescent protein (GFP) of Aequorea victoria, human mitochondrial FAD-linked glycerophosphate dehydrogenase (mGDH), a mGDHwt-EGFP construct, or two mutant mGDH-proteins fused with EGFP. The site of mutation was selected to affect cationic amino acids in the peptide signal sequence currently believed to play a key role in the subcellular distribution of mitochondrial proteins. All proteins were suitably expressed in the COS-7 cells. However, an increase in mGDH enzymatic activity above the control value in non-transfected COS-7 cell homogenates was only observed in cells transfected with mGDH, indicating that the catalytic activity of mGDH was masked in fused proteins. Confocal microscopy documented that, in the cells transfected with the mGDHwt-EGFP construct, the fusion protein was located exclusively in mitochondria, this contrasting with the nuclear labelling of cells expressing the green fluorescent protein alone. The mitochondrial anchoring of the mutated mGDH fused protein was altered, this alteration being most obvious in the mGDH313233-EGFP mutant. These findings raise the idea that a conformation change of the mGDH protein, as resulting from either an inherited or acquired alteration of its amino acid sequence, may affect its subcellular distribution and, hence, modify its immunogenic potential.

Fagan, T. F., et al. (1993). "Cloning, expression and sequence analysis of cDNA for the Ca (2+)-binding photoprotein, mitrocomin." FEBS Lett **333**(3): 301-305.

The primary structure of mitrocomin consists of 190 amino acid residues, with three Ca (2+)-binding sites and a tyrosine residue at the C-terminus. Mitrocomin shows an amino acid sequence homology of 67.9% and 60.7% when compared with aequorin

and clytin, respectively. The amino acid residues Cys152, His58, His169, Trp12, Trp86, Trp108, Trp129 and Trp173 are conserved in all three photoproteins, suggesting that they play a role in light emission.

Faimali, M., et al. (2014). "Ephyra jellyfish as a new model for ecotoxicological bioassays." Mar Environ Res **93**: 93-101.

The aim of this study was a preliminary investigation on the possibility of using the ephyra of Scyphozoan jellyfish Aurelia aurita (Linnaeus, 1758), the common moon jellyfish, as an innovative model organism in marine ecotoxicology. A series of sequential experiments have been carried out in laboratory in order to investigate the influence of different culturing and methodological parameters (temperature, photoperiod, ephyrae density and age) on behavioural end-points (% of Frequency of Pulsations) and standardize a testing protocol. After that, the organisms have been exposed to two well known reference toxic compounds (Cadmium Nitrate and SDS) in order to analyse the acute and behavioural responses during static exposure. Results of this work indicate that the proposed behavioural end-point, frequency of pulsations (Fp), is an easily measurable one and can be used coupled with an acute one (immobilization) and that ephyrae of jellyfish are very promising model organisms for ecotoxicological investigation.

Fan, J., et al. (2013). "Effects of collagen and collagen hydrolysate from jellyfish umbrella on histological and immunity changes of mice photoaging." Nutrients **5**(1): 223-233.

Jellyfish collagen (JC) was extracted from jellyfish umbrella and hydrolyzed to prepare jellyfish collagen hydrolysate (JCH). The effects of JC and JCH on UV-induced skin damage of mice were evaluated by the skin moisture, microscopic analyses of skin and immunity indexes. The skin moisture analyses showed that moisture retention ability of UV-induced mice skin was increased by JC and JCH. Further histological analysis showed that JC and JCH could repair the endogenous collagen and elastin protein fibers, and could maintain the natural ratio of type I to type III collagen. The immunity indexes showed that JC and JCH play a role in enhancing immunity of photoaging mice in vivo. JCH showed much higher protective ability than JC. These results suggest that JCH as a potential novel antiphotoaging agent from natural resources.

Fan, L., et al. (2017). "Activation of Na (+)/H (+) exchanger other than formation of transmembrane pore underlies the cytotoxicity of nematocyst venom from Chrysaora helvola Brandt jellyfish." Toxicon **133**: 162-168.

We previously reported unexpected apoptosis-like cell death induced by nematocyst venom (NV) from Chrysaora helvola Brandt (C. helvola) jellyfish. To assess whether the pore formation mechanism underlay the action of NV, the change in cell membrane permeability was studied in both chicken erythrocytes and human CNE-2 cells. Initially, paradoxical results were derived from osmoprotectant protection assays. Polyethylene glycol (PEG)2000, which completely inhibited the NV induced hemolysis, failed to protect CNE-2 cells. Detailed experiments showed that PEG protection from hemolysis is concentration dependent and indicated caution when estimating the pore size formed by NV with the osmotic protection method. NV-treated CNE-2 cells remained impermeable to dyes with various molecular weights (MWs) (622.6-40,000 Da). Furthermore, membrane depolarization and selective permeability to Na (+) other than K (+) were induced in CNE-2 cells. No oxidative damage to the cell membrane was detected. Amiloride, an inhibitor of Na (+)/H (+) exchanger (NHE), substantially protected both CNE-2 cells and erythrocytes from NV. Combined with the previously reported increase in intracellular pH, we supposed that NV activated plasma membrane NHE without forming transmembrane pores. Interestingly, glutathione (GSH) showed significant protection to CNE-2 cells while potentiating the hemolytic power of NV. This finding may suggest a key role of reactive oxygen species (ROS) in the cytotoxicity of NV. To the best of our knowledge, this is the first report that a hemolytic jellyfish venom acts through NHE in a manner other than compromising membrane integrity. The current work provides new insight into the arsenal of toxic jellyfishes.

Fang, C., et al. (2009). "Mapping GFP structure evolution during proton transfer with femtosecond Raman spectroscopy." Nature **462**(7270): 200-204.

Tracing the transient atomic motions that lie at the heart of chemical reactions requires high-resolution multidimensional structural information on the timescale of molecular vibrations, which commonly range from 10 fs to 1 ps. For simple chemical systems, it has been possible to map out in considerable detail the reactive potential-energy surfaces describing atomic motions and resultant reaction dynamics, but such studies remain challenging for complex chemical and biological transformations. A case in point is the green fluorescent protein (GFP) from the jellyfish Aequorea victoria, which is a widely used gene expression marker owing to its efficient bioluminescence. This feature is known to arise from excited-state proton

transfer (ESPT), yet the atomistic details of the process are still not fully understood. Here we show that femtosecond stimulated Raman spectroscopy provides sufficiently detailed and time-resolved vibrational spectra of the electronically excited chromophore of GFP to reveal skeletal motions involved in the proton transfer that produces the fluorescent form of the protein. In particular, we observe that the frequencies and intensities of two marker bands, the C-O and C = N stretching modes at opposite ends of the conjugated chromophore, oscillate out of phase with a period of 280 fs; we attribute these oscillations to impulsively excited low-frequency phenoxyl-ring motions, which optimize the geometry of the chromophore for ESPT. Our findings illustrate that femtosecond simulated Raman spectroscopy is a powerful approach to revealing the real-time nuclear dynamics that make up a multidimensional polyatomic reaction coordinate.

Fang, X., et al. (2017). "MiR-30a Positively Regulates the Inflammatory Response of Microglia in Experimental Autoimmune Encephalomyelitis." Neurosci Bull **33**(6): 603-615.

Multiple sclerosis (MS) is a classical inflammatory demyelinating disease of the central nervous system (CNS). Microglia are the main resident immune cells in the CNS and are closely associated with the pathogenesis of MS. In the present study, we found that miR-30a was highly expressed in jellyfish-like microglia in chronic active lesions of MS patients, as well as in the microglia of mice with experimental autoimmune encephalomyelitis (EAE) at the chronic phase. In vitro, the conditioned supernatant of mouse microglia overexpressing miR-30a promoted the apoptosis of oligodendrocyte precursor cells (OPCs), and inhibited OPC differentiation. In vivo, overexpressing miR-30a in transplanted microglia exacerbated the progression of EAE. Overexpression and knock-down experiments in primary cultured mouse microglia showed that miR-30a increased the expression of IL-1beta and iNOS, which are pro-inflammatory, while inhibiting the expression of Ym-1 and CD206. Mechanistically, miR-30a inhibited the expression of Ppargc1b, which is the co-activator of peroxisome proliferator-activated receptor gamma, resulting in pro-inflammatory effects. Our work shows that miR-30a is an important regulator of the inflammatory response in microglia, and may be a promising therapeutic target for inflammatory diseases like MS in the CNS.

Fannjiang, C., et al. (2019). "Augmenting biologging with supervised machine learning to study in situ behavior of the medusa Chrysaora fuscescens." J Exp Biol **222**(Pt 16).

Zooplankton play critical roles in marine ecosystems, yet their fine-scale behavior remains poorly understood because of the difficulty in studying individuals in situ Here, we combine biologging with supervised machine learning (ML) to propose a pipeline for studying in situ behavior of larger zooplankton such as jellyfish. We deployed the ITAG, a biologging package with high-resolution motion sensors designed for soft-bodied invertebrates, on eight Chrysaora fuscescens in Monterey Bay, using the tether method for retrieval. By analyzing simultaneous video footage of the tagged jellyfish, we developed ML methods to: (1) identify periods of tag data corrupted by the tether method, which may have compromised prior research findings, and (2) classify jellyfish behaviors. Our tools yield characterizations of fine-scale jellyfish activity and orientation over long durations, and we conclude that it is essential to develop behavioral classifiers on in situ rather than laboratory data.

Fautin, D. G. and J. M. Lowenstein (1992). "Scyphomedusae and their polyps are the same immunologically: implications for systematics." Comp Biochem Physiol B **102**(1): 13-14.

1. Polyp and medusa of the scyphozoans Aurelia aurita and Pelagia colorata (phylum Cnidaria) are indistinguishable by radioimmunoassay of whole animals, yet differ from other cnidarians against which they were tested. 2. We infer that proteins distinguishing species swamp those that differentiate the two (very distinct) life history phases. 3. Thus, at least for some taxa and some systematic techniques analyzing proteins, using organisms at the same developmental phase may be unnecessary, contrary to conventional wisdom.

Fei, Y. and T. E. Hughes (2000). "Nuclear trafficking of photoreceptor protein crx: the targeting sequence and pathologic implications." Invest Ophthalmol Vis Sci **41**(10): 2849-2856.

PURPOSE: To identify the targeting sequence controlling the nuclear transport of the photoreceptor-specific transcription factor cone-rod homeobox (Crx) protein and to address the question of whether disease-causing Crx mutations disrupt the nuclear trafficking of the Crx protein. METHODS: A series of cDNA fragments encoding Crx protein with deleted C termini were generated from mouse Crx cDNA by polymerase chain reaction (PCR). Point mutations were introduced into Crx coding sequence through PCR-based, site-directed mutagenesis. These mutated Crx fragments and the wild-type Crx were fused to cDNA encoding the jellyfish green fluorescent protein (GFP) and were transiently expressed in human embryonic kidney (HEK) 293T cells. Twelve to 48 hours after transfection, the living cells were counterstained with

the red fluorescent nucleic acid dye SYTO 59 and examined with epifluorescence and confocal microscopy to determine the subcellular localization of Crx fusion proteins. RESULTS: GFP expressed without a fusion partner was distributed evenly throughout the cells, whereas the wild-type Crx protein fused to GFP was localized only in the nucleus. GFP-tagged Crx proteins truncated at residues 107 or 165, demonstrated exclusive nuclear localization. In contrast, Crx fusion proteins truncated at residues 88, 79, 44, and 36, were located equally in both the cytoplasm and the nucleus. These results demonstrate that the nuclear localization signal (NLS) of Crx appears to reside in the amino acids between residue 88 and 107, which is surprising because the putative NLSs identified by prosite search are at residues 36 to 43 and 116 to 122. Further, a Crx fusion protein truncated at residue 99 was localized within the nucleus in the majority of the transfected cells, and two point mutations at residues 88 (K88T) and 98 (R98L) disrupted the nuclear localization, which indicates that the sequence between 88 and 98 in the C terminus of the Crx homeodomain contains a NLS that is essential for targeting Crx to the nucleus. However, the fusion protein truncated at residue 99 did not produce a complete nuclear localization in every transfected cell, suggesting that the Gln-rich domain at residues 99 to 106 is also required for the full accumulation of Crx protein in the nucleus. Two point mutations of Crx, R41W and E80A, that cause cone-rod dystrophy in humans and lie within the homeodomain but outside the NLS did not disrupt the nuclear localization of Crx protein, but a R90W mutation of Crx that causes human Leber congenital amaurosis (LCA) and resides within the NLS resulted in the fusion protein localized in both nuclei and cytoplasm in majority (51% to 69%) of the transfected cells. CONCLUSIONS: The wild-type Crx protein is localized within the nucleus. The putative NLSs of Crx at residues 36 to 43 and 116 to 122 are not essential. The minimal NLS necessary for the nuclear transport of Crx protein is located at residues 88 to 98 in the C terminus of the homeodomain. The R90W mutation of Crx found in LCA disrupts the nuclear transport of the mutant protein. The defective nuclear trafficking of Crx protein may be a part of the molecular mechanism of this early-onset retinal degeneration.

Fei, Y. and T. E. Hughes (2001). "Transgenic expression of the jellyfish green fluorescent protein in the cone photoreceptors of the mouse." Vis Neurosci **18**(4): 615-623.

The goal of this study was to determine whether the jellyfish green fluorescent protein (GFP) could be used in transgenic mice to label and purify cone photoreceptors from the living retina. We created a transgene containing the 5' regulatory sequence of the human red pigment gene (pR6.5 lacZ clone; kindly provided by J. Nathans & Y. Wang), fused to the GFP coding sequence. This transgene was used to generate seven lines of PCR-positive founders. Three of the lines had bright green fluorescent cone photoreceptors. The GFP fills the entire cell. Two mouse lines had only a few (-10-100) fluorescent cells per retina, and one line (R6.85933) had many thousands. In the latter, double labeling of the cones with RITC-conjugated peanut agglutinin reveals that in the ventral retina a small proportion of the cones express GFP, while in the dorsal retina the majority do. Cells dissociated from the retinae of line R6.85933 continue to fluoresce and can be readily detected and enriched with flow cytometry. The signal provides a log unit of separation between the fluorescent cone soma and the remaining retinal cells. Roughly 3% of the cells are this fluorescent, and it is possible to purify up to 30,000 cells from one mouse. RT-PCR analysis of the mRNA from these isolated cells detects both the middle and short wavelength opsins with little if any contamination from rhodopsin.

Feitl, K. E., et al. (2009). "Functional morphology and fluid interactions during early development of the scyphomedusa Aurelia aurita." Biol Bull **217**(3): 283-291.

Scyphomedusae undergo a predictable ontogenetic transition from a conserved, universal larval form to a diverse array of adult morphologies. This transition entails a change in bell morphology from a highly discontinuous ephyral form, with deep clefts separating eight discrete lappets, to a continuous solid umbrella-like adult form. We used a combination of kinematic, modeling, and flow visualization techniques to examine the function of the medusan bell throughout the developmental changes of the scyphomedusa Aurelia aurita. We found that flow around swimming ephyrae and their lappets was relatively viscous ($1 < Re < 10$) and, as a result, ephyral lappets were surrounded by thick, overlapping boundary layers that occluded flow through the gaps between lappets. As medusae grew, their fluid environment became increasingly influenced by inertial forces ($10 < Re < 10{,}000$) and, simultaneously, clefts between the lappets were replaced by organic tissue. Hence, although the bell undergoes a structural transition from discontinuous (lappets with gaps) to continuous (solid bell) surfaces during development, all developmental stages maintain functionally continuous paddling surfaces. This developmental pattern enables ephyrae to efficiently allocate tissue to bell diameter increase via lappet growth, while minimizing tissue allocation to inter-lappet spaces that maintain paddle function due to boundary layer

overlap.

Felician, F. F., et al. (2018). "Collagen from Marine Biological Sources and Medical Applications." Chem Biodivers **15**(5): e1700557.

Collagen is the most studied protein with a wide range of applications including pharmaceutical, biomedical, cosmetics, leather, and film industries due to its special characteristics that are high biocompatibility, good bioactivity, and weak antigenicity. Although collagen sources are abundant, the outbreak of varied diseases among land animals posed threat to its utilization in our daily life. Thus, a probe for an alternative source began, which in turn revealed the immense untapped marine sources, such as fish, jellyfish, and some marine Mammals. The present article deals with a brief description of collagen, its characteristics, marine sources, extraction, collagen peptides and their biological activities, potential use and application in various field.

Felician, F. F., et al. (2019). "The wound healing potential of collagen peptides derived from the jellyfish Rhopilema esculentum." Chin J Traumatol **22**(1): 12-20.

PURPOSE: Wound represents a major health challenge as they consume a large amount of healthcare resources to improve patient's quality of life. Many scientific studies have been conducted in search of ideal biomaterials with wound-healing activity for clinical use and collagen has been proven to be a suitable candidate biomaterial. This study intended to investigate the wound healing activity of collagen peptides derived from jellyfish following oral administration. METHODS: In this study, collagen was extracted from the jellyfish--Rhopilema esculentum using 1% pepsin. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and fourier transform infrared (FTIR) were used to identify and determine the molecular weight of the jellyfish collagen. Collagenase II, papain and alkaline proteinase were used to breakdown jellyfish collagen into collagen peptides. Wound scratch assay (in vitro) was done to determine migration potential of human umbilical vein endothelial cells (HUVEC) covering the artificial wound created on the cell monolayer following treatment with collagen peptides. In vivo studies were conducted to determine the effects of collagen peptides on wound healing by examining wound contraction, re-epithelialization, tissue regeneration and collagen deposition on the wounded skin of mice. Confidence level ($p < 0.05$) was considered significant using GraphPad Prism software. RESULTS: The yield of collagen was 4.31%. The SDS-PAGE and FTIR showed that extracted collagen from jellyfish was type I. Enzymatic hydrolysis of this collagen using collagenase II produced collagen peptides (CP1) and hydrolysis with alkaline proteinase/papain resulted into collagen peptides (CP2). Tricine SDS-PAGE revealed that collagen peptides consisted of protein fragments with molecular weight <25 kDa. Wound scratch assay showed that there were significant effects on the scratch closure on cells treated with collagen peptides at a concentration of 6.25 mug/mL for 48 h as compared to the vehicle treated cells. Overall treatment with collagen peptide on mice with full thickness excised wounds had a positive result in wound contraction as compared with the control.

Feng, J., et al. (2010). "Isolation and characterization of lethal proteins in nematocyst venom of the jellyfish Cyanea nozakii Kishinouye." Toxicon **55**(1): 118-125.

Cyanea nozakii Kishinouye, a jellyfish widely distributed in coastal areas of China, has garnered attention because of its stinging capacity and the resulting public health hazard. We used a recently developed technique to extract jellyfish venom from nematocysts; the present study investigates the lethality of C. nozakii venom. The nematocyst contents were extremely toxic to the grass carp, Ctenopharyngodon idellus, producing typical neurotoxin toxicity. The ID (50) was about 0.6microg protein/g fish. Toxin samples were stable when kept at -80(degrees)C, but after 48h, an 80% decline in lethality occurred at -20(degrees)C. Poor stability of the venom was observed within the range of 65-80(degrees)C and at pH 3.5. The venom was hydrolyzed by a proteolytic enzyme, trypsin. Fractionation of the venom yielded two protein bands with molecular weights of 60kDa and 50kDa. Our results provide the first evidence that C. nozakii produces lethal toxins. These characteristics highlight the need for the isolation and molecular characterization of new active toxins in C. nozakii.

Feng, J., et al. (2010). "Partial characterization of the hemolytic activity of the nematocyst venom from the jellyfish Cyanea nozakii Kishinouye." Toxicol In Vitro **24**(6): 1750-1756.

Using a recently developed technique to extract jellyfish venom from nematocysts, the present study investigated the hemolytic activity of Cyanea nozakii Kishinouye nematocyst venom on chicken erythrocytes. Venom extract caused a significant concentration-dependent hemolytic effect. The extract could retain its activity at -80 degrees C but was unstable when kept at 4 degrees C and -20 degrees C for 2 days. The hemolytic activity was inhibited by heating within the range of 37-100 degrees C. The extract was active over a pH range of 5.0-8.63 and the

pH optima for the extract was 7.8. Incubation of the venom with sphingomyelin specially inhibited hemolytic activity by up to 70%. Cu (2+) and Mn (2+) greatly reduced the hemolytic activity while Mg (2+), Sr (2+) and Ba (2+) produced a relatively low inhibiting effect on the hemolytic activity. Treatment with Ca (2+) induced a concentration-dependent increase in the hemolytic activity. In the presence of 5 mM EDTA, all the hemolytic activity was lost, however, the venom containing 1.5 mM EDTA was stable in the long-term storage. PLA (2) activity was also found in the nematocyst venom of C. nozakii. These characteristics provide us a fundamental knowledge in the C. nozakii nematocyst venom which would benefit future research.

Feng, S., et al. (2017). "Selective suppression of in situ proliferation of scyphozoan polyps by biofouling." Mar Pollut Bull **114**(2): 1046-1056.

An increase in marine artificial constructions has been proposed as a major cause of jellyfish blooms, because these constructions provide additional substrates for organisms at the benthic stage (polyps), which proliferate asexually and release a large amount of free-swimming medusae. These hard surfaces are normally covered by fouling communities, the components of which have the potential to impede the proliferation of polyps. In this study, we report an in situ experiment of polyp survival of four large scyphozoan species found in East Asian marginal seas that were exposed to biofouling, a universal phenomenon occurring on marine artificial constructions. Our results showed that the polyps of three species (Nemopilema nomurai, Cyanea nozaki, and Rhopilema esculentum) attached to the artificial surfaces were completely eliminated by biofouling within 7-8months, and only those of moon jellyfish (Aurelia sp.1) in the upper layers could multiply on both artificial materials and other organisms (e.g., ascidians and bryozoans). Fouling-associated competition and predation and suppressed asexual reproduction of podocysts were observed to contribute to the loss of polyps. This study shows that the natural distribution of polyps is defined by the biofouling community that colonizes the surfaces of artificial constructions. Consequently, the contribution of marine constructions to jellyfish bloom is limited only to the ability of the jellyfish species to reproduce asexually through budding and inhabit solid surfaces of fouling organisms in addition to inhabiting original artificial materials. We anticipate that fragile polyps will colonize and proliferate in harsh environments that are deleterious to biofouling, and we propose special attention to polyps in antifouling practices for excluding the possibility that they occupy the available ecological space.

Feng, Z., et al. (2012). "[Ciliate diversity and spatiotemporal variation in surface sediments of Yangtze River estuary hypoxic zone]." Ying Yong Sheng Tai Xue Bao **23**(12): 3441-3448.

By using denaturing gradient gel electrophoresis (DGGE) and sequencing as well as Ludox-QPS method, an investigation was made on the ciliate diversity and its spatiotemporal variation in the surface sediments at three sites of Yangtze River estuary hypoxic zone in April and August 2011. The ANOSIM analysis indicated that the ciliate diversity had significant difference among the sites ($R = 0.896$, $P = 0.0001$), but less difference among seasons ($R = 0.043$, $P = 0.207$). The sequencing of 18S rDNA DGGE bands revealed that the most predominant groups were planktonic Choreotrichia and Oligotrichia.

Frame, J., et al. (2018). "Thrust force characterization of free-swimming soft robotic jellyfish." Bioinspir Biomim **13**(6): 064001.

Five unique soft robotic jellyfish were manufactured with eight pneumatic network tentacle actuators extending radially from their centers. These jellyfish robots were able to freely swim untethered in the ocean, to steer from side to side, and to swim through orifices more narrow than the nominal diameter of the jellyfish. Each of the five jellyfish robots were manufactured with a different composition of body and tentacle actuator Shore hardness. A three-factor study was performed with these five jellyfish robots to determine the impact that actuator material Shore hardness, actuation frequency, and tentacle stroke actuation amplitude had upon the measured thrust force. It was found that all three of these factors significantly impacted mean thrust force generation, which peaked with a half-stroke actuation amplitude at a frequency of 0.8 Hz.

Frank, U. and B. Rinkevich (1999). "Scyphozoan jellyfish's mesoglea supports attachment, spreading and migration of anthozoans' cells in vitro." Cell Biol Int **23**(4): 307-311.

Mechanically and enzymatically dissociated cells from five anthozoan species were laid on seven substrates in vitro. Cells were taken from two sea anemones (Aiptasia sp. and Anemonia sulcata), a scleractinian coral (Stylophora pistillata) and two alcyonacean corals (Heteroxenia fuscescence and Nephthea sp). Substrates tested: glass (coverslips), plastic (uncoated tissue culture plates), type IV collagen, gelatin, fibronectin, mesoglea pieces from the scyphozoan jellyfish Rhopilema nomadica and acetic acid extract of jellyfish mesoglea. Except for the mesoglea pieces, cells did not respond to any one of the other substrates, retaining their rounded shape.

Following contact with mesoglea pieces, cells attached and spread. Subsequently they migrated into the mesogleal matrix at a rate of 5-10 microm/h during the first 2-5 h. No difference was found between the behavior of cells from the five different cnidarian species.

Frazao, B. and A. Antunes (2016). "Jellyfish Bioactive Compounds: Methods for Wet-Lab Work." Mar Drugs **14**(4).

The study of bioactive compounds from marine animals has provided, over time, an endless source of interesting molecules. Jellyfish are commonly targets of study due to their toxic proteins. However, there is a gap in reviewing successful wet-lab methods employed in these animals, which compromises the fast progress in the detection of related biomolecules. Here, we provide a compilation of the most effective wet-lab methodologies for jellyfish venom extraction prior to proteomic analysis-separation, identification and toxicity assays. This includes SDS-PAGE, 2DE, gel chromatography, HPLC, DEAE, LC-MS, MALDI, Western blot, hemolytic assay, antimicrobial assay and protease activity assay. For a more comprehensive approach, jellyfish toxicity studies should further consider transcriptome sequencing. We reviewed such methodologies and other genomic techniques used prior to the deep sequencing of transcripts, including RNA extraction, construction of cDNA libraries and RACE. Overall, we provide an overview of the most promising methods and their successful implementation for optimizing time and effort when studying jellyfish.

Frazao, B., et al. (2017). "Analysis of Pelagia noctiluca proteome Reveals a Red Fluorescent Protein, a Zinc Metalloproteinase and a Peroxiredoxin." Protein J **36**(2): 77-97.

Pelagia noctiluca is the most venomous jellyfish in the Mediterranean Sea where it forms dense blooms. Although there is several published research on this species, until now none of the works has been focused on a complete protein profile of the all body constituents of this organism. Here, we have performed a detailed proteomics characterization of the major protein components expressed by P. noctiluca. With that aim, we have considered the study of jellyfish proteins involved in defense, body constituents and metabolism, and furthered explore the significance and potential application of such bioactive molecules. P. noctiluca body proteins were separated by1D SDS-PAGE and 2DE followed by characterization by nanoLC-MS/MS and MALDI-TOF/TOF techniques. Altogether, both methods revealed 68 different proteins, including a Zinc Metalloproteinase, a Red Fluorescent Protein (RFP) and a Peroxiredoxin. These three proteins were identified for the first time in P. noctiluca. Zinc Metalloproteinase was previously reported in the venom of other jellyfish species. Besides the proteins described above, the other 65 proteins found in P. noctiluca body content were identified and associated with its clinical significance. Among all the proteins identified in this work we highlight: Zinc metalloproteinase, which has a ShK toxin domain and therefore should be implicated in the sting toxicity of P. noctiluca.; the RFP which are a very important family of proteins due to its possible application as molecular markers; and last but not least the discovery of a Peroxiredoxin in this organism makes it a new natural resource of antioxidant and anti-UV radiation agents.

Freeman, G. (1996). "The role of localized cell surface-associated glycoproteins during fertilization in the hydrozoan Aequorea." Dev Biol **179**(1): 17-26.

Hydrozoan eggs can be fertilized only at the site of polar body formation and first acquire this ability during second polar body formation. The eggs of Aequorea victoria form a discrete Triticum lectin binding moiety in the jelly coat near the first polar body as it is being given off and also a discrete concanavalin A binding moiety associated with the egg surface where the second polar body forms, which disappears immediately after fertilization. The germinal vesicle has an eccentric position in full grown Aequorea oocytes. The region of oocyte surface closest to the germinal vesicle is the site where the polar bodies normally form. When oocytes are centrifuged during oocyte maturation, the meiotic apparatus sometimes shifts to a different position with reference to the egg surface and polar bodies are given off at this new site. There is a corresponding shift in the position of the Triticum and concanavalin A lectin binding moieties, indicating that their formation is associated with local events occurring at the site of polar body formation. Treatment of Aequorea eggs with Triticum or concanavalin A causes a marked reduction in the ability of these eggs to be fertilized, suggesting that sugar-containing moieties, to which the lectins bind, play a role in fertilization. Removal of sugars on these moieties with mannosidase or N-acetylglucosaminidase, or the cleavage of the protein the sugars are attached to with trypsin, results in eggs that do not bind Triticum or concanavalin A and also show a marked reduction in the ability to be fertilized. These experiments suggest that the lectin binding moieties are glycoproteins.

Freeman, K. S., et al. (2009). "Characterization of eversion syndrome in captive Scyphomedusa jellyfish." Am J Vet Res **70**(9): 1087-1093.

OBJECTIVE: To determine whether

Scyphomedusa jellyfish with eversion syndrome had alterations in husbandry conditions, elemental content, or histologic appearance, compared with unaffected jellyfish. ANIMALS: 123 jellyfish (44 with eversion syndrome and 79 without) at 6 institutions. PROCEDURES: Elemental analyses were performed on 24 jellyfish with eversion syndrome and 49 without, and histologic examinations were performed on 20 jellyfish with eversion syndrome and 30 without. A questionnaire distributed to 39 institutions with Scyphomedusa jellyfish was used to gather information about husbandry, environmental conditions, and prevalence of eversion syndrome. RESULTS: For the 39 institutions that responded to the questionnaire, prevalence of eversion syndrome ranged from 0% to 30%. For Aurelia aurita, eversion was more common at institutions with only captive-raised and no wild-caught jellyfish. Eversion was most common among young (approx 1- to 2-month-old) growing jellyfish and older (> 6-month-old) jellyfish. Elemental analysis revealed only minor differences between affected and unaffected jellyfish, with great variation among jellyfish from the same institution and among jellyfish from different institutions. Striated muscle degeneration and necrosis and extracellular matrix (mesoglea) degeneration were evident on histologic examination of affected jellyfish. CONCLUSIONS AND CLINICAL RELEVANCE: Results suggested that eversion syndrome is a complex phenomenon associated with degenerative changes of the bell matrix.

Freeman, S. E. and R. J. Turner (1969). "A pharmacological study of the toxin in a Cnidarian, Chironex fleckeri Southcott." Br J Pharmacol **35**(3): 510-520.

1. A study has been made of the pharmacological actions of toxic preparations obtained from the box jellyfish Chironex fleckeri Southcott. Two toxin preparations were used. One was a tentacle extract which was partially purified by Sephadex gel filtration; the second was obtained by a process analogous to snake milking, and is probably similar in composition to the material injected into victims.2. All preparations were extremely toxic; death in animals, following minimally lethal doses, occurred in minutes. Respiratory arrest of central origin appeared to be the terminal event in all species tested. This was accompanied by marked signs of cardiotoxicity. The heart was slowed, irregular, and showed varying degrees of conduction delay. Terminally it showed atrioventricular block.3. Blood pressure changes were biphasic. An initial rise in carotid pressure was followed by a profound fall; a second rise to an above normal level frequently followed this. These blood pressure oscillations were damped down by prior treatment with hexamethonium but the hypertensive response remained.4. Blood samples taken before terminal apnoea showed a variable degree of haemolysis and a raised K (+) level.5. Experiments with isolated organ preparations suggested that the toxin had a non-specific lytic effect on cells, but did not contain pharmacologically active substances of small molecular weight such as 5-hydroxytryptamine.6. It is suggested that the toxin (s) act by altering membrane permeability; the signs at death may reflect the sensitivity of the target organs to such a change.

Freitag, N. E. and K. E. Jacobs (1999). "Examination of Listeria monocytogenes intracellular gene expression by using the green fluorescent protein of Aequorea victoria." Infect Immun **67**(4): 1844-1852.

The ActA protein of Listeria monocytogenes is an essential virulence factor and is required for intracellular bacterial motility and cell-to-cell spread. plcB, cotranscribed with actA, encodes a broad-specificity phospholipase C that contributes to lysis of host cell vacuoles and cell-to-cell spread. Construction of a transcriptional fusion between actA-plcB and the green fluorescent protein gene of Aequorea victoria has facilitated the detailed examination of patterns of actA/plcB expression within infected tissue culture cells. actA/plcB expression began approximately 30 min postinfection and was dependent upon entry of L. monocytogenes into the host cytosol. L. monocytogenes Deltahly mutants, which are unable to escape from host cell vacuoles, did not express actA/plcB at detectable levels within infected tissue culture cells; however, complementation of the hly defect allowed entry of the bacteria into the host cytoplasm and subsequent actA/plcB expression. These results emphasize the ability of L. monocytogenes to sense the different host cell compartment environments encountered during the course of infection and to regulate virulence gene expression in response.

Frenk, E., et al. (1990). "Delayed skin reaction caused by a coelenterate." Dermatologica **181**(3): 241-242.

We report a delayed skin reaction, histologically characterized by liquefaction degeneration of the basal layer, which was observed in a 30-year-old man returning from Guadeloupe. It was most likely due to contact with a marine animal.

Friedel, N., et al. (2016). "Severe anaphylactic reaction to mediterranean jellyfish (Ropilhema nomadica) envenomation: Case report." Toxicol Rep **3**: 427-429.

We present a 15-year-old female patient with an anaphylactic reaction to a jellyfish sting, sustained

while surfing in the Mediterranean Sea. She experienced immediate difficulty in breathing, hoarseness and itching and was taken by ambulance to the emergency department, receiving intramuscular adrenaline on the way. She presented with periorbital swelling and facial edema and improved with systemic steroids and antihistamines. She was discharged 2 days later with allergy service follow up at our institution. This is the first case report documenting anaphylaxis due to Mediterranean jellyfish envenomation.

Fringuelli, E., et al. (2012). "Development of a quantitative real-time PCR for the detection of Tenacibaculum maritimum and its application to field samples." J Fish Dis **35**(8): 579-590.

The development and the application of a quantitative real-time PCR for the detection of Tenacibaculum maritimum are described. A set of primers and probe was designed to amplify a 155-bp fragment specific to the T. maritimum 16S rRNA gene. The test was shown to be very sensitive, able to detect as little as 4.8 DNA copies number muL (-1). In addition, the assay was found to have a high degree of repeatability and reproducibility, with a linear dynamic range (R (2) = 0.999) extending over 6 log (10) dilutions and a high efficiency (100%). The assay was applied to DNA samples extracted from 48 formalin-fixed paraffin-embedded (FFPE) Atlantic salmon, Salmo salar, gill tissues showing varying degrees of gill pathology (scored 0-3) and from 26 jellyfish samples belonging to the species Phialella quadrata and Muggiaea atlantica. For each sample, the bacterial load was normalised against the level of the salmonid elongation factor alpha 1 (ELF) detected by a second real-time PCR using previously published primers and probe. Tenacibaculum maritimum DNA was detected in 89% of the blocks with no signs of gill disease as well as in 95% of the blocks with mild-to-severe gill pathology. Association between bacterial load and gill pathology severity was investigated. T. maritimum DNA was detected at low level in four of the 26 jellyfish tested.

Fuchida, S., et al. (2017). "Leaching of Metals and Metalloids from Hydrothermal Ore Particulates and Their Effects on Marine Phytoplankton." ACS Omega **2**(7): 3175-3182.

Seafloor massive sulfide deposits have attracted much interest as mineral resources. Therefore, the potential environmental impacts of full-scale mining should be considered. In this study, we focused on metal and metalloid contamination that could be triggered by accidental leakage and dispersion of hydrothermal ore particulates from mining vessels into surface seawater. We determined the leaching potential of metals and metalloids from four hydrothermal ores collected from the Okinawa Trough into aerobic seawater and then evaluated the toxic effects of ore leachates on a phytoplankton species, Skeletonema marinoi-dohrnii complex, which is present ubiquitously in the ocean. Large amounts of metals and metalloids were released from the ground hydrothermal ores into seawater within 5 min under aerobic conditions. The main components of leachates were Zn + Pb, As + Sb, and Zn + Cu, which were obtained from the Fe-Zn-Pb-rich and Zn-Pb-rich zero-age, Ba-rich, and Fe-rich ores, respectively. The leachates had different chemical compositions from those of the ore. The rapid release and difference in chemical compositions between the leachates and the ores indicated that substances were not directly dissolved from the sulfide-binding mineral phase but from labile phases mainly on the adsorption-desorption interface of the ores under these conditions. All ore leachates inhibited the growth of S. marinoi-dohrnii complex but with different magnitudes of toxic effects. These results indicate that the fine particulate matter of hydrothermal ores is a potential source of toxic contamination that may damage primary production in the ocean. Therefore, we insist on the necessity for the prior evaluation of toxic element leachability from mineral ores into seawater to minimize mining impacts on the surface environment.

Fuchs, B., et al. (2014). "Regulation of polyp-to-jellyfish transition in Aurelia aurita." Curr Biol **24**(3): 263-273.

BACKGROUND: The life cycle of scyphozoan cnidarians alternates between sessile asexual polyps and pelagic medusa. Transition from one life form to another is triggered by environmental signals, but the molecular cascades involved in the drastic morphological and physiological changes remain unknown. RESULTS: We show in the moon jelly Aurelia aurita that the molecular machinery controlling transition of the sessile polyp into a free-swimming jellyfish consists of two parts. One is conserved and relies on retinoic acid signaling. The second, novel part is based on secreted proteins that are strongly upregulated prior to metamorphosis in response to the seasonal temperature changes. One of these proteins functions as a temperature-sensitive "timer" and encodes the precursor of the strobilation hormone of Aurelia. CONCLUSIONS: Our findings uncover the molecule framework controlling the polyp-to-jellyfish transition in a basal metazoan and provide insights into the evolution of complex life cycles in the animal kingdom.

Fujiki, A., et al. (2019). "Branching pattern and morphogenesis of medusa tentacles in the jellyfish Cladonema pacificum (Hydrozoa, Cnidaria)."

Zoological Lett **5**: 12.

Background: Branched structures are found in many natural settings, and the molecular and cellular mechanisms underlying their formation in animal development have extensively studied in recent years. Despite their importance and the accumulated knowledge from studies on several organs of Drosophila and mammals, much remains unknown about branching mechanisms in other animal species. We chose to study the jellyfish species Cladonema pacificum. Unlike many other jellyfish, this species has branched medusa tentacles, and its basal phylogenetic position in animal evolution makes it an ideal organism for studying and understanding branching morphogenesis more broadly. Branched tentacles are unique compared to other well-studied branched structures in that they have two functionally distinct identities: one with adhesive organs for attaching to a substratum, and another with nematocyst clusters for capturing prey. Results: We began our analyses on C. pacificum tentacles by observing their branching during growth. We found that tentacle branches form through repeated addition of new branches to the proximal region of the main tentacle while it is elongating. At the site of branch bud formation, we observed apical thickening of the epidermal epithelial layer, possibly caused by extension of the epithelial cells along the apico-basal axis. Interestingly, tentacle branch formation required receptor tyrosine kinase signaling, which is an essential factor for branching morphogenesis in Drosophila and mammals. We also found that new branches form adhesive organs first, and then are transformed into branches with nematocyst clusters as they develop. Conclusions: These results highlight unique features in branch generation in C. pacificum medusa tentacles and illuminate conserved and fundamental mechanisms by which branched structures are created across a variety of animal species.

Fujimasa, I. and K. Imachi (1991). "[Artificial hearts--toward future technologies]." Nihon Geka Gakkai Zasshi **92**(9): 1263-1266.

What are the most essential technologies for developing the implantable artificial heart in future? The first is the development of autonomic and dispersed micro actuators for acting as sarcomeres of the heart muscle. An electric motor driven artificial heart transmitted the power with belts had been developed as a preliminary mechanism. A micro actuation using noise energy has been developed for simulating the structure and the function of striate-muscle sarcomeres. The chemical energy conversion mechanism must be applied instead of the conventional electro-mechanical mechanisms, when we implant the total artificial heart permanently. As a implantable assisted artificial heart using tentatively, we have developed an axial flow pump system. The pump system acts as a systemic and a pulmonary pump produced pulsatile flow switching an axial pump output. The second is the search of biocompatible materials, which do not only mean blood compatibility but also tissue compatibility. The great masses in chest cavity have inevitably occurred infection. The autonomic and dispersed control system is the third item. We have developed a jellyfish valve with low fluid dynamical resistances for improving the pump dynamic characteristics.

Fujisawa, T., et al. (2016). "Role of Coherent Low-Frequency Motion in Excited-State Proton Transfer of Green Fluorescent Protein Studied by Time-Resolved Impulsive Stimulated Raman Spectroscopy." J Am Chem Soc **138**(12): 3942-3945.

Green fluorescent protein (GFP) from jellyfish Aequorea victoria, an essential bioimaging tool, luminesces via excited-state proton transfer (ESPT) in which the phenolic proton of the p-hydroxybenzylideneimidazolinone chromophore is transferred to Glu222 through a hydrogen-bond network. In this process, the ESPT mediated by the low-frequency motion of the chromophore has been proposed. We address this issue using femtosecond time-resolved impulsive stimulated Raman spectroscopy. After coherently exciting low-frequency modes (<300 cm (-1)) in the excited state of GFP, we examined the excited-state structural evolution and the ESPT dynamics within the dephasing time of the low-frequency vibration. A clear anharmonic vibrational coupling is found between one high-frequency mode of the chromophore (phenolic CH bend) and a low-frequency mode at approximately 104 cm (-1). However, the data show that this low-frequency motion does not substantially affect the ESPT dynamics.

Fujita, S., et al. (2019). "Cell proliferation controls body size growth, tentacle morphogenesis, and regeneration in hydrozoan jellyfish Cladonema pacificum." PeerJ **7**: e7579.

Jellyfish have existed on the earth for around 600 million years and have evolved in response to environmental changes. Hydrozoan jellyfish, members of phylum Cnidaria, exist in multiple life stages, including planula larvae, vegetatively-propagating polyps, and sexually-reproducing medusae. Although free-swimming medusae display complex morphology and exhibit increase in body size and regenerative ability, their underlying cellular mechanisms are poorly understood. Here, we investigate the roles of cell proliferation in body-size growth, appendage

morphogenesis, and regeneration using Cladonema pacificum as a hydrozoan jellyfish model. By examining the distribution of S phase cells and mitotic cells, we revealed spatially distinct proliferating cell populations in medusae, uniform cell proliferation in the umbrella, and clustered cell proliferation in tentacles. Blocking cell proliferation by hydroxyurea caused inhibition of body size growth and defects in tentacle branching, nematocyte differentiation, and regeneration. Local cell proliferation in tentacle bulbs is observed in medusae of two other hydrozoan species, Cytaeis uchidae and Rathkea octopunctata, indicating that it may be a conserved feature among hydrozoan jellyfish. Altogether, our results suggest that hydrozoan medusae possess actively proliferating cells and provide experimental evidence regarding the role of cell proliferation in body-size control, tentacle morphogenesis, and regeneration.

Fukuda, H., et al. (2000). "Folding of green fluorescent protein and the cycle3 mutant." Biochemistry **39**(39): 12025-12032.

Although the correct folding of green fluorescent protein (GFP) is required for formation of the chromophore, it is known that wild-type GFP cannot mature efficiently in vivo in Escherichia coli at 37 degrees C or higher temperatures that the jellyfish in the Pacific Northwest have never experienced. Recently, by random mutagenesis by the polymerase chain reaction (PCR) method, a mutant called Cycle3 was constructed. This mutant had three mutations, F99S, M153T, and V163A, on or near the surface of the GFP molecule and was able to mature correctly even at 37 degrees C [Crameri et al. (1996) Nat. Biotechnol. 143, 315-319]. In the present study, we investigated the differences in their folding behavior in vitro. We observed the folding and unfolding reactions of both wild-type GFP and the Cycle3 mutant by using green fluorescence as an indicator of the formation of the native structure and examining hydrogen-exchange reactions by Fourier transform infrared spectroscopy. Both proteins showed unusually slow refolding and unfolding rates, and their refolding rates were almost identical under the native state at 25 and at 35 degrees C.

Galle, S., et al. (2005). "The homeobox gene Msx in development and transdifferentiation of jellyfish striated muscle." Int J Dev Biol **49**(8): 961-967.

Bilaterian Msx homeobox genes are generally expressed in areas of cell proliferation and in association with multipotent progenitor cells. Likewise, jellyfish Msx is expressed in progenitor cells of the developing entocodon, a cell layer giving rise to the striated and smooth muscles of the medusa. However, in contrast to the bilaterian homologs, Msx gene expression is maintained at high levels in the differentiated striated muscle of the medusa in vivo and in vitro. This tissue exhibits reprogramming competence. Upon induction, the Msx gene is immediately switched off in the isolated striated muscle undergoing transdifferentiation, to be upregulated again in the emerging smooth muscle cells which, in a stem cell like manner, undergo quantal cell divisions producing two cell types, a proliferating smooth muscle cell and a differentiating nerve cell. This study indicates that the Msx protein may be a key component of the reprogramming machinery responsible for the extraordinary transdifferentation and regeneration potential of striated muscle in the hydrozoan jellyfish.

Gallin, W. (1991). "Sequence of an acidic ribosomal protein from the jellyfish Polyorchis penicillatus." Biochem Cell Biol **69**(2-3): 211-215.

We have isolated a cDNA clone from the jellyfish Polyorchis penicillatus that encodes the homologue of the A1 acidic ribosomal protein previously characterized in human, brine shrimp, fruit fly, and yeast. The sequence of this protein is strongly conserved among the five eukaryotic species for which it has been determined. Conservation is greatest in the amino-terminal 51 amino acids and the carboxyl-terminal 25 amino acids. This suggests that these regions are necessary for interactions with other components of the protein synthetic machinery, while the central part of the protein has a less specific role to play. Comparison of the sequences obtained from the different species indicate that the metazoan lineages all appear to have arisen at approximately the same time and significantly later than the time of divergence of yeast from the common ancestor of the Metazoa.

Galliot, B. and D. Miller (2000). "Origin of anterior patterning. How old is our head?" Trends Genet **16**(1): 1-5.

Most animals that display a bilateral symmetry (bilaterians) share homologous regulatory genes involved in head development. Recently, homologues of several of these genes have been cloned from animals that are radially organized, such as coral, sea anemones, jellyfish or hydra (cnidarians). Surprisingly, some of these are expressed apically and/or during apical patterning in hydrozoans, suggesting that head patterning is much older than previously thought.

Galliot, B. and M. Quiquand (2011). "A two-step process in the emergence of neurogenesis." Eur J Neurosci **34**(6): 847-862.

Cnidarians belong to the first phylum differentiating a nervous system, thus providing suitable model systems to trace the origins of

neurogenesis. Indeed corals, sea anemones, jellyfish and hydra contract, swim and catch their food thanks to sophisticated nervous systems that share with bilaterians common neurophysiological mechanisms. However, cnidarian neuroanatomies are quite diverse, and reconstructing the urcnidarian nervous system is ambiguous. At least a series of characters recognized in all classes appear plesiomorphic: (1) the three cell types that build cnidarian nervous systems (sensory-motor cells, ganglionic neurons and mechanosensory cells called nematocytes or cnidocytes); (2) an organization of nerve nets and nerve rings [those working as annular central nervous system (CNS)]; (3) a neuronal conduction via neurotransmitters; (4) a larval anterior sensory organ required for metamorphosis; (5) a persisting neurogenesis in adulthood. By contrast, the origin of the larval and adult neural stem cells differs between hydrozoans and other cnidarians; the sensory organs (ocelli, lens-eyes, statocysts) are present in medusae but absent in anthozoans; the electrical neuroid conduction is restricted to hydrozoans. Evo-devo approaches might help reconstruct the neurogenic status of the last common cnidarian ancestor. In fact, recent genomic analyses show that if most components of the postsynaptic density predate metazoan origin, the bilaterian neurogenic gene families originated later, in basal metazoans or as eumetazoan novelties. Striking examples are the ParaHox Gsx, Pax, Six, COUP-TF and Twist-type regulators, which seemingly exert neurogenic functions in cnidarians, including eye differentiation, and support the view of a two-step process in the emergence of neurogenesis.

Gambardella, C., et al. (2015). "Effect of silver nanoparticles on marine organisms belonging to different trophic levels." Mar Environ Res **111**: 41-49.

Silver nanoparticles (Ag-NPs) are increasingly used in a wide range of consumer products and such an extensive use raises questions about their safety and environmental toxicity. We investigated the potential toxicity of Ag-NPs in the marine ecosystem by analyzing the effects on several organisms belonging to different trophic levels. Algae (Dunaliella tertiolecta, Skeletonema costatum), cnidaria (Aurelia aurita jellyfish), crustaceans (Amphibalanus amphitrite and Artemia salina) and echinoderms (Paracentrotus lividus) were exposed to Ag-NPs and different end-points were evaluated: algal growth, ephyra jellyfish immobilization and frequency of pulsations, crustaceans mortality and swimming behavior, and sea urchin sperm motility. Results showed that all the end-points were able to underline a dose-dependent effect. Jellyfish were the most sensitive species, followed by barnacles, sea urchins, green algae, diatoms and brine shrimps. In conclusion, Ag-NPs exposure can influence different trophic levels within the marine ecosystem.

Gambini, C., et al. (2012). "Micro- and macrorheology of jellyfish extracellular matrix." Biophys J **102**(1): 1-9.

Mechanical properties of the extracellular matrix (ECM) play a key role in tissue organization and morphogenesis. Rheological properties of jellyfish ECM (mesoglea) were measured in vivo at the cellular scale by passive microrheology techniques: microbeads were injected in jellyfish ECM and their Brownian motion was recorded to determine the mechanical properties of the surrounding medium. Microrheology results were compared with macrorheological measurements performed with a shear rheometer on slices of jellyfish mesoglea. We found that the ECM behaved as a viscoelastic gel at the macroscopic scale and as a much softer and heterogeneous viscoelastic structure at the microscopic scale. The fibrous architecture of the mesoglea, as observed by differential interference contrast and scanning electron microscopy, was in accord with these scale-dependent mechanical properties. Furthermore, the evolution of the mechanical properties of the ECM during aging was investigated by measuring microrheological properties at different jellyfish sizes. We measured that the ECM in adult jellyfish was locally stiffer than in juvenile ones. We argue that this stiffening is a consequence of local aggregations of fibers occurring gradually during aging of the jellyfish mesoglea and is enhanced by repetitive muscular contractions of the jellyfish.

Gamero-Mora, E., et al. (2019). "Regenerative Capacity of the Upside-down Jellyfish Cassiopea xamachana." Zool Stud **58**: e37.

This study provides the first observation that umbrellar tissue can lead to the formation of virtually all body structures in jellyfish of the order Rhizostomeae. The regeneration process was observed in two specimens of the upside-down jellyfish Cassiopea xamachana Bigelow, 1892, one housed at the Vienna Zoo, Austria and the other in a laboratory at the University of Sao Paulo, Brazil. The process was triggered by an injury and ended with the formation of two new sets of body structures. Our observation offers evidence that C. xamachana has a hidden regenerative capacity exceeding that previously recorded.

Ganesh, S., et al. (2017). "Jellyfish sign for intraoperative identification of posterior lenticonus." Int Ophthalmol **37**(5): 1239-1241.

Posterior lenticonus is a rare progressive disease characterized by protrusion of posterior lens capsule

along with lens cortex into the vitreous cavity. It may be associated with local thinning or absence of posterior lens capsule. It generally occurs sporadically, but familial cases have also been reported. If visually significant or if amblyopia is present, lens removal is indicated. Treatment consists of clear or cataractous lens extraction, optical correction along with prompt amblyopia therapy. In this case, we propose a "jellyfish sign" seen intraoperatively, which is referred to the characteristic movement of the posterior capsular cataractous material on injection of balanced salt solution in the capsular bag.

Gao, B., et al. (2005). "Transfection and expression of exogenous gene in laying hens oviduct in vitro and in vivo." J Zhejiang Univ Sci B **6**(2): 137-141.

To examine whether or not the regulatory sequence of chicken ovalbumin gene can drive transgene expression specifically in hen oviduct, the authors constructed an oviduct-specific expression vector (pOV), containing 3.0 kilobases (kb) of the 5'-flanking sequence and 3.0 kb of the 3'-flanking sequence of the chicken ovalbumin gene. Jellyfish green fluorescence protein (EGFP) reporter gene and bacterial LacZ reporter gene were respectively inserted into the downstream of the 5'-regulatory region. The recombinants were named as pOVEGFP and pOVLacZ. Two transfer systems, in vitro and in vivo, were used to verify the function of the vector. In vitro, the plasmid DNA pOVEGFP and pEGFP-N1 were transfected respectively by the polyethyleneimine procedure into the primary chicken oviduct epithelium (PCOE) and fibroblasts cells isolated from laying hens. In vivo, the recombinant vector pOVLacZ was injected into egg-laying hens via wing vein and the tissues were collected for RT-PCR analysis. The results showed that expression of pEGFP-N1 was achieved at low level in oviduct epithelial cells and at high level in fibroblasts, but that the recombinant vector was not expressed in both cells. RT-PCR analysis showed that the LacZ gene was transcribed in the oviduct, but not in the heart, liver, kidney and spleen of the injected hens. Accordingly, the beta-galactosidase activity was only detected in the oviduct magnum (116.7 mU/ml) and eggs (16.47 mU/ml). These results indicated that the cloned regulation regions of chicken ovalbumin gene could drive exogenous gene expression specifically in the oviducts of hens. In vivo gene injection via wing vein may serve as a rapid production system of recombinant proteins in chicken eggs. In addition, the cultured primary oviduct cells from laying hens were not efficient temporary expression systems for analyzing the function of regulating elements of ovalbumin gene.

Gao, X. and G. Wang (2018). "Investigation on the expression stability of common reference genes in Aurelia sp.1 under hypoxia." Cell Mol Biol (Noisy-le-grand) **64**(12): 26-31.

RT-qPCR (Quantitative real-time polymerase chain reaction) is a reliable molecular biology technique used for gene expression detection due to its high sensibility and good reproducibility. However, suitable reference genes for RT-qPCR are often not available to investigate the expression of target genes in jellyfish under different conditions. To determine the responsible genes of jellyfish under hypoxia, primers to amplify the actin gene was designed for the amplification according to the conserved actin amino acid sequences of cnidarian. Then, we cloned and sequenced the partial cDNA sequence of beta-actin gene containing 849 bp nucleic acids was cloned and sequenced, and the four common housekeeping genes (18S rRNA, beta-actin, alpha-tubulin and GAPDH) were detected. To obtain suitable reference genes, we compared the four genes under normoxia and hypoxia were determined and compared using RT-qPCR. The evaluation result shows that alpha-tubulin gene can be used as single reference gene, and alpha-tubulin and beta-actin can be served as multiple reference genes to study relative gene expression related to hypoxic tolerance of Aurelia sp.1. This research will establish foundation to reveal the molecular mechanism of jellyfish under hypoxia.

Garamszegi, N., et al. (1997). "Application of a chimeric green fluorescent protein to study protein-protein interactions." Biotechniques **23**(5): 864-866, 868-870, 872.

The green fluorescent protein (GFP) of the jellyfish Aequorea victoria is an emerging tool to monitor gene expression in situ and in vivo. Because of its fluorescence properties, when GFP is fused in-frame to a specific protein of interest, various aspects of the behavior of this protein can be analyzed noninvasively. Here we describe a fusion between GFP and human calmodulin-like protein (CLP) and show that this protein retains fluorescence and known characteristics of CLP, including Ca (2+)-dependent interaction with phenyl-Sepharose and interaction with a specific cellular target protein. The results suggest a novel application for GFP fusion proteins in the rapid, nonradioactive detection of interacting proteins on gel overlays.

Garcia-Arredondo, A., et al. (2014). "Characteristics of hemolytic activity induced by the aqueous extract of the Mexican fire coral Millepora complanata." J Venom Anim Toxins Incl Trop Dis **20**(1): 49.

BACKGROUND: Millepora complanata is a

plate-like fire coral common throughout the Caribbean. Contact with this species usually provokes burning pain, erythema and urticariform lesions. Our previous study suggested that the aqueous extract of M. complanata contains non-protein hemolysins that are soluble in water and ethanol. In general, the local damage induced by cnidarian venoms has been associated with hemolysins. The characterization of the effects of these components is important for the understanding of the defense mechanisms of fire corals. In addition, this information could lead to better care for victims of envenomation accidents. METHODS: An ethanolic extract from the lyophilized aqueous extract was prepared and its hemolytic activity was compared with the hemolysis induced by the denatured aqueous extract. Based on the finding that ethanol failed to induce nematocyst discharge, ethanolic extracts were prepared from artificially bleached and normal M. complanata fragments and their hemolytic activity was tested in order to obtain information about the source of the heat-stable hemolysins. RESULTS: Rodent erythrocytes were more susceptible to the aqueous extract than chicken and human erythrocytes. Hemolytic activity started at ten minutes of incubation and was relatively stable within the range of 28-50 degrees C. When the aqueous extract was preincubated at temperatures over 60 degrees C, hemolytic activity was significantly reduced. The denatured extract induced a slow hemolytic activity (HU50 = 1,050.00 +/- 45.85 mug/mL), detectable four hours after incubation, which was similar to that induced by the ethanolic extract prepared from the aqueous extract (HU50 = 1,167.00 +/- 54.95 mug/mL). No significant differences were observed between hemolysis induced by ethanolic extracts from bleached and normal fragments, although both activities were more potent than hemolysis induced by the denatured extract. CONCLUSIONS: The results showed that the aqueous extract of M. complanata possesses one or more powerful heat-labile hemolytic proteins that are slightly more resistant to temperature than jellyfish venoms. This extract also contains slow thermostable hemolysins highly soluble in ethanol that are probably derived from the body tissues of the hydrozoan.

Garcia-Rodriguez, J., et al. (2018). "Gonadal histology of box jellyfish (Cnidaria: Cubozoa) reveals variation between internal fertilizing species Alatina alata (Alatinidae) and Copula sivickisi (Tripedaliidae)." J Morphol **279**(6): 841-856.

Cubozoans (box jellyfish) are gonochoristic cnidarians with distinct reproductive strategies. This comparative histological study examines the gonad organization of Alatina alata and Copula sivickisi, two box jellyfish species that exhibit different modes of internal fertilization. A. alata reproduces via spermcasting aggregations while C. sivickisi reproduces via copulation; in both cases, internal fertilization occurs in the gastrovascular cavity. Herein, we provide the first histological description of subgastric sacs-structures unique to C. sivickisi. Although previously thought to function as sperm storage sacs, our findings reveal that subgastric sacs are nematocyst nests lacking sperm entirely. Conversely, we discovered that velarial spots in C. sivickisi females correspond to actual sperm storage structures. Histological examination of cubozoan sperm packages revealed that while sperm packages from both species have motile flagella, A. alata males produce nonencapsulated sperm bundles (i.e., "spermatozeugmata"), and C. sivickisi males produce encapsulated packages (i.e., "spermatophores"). Our findings corroborate the presence of several types of nematocysts in C. sivickisi embryo strands and spermatophores, and indicate their provenance to be both female and male gonads respectively, as well as subgastric sacs (i.e., nematocyst nests). In contrast to our findings of velarial spots as sperm storages structures in C. sivickisi females, and of nematocysts in the gonads of both sexes, we report that A. alata medusae lack both sperm storage structures and gonadal nematocysts. Finally, we discuss our findings on reproductive morphology of C. sivickisi and A. alata in light of the respective reproductive behavior of these two cubozoan species.

Garm, A., et al. (2008). "Unique structure and optics of the lesser eyes of the box jellyfish Tripedalia cystophora." Vision Res **48**(8): 1061-1073.

The visual system of box jellyfish comprises a total of 24 eyes. These are of four types and each probably has a special function. To investigate this hypothesis the morphology and optics of the lesser eyes, the pit and slit eyes, were examined. The pit eyes hold one cell type only and are probably mere light meters. The slit eyes, comprising four cell types, are complex and highly asymmetric. They also hold a lens-like structure, but its optical power is minute. Optical modeling suggests spatial resolution, but only in one plane. These unique and intriguing traits support strong peripheral filtering.

Garm, A. and J. Bielecki (2008). "Swim pacemakers in box jellyfish are modulated by the visual input." J Comp Physiol A Neuroethol Sens Neural Behav Physiol **194**(7): 641-651.

A major part of the cubozoan central nervous system is situated in the eye-bearing rhopalia. One of the neuronal output channels from the rhopalia carries a swim pacemaker signal, which has a one-to-one relation with the swim contractions of the bell shaped body. Given the advanced visual system of box

jellyfish and that the pacemaker signal originates in the vicinity of these eyes, it seems logical to assume that the pacemakers are modified by the visual input. Here, the firing frequency and distribution of inter-signal intervals (ISIs) of single pacemakers are examined in the Caribbean box jellyfish, Tripedalia cystophora. It is shown that the absolute ambient light intensity, if kept constant, has no influence on the signal, but if the intensity changes, it has a major impact on both frequency and ISIs. If the intensity suddenly drops there is an increase in firing frequency, and the ISIs become more homogeneously distributed. A rise in intensity, on the other hand, produces a steep decline in the frequency and makes the ISIs highly variable. These electrophysiological data are correlated with behavioral observations from the natural habitat of the medusae.

Garm, A., et al. (2012). "Opposite patterns of diurnal activity in the box jellyfish Tripedalia cystophora and Copula sivickisi." Biol Bull **222**(1): 35-45.

Cubozoan medusae have a stereotypic set of 24 eyes, some of which are structurally similar to vertebrate and cephalopod eyes. Across the approximately 25 described species, this set of eyes varies surprisingly little, suggesting that they are involved in an equally stereotypic set of visual tasks. During the day Tripedalia cystophora is found at the edge of mangrove lagoons where it accumulates close to the surface in sun-lit patches between the prop roots. Copula sivickisi (formerly named Carybdea sivickisi) is associated with coral reefs and has been observed to be active at night. At least superficially, the eyes of the two species are close to identical. We studied the diurnal activity pattern of these two species both in the wild and under controlled conditions in laboratory experiments. Despite the very similar visual systems, we found that they display opposite patterns of diurnal activity. T. cystophora is active exclusively during the day, whereas C. sivickisi is actively swimming at night, when it forages and mates. At night T. cystophora is found on the muddy bottom of the mangrove lagoon. C. sivickisi spends the day attached to structures such as the underside of stones and coral skeletons. This species difference seems to have evolved to optimize foraging, since the patterns of activity follow those of the available prey items in their respective habitats.

Garm, A., et al. (2016). "Hunting in Bioluminescent Light: Vision in the Nocturnal Box Jellyfish Copula sivickisi." Front Physiol **7**: 99.

Cubomedusae all have a similar set of six eyes on each of their four rhopalia. Still, there is a great variation in activity patterns with some species being strictly day active while others are strictly night active. Here we have examined the visual ecology of the medusa of the night active Copula sivickisi from Okinawa using optics, morphology, electrophysiology, and behavioral experiments. We found the lenses of both the upper and the lower lens eyes to be image forming but under-focused, resulting in low spatial resolution in the order of 10-15 degrees. The photoreceptor physiology is similar in the two lens eyes and they have a single opsin peaking around 460 nm and low temporal resolution with a flicker fusion frequency (fff) of 2.5 Hz indicating adaptions to vision in low light intensities. Further, the outer segments have fluid filled swellings, which may concentrate the light in the photoreceptor membrane by total internal reflections, and thus enhance the signal to noise ratio in the eyes. Finally our behavioral experiments confirmed that the animals use vision when hunting. When they are active at night they seek out high prey-concentration by visual attraction to areas with abundant bioluminescent flashes triggered by their prey.

Garm, A., et al. (2007). "The lens eyes of the box jellyfish Tripedalia cystophora and Chiropsalmus sp. are slow and color-blind." J Comp Physiol A Neuroethol Sens Neural Behav Physiol **193**(5): 547-557.

Box jellyfish, or cubomedusae, possess an impressive total of 24 eyes of four morphologically different types. Compared to other cnidarians they also have an elaborate behavioral repertoire, which for a large part seems to be visually guided. Two of the four types of cubomedusean eyes, called the upper and the lower lens eye, are camera type eyes with spherical fish-like lenses. Here we explore the electroretinograms of the lens eyes of the Caribbean species, Tripedalia cystophora, and the Australian species, Chiropsalmus sp. using suction electrodes. We show that the photoreceptors of the lens eyes of both species have dynamic ranges of about 3 log units and slow responses. The spectral sensitivity curves for all eyes peak in the blue-green region, but the lower lens eye of T. cystophora has a small additional peak in the near UV range. All spectral sensitivity curves agree well with the theoretical absorbance curve of a single opsin, strongly suggesting color-blind vision in box jellyfish with a single receptor type. A single opsin is supported by selective adaptation experiments.

Garm, A. and P. Ekstrom (2010). "Evidence for multiple photosystems in jellyfish." Int Rev Cell Mol Biol **280**: 41-78.

Cnidarians are often used as model animals in studies of eye and photopigment evolution. Most cnidarians display photosensitivity at some point in their lifecycle ranging from extraocular photoreception

to image formation in camera-type eyes. The available information strongly suggests that some cnidarians even possess multiple photosystems. The evidence is strongest within Cubomedusae where all known species posses 24 eyes of four morphological types. Physiological experiments show that each cubomedusan eye type likely constitutes a separate photosystem controlling separate visually guided behaviors. Further, the visual system of cubomedusae also includes extraocular photoreception. The evidence is supported by immunocytochemical and molecular data indicating multiple photopigments in cubomedusae as well as in other cnidarians. Taken together, available data suggest that multiple photosystems had evolved already in early eumetazoans and that their original level of organization was discrete sets of special-purpose eyes and/or photosensory cells.

Garm, A., et al. (2006). "Rhopalia are integrated parts of the central nervous system in box jellyfish." Cell Tissue Res **325**(2): 333-343.

In cubomedusae, the central nervous system (CNS) is found both in the bell (the ring nerve) and in the four eye-bearing sensory structures (the rhopalia). The ring nerve and the rhopalia are connected via the rhopalial stalks and examination of the structure of the rhopalial stalks therefore becomes important when trying to comprehend visual processing. In the present study, the rhopalial stalk of the cubomedusae Tripedalia cystophora has been examined by light microscopy, transmission electron microscopy, and electrophysiology. A major part of the ring nerve is shown to continue into the stalk and to contact the rhopalial neuropil directly. Ultrastructural analysis of synapse distribution in the rhopalial stalk has failed to show any clustering, which indicates that integration of the visual input is probably spread throughout the CNS. Together, the results indicate that cubomedusae have one coherent CNS including the rhopalia. Additionally, a novel gastrodermal nerve has been found in the stalk; this nerve is not involved in visual processing but is likely to be mechanosensory and part of a proprioceptory system.

Garm, A., et al. (2013). "Pattern- and contrast-dependent visual response in the box jellyfish Tripedalia cystophora." J Exp Biol **216**(Pt 24): 4520-4529.

Cubomedusae possess a total of 24 eyes, some of which are structurally similar to vertebrate eyes. Accordingly, the medusae also display a range of light-guided behaviours including obstacle avoidance, diurnal activity patterns and navigation. Navigation is supported by spatial resolution and image formation in the so-called upper lens eye. Further, there are indications that obstacle avoidance requires image information from the lower lens eye. Here we use a behavioural assay to examine the obstacle avoidance behaviour of the Caribbean cubomedusa Tripedalia cystophora and test whether it requires spatial resolution. The possible influence of the contrast and orientation of the obstacles is also examined. We show that the medusae can only perform the behaviour when spatial information is present, and fail to avoid a uniformly dark wall, directly proving the use of spatial vision. We also show that the medusae respond stronger to high contrast lines than to low contrast lines in a graded fashion, and propose that the medusae use contrast as a semi-reliable measure of distance to the obstacle.

Garm, A., et al. (2015). "Mating in the box jellyfish Copula sivickisi--Novel function of cnidocytes." J Morphol **276**(9): 1055-1064.

Within cubozoans, a few species have developed a sexual reproduction system including mating and internal fertilization. One species, Copula sivickisi, is found in a large area of the indo pacific. They have separate sexes and when mature males and females meet they entangle their tentacles and the males transfer a sperm package, a spermatozeugmata, which is ingested by the female fertilizing her eggs internally. After 2-3 days, the females lay an embryo strand that sticks to the substrate and after another 2-3 days, the fully developed larvae leave the strand. We have examined the ultrastructure of the gonads and spermatozeugmata to look for structural adaptations to this specialized way of reproduction and understand how the fertilization takes place. Surprisingly, we discovered that the male gonads were heavily packed with cnidocytes of the isorhiza type and that they are transferred to the spermatozeugmata. The spermatozeugmata does not dissolve in the female gastrovascular cavity but is attached to the female gonad probably using the isorhizas. Here, the sperm cells are partly digested and the nuclei are released. The actual fertilization seems to happen through phagocytosis of the released nuclei by the epithelial cells. The female gonads are likewise packed with cnidocytes but of the eurytele type. They do not mature inside the female and putatively serve to protect the developing larvae once the embryo strand is laid. This specialized way of fertilization is to our knowledge novel and so is this first account of cnidocytes being directly involved in cnidarian reproduction.

Garm, A. and S. Mori (2009). "Multiple photoreceptor systems control the swim pacemaker activity in box jellyfish." J Exp Biol **212**(Pt 24): 3951-3960.

Like all other cnidarian medusae, box jellyfish propel themselves through the water by contracting their bell-shaped body in discrete swim pulses. These pulses are controlled by a swim pacemaker system situated in their sensory structures, the rhopalia. Each medusa has four rhopalia each with a similar set of six eyes of four morphologically different types. We have examined how each of the four eye types influences the swim pacemaker. Multiple photoreceptor systems, three of the four eye types, plus the rhopalial neuropil, affect the swim pacemaker. The lower lens eye inhibits the pacemaker when stimulated and provokes a strong increase in the pacemaker frequency upon light-off. The upper lens eye, the pit eyes and the rhopalial neuropil all have close to the opposite effect. When these responses are compared with all-eye stimulations it is seen that some advanced integration must take place.

Garm, A., et al. (2007). "Visually guided obstacle avoidance in the box jellyfish Tripedalia cystophora and Chiropsella bronzie." J Exp Biol **210**(Pt 20): 3616-3623.

Box jellyfish, cubomedusae, possess an impressive total of 24 eyes of four morphologically different types. Two of these eye types, called the upper and lower lens eyes, are camera-type eyes with spherical fish-like lenses. Compared with other cnidarians, cubomedusae also have an elaborate behavioral repertoire, which seems to be predominantly visually guided. Still, positive phototaxis is the only behavior described so far that is likely to be correlated with the eyes. We have explored the obstacle avoidance response of the Caribbean species Tripedalia cystophora and the Australian species Chiropsella bronzie in a flow chamber. Our results show that obstacle avoidance is visually guided. Avoidance behavior is triggered when the obstacle takes up a certain angle in the visual field. The results do not allow conclusions on whether color vision is involved but the strength of the response had a tendency to follow the intensity contrast between the obstacle and the surroundings (chamber walls). In the flow chamber Tripedalia cystophora displayed a stronger obstacle avoidance response than Chiropsella bronzie since they had less contact with the obstacles. This seems to follow differences in their habitats.

Garm, A., et al. (2011). "Box jellyfish use terrestrial visual cues for navigation." Curr Biol **21**(9): 798-803.

Box jellyfish have an impressive set of 24 eyes of four different types, including eyes structurally similar to those of vertebrates and cephalopods [1, 2]. However, the known visual responses are restricted to simple phototaxis, shadow responses, and object avoidance responses [3-8], and it has been a puzzle why they need such a complex set of eyes. Here we report that medusae of the box jellyfish Tripedalia cystophora are capable of visually guided navigation in mangrove swamps using terrestrial structures seen through the water surface. They detect the mangrove canopy by an eye type that is specialized to peer up through the water surface and that is suspended such that it is constantly looking straight up, irrespective of the orientation of the jellyfish. The visual information is used to navigate to the preferred habitat at the edge of mangrove lagoons.

Garm, A., et al. (2007). "The ring nerve of the box jellyfish Tripedalia cystophora." Cell Tissue Res **329**(1): 147-157.

Box jellyfish have the most elaborate sensory system and behavioural repertoire of all cnidarians. Sensory input largely comes from 24 eyes situated on four club-shaped sensory structures, the rhopalia, and behaviour includes obstacle avoidance, light shaft attractance and mating. To process the sensory input and convert it into the appropriate behaviour, the box jellyfish have a central nervous system (CNS) but this is still poorly understood. The CNS has two major components: the rhopalial nervous system and the ring nerve. The rhopalial nervous system is situated within the rhopalia in close connection with the eyes, whereas the ring nerve encircles the bell. We describe the morphology of the ring nerve of the box jellyfish Tripedalia cystophora as ascertained by normal histological techniques, immunohistochemistry and transmission electron microscopy. By light microscopy, we have estimated the number of cells in the ring nerve by counting their nuclei. In cross sections at the ultrastructural level, the ring nerve appears to have three types of neurites: (1) small "normal"-looking neurites, (2) medium-sized neurites almost completely filled by electron-lucent vacuoles and (3) giant neurites. In general, only one giant neurite is seen on each section; this type displays the most synapses. Epithelial cells divide the ring nerve into compartments, each having a tendency to contain neurites of similar morphology. The number and arrangement of the compartments vary along the length of the ring nerve.

Gast, R. J. (2006). "Molecular phylogeny of a potentially parasitic dinoflagellate isolated from the solitary radiolarian, Thalassicolla nucleata." J Eukaryot Microbiol **53**(1): 43-45.

Thalassicolla nucleata, a solitary radiolarian, has been described as being parasitized by two dinoflagellates, Solenodinium (Syndiniales) and Caryotoma (Blastodiniales). Several T. nucleata were stripped of their extracapsular material and allowed to

regenerate their rhizopodial structures without symbionts. Within a week, two were observed to disintegrate, leaving behind non-pigmented swimming dinoflagellate cells. Identical full-length ribosomal sequences were recovered from both samples. Upon alignment and phylogenetic analysis, it was determined that these putative parasite sequences were distinct from Scrippsiella nutricula (the dinoflagellate symbiont of the host), and also from all other dinoflagellate parasites sequenced to date.

Gawinski, C., et al. (2019). "Biodiversity of gelatinous macrozooplankton: Quantitative assessment of data and distribution patterns in the southern and central North Sea during August 2018." Data Brief **25**: 104186.

This article describes the biodiversity of gelatinous macrozooplankton and presents quantitative field data on their community composition and distribution pattern in the North Sea during August 2018. The data set consists of jellyfish and comb jelly species abundance estimates which are based on sampling at 62 stations in the central and southern North Sea covering Danish waters, the German Bight, waters off the Dutch coast as well as the western North Sea off the UK coast and the central North Sea. The sampling gear was a 13 m long MIK-net (modified Methot Isaac Kidd net; O 2 m, mesh size 1 mm, mesh size cod end 500 mum) deployed in double oblique hauls from the surface to 5 m above the sea floor. Samples were visually analysed for gelatinous macrozooplankton (>2 mm) using a light table. Samples were processed within 1 hour after catch. In total, 6239 gelatinous macrozooplankton specimen were caught. Spatial distribution pattern described in this article include the jellyfish species Aequorea sp., Aurelia aurita, Beroe sp., Chrysaora hysoscella, Clytia hemisphaerica, Cyanea capillata, Cyanea lamarckii, Eirene viridula, Leuckartiara octona, Melicertum octocostatum, Obelia sp. as well as the comb jelly species Mnemiopsis leidyi and Pleurobrachia pileus. Further, size frequency distributions of abundant taxa are provided together with a summary of abundances as well as average, maximum and minimum sizes of all species. This dataset has not previously been published and is of high value for comparison with other - and future - investigations of gelatinous macrozooplankton in the North Sea. The data were obtained during an internationally coordinated, standard fishery survey which is carried out annually (Quarter 3 - North Sea - International Bottom Trawl Survey - Q3 NS-IBTS). The gained information could be used as baseline for a monitoring of potential changes in gelatinous macrozooplankton abundances to address the long standing question if gelatinous zooplankton are on the rise due to climate change induced stressors.

Ge, J., et al. (2018). "Transcriptome analysis of scyphozoan jellyfish Rhopilema esculentum from polyp to medusa identifies potential genes regulating strobilation." Dev Genes Evol **228**(6): 243-254.

Strobilation is a unique asexual reproduction mode of scyphozoan jellyfish, through which benthic polyp develops into pelagic medusa. It is an orderly metamorphosis process triggered by environmental signals. However, the knowledges of molecular mechanisms under the drastic morphological and physiological changes are still limited. In this study, the transcriptomes from polyps to juvenile medusae at different stages were characterized by RNA-seq in scyphozoan jellyfish Rhopilema esculentum. Among 96,076 de novo assembled unigenes, 7090 differentially expressed genes (DEGs) were identified during the developmental stages. The co-expression pattern analysis of DEGs yielded 15 clusters with different expression patterns. Among them, a cluster with 388 unigenes was related to strobila. In this specific cluster, the GO terms related to "sequence-specific DNA binding transcription factor activity" and "sequence-specific DNA binding" were significantly enriched. Transcription factors, including segmentation protein even-skipped-like, segmentation polarity protein engrailed-like, homeobox proteins Otx-like, Twist-like and Cnox2-Pc-like, as well as genes such as RxR-like and Dmrtf-like, were identified to be potentially involved in strobilation. Their expression patterns and the other 11 TFs/genes involved in strobilation were confirmed with qRT-PCR methods. The present study pointed out the role of transcription factors in strobilation and produced a list of novel candidate genes for further studies. It could provide valuable information for understanding the molecular mechanisms of jellyfish strobilation.

Ge, M., et al. (2019). "Comparative proteomic analysis of Aurelia coerulea for its locomotion system molecular structure-function inference." J Proteomics **209**: 103509.

BACKGROUND: Rhythmic contraction and autonomous movement play a key role in the predation, production and displacement of jellyfish. METHODS: Four independent body parts of the jellyfish Aurelia coerulea, including Bell, Tentacle, Oral arm and Gastric pouch were extracted and have been carried out a compared proteomics by liquid chromatography-mass spectrometry/mass-spectrometry (LC-MS/MS). ResultsA total of 13,429 peptides and 1916 proteins with molecular weights in the range of 10.6-980.9kDa were identified, where 1916, 1562, 1474 and 1441 proteins were matched in the Gastric pouch, Tentacle, Oral arm and Bell, respectively. Gene Ontology (GO)

analysis showed that translation, cytoplasma and ATP binding occupy the top differential terms of the three subdomains Biological process, Cellular Component and Molecular Function. A total of 326 pathways were successfully mapped that are mainly associated with intracellular synthesis, metabolism as well as intracellular functions. Moreover, a total of 27 contractile machinery associated proteins including 22 myosin, 3 actin and 2 tropomyosin were identified. CONCLUSIONS: Our results provide a composition profile in the four independent body parts of the jellyfish A. coerulea, of which the identified muscular proteins will greatly help in the understanding of the structural and functional relationship, as well as their operating mechanisms in the jellyfish locomotion system. SIGNIFICANCE: Omics studies have gained a new overall insight into the function of gene and protein networks during the development of motor systems in both bilateral and radial symmetrical animals. A compared proteomics using the label-free method of nano-LC-MS/MS has been performed through the four independent body parts of the moon jellyfish A. coerulea, including Bell, Tentacle, Oral arm and Gastric pouch. In addition to conventional bioinformatics analyses such as GO and KEGG, we have scanned the locomotion-related components, aligned their sequences, simulated three dimensional structures as well as did the molecular phylogenetic analyses. Our investigation provides a composition profile in the four independent body parts of the jellyfish A. coerulea, of which the identified muscular proteins will greatly help in the understanding of the structural and functional relationship, as well as their operating mechanisms in the jellyfish locomotion system.

Gehring, W. J. (2002). "The genetic control of eye development and its implications for the evolution of the various eye-types." Int J Dev Biol **46**(1): 65-73.

Mutations in the Pax 6 homologs of mammals and insects prevent eye development and targeted expression of both mammal and insect Pax 6 homologs is capable of inducing functional ectopic eyes. Supported by RNA interference experiments in planarians and nemerteans, these findings indicate that Pax 6 is a universal master control gene for eye morphogenesis. Since all metazoan eyes use rhodopsin as a photoreceptor molecule and the same master control gene for eye development, we postulate a monophyletic origin of the various eye types. The finding of well developed eyes in jellyfish which essentially lack a brain, leads us to propose that the eye as a sensory organ evolved before the brain which is an information processing organ. The finding of highly developed eyes with a lens, vitreous body, stacked membranes like a retina and shielding pigment in unicellular dinoflagellates, raises the possibility that the prototypic eyes might have been acquired from symbionts.

Gehring, W. J. (2005). "New perspectives on eye development and the evolution of eyes and photoreceptors." J Hered **96**(3): 171-184.

Recent experiments on the genetic control of eye development have opened up a completely new perspective on eye evolution. The demonstration that targeted expression of one and the same master control gene, that is, Pax6 can induce the formation of ectopic eyes in both insects and vertebrates, necessitates a reconsideration of the dogma of a polyphyletic origin of the various eye types in all the animal phyla. The involvement of Pax6 and six1 and six3 genes, which encode highly conserved transcription factors, in the genetic control of eye development in organisms ranging from planarians to humans argues strongly for a monophyletic origin of the eye. Because transcription factors can control the expression of any target gene provided it contains the appropriate gene regulatory elements, the conservation of the genetic control of eye development by Pax6 among all bilaterian animals is not due to functional constraints but a consequence of its evolutionary history. The prototypic eyes postulated by Darwin to consist of two cells only, a photoreceptor and a pigment cell, were accidentally controlled by Pax6 and the subsequent evolution of the various eye types occurred by building onto this original genetic program. A hypothesis of intercalary evolution is proposed that assumes that the eye morphogenetic pathway is progressively modified by intercalation of genes between the master control genes on the top of the hierarchy and the structural genes like rhodopsin at the bottom. The recruitment of novel genes into the eye morphogenetic pathway can be due to at least two different genetic mechanisms, gene duplication and enhancer fusion.In tracing back the evolution of eyes beyond bilaterians, we find highly developed eyes in some box-jellyfish as well as in some Hydrozoans. In Hydrozoans the same orthologous six genes (six1 and six3) are required for eye regeneration as in planarians, and in the box jellyfish Tripedalia a pax B gene, which may be a precursor of Pax6, was found to be expressed in the eyes. In contrast to the adults, which have highly evolved eyes, the Planula larva of Tripedalia has single- celled photoreceptors similar to some unicellular protists. For the origin of photoreceptor cells in metazoa, I propose two hypotheses, one based on cellular differentiation and a more speculative one based on symbiosis. The former assumes that photoreceptor cells originated from a colonial protist in which all the cells were photosensitive and subsequent cellular differentiation to give rise to

photoreceptor cells. The symbiont hypothesis, which I call the Russian doll model, assumes that photosensitivity arose first in photosynthetic cyanobacteria that were subsequently taken up into red algae as primary chloroplasts. The red algae in turn were taken up by dinoflagellates as secondary chloroplasts and in some species evolved into the most sophisticated eye organelles, as found, for example, in some dinoflagellates like Erythropsis and Warnovia, which lack chloroplasts. Because dinoflagellates are commonly found as symbionts in cnidarians, the dinoflagellates may have transferred their photoreceptor genes to cnidarians. In cnidarians such as Tripedalia the step from photoreceptor organelles to multicellular eyes has occurred. These two hypotheses, the cellular differentiation and the symbiont hypothesis, are not mutually exclusive and are the subject of further investigations.

Gemmell, B. J., et al. (2016). "Can gelatinous zooplankton influence the fate of crude oil in marine environments?" Mar Pollut Bull **113**(1-2): 483-487.

Gelatinous zooplankton are known for their capacity to excrete copious amounts of mucus that can be utilized by other organisms. The release of mucus is exacerbated by stressful conditions. Despite the recognized importance of cnidarian mucus to production and material flux in marine ecosystems, the role of gelatinous zooplankton in influencing the fate of oil spills is unknown. In this study we used laboratory experiments to observe the influence of mucus from the moon jellyfish (Aurelia aurita) on the aggregation and degradation of crude oil. The results show that jellyfish swimming in a dispersed solution of oil droplets produced copious amounts of mucus and the mucus aggregates that were shed by the animals contained 26 times more oil than the surrounding water. Incubation experiments showed that hydrocarbon degrading bacteria cell densities more than doubled in the presence of mucus and after 14days, resulted in a significant increase in oil degradation. These results suggest that jellyfish can aggregate dispersed oil droplets and embed them within a matrix that favors hydrocarbon degrading bacteria. While this study lends support to the hypothesis that the presence of gelatinous zooplankton can impact oil spills large scale mesocosm studies will be needed to fully quantify the influence on a natural system.

Gemmell, B. J., et al. (2018). "Widespread utilization of passive energy recapture in swimming medusae." J Exp Biol **221**(Pt 1).

Recently, it has been shown that some medusae are capable of swimming very efficiently, i.e. with a low cost of transport, and that this is in part due to passive energy recapture (PER) which occurs during bell relaxation. We compared the swimming kinematics among a diverse array of medusae, varying in taxonomy, morphology and propulsive and foraging modes, in order to evaluate the prevalence of PER in medusae. We found that while PER was common among taxa, the magnitude of the contribution to overall swimming varied greatly. The ability of medusae to utilize PER was not related to morphology and swimming performance but was controlled by their swimming kinematics. Utilizing PER required the medusae to pause after bell expansion and individuals could modulate their PER by changing their pause duration. PER can greatly enhance swimming efficiency but there appear to be trade-offs associated with utilizing PER.

Gemmell, B. J., et al. (2015). "Suction-based propulsion as a basis for efficient animal swimming." Nat Commun **6**: 8790.

A central and long-standing tenet in the conceptualization of animal swimming is the idea that propulsive thrust is generated by pushing the surrounding water rearward. Inherent in this perspective is the assumption that locomotion involves the generation of locally elevated pressures in the fluid to achieve the expected downstream push of the surrounding water mass. Here we show that rather than pushing against the surrounding fluid, efficient swimming animals primarily pull themselves through the water via suction. This distinction is manifested in dominant low-pressure regions generated in the fluid surrounding the animal body, which are observed by using particle image velocimetry and a pressure calculation algorithm applied to freely swimming lampreys and jellyfish. These results suggest a rethinking of the evolutionary adaptations observed in swimming animals as well as the mechanistic basis for bio-inspired and biomimetic engineered vehicles.

Gemmell, B. J., et al. (2019). "A ctenophore (comb jelly) employs vortex rebound dynamics and outperforms other gelatinous swimmers." R Soc Open Sci **6**(3): 181615.

Gelatinous zooplankton exhibit a wide range of propulsive swimming modes. One of the most energetically efficient is the rowing behaviour exhibited by many species of schyphomedusae, which employ vortex interactions to achieve this result. Ctenophores (comb jellies) typically use a slow swimming, cilia-based mode of propulsion. However, species within the genus Ocyropsis have developed an additional propulsive strategy of rowing the lobes, which are normally used for feeding, in order to rapidly escape from predators. In this study, we used high-speed digital particle image velocimetry to

examine the kinematics and fluid dynamics of this rarely studied propulsive mechanism. This mechanism allows Ocyropsis to achieve size-adjusted speeds that are nearly double those of other large gelatinous swimmers. The investigation of the fluid dynamic basis of this escape mode reveals novel vortex interactions that have not previously been described for other biological propulsion systems. The arrangement of vortices during escape swimming produces a similar configuration and impact as that of the well-studied 'vortex rebound' phenomenon which occurs when a vortex ring approaches a solid wall. These results extend our understanding of how animals use vortex-vortex interactions and provide important insights that can inform the bioinspired engineering of propulsion systems.

Gemmell, B. J., et al. (2014). "Exploring vortex enhancement and manipulation mechanisms in jellyfish that contributes to energetically efficient propulsion." Commun Integr Biol **7**: e29014.

The ability of animals to propel themselves efficiently through a fluid medium is ecologically advantageous. Flexible components that influence vortex interactions are widespread among animal propulsors. However the mechanisms by which vortices are enhanced and appropriately positioned for thrust generation are still poorly understood. Here, we describe how kinematic propulsor movements of a jellyfish can enhance and reposition a vortex ring that allows the recapture of wake energy for secondary thrust generation and efficient locomotion. We use high-speed video and digital particle image velocimetry (DPIV) to resolve kinematics simultaneously with fluid structures. These results provide new insight into how animals can manipulate fluid structures to reduce metabolic energy demands of swimming muscles and may have implications in bio-inspired design.

Gemmell, B. J., et al. (2013). "Passive energy recapture in jellyfish contributes to propulsive advantage over other metazoans." Proc Natl Acad Sci U S A **110**(44): 17904-17909.

Gelatinous zooplankton populations are well known for their ability to take over perturbed ecosystems. The ability of these animals to outcompete and functionally replace fish that exhibit an effective visual predatory mode is counterintuitive because jellyfish are described as inefficient swimmers that must rely on direct contact with prey to feed. We show that jellyfish exhibit a unique mechanism of passive energy recapture, which is exploited to allow them to travel 30% further each swimming cycle, thereby reducing metabolic energy demand by swimming muscles. By accounting for large interspecific differences in net metabolic rates, we demonstrate, contrary to prevailing views, that the jellyfish (Aurelia aurita) is one of the most energetically efficient propulsors on the planet, exhibiting a cost of transport (joules per kilogram per meter) lower than other metazoans. We estimate that reduced metabolic demand by passive energy recapture improves the cost of transport by 48%, allowing jellyfish to achieve the large sizes required for sufficient prey encounters. Pressure calculations, using both computational fluid dynamics and a newly developed method from empirical velocity field measurements, demonstrate that this extra thrust results from positive pressure created by a vortex ring underneath the bell during the refilling phase of swimming. These results demonstrate a physical basis for the ecological success of medusan swimmers despite their simple body plan. Results from this study also have implications for bioinspired design, where low-energy propulsion is required.

Gemmell, B. J., et al. (2015). "Control of vortex rings for manoeuvrability." J R Soc Interface **12**(108): 20150389.

Manoeuvrability is critical to the success of many species. Selective forces acting over millions of years have resulted in a range of capabilities currently unmatched by machines. Thus, understanding animal control of fluids for manoeuvring has both biological and engineering applications. Within inertial fluid regimes, propulsion involves the formation and interaction of vortices to generate thrust. We use both volumetric and planar imaging techniques to quantify how jellyfish (Aurelia aurita) modulate vortex rings during turning behaviour. Our results show that these animals distort individual vortex rings during turns to alter the force balance across the animal, primarily through kinematic modulation of the bell margin. We find that only a portion of the vortex ring separates from the body during turns, which may increase torque. Using a fluorescent actin staining method, we demonstrate the presence of radial muscle fibres lining the bell along the margin. The presence of radial muscles provides a mechanistic explanation for the ability of scyphomedusae to alter their bell kinematics to generate non-symmetric thrust for manoeuvring. These results illustrate the advantage of combining imaging methods and provide new insights into the modulation and control of vorticity for low-speed animal manoeuvring.

Genikhovich, G. and U. Technau (2011). "Complex functions of Mef2 splice variants in the differentiation of endoderm and of a neuronal cell type in a sea anemone." Development **138**(22): 4911-4919.

In triploblastic animals, mesoderm gives rise to

many tissues and organs, including muscle. By contrast, the representatives of the diploblastic phylum Cnidaria (corals, sea anemones, jellyfish and hydroids) lack mesoderm but possess muscle. In vertebrates and insects, the transcription factor Mef2 plays a pivotal role in muscle differentiation; however, it is also an important regulator of neuron differentiation and survival. In the sea anemone Nematostella vectensis, an organism that lacks mesoderm but has muscles and neurons, Mef2 (Nvmef2) has been reported in single ectodermal cells of likely neural origin. To our surprise, we found that Nvmef2 is alternatively spliced, forming differentially expressed variants. Using morpholino-mediated knockdown and mRNA injection, we demonstrate that specific splice variants of Nvmef2 are required for the proliferation and differentiation of endodermal cells and for the development of ectodermal nematocytes, a neuronal cell type. Moreover, we identified a small conserved motif in the transactivation domain that is crucially involved in the endodermal function of Nvmef2. The identification of a crucial and conserved motif in the transactivation domain predicts a similarly important role in vertebrate Mef2 function. This is the first functional study of a determinant of several mesodermal derivatives in a diploblastic animal. Our data suggest that the involvement of alternative splice variants of Mef2 in endomesoderm and neuron differentiation predates the cnidarian-bilaterian split.

Geoffroy, M. C., et al. (2000). "Use of green fluorescent protein to tag lactic acid bacterium strains under development as live vaccine vectors." Appl Environ Microbiol **66**(1): 383-391.

The lactic acid bacteria (LAB) are safe microorganisms which are mainly used for the preparation of fermented foods and for probiotic applications. The potential of LAB as live vehicles for the production and delivery of therapeutic molecules such as antigens is also being actively investigated today. However, very little is known about the fate of live LAB when administered in vivo and about the interaction of these microorganisms with the nasal or gastrointestinal ecosystem. For future applications, it is essential to be able to discriminate the biotherapeutic strain from the endogenous microflora and to unravel the mechanisms underlying the postulated health-beneficial effect. We therefore started to investigate both aspects in a mouse model with two LAB species presently under development as live vaccine vectors, i.e., Lactococcus lactis and Lactobacillus plantarum. We have constructed different expression vectors carrying the gfp (green fluorescent protein [GFP]) gene from the jellyfish Aequoria victoria, and we found that this visible marker was best expressed when placed under the control of the inducible strong nisA promoter from L. lactis. Notably, a threshold amount of GFP was necessary to obtain a bright fluorescent phenotype. We further demonstrated that fluorescent L. plantarum NCIMB8826 can be enumerated and sorted by flow cytometry. Moreover, tagging of this strain with GFP allowed us to visualize its phagocytosis by macrophages in vitro and ex vivo and to trace it in the gastrointestinal tract of mice upon oral administration.

Gerhardt, B., et al. (1998). "The vesicle transport protein Vps33p is an ATP-binding protein that localizes to the cytosol in an energy-dependent manner." J Biol Chem **273**(25): 15818-15829.

Molecular mechanisms of vesicle transport between the prevacuolar compartment and the vacuole in yeast or the lysosome in mammalian cells are poorly understood. To learn more about the specificity of this intercompartmental step, we have examined the subcellular localization of a SEC1 homologue, Vps33p, a protein implicated to function in transport between the prevacuolar compartment and the vacuole. Following short pulses, 80-90% of newly synthesized Vps33p cofractionated with a cytosolic enzyme marker after making permeabilized yeast cells. However, during a chase, 20-40% of Vps33p fractionated with permeabilized cell membranes in a time-dependent fashion with a half-time of approximately 40 min. Depletion of cellular ATP increased the association rate to a half-time of approximately 4 min and caused 80-90% of newly synthesized Vps33p to be associated with permeabilized cell membranes. The association of Vps33p with permeabilized cell membranes was reversible after restoring cells with glucose before permeabilization. The N-ethylmaleimide-sensitive fusion protein homologue, Sec18p, a protein with known ATP binding and hydrolysis activity, displayed the same reversible energy-dependent sedimentation characteristics as Vps33p. We determined that the photosensitive analog, 8-azido-[alpha-32P]ATP, could bind directly to Vps33p with low affinity. Interestingly, excess unlabeled ATP could enhance photoaffinity labeling of 8-azido-[alpha-32P]ATP to Vps33p, suggesting cooperative binding, which was not observed with excess GTP. Importantly, we did not detect significant photolabeling after deleting amino acid regions in Vps33p that show similarity to ATP interaction motifs. We visualized these events in living yeast cells after fusing the jellyfish green fluorescent protein (GFP) to the C terminus of full-length Vps33p. In metabolically active cells, the fully functional Vps33p-GFP fusion protein appeared to stain throughout the cytoplasm with one or two very bright fluorescent spots near the vacuole. After depleting cellular ATP, Vps33p-GFP appeared to localize with a

punctate morphology, which was also reversible upon restoring cells with glucose. Overall, these data support a model where Vps33p cycles between soluble and particulate forms in an ATP-dependent manner, which may facilitate the specificity of transport vesicle docking or targeting to the yeast lysosome/vacuole.

Germain, G. and M. Anctil (1996). "Evidence for Intercellular Coupling and Connexin-like Protein in the Luminescent Endoderm of Renilla koellikeri (Cnidaria, Anthozoa)." Biol Bull **191**(3): 353-366.

Gap junction plaques are abundant in Hydrozoa, where they play an important role in signal propagation through epithelia and nerve nets, but they have not been found in the two other classes of Cnidaria, the Scyphozoa and the Anthozoa. Here several lines of evidence are presented that point to the existence of intercellular coupling in tissues of the anthozoan Renilla koellikeri, especially in the luminescent endoderm. Dye-exchange experiments show that calcein vital stains spread between cultured cells after their reassociation. Polyp luminescence evoked by KCI depolarization, electrical stimulation, or {beta}-adrenergic agonists was largely and reversibly suppressed in the presence of the gap junction uncouplers octanol, heptanol, and low pH sodium acetate. A connexin43-like protein was isolated on Western blots of R. koellikeri membrane extracts by using a monoclonal connexin-43 antibody. Loading this antibody in R. koellikeri tissues resulted in the suppression of luminescence evoked by electrical stimulation. Immunohistochemical investigations using this antibody revealed mostly punctate immunostaining associated with endodermal cells of the luminescent tissue and with the mesogleal nerve net. Electron microscopic observations confirmed the absence of conventional gap junction plaques in these tissues, but revealed the presence of tiny zones of close membrane apposition between light-emitting and other endodermal cells, with gaps of 2-4 nm. Taken together, these results are consistent with the notion of the existence in R. koellikeri of intercellular coupling (1) involved in local transmission of luminescence signals, and (2) mediated by connexin43-based connexons that are not assembled into typical gap junction plaques.

Germanguz, I., et al. (2007). "Four twist genes in zebrafish, four expression patterns." Dev Dyn **236**(9): 2615-2626.

Twist genes code for regulatory bHLH proteins essential for embryonic development and conserved across the metazoa. There are four genes that constitute the zebrafish twist family: twist1a, twist1b, twist2--orthologs of the mammalian twist1 and twist2 genes; and twist3--a gene from a new clade that does not exist in mammals. Presented here are their embryonic mRNA expression profiles. The study extends the known conservation of twist developmental patterns in tetrapods to the fish, e.g., expression in cephalic neural crest, sclerotome and lateral plate mesoderm. Some other expression domains are unique, like hypochord and dorsal aorta; some, like the notochord, may be ancestral patterns retained from protochordates; and the expression in invaginating/migrating cells may have been retained from the jellyfish. Perhaps this is one of the more ancient functions of twist--conserved from diploblasts to humans--to facilitate cell movement.

German-Retana, S., et al. (2000). "Effects of green fluorescent protein or beta-glucuronidase tagging on the accumulation and pathogenicity of a resistance-breaking Lettuce mosaic virus isolate in susceptible and resistant lettuce cultivars." Mol Plant Microbe Interact **13**(3): 316-324.

The RNA genome of a resistance-breaking isolate of Lettuce mosaic virus (LMV-E) was engineered to express the jellyfish green fluorescent protein (GFP) or beta-glucuronidase (GUS) fused to the helper-component proteinase (HC-Pro) to study LMV invasion and spread in susceptible and resistant lettuce cultivars. Virus accumulation and movement were monitored by either histochemical GUS assays or detection of GFP fluorescence under UV light. The GFP- and GUS-tagged viruses spread systemically in the susceptible lettuce cultivars Trocadero and Vanguard, where they induced attenuated symptoms, compared with the wild-type virus. Accumulation of the GFP-tagged virus was reduced but less affected than in the case of the GUS-tagged virus. Systemic movement of both recombinant viruses was very severely affected in Vanguard 75, a lettuce cultivar nearly isogenic to Vanguard but carrying the resistance gene mo1(2). Accumulation of the recombinant viruses in systemically infected leaves was either undetectable (GUS-tag) or erratic, strongly delayed, and inhibited by as much as 90% (GFP-tag). As a consequence, and contrary to the parental virus, the recombinant viruses were not able to overcome the protection afforded by the mo1(2) gene. Taken together, these results indicate that GUS or GFP tagging of the HC-Pro of LMV has significant negative effects on the biology of the virus, abolishing its resistance-breaking properties and reducing its pathogenicity in susceptible cultivars.

Gerrard, E., et al. (2018). "Convergent evolution of tertiary structure in rhodopsin visual proteins from vertebrates and box jellyfish." Proc Natl Acad Sci U S A **115**(24): 6201-6206.

Box jellyfish and vertebrates are separated

by >500 million years of evolution yet have structurally analogous lens eyes that employ rhodopsin photopigments for vision. All opsins possess a negatively charged residue-the counterion-to maintain visible-light sensitivity and facilitate photoisomerization of their retinaldehyde chromophore. In vertebrate rhodopsins, the molecular evolution of the counterion position-from a highly conserved distal location in the second extracellular loop (E181) to a proximal location in the third transmembrane helix (E113)-is established as a key driver of higher fidelity photoreception. Here, we use computational biology and heterologous action spectroscopy to determine whether the appearance of the advanced visual apparatus in box jellyfish was also accompanied by changes in the opsin tertiary structure. We found that the counterion in an opsin from the lens eye of the box jellyfish Carybdea rastonii (JellyOp) has also moved to a unique proximal location within the transmembrane bundle-E94 in TM2. Furthermore, we reveal that this Schiff base/counterion system includes an additional positive charge-R186-that has coevolved with E94 to functionally separate E94 and E181 in the chromophore-binding pocket of JellyOp. By engineering this pocket-neutralizing R186 and E94, or swapping E94 with the vertebrate counterion E113-we can recreate versions of the invertebrate and vertebrate counterion systems, respectively, supporting a relatively similar overall architecture in this region of animal opsins. In summary, our data establish the third only counterion site in animal opsins and reveal convergent evolution of tertiary structure in opsins from distantly related species with advanced visual systems.

Gershwin, L. A. (2001). "Systematics and biogeography of the jellyfish Aurelia labiata (Cnidaria: Scyphozoa)." Biol Bull **201**(1): 104-119.

The hypothesis that the common eastern North Pacific Aurelia is A. aurita is falsified with morphological analysis. The name Aurelia labiata is resurrected, and the species is redescribed, to refer to medusae differing from A. aurita by a suite of characters related to a broad and elongated manubrium. Specifically, the oral arms are short, separated by and arising from the base of the fleshy manubrium, and the planulae are brooded upon the manubrium itself, rather than on the oral arms. Aurelia aurita possesses no corresponding enlarged structure. Furthermore, the number of radial canals is typically much greater in A. labiata, and thus the canals often appear more anastomosed than in A. aurita. Finally, most A. labiata medusae possess a 16-scalloped bell margin, whereas the margin is 8-scalloped in most A. aurita. Separation of the two forms has previously been noted on the basis of allozyme and isozyme analyses and on the histology of the neuromuscular system. Partial 18S rDNA sequencing corroborates these findings. Three distinct morphotypes of A. labiata, corresponding to separate marine bioprovinces, have been identified among 17 populations from San Diego, California, to Prince William Sound, Alaska. The long-undisputed species A. limbata may be simply a color morph of A. labiata, or a species within a yet-unelaborated A. labiata species complex. The first known introduction of Aurelia cf. aurita into southern California waters is documented. Although traditional jellyfish taxonomy tends to recognize many species as cosmopolitan or nearly so, these results indicate that coastal species, such as A. labiata, may experience rapid divergence among isolated populations, and that the taxonomy of such species should therefore be scrutinized with special care.

Gershwin, L. A., et al. (2014). "Dangerous jellyfish blooms are predictable." J R Soc Interface **11**(96).

The potentially fatal Irukandji syndrome is relatively common in tropical waters throughout the world. It is caused by the sting of the Irukandji jellyfish, a family of box jellyfish that are almost impossible to detect in the water owing to their small size and transparency. Using collated medical records of stings and local weather conditions, we show that the presence of Irukandji blooms in coastal waters can be forecast on the basis of wind conditions. On the Great Barrier Reef, blooms largely coincide with relaxation of the prevailing southeasterly trade winds, with average conditions corresponding to near zero alongshore wind on the day prior to the sting. These conditions are consistent with hypotheses long held by local communities and provide a basis for designing management interventions that have the potential to eliminate the majority of stings.

Gershwin, L. A. and P. Dawes (2008). "Preliminary observations on the response of Chironex fleckeri (Cnidaria: Cubozoa: Chirodropida) to different colors of light." Biol Bull **215**(1): 57-62.

Cubozoans are well known for their attraction to light and light-colored objects. Two highly venomous types are a public safety concern in Australian waters and elsewhere: Chironex fleckeri, long considered the world's deadliest animal and colloquially called the box jellyfish; and the irukandjis, a group of at least 10 species that cause various degrees of debilitating illness. We were asked by the tourism industry whether there might be a color of light that box jellyfish and irukandjis are not attracted to, such that nighttime diving activities might pose less risk of being stung. Our preliminary trials with Chironex fleckeri indicated a marked positive response to lights

of white, red, yellow, green, orange, and blue. All colors elicited a strong and directed attraction to light; however, medusae slowed down their pulsation rate, streamed out their tentacles, and performed a series of figure-eight patterns back and forth through the lighted area when exposed to blue light, which we interpreted as feeding behavior. This compares curiously with a report subsequent to our testing, in which the small, mangrove-inhabiting cubomedusa Tripedalia cystophora and the beach-dwelling Chiropsella bronzie demonstrate a peak sensitivity to blue-green light in the region of 500 nm, and that the former is behaviorally attracted to blue and green light, but ignores red. This leaves open the possibility that Irukandji species, which are more closely related to Tripedalia than to Chironex, may be blind to red.

Gershwin, L. A., et al. (2013). "Biology and ecology of Irukandji jellyfish (Cnidaria: Cubozoa)." Adv Mar Biol **66**: 1-85.

Irukandji stings are a leading occupational health and safety issue for marine industries in tropical Australia and an emerging problem elsewhere in the Indo-Pacific and Caribbean. Their mild initial sting frequently results in debilitating illness, involving signs of sympathetic excess including excruciating pain, sweating, nausea and vomiting, hypertension and a feeling of impending doom; some cases also experience acute heart failure and pulmonary oedema. These jellyfish are typically small and nearly invisible, and their infestations are generally mysterious, making them scary to the general public, irresistible to the media, and disastrous for tourism. Research into these fascinating species has been largely driven by the medical profession and focused on treatment. Biological and ecological information is surprisingly sparse, and is scattered through grey literature or buried in dispersed publications, hampering understanding. Given that long-term climate forecasts tend toward conditions favourable to jellyfish ecology, that long-term legal forecasts tend toward increasing duty-of-care obligations, and that bioprospecting opportunities exist in the powerful Irukandji toxins, there is a clear need for information to help inform global research and robust management solutions. We synthesise and contextualise available information on Irukandji taxonomy, phylogeny, reproduction, vision, behaviour, feeding, distribution, seasonality, toxins, and safety. Despite Australia dominating the research in this area, there are probably well over 25 species worldwide that cause the syndrome and it is an understudied problem in the developing world. Major gaps in knowledge are identified for future research: our lack of clarity on the socio-economic impacts, and our need for time series and spatial surveys of the species, make this field particularly enticing.

Getino-Mamet, L. N., et al. (2017). "Isolation and characterization of 14 tetranucleotide microsatellite loci for the cannonball jellyfish (Stomolophus sp.) by next generation sequencing." Mol Biol Rep **44**(2): 257-260.

The Cannonball jellyfish (Stomolophus sp.) is a species of jellyfish with high relevance in artisanal fishing. Studies of their populations do not extend beyond the morphological descriptions knowing that presents a great morphological variability. However, there are no genetic studies to determine the number of independent populations, so microsatellite markers become a suitable option. Since there are no species-specific microsatellite loci, in this paper, 14 new microsatellite loci are characterized. Microsatellite loci were isolated de novo through next generation sequencing, by two runs on Illumina MiSeq. A total of 506,771,269 base pair were obtained, from which 142,616 were microsatellite loci, and 1546 of them could design primers. We tested 14 primer pairs on 32 individuals from Bahia de La Paz, Gulf of California. We observed low genetic variation among loci (mean number of alleles per locus = 4.33, mean observed heterozygosity 0.381, mean expected heterozygosity 0.501). These loci are the first ones described for the species and will be helpful to carry out genetic diversity and population genetics studies.

Gold, D. A., et al. (2015). "Structural and Developmental Disparity in the Tentacles of the Moon Jellyfish Aurelia sp.1." PLoS One **10**(8): e0134741.

Tentacles armed with stinging cells (cnidocytes) are a defining trait of the cnidarians, a phylum that includes sea anemones, corals, jellyfish, and hydras. While cnidarian tentacles are generally characterized as structures evolved for feeding and defense, significant variation exists between the tentacles of different species, and within the same species across different life stages and/or body regions. Such diversity suggests cryptic distinctions exist in tentacle function. In this paper, we use confocal and transmission electron microscopy to contrast the structure and development of tentacles in the moon jellyfish, Aurelia species 1. We show that polyp oral tentacles and medusa marginal tentacles display markedly different cellular and muscular architecture, as well as distinct patterns of cellular proliferation during growth. Many structural differences between these tentacle types may reflect biomechanical solutions to different feeding strategies, although further work would be required for a precise mechanistic understanding. However, differences in cell proliferation dynamics suggests that the two tentacle forms lack a conserved mechanism of development, challenging the textbook-notion that

cnidarian tentacles can be homologized into a conserved bauplan.

Gold, D. A., et al. (2016). "Cell tracking supports secondary gastrulation in the moon jellyfish Aurelia." Dev Genes Evol **226**(6): 383-387.

The moon jellyfish Aurelia exhibits a dramatic reorganization of tissue during its metamorphosis from planula larva to polyp. There are currently two competing hypotheses regarding the fate of embryonic germ layers during this metamorphosis. In one scenario, the original endoderm undergoes apoptosis and is replaced by a secondary endoderm derived from ectodermal cells. In the second scenario, both ectoderm and endoderm remain intact through development. In this study, we performed a pulse-chase experiment to trace the fate of larval ectodermal cells. We observed that prior to metamorphosis, ectodermal cells that proliferated early in larval development concentrate at the future oral end of the polyp. During metamorphosis, these cells migrate into the endoderm, extending all the way to the aboral portion of the gut. We therefore reject the hypothesis that larval endoderm remains intact during metamorphosis and provide additional support for the "secondary gastrulation" hypothesis. Aurelia appears to offer the first and only described case where a cnidarian derives its endoderm twice during normal development, adding to a growing body of evidence that germ layers can be dramatically reorganized in cnidarian life cycles.

Goldberg, R. B., et al. (1975). "DNA sequence organization in the genomes of five marine invertebrates." Chromosoma **51**(3): 225-251.

The arrangement of repetitive and non-repetitive sequence was studied in the genomic DNA of the oyster (Crassostrea virginica), the surf clam (Spisula solidissima), the horseshoe crab (Limulus polyphemus), a nemertean worm (Cerebratulus lacteus) and a jelly-fish (Aurelia aurita). Except for the jellyfish these animals belong to the protostomial branch of animal evolution, for which little information regarding DNA sequence organization has previously been available. The reassociation kinetics of short (250-300 nucleotide) and long (2,000-3,000 nucleotide) DNA fragments was studied by the hydroxyapatite method. It was shown that in each case a major fraction of the DNA consists of single copy sequences less than about 3,000 nucleotides in length, interspersed with short repetitive sequences. The lengths of the repetitive sequences were estimated by optical hyperchromicity and S1 nuclease measurements made on renaturation products. All the genomes studied include a prominent fraction of interspersed repetitive sequences about 300 nucleotides in length, as well as longer repetitive sequence regions.

Goldstein, J. and U. K. Steiner (2019). "Ecological drivers of jellyfish blooms - The complex life history of a 'well-known' medusa (Aurelia aurita)." J Anim Ecol.

Jellyfish blooms are conspicuous demographic events with significant ecological and socio-economic impact. Despite worldwide concern about an increased frequency and intensity of such mass occurrences, predicting their booms and busts remains challenging. Forecasting how jellyfish populations may respond to environmental change requires considering their complex life histories. Metagenic life cycles, which include a benthic polyp stage, can boost jellyfish mass occurrences via asexual recruitment of pelagic medusae. Here we present stage-structured matrix population models with monthly, individual-based demographic rates of all life stages of the moon jellyfish Aurelia aurita L. (sensu stricto). We investigate the life-stage dynamics of these complex populations under low and high food conditions to illustrate how changes in medusa density depend on non-medusa stage dynamics. We show that increased food availability can be an important ecological driver of jellyfish mass occurrences, as it can temporarily shift the population structure from polyp- to medusa-dominated. Projecting populations for a winter warming scenario additionally enhanced the booms and busts of jellyfish blooms. We identify demographic key variables that control the intensity and frequency of jellyfish blooms in response to environmental drivers such as habitat eutrophication and climate change. By contributing to an improved understanding of mass occurrence phenomena, our findings provide perspective for future management of ecosystem health.

Grigoriev, N. G., et al. (1999). "Modulation of jellyfish potassium channels by external potassium ions." J Neurophysiol **82**(4): 1728-1739.

The amplitude of an A-like potassium current (I (Kfast)) in identified cultured motor neurons isolated from the jellyfish Polyorchis penicillatus was found to be strongly modulated by extracellular potassium ([K (+)] (out)). When expressed in Xenopus oocytes, two jellyfish Shaker-like genes, jShak1 and jShak2, coding for potassium channels, exhibited similar modulation by [K (+)] (out) over a range of concentrations from 0 to 100 mM. jShak2-encoded channels also showed a decreased rate of inactivation and an increased rate of recovery from inactivation at high [K (+)] (out). Using site-directed mutagenesis we show that inactivation of jShak2 can be ascribed to an unusual combination of a weak "implicit" N-type inactivation mechanism and a

strong, fast, potassium-sensitive C-type mechanism. Interaction between the two forms of inactivation is responsible for the potassium dependence of cumulative inactivation. Inactivation of jShak1 was determined primarily by a strong "ball and chain" mechanism similar to fruit fly Shaker channels. Experiments using fast perfusion of outside-out patches with jShak2 channels were used to establish that the effects of [K (+)] (out) on the peak current amplitude and inactivation were due to processes occurring at either different sites located at the external channel mouth with different retention times for potassium ions, or at the same site (s) where retention time is determined by state-dependent conformations of the channel protein. The possible physiological implications of potassium sensitivity of high-threshold potassium A-like currents is discussed.

Grigoriev, N. G., et al. (1999). "Residues in a jellyfish shaker-like channel involved in modulation by external potassium." J Neurophysiol **82**(4): 1740-1747.

The jellyfish gene, jShak2, coded for a potassium channel that showed increased conductance and a decreased inactivation rate as [K (+)] (out) was increased. The relative modulatory effectiveness of K (+), Rb (+), Cs (+), and Na (+) indicated that a weak-field-strength site is present. Cysteine substituted mutants (L369C and F370C) of an N-terminal truncated construct, (jShak2Delta2-38) which only showed C-type inactivation, were used to establish the position and nature of this site (s). In comparison with jShak2Delta2-38 and F370C, L369C showed a greater relative increase in peak current when [K (+)] (out) was increased from 1 to 100 mM because the affinity of this site was reduced at low [K (+)] (out). Increasing [K (+)] (out) had little effect on the rate of inactivation of L369C; however, the appearance of a second, hyperbolic component to the inactivation curve for F370C indicated that this mutation had increased the affinity of the low-affinity site by bringing the backbone oxygens closer together. Methanethiosulphonate reagents were used to form positively (MTSET), negatively (MTSES), and neutrally (MTSM) charged side groups on the cysteine-substituted residues at the purported K (+) binding site (s) in the channel mouth and conductance and inactivation kinetic measurements made. The reduced affinity of the site produced by the mutation L369C was probably due to the increased hydrophobicity of cysteine, which changed the relative positions of carbonyl oxygens since MTSES modification did not form a high-field-strength site as might be expected if the cysteine residues project into the pore. Addition of the side chain -CH (2)-S-S-CH (3), which is similar to the side chain of methionine, a conserved residue in many potassium channels, resulted in an increased peak current and reduced inactivation rate, hence a higher affinity binding site. Modification of cysteine substituted mutants occurred more readily from the inactivated state confirming that side chains probably rotate into the pore from a buried position when no K ions are in the pore. In conclusion we were able to show that, as for certain potassium channels in higher taxonomic groups, the site (s) responsible for modulation by [K (+)] (out) is situated just outside the selectivity filter and is represented by the residues L (369) and F (370) in the jellyfish Shaker channel, jShak2.

Grimmelikhuijzen, C. J., et al. (1988). "Isolation of pyroGlu-Leu-Leu-Gly-Gly-Arg-Phe-NH2 (Pol-RFamide), a novel neuropeptide from hydromedusae." Brain Res **475**(1): 198-203.

The hydromedusa Polyorchis penicillatus is a good model system to study neurotransmission in coelenterates. Using a radioimmunoassay for the peptide sequence Arg-Phe-NH2 (RFamide), two peptides have now been purified from acetic acid extracts of this medusa. The structure of one of these peptides was established as pyroGlu-Leu-Leu-Gly-Gly-Arg-Phe-NH2, and was named Pol-RFamide. This peptide belongs to the same peptide family as a recently isolated neuropeptide from sea anemones (pyroGlu-Gly-Arg-Phe-NH2). Using antisera to Pol-RFamide, the peptide was found to be exclusively localized in neurones of Polyorchis, among them neurones associated with smooth-muscle fibres. This suggests that Pol-RFamide might be a transmitter or modulator at neuromuscular junctions.

Grimmelikhuijzen, C. J., et al. (1992). "Isolation of the neuropeptide less than Glu-Trp-Leu-Lys-Gly-Arg-Phe-NH2 (Pol-RFamide II) from the hydromedusa Polyorchis penicillatus." Biochem Biophys Res Commun **183**(2): 375-382.

Using a radioimmunoassay for the sequence Arg-Phe-NH2 (RFamide), we have isolated the peptide less than Glu-Trp-Leu-Lys-Gly-Arg-Phe-NH2 (Pol-RFamide II) from acetic acid extracts of the hydromedusa Polyorchis penicillatus. This peptide is a neuropeptide and constitutes a peptide family together with less than Glu-Leu-Leu-Gly-Gly-Arg-Phe-NH2 (Pol-RFamide I), the first neuropeptide isolated from Polyorchis, and less than Glu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide isolated from sea anemones and sea pansies.

Grimmelikhuijzen, C. J. and A. N. Spencer (1984). "FMRFamide immunoreactivity in the nervous system of the medusa Polyorchis penicillatus." J Comp Neurol **230**(3): 361-371.

Three different antisera to the molluscan neuropeptide Phe-Met-Arg-Phe-amide (FMRFamide) and two different antisera to the fragment RFamide were used to stain sections or whole mounts of the hydrozoan medusa Polyorchis penicillatus. All antisera stained the same neuronal structures. Strong immunoreactivity was found in neurons of the ectodermal nerve nets of the manubrium and tentacles, in neurons of the sensory epithelium, and in neurons at the periphery of the sphincter muscle. Strong immunoreactivity was also present in processes and perikarya of the whole outer nerve ring, in the ocellar nerves, and in nerve cells lying at the periphery of the ocellus. The inner nerve ring contained a moderate number of immunoreactive processes and perikarya, which were distinct from the swimming motor neurons. In contrast to the situation in the hydrozoan polyp Hydra attenuata, no immunoreactivity was found with several antisera to oxytocin/vasopressin and bombesin/gastrin-releasing peptide. The morphology and location of most FMRFamide-immunoreactive neurons in Polyorchis coincides with two identified neuronal systems, which have been recently discovered from neurophysiological studies.

Kim, H. M., et al. (2019). "The genome of the giant Nomura's jellyfish sheds light on the early evolution of active predation." BMC Biol **17**(1): 28.

BACKGROUND: Unique among cnidarians, jellyfish have remarkable morphological and biochemical innovations that allow them to actively hunt in the water column and were some of the first animals to become free-swimming. The class Scyphozoa, or true jellyfish, are characterized by a predominant medusa life-stage consisting of a bell and venomous tentacles used for hunting and defense, as well as using pulsed jet propulsion for mobility. Here, we present the genome of the giant Nomura's jellyfish (Nemopilema nomurai) to understand the genetic basis of these key innovations. RESULTS: We sequenced the genome and transcriptomes of the bell and tentacles of the giant Nomura's jellyfish as well as transcriptomes across tissues and developmental stages of the Sanderia malayensis jellyfish. Analyses of the Nemopilema and other cnidarian genomes revealed adaptations associated with swimming, marked by codon bias in muscle contraction and expansion of neurotransmitter genes, along with expanded Myosin type II family and venom domains, possibly contributing to jellyfish mobility and active predation. We also identified gene family expansions of Wnt and posterior Hox genes and discovered the important role of retinoic acid signaling in this ancient lineage of metazoans, which together may be related to the unique jellyfish body plan (medusa formation). CONCLUSIONS: Taken together, the Nemopilema jellyfish genome and transcriptomes genetically confirm their unique morphological and physiological traits, which may have contributed to the success of jellyfish as early multi-cellular predators.

Kim, J. H., et al. (2018). "Fatal Pulmonary Edema in a Child After Jellyfish Stings in Korea." Wilderness Environ Med **29**(4): 527-530.

Jellyfish have been increasing at a global scale in recent years. These blooms not only have deleterious effects on marine ecosystems, they also increase the risk of jellyfish stings and accompanying envenomation. Here, we report a fatal case of pulmonary edema caused by jellyfish envenomation in a child in Korea. The patient died 4 h after envenomation despite cardiopulmonary resuscitation. Nemopilema nomurai was the suspected species of jellyfish encountered by the patient, although we are unable to confirm this. With this case report, we aim to inform on the serious issue of toxicity associated with jellyfish species that bloom mainly along Korean, east Chinese, and Japanese shores and to discuss appropriate first aid methods in case of jellyfish stings.

Kim, S. K. and J. C. Wang (1998). "Localization of F plasmid SopB protein to positions near the poles of Escherichia coli cells." Proc Natl Acad Sci U S A **95**(4): 1523-1527.

The subcellular localization of the SopB protein, which is encoded by the Escherichia coli F plasmid and is involved in the partition of the single-copy plasmid, was directly visualized through the expression of the protein fused to the jellyfish green fluorescent protein (GFP). The fusion protein, but not GFP itself, was found to localize to positions close but not at the poles of exponentially growing cells. Neither the presence of other F-encoded proteins nor the binding of SopB to its recognition sites within the sopC locus of F is required for this localization. Examination of derivatives of the fusion protein lacking various regions of SopB suggests that the signal for the cellular localization of SopB resides in a region close to its N terminus. It is plausible that the near polar localization of SopB may serve the function of keeping a segregated pair of F plasmids apart while the cell septum is being formed. The plausible relation between the specific location of SopB and its suppression of sopC-linked genes when overexpressed is also discussed.

Kim, S. S., et al. (2001). "Generation of replication-defective helper-free vectors based on simian immunodeficiency virus." Virology **282**(1): 154-167.

A systematic study on generating simian immunodeficiency virus (SIV)-based vectors was

carried out. The goal was to generate helper-free, replication-defective SIVmac-based vectors at high titers. The general approach was to cotransfect into human 293T cells a plasmid carrying the vector construct along with two helper plasmids that together expressed the SIVmac virion proteins. Initial vectors carried the bacterial beta-galactosidase gene (beta-gal). These vectors had a technical difficulty: "pseudotransduction" of beta-gal protein produced during the 293T cell transfections. As a result, infection of cultures with these vector stocks also resulted in passive transfer into, and X-gal staining of, cells that had not actually been infected by the vector. A second generation of vectors expressing the enhanced jellyfish green fluorescence protein (EGFP) was not subject to this artifact. A systematic study of the SIVmac-based EGFP vectors was carried out. Helper-free vector stocks were obtained when helper plasmids lacking the SIVmac packaging signals were used. By employing envelope helper plasmids derived from different SIVmac isolates, it was possible to generate SIVmac-based vectors pseudotyped with envelope proteins of different cell tropism. Optimization of vector and helper plasmid structures, transfection conditions, and infection procedures ultimately yielded vector titers in excess of 10(6)/ml.

Kim, S. S., et al. (2001). "Use of helper-free replication-defective simian immunodeficiency virus-based vectors to study macrophage and T tropism: evidence for distinct levels of restriction in primary macrophages and a T-cell line." J Virol **75**(5): 2288-2300.

Cell tropism of human and simian immunodeficiency viruses (HIV and SIV, respectively) is governed in part by interactions between the viral envelope protein and the cellular receptors. However, there is evidence that envelope-host cell interactions also affect postentry steps in viral replication. We used a helper-free replication-defective SIV macaque (SIVmac)-based retroviral vector carrying the enhanced jellyfish green fluorescent protein inserted into the nef region (V1EGFP) to examine SIV tropism in a single cycle of infection. Vector stocks containing envelope proteins from three different SIVmac clones, namely, SIVmac239 (T-lymphocyte tropic [T-tropic]), SIVmac316 (macrophage tropic [M-tropic]), and SIVmac1A11 (dualtropic), were tested. SIVmac239 replicates efficiently in many human T-cell lines, but it does not efficiently infect primary rhesus macrophages. Conversely, SIVmac316 efficiently infects primary macrophages, but it does not replicate in Molt4-Clone8 (M4C8) T cells. SIVmac1A11 replicates efficiently in both cell types. When primary macrophages were infected with V1EGFP pseudotyped by SIVmac316 or SIVmac1A11 envelopes, the infection was substantially (ca. 200- to 300-fold) more efficient than for the SIVmac239 pseudotype. Thus, in primary macrophages, a major component of M versus T tropism involves relatively early events in the infection cycle. Quantitative PCR studies indicated that synthesis and transport of vector DNA into the nucleus were similar for macrophages infected with the clone 239 and 316 pseudotypes, suggesting that the restriction for SIVmac239 infection is after reverse transcription and nuclear import of viral DNA. When the same vector pseudotypes were used to infect M4C8 cells, they all showed approximately equivalent infectivities, even though replication-competent SIVmac316 does not continue to replicate in these cells. Therefore, in M4C8 cells, restriction involves a late step in the infection cycle (after proviral integration and expression). Thus, depending on the cell type infected, envelope-dependent cell interactions that govern SIV M and T tropism may involve different steps in infection.

Lin, L., et al. (2010). "Ultrasound-mediated DNA transformation in thermophilic gram-positive anaerobes." PLoS One **5**(9): e12582.

BACKGROUND: Thermophilic, Gram-positive, anaerobic bacteria (TGPAs) are generally recalcitrant to chemical and electrotransformation due to their special cell-wall structure and the low intrinsic permeability of plasma membranes. METHODOLOGY/PRINCIPAL FINDINGS: Here we established for any Gram-positive or thermophiles an ultrasound-based sonoporation as a simple, rapid, and minimally invasive method to genetically transform TGPAs. We showed that by applying a 40 kHz ultrasound frequency over a 20-second exposure, Texas red-conjugated dextran was delivered with 27% efficiency into Thermoanaerobacter sp. X514, a TGPA that can utilize both pentose and hexose for ethanol production. Experiments that delivered plasmids showed that host-cell viability and plasmid DNA integrity were not compromised. Via sonoporation, shuttle vectors pHL015 harboring a jellyfish gfp gene and pIKM2 encoding a Clostridium thermocellum beta-1,4-glucanase gene were delivered into X514 with an efficiency of 6x10(2) transformants/microg of methylated DNA. Delivery into X514 cells was confirmed via detecting the kanamycin-resistance gene for pIKM2, while confirmation of pHL015 was detected by visualization of fluorescence signals of secondary host-cells following a plasmid-rescue experiment. Furthermore, the foreign beta-1,4-glucanase gene was functionally expressed in X514, converting the host into a prototypic thermophilic consolidated bioprocessing organism that is not only ethanologenic but cellulolytic. CONCLUSIONS/SIGNIFICANCE: In this study, we

developed an ultrasound-based sonoporation method in TGPAs. This new DNA-delivery method could significantly improve the throughput in developing genetic systems for TGPAs, many of which are of industrial interest yet remain difficult to manipulate genetically.

Lin, Q., et al. (2018). "[Ecological carrying capacity of shellfish in the Yellow River estuary and its adjacent waters.]." Ying Yong Sheng Tai Xue Bao **29**(9): 3131-3138.

Yellow River Estuary and adjacent waters are famous shellfish production areas. Mactra veseriformis, Ruditapes philippinarum, and Meretix meretrix are important species for stocking enhancement. At present, the annual output of shellfish bottom sowing culture has reached 300 thousand tons, with an output value of 1.54 billion RMB. Over stocking of shellfish will cause environmental changes in marine, increase shellfish mortality and endanger ecosystem health. Accordingly, the assessment of the carrying capacity for shellfish based on ecosystem underpins responsible marine fisheries enhancement. In this study, an Ecopath mass-balance model of the Yellow River estuary and adjacent waters ecosystem constructed by Ecopath with Ecosim software was used to analyze the summary statistics parameters of the ecosystem, mixed trophic interactions, and to calculate the ecological carrying capacity of shellfish. The results showed that the ratio of total primary production/total respiration (TPP/TR) was 3.45, that of total primary production/total biomass (TPP/B) was 38.91, with the low Finn cycling index (0.028), high surplus production being 961.24 t.km (-2).a (-1) and low system connecting index (0.38), indicating that this ecosystem was at an unstable development stage. The increases of shellfish biomass would have positive impacts on Gobiidae, shrimps, crabs, and negative impacts on pelagic fishes, demersal fishes, edible jellyfish, zooplankton. Current biomass of shellfish was 5.5 t.km (-2), with the potential enhancement. Based on the Ecopath model, the primary assessment of carrying capacity of shellfish was 18.22 t.km (-2) in Yellow River estuary and its adjacent waters. This study provides scientific references for the sustainable development of fisheries resources in the Yellow River estuary.

Lin, Y. C., et al. (2001). "The anatomy of the nervous system of the hydrozoan jellyfish, Polyorchis penicillatus, as revealed by a monoclonal antibody." Invert Neurosci **4**(2): 65-75.

Dissociated cells from the margin and tentacles of the hydromedusa Polyorchis penicillatus were centrifuged in a Percoll gradient to remove cnidocytes. The resulting formaldehyde-fixed cells were used to inoculate mice to produce monoclonal antibodies. One of the hybridomas, which secreted antibodies against all neurons, was cloned and designated as mAb 5C6. Immunohistochemical labelling with mAb 5C6 of whole-mount preparations and paraffin sections provided a far more complete picture of the organisation of the hydromedusan nervous system than was previously available when using neuronal labelling techniques that restrict labelling to certain neuronal types. Besides confirming anatomical features described in earlier studies these techniques allowed us to discover a number of new structures and to determine connections that were only suspected. Such findings included:1. The discovery of an arch-like connection between the swimming motor neuron network at the apices of the subumbrellar muscle sheets 2. An orthogonal network connecting each pair of radial nerves in each radius 3. Continuity of a central branch of the radial nerve with the radial innervation of the manubrium 4. Details of the sensory neuronal contribution to the microanatomy of the ocelli and cnidocyte batteries 5. Presence of specialised receptor cells in the margin at the bases of tentacles 6. Neurons apparently innervating the radial muscles of the velum 7. Isolated neurons in the peduncle and gonads

Lin, Y. C., et al. (2000). "Wound healing in jellyfish striated muscle involves rapid switching between two modes of cell motility and a change in the source of regulatory calcium." Dev Biol **225**(1): 87-100.

Small wounds (1.2 mm in diameter) made in the sheet of myoepithelial cells forming the "swimming" muscle of the jellyfish, Polyorchis penicillatus, were closed within 10 h by epithelial cells migrating centripetally to the wound center. Some 24 to 48 h later these cells redifferentiated into fully contractile muscle cells. Labeling with bromodeoxyuridine failed to reveal any cell proliferation during this process. Phenotype switching (within 1 h) from contractile muscle cells to migratory cells did not require synthesis of new protein as shown by treatment with 40 microM cycloheximide. Excitation-contraction coupling in undamaged muscle depended on entry of Ca (2+) through voltage-gated ion channels, as shown by a block of contractility by 40 microM nitrendipine and also on calcium released from intracellular stores since caffeine (10 mM) caused a 25% reduction in contractile force. In contrast, migratory cells did not require a source of extracellular calcium since migration was unimpeded by low (1 microM) free Ca (2+) or nitrendipine. Instead, modulatory calcium was derived from intracellular stores since caffeine (10 mM) and thapsigargin (10 microM) slowed migration. This lack of dependence on calcium influx in

migratory cells was further confirmed by a dramatic down-regulation in voltage-gated inward current as shown by whole-cell patch recordings.

Lin, Y. C. and A. N. Spencer (2001). "Calcium currents from jellyfish striated muscle cells: preservation of phenotype, characterisation of currents and channel localisation." J Exp Biol **204**(Pt 21): 3717-3726.

When striated muscle cells of the jellyfish Polyorchis penicillatus were dissociated at 30 degrees C they retained their in vivo morphology and the integrity of ionic currents. This contrasted with cells dissociated at room temperature that rarely expressed any inward currents. Whole-cell, patch-clamp recordings from dissociated muscle cells revealed that the inward component of the total ionic current consisted of only one calcium current. This calcium current activated at -70 mV, peaked at -30 mV, and inactivated within 5 ms. In comparison with barium and strontium ions, calcium ions were the preferred current carriers. Calcium channels can be blocked by dihydropyridines and nickel ions at micromolar levels. Several properties of this current are reminiscent of T-type calcium currents. Localisation of this channel using the fluorescent channel blocker fDHP and the fluorescent dye RH414 indicated that myofibres had a higher density of these channels than the somata.

Lin, Y. C. and A. N. Spencer (2001). "Localisation of intracellular calcium stores in the striated muscles of the jellyfish Polyorchis penicillatus: possible involvement in excitation-contraction coupling." J Exp Biol **204**(Pt 21): 3727-3736.

When jellyfish striated muscles were stimulated directly, the amplitude of contractile tension increased as the stimulation frequency increased. Application of 10 mmol l (-1) caffeine reduced the amplitude of contractile tension and abolished this facilitatory relationship, indicating that calcium stores participate in excitation-contraction coupling. Calcium stores were identified ultrastructurally using enzymatic histochemistry to localize CaATPases, and potassium dichromate to precipitate calcium. Electron energy-loss spectroscopy was used to verify the presence of calcium in precipitates. Both CaATPase and calcium were localised in membrane-bound vesicles beneath the sarcolemma. We concluded that sub-sarcolemmal vesicles could act as calcium stores and participate in excitation-contraction coupling.

Lin, Z. F. and S. H. Wang (2019). "Research progress in scyphozoan polyp strobilation-induced factors and regulation mechanism." Ying Yong Sheng Tai Xue Bao **30**(3): 1057-1066.

Strobilation is a key stage for polyp-to-jellyfish transition. Knowledge about the strobilation-induced factors and the underlying molecular regulation mechanism could help control jellyfish bloom in nature, improve jellyfish artificial breeding, as well as get insight about the ancestral molecular origin of metamorphosis of amphibians, insect and cnidarians. Natural factors, including temperature, illumination, salinity, and symbiotic zooxanthellae, could induce strobilation. The mode of strobilation and how these natural factors irritate strobilation are distinct in different jellyfish species. Chemicals including indole derivates, 9-cis retinoic acid, elemental iodine, hydrogen peroxide, could also induce strobilation in laboratory. Indole derivates are effective inducers to most scyphozoan species. The molecular mechanism of strobilation is unclear. Results from moon jelly reveal that RxR signaling pathway plays an important role during strobilation. A secreted moon jelly-special protein named CL390 may serve as a strobilation-induced hormone precursor. These results imply that morphological differences in medusa production may mask similarities at the cellular level in different jellyfish species. The molecular mechanism of metamorphosis in jellyfish may share some consistency with amphibians and insects.

Link, C. D., et al. (1999). "Direct observation of stress response in Caenorhabditis elegans using a reporter transgene." Cell Stress Chaperones **4**(4): 235-242.

Transgenic Caenorhabditis elegans expressing jellyfish Green Fluorescent Protein under the control of the promoter for the inducible small heat shock protein gene hsp-16-2 have been constructed. Transgene expression parallels that of the endogenous hsp-16 gene, and, therefore, allows direct visualization, localization, and quantitation of hsp-16 expression in living animals. In addition to the expected upregulation by heat shock, we show that a variety of stresses, including exposure to superoxide-generating redox-cycling quinones and the expression of the human beta amyloid peptide, specifically induce the reporter transgene. The quinone induction is suppressed by coincubation with L-ascorbate. The ability to directly observe the stress response in living animals significantly simplifies the identification of both exogenous treatments and genetic alterations that modulate stress response, and possibly life span, in C. elegans.

Lipinski, D. and K. Mohseni (2009). "Flow structures and fluid transport for the hydromedusae Sarsia tubulosa and Aequorea victoria." J Exp Biol **212**(Pt 15): 2436-2447.

The flow structures produced by the hydromedusae Sarsia tubulosa and Aequorea victoria

are examined using direct numerical simulation and Lagrangian coherent structures (LCS). Body motion of each hydromedusa is digitized and input to a CFD program. Sarsia tubulosa uses a jetting type of propulsion, emitting a single, strong, fast-moving vortex ring during each swimming cycle while a secondary vortex of opposite rotation remains trapped within the subumbrellar region. The ejected vortex is highly energetic and moves away from the hydromedusa very rapidly. Conversely, A. victoria, a paddling type hydromedusa, is found to draw fluid from the upper bell surface and eject this fluid in pairs of counter-rotating, slow-moving vortices near the bell margins. Unlike S. tubulosa, both vortices are ejected during the swimming cycle of A. victoria and linger in the tentacle region. In fact, we find that A. victoria and S. tubulosa swim with Strouhal numbers of 1.1 and 0.1, respectively. This means that vortices produced by A. victoria remain in the tentacle region roughly 10 times as long as those produced by S. tubulosa, which presents an excellent feeding opportunity during swimming for A. victoria. Finally, we examine the pressure on the interior bell surface of both hydromedusae and the velocity profile in the wake. We find that S. tubulosa produces very uniform pressure on the interior of the bell as well as a very uniform jet velocity across the velar opening. This type of swimming can be well approximated by a slug model, but A. victoria creates more complicated pressure and velocity profiles. We are also able to estimate the power output of S. tubulosa and find good agreement with other hydromedusan power outputs. All results are based on numerical simulations of the swimming jellyfish.

Lipinski, D. and K. Mohseni (2010). "A ridge tracking algorithm and error estimate for efficient computation of Lagrangian coherent structures." Chaos **20**(1): 017504.

A ridge tracking algorithm for the computation and extraction of Lagrangian coherent structures (LCS) is developed. This algorithm takes advantage of the spatial coherence of LCS by tracking the ridges which form LCS to avoid unnecessary computations away from the ridges. We also make use of the temporal coherence of LCS by approximating the time dependent motion of the LCS with passive tracer particles. To justify this approximation, we provide an estimate of the difference between the motion of the LCS and that of tracer particles which begin on the LCS. In addition to the speedup in computational time, the ridge tracking algorithm uses less memory and results in smaller output files than the standard LCS algorithm. Finally, we apply our ridge tracking algorithm to two test cases, an analytically defined double gyre as well as the more complicated example of the numerical simulation of a swimming jellyfish. In our test cases, we find up to a 35 times speedup when compared with the standard LCS algorithm.

Lippincott-Schwartz, J. (2001). "The secretory membrane system studied in real-time. Robert Feulgen Prize Lecture, 2001." Histochem Cell Biol **116**(2): 97-107.

The discovery and development of green fluorescent protein (GFP) from the jellyfish, Aequorea victoria, has revolutionized studies on protein localization and dynamics by allowing direct observation of a protein's life history and pathway in living cells, previously only deduced from genetic, biochemical, or immunolabeling studies. Applied to the secretory membrane system, which regulates delivery of newly synthesized proteins and lipids to the cell surface, GFP-based studies are providing important new insights into the maintenance and biogenesis of organelles, as well as the origin, pathway, and fate of secretory transport intermediates.

Lippmann, J. M., et al. (2011). "Fatal and severe box jellyfish stings, including Irukandji stings, in Malaysia, 2000-2010." J Travel Med **18**(4): 275-281.

BACKGROUND: Jellyfish are a common cause of injury throughout the world, with fatalities and severe systemic events not uncommon after tropical stings. The internet is a recent innovation to gain information on real-time health issues of travel destinations, including Southeast Asia. METHODS: We applied the model of internet-based retrospective health data aggregation, through the Divers Alert Network Asia-Pacific (DAN AP), together with more conventional methods of literature and media searches, to document the health significance, and clinical spectrum, of box jellyfish stings in Malaysia for the period January 1, 2000 to July 30, 2010. RESULTS: Three fatalities, consistent with chirodropid envenomation, were identified for the period-all tourists to Malaysia. Non-fatal chirodropid stings were also documented. During 2010, seven cases consistent with moderately severe Irukandji syndrome were reported to DAN and two representative cases are discussed here. Photographs of chirodropid (multi-tentacled), carybdeid (four-tentacled) box jellyfish, and of severe sting lesions were also submitted to DAN during this period. CONCLUSIONS: This study suggests that the frequency and severity of jellyfish stings affecting tourists in Southeast Asia have been significantly underestimated. Severe and fatal cases of chirodropid-type stings occur in coastal waters off Peninsular Malaysia and Sabah, Borneo. Indeed, the first Malaysian cases consistent with Irukandji-like syndrome are reported here. Reports to DAN, a provider of emergency advice to divers, offer one

method to address the historic lack of formalized reporting mechanisms for such events, for photo-documentation of the possible culprit species and treatment advice. The application of marine stinger prevention and treatment principles throughout the region may help reduce the incidence and severity of such stings. Meanwhile travelers and their medical advisors should be aware of the hazards of these stings throughout the Asia-Pacific.

Lisenkova, A. A., et al. (2017). "Complete mitochondrial genome and evolutionary analysis of Turritopsis dohrnii, the "immortal" jellyfish with a reversible life-cycle." Mol Phylogenet Evol **107**: 232-238.

Turritopsis dohrnii (Cnidaria, Hydrozoa, Hydroidolina, Anthoathecata) is the only known metazoan that is capable of reversing its life cycle via morph rejuvenation from the adult medusa stage to the juvenile polyp stage. Here, we present a complete mitochondrial (mt) genome sequence of T. dohrnii, which harbors genes for 13 proteins, two transfer RNAs, and two ribosomal RNAs. The T. dohrnii mt genome is characterized by typical features of species in the Hydroidolina subclass, such as a high A+T content (71.5%), reversed transcriptional orientation for the large rRNA subunit gene, and paucity of CGN codons. An incomplete complementary duplicate of the cox1 gene was found at the 5' end of the T. dohrnii mt chromosome, as were variable repeat regions flanking the chromosome. We identified species-specific variations (nad5, nad6, cob, and cox1 genes) and putative selective constraints (atp8, nad1, nad2, and nad5 genes) in the mt genes of T. dohrnii, and predicted alterations in tertiary structures of respiratory chain proteins (NADH4, NADH5, and COX1 proteins) of T. dohrnii. Based on comparative analyses of available hydrozoan mt genomes, we also determined the taxonomic relationships of T. dohrnii, recovering Filifera IV as a paraphyletic taxon, and assessed intraspecific diversity of various Hydrozoa species.

Litschauer-Poursadrollah, M., et al. (2010). "[Jellyfish and poison-producing animals that endanger swimmers]." Dtsch Med Wochenschr **135**(21): 1073-1077.

Exposure to fresh water as well as to sea water can cause unpleasant consequences. The water of lakes or biotopes may be the reason for severe itching reactions on exposed skin, caused by cercariae. Exposure to seawater may lead to skin affections including itching or burning urticarial lesions as well as life threatening reactions. The causes for these reactions are especially species of jellyfish.

Little, M. (2002). "Is there a role for the use of pressure immobilization bandages in the treatment of jellyfish envenomation in Australia?" Emerg Med (Fremantle) **14**(2): 171-174.

BACKGROUND: The aim of this paper was to review the literature relating to the use of pressure immobilization bandages in the first aid management of jellyfish sting in Australia and to attempt to make a recommendation about their use based on the current literature. METHODS: A descriptive review of all published cases of jellyfish envenomation in Australia was performed, with specific focus on the discussion of pressure immobilization bandages in the management of such cases. A Medline search was performed using the key words listed for this article. Selected articles were reviewed and further publications were identified from the published reference lists given in the selected articles. RESULTS: The published articles were grouped into three groups: in vitro evidence, case reports and editorial comment (either in journals or book). Fifteen references were identified that discussed the use of pressure immobilization bandages in the management of jellyfish envenomation. Other articles were identified that had significant management issues discussion. CONCLUSION: Most of the 'jellyfish' literature is in relation to envenomation by Chironex fleckeri. This jellyfish is usually found in tropical Australia and has resulted in the deaths of 67 people in Australia. The last death was near Cairns in 2000. Unfortunately, there are few good data on marine envenomations, with most of the literature being Chironex envenomation case reports. There are minimal data on the effect of pressure immobilization bandages on other jellyfish envenomations. There is no good evidence to support the use of pressure immobilization bandages in the management of jellyfish sting in Australia [corrected].

Low, A., et al. (2009). "Enhanced replication and pathogenesis of Moloney murine leukemia virus in mice defective in the murine APOBEC3 gene." Virology **385**(2): 455-463.

Human APOBEC3G (hA3G), a member of the AID/APOBEC family of deaminases, is a restriction factor for human immunodeficiency virus (HIV). In the absence of the viral Vif protein hA3G is packaged into virions and during reverse transcription in a recipient cell it deaminates cytosines, leading to G-->A hypermutation and inactivation of the viral DNA. Unlike humans, who carry seven APOBEC3 genes, mice only carry one, mA3. Thus the role of mA3 in restriction of retroviral infection could be studied in mA3 -/- knockout mice, where the gene is inactivated. M-MuLV-infected mA3 -/- mice showed substantially higher levels of infection at very early times compared

to wild-type mice (ca. 2 logs at 0-10 days), particularly in the bone marrow and spleen. Restriction of M-MuLV infection was studied ex vivo in primary bone marrow-derived dendritic cells (BMDCs) that express or lack mA3, using an M-MuLV-based retroviral vector expressing enhanced jellyfish green fluorescent protein (EGFP). The results indicated that mA3 within the virions as well as mA3 in the recipient cell contribute to resistance to infection in BMDCs. Finally, M-MuLV-infected mA3 +/+ mice developed leukemia more slowly compared to animals lacking one or both copies of mA3 although the resulting disease was similar (T-lymphoma). These studies indicate that mA3 restricts replication and pathogenesis of M-MuLV in vivo.

Lowder, M., et al. (2000). "Effect of starvation and the viable-but-nonculturable state on green fluorescent protein (GFP) fluorescence in GFP-tagged Pseudomonas fluorescens A506." Appl Environ Microbiol **66**(8): 3160-3165.

The green fluorescent protein (GFP) gene, gfp, of the jellyfish Aequorea victoria is being used as a reporter system for gene expression and as a marker for tracking prokaryotes and eukaryotes. Cells that have been genetically altered with the gfp gene produce a protein that fluoresces when it is excited by UV light. This unique phenotype allows gfp-tagged cells to be specifically monitored by nondestructive means. In this study we determined whether a gfp-tagged strain of Pseudomonas fluorescens continued to fluoresce under conditions under which the cells were starved, viable but nonculturable (VBNC), or dead. Epifluorescent microscopy, flow cytometry, and spectrofluorometry were used to measure fluorescence intensity in starved, VBNC, and dead or dying cells. Results obtained by using flow cytometry indicated that microcosms containing VBNC cells, which were obtained by incubation under stress conditions (starvation at 37.5 degrees C), fluoresced at an intensity that was at least 80% of the intensity of nonstressed cultures. Similarly, microcosms containing starved cells incubated at 5 and 30 degrees C had fluorescence intensities that were 90 to 110% of the intensity of nonstressed cells. VBNC cells remained fluorescent during the entire 6-month incubation period. In addition, cells starved at 5 or 30 degrees C remained fluorescent for at least 11 months. Treatment of the cells with UV light or incubation at 39 or 50 degrees C resulted in a loss of GFP from the cells. There was a strong correlation between cell death and leakage of GFP from the cells, although the extent of leakage varied depending on the treatment. Most dead cells were not GFP fluorescent, but a small proportion of the dead cells retained some GFP at a lower concentration than the concentration in live cells. Our results suggest that gfp-tagged cells remain fluorescent following starvation and entry into the VBNC state but that fluorescence is lost when the cells die, presumably because membrane integrity is lost.

Lowik, C. W., et al. (2009). "Whole body optical imaging in small animals and its translation to the clinic: intra-operative optical imaging guided surgery." Eur J Cancer **45 Suppl 1**: 391-393.

Whole body optical imaging using bioluminescence or fluorescence is one of the most rapidly emerging technologies to non-invasively follow all kinds of molecular and cellular processes in small animals. Using tomographic approaches it is now also possible to get better quantitative data. Due to its sensitivity and simplicity it is now also widely used in drug development and drug screening. Finally, using near infrared fluorescent probes that have much deeper penetration also opens up new exciting applications such as intra-operative image guided surgery for sentinel lymph node mapping and radical resection of tumours. Recent advances in imaging strategies that reveal cellular and molecular biological events in real-time facilitate our understanding of biological processes occurring in living animals. The development of molecular tags, such as green fluorescent protein (GFP) from the jellyfish Aequorea victoria, red fluorescent proteins (RFP) from the Discosoma species (dsRed2) and luciferase (Luc) from the firefly Photinus pyralis (fLuc) and the sea pansy Renilla (rLuc), has revolutionised research over the past decade, allowing complex biochemical processes to be associated with the functioning of proteins in living cells. Optical technologies, both microscopic and macroscopic, are developing fast. Recent technical advances for imaging weak visible light sources using cooled charged coupled device (CCCD) cameras, peltier cooled detectors and micro-plate channel intensifiers allow detection of photon emission from inside the tissues of small animals. Whole body fluorescent imaging (FLI) and bioluminescent imaging (BLI) are now applied to study cell- and tissue-specific gene promoter activity and also to follow trafficking, differentiation and fate of i.e. GFP or RFP and/or luciferase expressing cells, or biological processes like apoptosis, protein-protein interaction, angiogenesis, proteolysis and gene-transfer. Optical imaging (OI) and optical reporter systems are also very cost-effective and time-efficient and they are particularly well suited for small animal imaging and for in vitro assays to validate different reporter systems.

Lu, H. L., et al. (2011). "A calcium bioluminescence assay for functional analysis of mosquito (Aedes aegypti) and tick (Rhipicephalus microplus) G protein-coupled receptors." J Vis Exp

(50).

Arthropod hormone receptors are potential targets for novel pesticides as they regulate many essential physiological and behavioral processes. The majority of them belong to the superfamily of G protein-coupled receptors (GPCRs). We have focused on characterizing arthropod kinin receptors from the tick and mosquito. Arthropod kinins are multifunctional neuropeptides with myotropic, diuretic, and neurotransmitter function. Here, a method for systematic analyses of structure-activity relationships of insect kinins on two heterologous kinin receptor-expressing systems is described. We provide important information relevant to the development of biostable kinin analogs with the potential to disrupt the diuretic, myotropic, and/or digestive processes in ticks and mosquitoes. The kinin receptors from the southern cattle tick, Boophilus microplus (Canestrini), and the mosquito Aedes aegypti (Linnaeus), were stably expressed in the mammalian cell line CHO-K1. Functional analyses of these receptors were completed using a calcium bioluminescence plate assay that measures intracellular bioluminescence to determine cytoplasmic calcium levels upon peptide application to these recombinant cells. This method takes advantage of the aequorin protein, a photoprotein isolated from luminescent jellyfish. We transiently transfected the aequorin plasmid (mtAEQ/pcDNA1) in cell lines that stably expressed the kinin receptors. These cells were then treated with the cofactor coelenterazine, which complexes with intracellular aequorin. This bond breaks in the presence of calcium, emitting luminescence levels indicative of the calcium concentration. As the kinin receptor signals through the release of intracellular calcium, the intensity of the signal is related to the potency of the peptide. This protocol is a synthesis of several previously described protocols with modifications; it presents step-by-step instructions for the stable expression of GPCRs in a mammalian cell line through functional plate assays (Staubly et al., 2002 and Stables et al., 1997). Using this methodology, we were able to establish stable cell lines expressing the mosquito and the tick kinin receptors, compare the potency of three mosquito kinins, identify critical amino acid positions for the ligand-receptor interaction, and perform semi-throughput screening of a peptide library. Because insect kinins are susceptible to fast enzymatic degradation by endogenous peptidases, they are severely limited in use as tools for pest control or endocrinological studies. Therefore, we also tested kinin analogs containing amino isobutyric acid (Aib) to enhance their potency and biostability. This peptidase-resistant analog represents an important lead in the development of biostable insect kinin analogs and may aid in the development of neuropeptide-based arthropod control strategies.

Lu, X., et al. (2014). "Escape variants of the XPR1 gammaretrovirus receptor are rare due to reliance on a splice donor site and a short hypervariable loop." Virology **468-470**: 63-71.

Entry determinants in the XPR1 receptor for the xenotropic/polytropic mouse leukemia viruses (XP-MLVs) lie in its third and fourth putative extracellular loops (ECLs). The critical ECL3 receptor determinant overlies a splice donor and is evolutionarily conserved in vertebrate XPR1 genes; 2 of the 3 rare replacement mutations at this site destroy this receptor determinant. The 13 residue ECL4 is hypervariable, and replacement mutations carrying an intact ECL3 site alter but do not abolish receptor activity, including replacement of the entire loop with that of a jellyfish (Cnidaria) XPR1. Because ECL4 deletions are found in all X-MLV-infected Mus subspecies, we deleted each ECL4 residue to determine if deletion-associated restriction is residue-specific or is effected by loop size. All deletions influence receptor function, although different deletions affect different XP-MLVs. Thus, receptor usage of a constrained splice site and a loop that tolerates mutations severely limits the likelihood of host escape mutations.

Ma, J., et al. (2019). "A longitudinal assessment of aluminum contents in foodstuffs and aluminum intake of residents in Tianjin metropolis." Food Sci Nutr **7**(3): 997-1003.

Aim: In this report, we retrieved and analyzed the data of aluminum contents in foodstuffs over a 6-year span between 2010 and 2015 and assessed the risk of dietary aluminum exposure in residents of Tianjin metropolis. Methods: A multistage random clustering method was used to survey Tianjin residents between 2010 and 2015. Samples were mainly purchased from breakfast vendors, farmers' markets, and supermarkets in Tianjin between 2009 and 2015. A total of 1,814 persons aged at least 2 years from 1,262 households from randomly chosen communities were asked to complete the questionnaire on food consumption. Aluminum contents in the food samples were determined. Results: Totally 21.14% of food samples exceeded the recommended aluminum residue limit over the study period. The mean aluminum levels in the food samples over the 6-year span were 111.9 7 +/- 265.26 mg/kg, and the mean P95 was 597.00 mg/kg. Totally 21.14% of the food samples exceeded the recommended aluminum residue limit (100 mg/kg). The lowest mean aluminum levels in food were detected in 2010, and the highest levels were found in 2015. The highest mean aluminum levels were found in jellyfish. The highest total mean aluminum intake in food was 83.61 mg/day in those aged at least 50 years

and younger than 66 years. Meanwhile, children aged at least 2 years and less than 8 years had the highest mean weekly aluminum intake (18.19 mg/kg body weight/week); they also had the highest MOS (18.19). Conclusion: The findings indicate that despite the implementation since 2014 of the new policy on the use of aluminum food additives in China, residents in Tianjin still face high levels of aluminum exposure in foodstuffs with young children particularly vulnerable. Public awareness of the new policy should be enhanced, and more vigorous supervision of the use of aluminum food additives should be undertaken.

Ma, X., et al. (2016). "Gold nanocrystals with DNA-directed morphologies." Nat Commun **7**: 12873.

Precise control over the structure of metal nanomaterials is important for developing advanced nanobiotechnology. Assembly methods of nanoparticles into structured blocks have been widely demonstrated recently. However, synthesis of nanocrystals with controlled, three-dimensional structures remains challenging. Here we show a directed crystallization of gold by a single DNA molecular regulator in a sequence-independent manner and its applications in three-dimensional topological controls of crystalline nanostructures. We anchor DNA onto gold nanoseed with various alignments to form gold nanocrystals with defined topologies. Some topologies are asymmetric including pushpin-, star- and biconcave disk-like structures, as well as more complex jellyfish- and flower-like structures. The approach of employing DNA enables the solution-based synthesis of nanocrystals with controlled, three-dimensional structures in a desired direction, and expands the current tools available for designing and synthesizing feature-rich nanomaterials for future translational biotechnology.

Macali, A., et al. (2018). "Episodic records of jellyfish ingestion of plastic items reveal a novel pathway for trophic transference of marine litter." Sci Rep **8**(1): 6105.

Invertebrates represent the most plentiful component of marine biodiversity. To date, only few species have been documented for marine litter intake. Here, we report for the first time the presence of macroplastic debris in a jellyfish species. Such novel target to plastic pollution highlights an under studied vector of marine litter along marine trophic web, raising further concern over the impact on marine wildlife.

Mackie, G. and R. Meech (1995). "Central circuitry in the jellyfish Aglantha. I: The relay system." J Exp Biol **198**(Pt 11): 2261-2270.

1. The relay system is an interneuronal pathway in the margin of the jellyfish Aglantha digitale. It excites a second interneuronal pathway, the carrier system, and is itself excited by pacemaker neurones concerned with slow swimming. It also excites a slow conduction pathway in the tentacles causing graded, tonic contractions of all the tentacles during slow swimming. 2. The pacemakers, the carrier system and the relay system all contribute to the production of excitatory postsynaptic potentials (EPSPs) in a giant axon that runs in the outer nerve ring (ring giant axon). These EPSPs may cause the latter to spike during slow swimming. If it does so, it will fire tentacle giant axons, producing twitch contractions of the tentacles. Such contractions probably help to contract the tentacles rapidly at the start of slow swimming. This is an unusual case of a giant axon that normally mediates escape behaviour being appropriated for use during a non-escape activity. 3. The relay system can conduct impulses on its own but their conduction velocity is greatly increased when preceded by either pacemaker or ring giant spikes. This phenomenon, termed the 'piggyback effect', may be due to extracellular field effects rather than to actions mediated by chemical or electrical synapses. 4. Recordings from the epithelial cells that ensheath the ring giant and outer nerve ring neurones show miniature synaptic potentials and other events that seem to reflect events in the nervous system, but no functions can be assigned to them. 5. There is no obvious counterpart to the relay system in medusae lacking escape circuitry.

Mackie, G. and R. Meech (1995). "Central circuitry in the jellyfish Aglantha. II: The ring giant and carrier systems." J Exp Biol **198**(Pt 11): 2271-2278.

1. The ring giant axon in the outer nerve ring of the jellyfish Aglantha digitale is a multinucleate syncytium 85 % of which is occupied by an electron-dense fluid-filled vacuole apparently in a Gibbs Donnan equilibrium with the surrounding band of cytoplasmic cortex. Micropipette recordings show small (-15 to -25 mV) and large (-62 to -66 mV) resting potentials. Low values, obtained with a high proportion of the micropipette penetrations, are assumed to be from the central vacuole; high values from the cytoplasmic cortex. Background electrical activity includes rhythmic oscillations and synaptic potentials representing hair cell input caused by vibration. 2. After the ring giant axon has been cut, propagating action potentials evoked by stimulation are conducted past the cut and re-enter the axon on the far side. The system responsible (the carrier system) through-conducts at a velocity approximately 25 % of that of the ring giant axon and is probably composed of small neurones running in parallel with it. Numerous small neurones are seen by electron

microscopy, some making one-way and some two-way synapses with the ring giant. 3. Despite their different conduction velocities, the two systems normally appear to fire in synchrony and at the velocity of the ring giant axon. We suggest that, once initiated, ring giant spikes propagate rapidly around the margin, firing the carrier neurones through serial synapses and giving them, in effect, the same high conduction velocity. Initiation of ring giant spikes can, however, require input from the carrier system. The spikes are frequently seen to be mounted on slow positive potentials representing summed carrier postsynaptic potentials. 4. The carrier system fires one-for-one with the giant axons of the tentacles and may mediate impulse traffic between the latter and the ring giant axon. We suggest that the carrier system may also provide the pathways from the ring giant to the motor giant axons used in escape swimming. 5. The findings show that the ring giant axon functions in close collaboration with the carrier system, increasing the latter's effective conduction velocity, and that interactions with other neuronal sub-systems are probably mediated exclusively by the carrier system.

Mackie, G. O. (1975). "Neurobiology of Stomotoca. II. Pacemakers and conduction pathways." J Neurobiol **6**(4): 357-378.

Evidence is presented for separate conduction pathways for swimming and for tentacle coordination in the marginal nerves of the jellyfish Stomotoca. The effector muscles are fired through junctions sensitive to excess Mg++, probably represented by the neuromuscular synapses observed by electron microscopy. The swimming effector (striated muscle) fires one-to-one with nerve input signals and myoid conduction occurs. Tentacle responses (smooth muscle contractions) involve facilitation, presumably at the neuro-effector junction; responses are graded and nonpropagating. Electrical correlates of two further conducting systems using the marginal nerves have been recorded. Their functions are unknown. One, the bridge system, extends up the four radii and encircles the peduncle; the other (ring system) is confined to the margin. A fifth conducting system is inferred in the case of the pointing response and its distribution is plotted. Signals have not been obtained from it. Pointing is accompanied by a burst of muscle potentials in the radial smooth muscles and is exhibited after a lengthy latency, indicating a local pacemaker. A sixth conducting pathway is the epithelial system, which mediates crumpling, a response involving the radial muscles without pacemaker intervention. Characteristic conduction velocities and wave forms are noted for the first four systems and for epithelial pulses. All systems, except perhaps the pointing conduction system, through-conduct under excess Mg++. Spontaneous activity patterns are described for the swimming, tentacle pulse, and ring systems. Abrupt increases in light intensity inhibit spontaneous activity, sudden decreases augmenting it. In the absence of specialized photoreceptors, light is presumed to act directly on central neurons. Epithelial pulses inhibit swimming, apparently by blocking the generation or conduction of the primary nervous events. This observation, taken in conjunction with evidence of feedback inhibition of the primary swimming system by the cells it fires, is discussed in relation to possible mechanisms whereby the output of nerve cells might be altered by activity in the excitable epithelial cells which envelop them.

Mackie, G. O. (2004). "Central neural circuitry in the jellyfish Aglantha: a model 'simple nervous system'." Neurosignals **13**(1-2): 5-19.

Like other hydrozoan medusae, Aglantha lacks a brain, but the two marginal nerve rings function together as a central nervous system. Twelve neuronal and two excitable epithelial conduction systems are described and their interactions summarized. Aglantha differs from most medusae in having giant axons. It can swim and contract its tentacles in two distinct ways (escape and slow). Escape responses are mediated primarily by giant axons but conventional interneurons are also involved in transmission of information within the nerve rings during one form of escape behavior. Surprisingly, giant axons provide the motor pathway to the swim muscles in both escape and slow swimming. This is possible because these axons can conduct calcium spikes as well as sodium spikes and do so on an either/or basis without overlap. The synaptic and ionic bases for these responses are reviewed. During feeding, the manubrium performs highly accurate flexions to points at the margin. At the same time, the oral lips flare open. The directional flexions are conducted by FMRFamide immunoreactive nerves, the lip flaring by an excitable epithelium lining the radial canals. Inhibition of swimming during feeding is due to impulses propagated centrifugally in the same epithelium. Aglantha probably evolved from an ancestor possessing a relatively simple wiring plan, as seen in other hydromedusae. Acquisition of giant axons resulted in considerable modification of this basic plan, and required novel solutions to the problems of integrating escape with non-escape circuitry.

Mackie, G. O., et al. (2003). "Central circuitry in the jellyfish Aglantha digitale IV. Pathways coordinating feeding behaviour." J Exp Biol **206**(Pt 14): 2487-2505.

The hydromedusan jellyfish Aglantha digitale feeds on small planktonic organisms carried to the

margin by tentacle flexions. During feeding, the manubrium bends across ("points") and seizes the prey with flared lips. In immobilized preparations, pointing to a source of electrical stimulation was accurate, 70% of the time, to within 15 degrees. Cutting experiments showed that the conduction pathways concerned with pointing and lip flaring are located in eight radial strands consisting of a radial canal, a giant nerve axon and a bundle of small axons with FMRFamide-like immunoreactivity. Application of food juices to sites on the margin and tentacles evoked trains of impulses in the axon bundles (F events; conduction velocity 15.5+/-3.7 cm s (-1)) and in the epithelium lining the radial canals (E events; conduction velocity 28.5+/-3.5 cm s (-1)). Impulses were conducted circularly in the outer nerve ring (F events) or in the ring canal (E events). Unilateral flexions of the manubrium during pointing arise from preferential excitation of one or more of eight longitudinal "muscle bands" in the wall of the manubrium and peduncle. Lip flaring represents symmetrical contraction of all eight bands. Cutting experiments revealed that F events mediate pointing; E events mediate lip flaring. Thus the endodermal radial canals, which in other hydromedusae mediate protective 'crumpling', provide the conduction pathway for manubrial lip flaring. Aglantha's alternative protective response--escape swimming--makes crumpling unnecessary, releasing the pathway for use in feeding. Trains of E events, generated in the manubrium during ingestion, propagate to the margin and inhibit rhythmic (slow) swimming with a duration that depended on their number and frequency. Inhibition of swimming appeared to facilitate transfer of food from the margin to the mouth, but how it comes about is unclear.

Mackie, G. O. and R. W. Meech (1985). "Separate sodium and calcium spikes in the same axon." Nature **313**(6005): 791-793.

Aglantha digitale is a jellyfish (order Hydromedusae) capable of two distinct kinds of locomotion; 'slow' swimming which is generated endogenously and is used in fishing behaviour, and 'fast' swimming which is evoked by predators and serves for escape. Both forms of swimming are produced by contraction of the bell-shaped body wall and expulsion of a jet of water from an opening at the base of the animal. During slow swimming, the contractions are weak and the animal moves about 15 mm, roughly one body length, but during a fast swim there is a more violent contraction which can propel the animal five times as far. Both forms of contraction depend on impulses in the eight giant motor axons that synapse directly with the muscle sheet making up the inner surface of the body wall. We report here that the giant motor axons are able to mediate both kinds of activity because they can conduct two different sorts of impulse. Fast swimming requires a rapidly conducted Na+-dependent action potential whereas slow swimming depends on a low amplitude Ca2+ 'spike'. This is the first report of an axon capable of two kinds of impulse propagation and it provides a physiological function for low potential Ca2+ activation.

Mackie, G. O. and R. W. Meech (2000). "Central circuitry in the jellyfish Aglantha digitale. III. The rootlet and pacemaker systems." J Exp Biol **203**(Pt 12): 1797-1807.

Tactile stimulation of the subumbrella of Aglantha digitale was found to evoke an escape swimming response similar to that evoked by stimulation of the outer surfaces of the margin but that does not involve the ring giant axon. Evidence is presented that conduction around the margin takes place via an interconnected system of rootlet interneurones. Confocal microscopy of carboxyfluorescein-filled axons showed that the rootlet neurones run out from the bases of the motor giant axons within the inner nerve ring and come into close contact with those of the neighbouring motor giant axons on either side. Transmission between the rootlet neurones has the properties of chemical synaptic transmission. A distinct type of fast excitatory postsynaptic potential (rootlet PSP) was recorded in motor giant axons following stimulation of nearby axons in 3-5 mmol l (-) (1) Mn (2+), which lowered the PSP below spike threshold. Immune labelling with anti-syntaxin 1 showed structures tentatively identified as synapses in the inner nerve ring, including some on the rootlet neurones. Neuromuscular junctions were not labelled. A secondary consequence of stimulating motor giant axons was the triggering of events in the pacemaker system. Triggering was blocked in 105 mmol l (-) (1) Mg (2+), indicating a synaptic link. Activity in the pacemaker system led indirectly to tentacle contractions (as described in earlier papers in this series), but the contractions were not as sudden or as violent as those seen when escape swimming was mediated by the ring giant axon. Events triggered in the pacemaker system fed back into the motor giants, producing postsynaptic potentials that appeared as humps in the spike after-potential. The conduction velocity of events propagating in the relay system was increased when the rootlet pathway was simultaneously excited (piggyback effect). With the addition of the rootlet pathway, the number of identified systems concerned with locomotion, feeding and tentacle contractions comes to fourteen, and the list is probably nearly complete.

Mackie, G. O. and R. W. Meech (2008). "Nerves

in the endodermal canals of hydromedusae and their role in swimming inhibition." Invert Neurosci **8**(4): 199-209.

N eoturris breviconis (Anthomedusae) has a nerve plexus in the walls of its endodermal canals. The plexus is distinct from the ectodermal nerve plexuses supplying the radial and circular muscles in the ectoderm and no connections have been observed between them. Stimulation of the endodermal plexus evokes electrical events recorded extracellularly as "E" potentials. These propagate through all areas where the plexus has been shown by immunohistology to exist and nowhere else. When Neoturris is ingesting food, trains of "E" potentials propagate down the radial canals to the margin and cause inhibition of swimming. This response is distinct from the inhibition of swimming associated with contractions of the radial muscles but both may play a part in feeding and involve chemoreceptors. Preliminary observations suggest that the "E" system occurs in other medusae including Aglantha digitale (Trachymedusae) where the conduction pathway was previously thought to be an excitable epithelium.

Macrokanis, C. J., et al. (2004). "Irukandji syndrome in northern Western Australia: an emerging health problem." Med J Aust **181**(11-12): 699-702.

OBJECTIVES: (1) To assess the number and severity of episodes of Irukandji syndrome in Broome, Western Australia. (2) To correlate demographic, seasonal, geographic and climatic features of Irukandji stings. (3) To assess treatment of Irukandji syndrome at Broome Health Service. (4) To assess the public health impact. DESIGN AND SETTING: (1) A retrospective analysis of jellyfish data forms and charts of 111 patients, identified from Broome Health Service Emergency Department with a discharge diagnosis of marine sting between 1 January 2001 and 1 July 2003. (2) Correlation between climate and Irukandji envenomation data. MAIN OUTCOME MEASURES: Number of patients with Irukandji syndrome; their demographic and environmental features; the clinical syndrome; treatment requirements. RESULTS: 111 patients were prospectively identified with marine stings; 88 were identified with Irukandji syndrome. Non-Irukandji syndrome data were excluded for analysis. The "jellyfish season" extends from January to May, although stings occur all year round. Only 38% of patients had vinegar applied to the sting site before hospital presentation. Signs and symptoms were variable between individuals, with 20% having no signs of sting at all and welts found in 16%. Fifty per cent of patients were hypertensive at presentation. Distress was found in the majority of patients, with 90% requiring opioid analgesia (morphine equivalent: mean, 20 mg; median, 13 mg) and 17% requiring admission. There was one evacuation to Perth with cardiotoxic marine envenomation resulting in pulmonary oedema, which necessitated 4 days in intensive care. Stings were significantly more common when the ambient median temperature was greater than 28.3 degrees C, after midday, on an incoming high tide and on windy days. CONCLUSION: The rate of envenomation in northern WA is likely to be the highest currently documented in Australia. There is syndromic variability when compared with the north Queensland experience. This implies different causative jellyfish species that are not yet identified. Stings in Broome can be severe and life threatening; there are significant commercial and public health implications as a result. Management at Broome Hospital is contemporary and effective.

Malul, D., et al. (2019). "The Levantine jellyfish Rhopilema nomadica and Rhizostoma pulmo swim faster against the flow than with the flow." Sci Rep **9**(1): 20337.

Jellyfish locomotion and orientation have been studied in the past both in the laboratory, testing mostly small jellyfish, and in the field, where it was impossible to control the seawater currents. Utilizing an outdoor water flume, we tested the locomotion of jellyfish when swimming against and with currents of up to 4.5 cm s (-1). We used adult jellyfish from two of the most abundant species in the eastern Mediterranean, Rhopilema nomadica and Rhizostoma pulmo, and measured their pulsation frequency and swimming speed relative to the water. While pulsation frequency was not affected by the water velocity, jellyfish swam faster against the current than with it. This finding suggests that jellyfish possess a sensory ability, whose mechanism is currently unknown, enabling them to gauge the flow and react to it, possibly in order to reduce the risk of stranding.

Malvezzi-Campeggi, F., et al. (2001). "Light-induced flickering of DsRed provides evidence for distinct and interconvertible fluorescent states." Biophys J **81**(3): 1776-1785.

Green fluorescent protein (GFP) from jellyfish Aequorea victoria, the powerful genetically encoded tag presently available in a variety of mutants featuring blue to yellow emission, has found a red-emitting counterpart. The recently cloned red fluorescent protein DsRed, isolated from Discosoma corals (), with its emission maximum at 583 nm, appears to be the long awaited tool for multi-color applications in fluorescence-based biological research. Studying the emission dynamics of DsRed by fluorescence correlation spectroscopy (FCS), it can be verified that this protein exhibits strong light-dependent flickering similar to what is observed in

several yellow-shifted mutants of GFP. FCS data recorded at different intensities and excitation wavelengths suggest that DsRed appears under equilibrated conditions in at minimum three interconvertible states, apparently fluorescent with different excitation and emission properties. Light absorption induces transitions and/or cycling between these states on time scales of several tens to several hundreds of microseconds, dependent on excitation intensity. With increasing intensity, the emission maximum of the static fluorescence continuously shifts to the red, implying that at least one state emitting at longer wavelength is preferably populated at higher light levels. In close resemblance to GFP, this light-induced dynamic behavior implies that the chromophore is subject to conformational rearrangements upon population of the excited state.

Malzahn, A. M., et al. (2010). "Differential effects of nutrient-limited primary production on primary, secondary or tertiary consumers." Oecologia **162**(1): 35-48.

Nutritional imbalances between predator and prey are the rule rather than the exception at the lower end of food webs. We investigated the role of different grazers in the propagation of nutritionally imbalanced primary production by using the same primary producers in a three-trophic-level food chain and a four-trophic-level food chain experimental setup. The three-trophic-level food chain consisted of a classic single-cell primary producer (Rhodomonas salina), a metazoan grazer (the copepod Acartia tonsa) and a top predator (the jellyfish Gonionemus vertens), while we added a protozoan grazer (Oxyrrhis marina) as primary consumer to the food chain to establish the four-trophic-level food chain. This setup allowed us to investigate how nutrient-limitation effects change from one trophic level to another, and to investigate the performance of two components of our experimental food chains in different trophic positions. Stoichiometry and fatty acid profiles of the algae showed significant differences between the nutrient-depleted [no N and no P addition (-P), respectively] and the nutrient-replete (f/2) treatments. The differences in stoichiometry could be traced when O. marina was the first consumer. Copepods feeding on these flagellates were not affected by the nutritional imbalance of their prey in their stoichiometry, their respiration rates nor in their developmental rates. In contrast, when copepods were the primary consumer, those reared on the -P algae showed significantly higher respiration rates along with significantly lower developmental rates. In neither of our two experimental food chains did the signals from the base of the food chains travel up to jelly fish, our top predator.

Mamish, S., et al. (2015). "Radioactivity in three species of eastern Mediterranean jellyfish." J Environ Radioact **149**: 1-7.

Activity concentrations of (137)Cs, (40)K, (210)Po, (210)Pb, (234)U and (238)U were determined in umbrella and oral arms of three widely distributed jellyfish species; namely Rhopilema nomadica Galil, 1990, Aurelia aurita Linne, 1758 and Aequorea forskalea Peron & Lesueur, 1810 collected from February 2011 to January 2012 in four sampling locations along the Syrian coast (Eastern Mediterranean Sea). The results have shown significant variations in radionuclides activity concentrations amongst the species. The average activity concentrations of (40)K, (210)Po, (210)Pb, (234)U and (238)U in the umbrella of R. nomadica species were higher than the average activity concentrations in the umbrella of A. aurita species by about 3.2, 1.4, 1.8, 3.2 and 3.2 folds, and A. forskalea species by about 45.5, 15.4, 19, 7.4 and 7.6 folds, respectively. The average activity concentrations of (40)K, (210)Po, (210)Pb, (234)U and (238)U in oral arms of R. nomadica species were higher than the average activity concentrations in oral arms of A. aurita species by about 3.8, 1.7, 1.9, 2.8 and 2.9 folds, respectively. (137)Cs activity concentrations were below the detection limit in all measured samples. In addition, activity concentrations of (137)Cs, (40)K, (210)Po, (210)Pb, (234)U and (238)U were also determined in 44 surface seawater samples and the activity concentrations ranged between 10.6 and 11.9 Bq l (-1) for (40)K, 1.1 and 1.4 mBq l (-1) for (210)Po, 0.5 and 0.7 mBq l (-1) for (210)Pb, 40.8 and 44.5 mBq l (-1) for (234)U, and 36.9 and 38.4 mBq l (-1) for (238)U, while (137)Cs activity concentrations were below the detection limit in all measured samples. Moreover, the umbrella and oral arms readily accumulated (40)K, (210)Po, (210)Pb, (234)U and (238)U above ambient seawater levels in the sequence of (210)Po > (210)Pb > (4) K > (234)U and (238)U. Concentration ratio (CR) values were relatively high for (210)Po and (210)Pb and reached 10(3) and 10(2), respectively for the jellyfish R. nomadica species compared to A. aurita and A. forskalea species. Therefore, R. nomadica can be used as biomonitor for these two radionuclides in the Eastern Mediterranean Sea. However, the obtained data can be considered the first reported baseline values for radioactivity in jellyfish.

Manabe, Y., et al. (2014). "A Case of Delayed Flare-up Allergic Dermatitis Caused by Jellyfish Sting." Tokai J Exp Clin Med **39**(3): 90-94.

A 7-year-old boy, taking lessons at a yacht school at Enoshima in Kanagawa prefecture in Japan,

recognized a linear eruption on his left lower leg during practice in August 2012. As it gradually enlarged, he visited a local medical clinic. The eruption initially improved with topical treatment but exacerbated in October of the same year. Although topical treatment was started again, there was minimal improvement, so the patient visited our hospital in December. At his first visit, he had a hard linear nodule on his left lower leg, and papules with excoriation were scattered over the lower limbs. Considering eczema, topical steroid treatment and occlusive dressing technique were started but the nodule remained. Based on the clinical course, clinical features, and laboratory findings, the lesion was considered to be delayed flare-up allergic dermatitis caused by a jellyfish sting [1].

Manner, J. and T. M. Yelbuz (2019). "Functional Morphology of the Cardiac Jelly in the Tubular Heart of Vertebrate Embryos." J Cardiovasc Dev Dis **6**(1).

The early embryonic heart is a multi-layered tube consisting of (1) an outer myocardial tube; (2) an inner endocardial tube; and (3) an extracellular matrix layer interposed between the myocardium and endocardium, called "cardiac jelly" (CJ). During the past decades, research on CJ has mainly focused on its molecular and cellular biological aspects. This review focuses on the morphological and biomechanical aspects of CJ. Special attention is given to (1) the spatial distribution and fiber architecture of CJ; (2) the morphological dynamics of CJ during the cardiac cycle; and (3) the removal/remodeling of CJ during advanced heart looping stages, which leads to the formation of ventricular trabeculations and endocardial cushions. CJ acts as a hydraulic skeleton, displaying striking structural and functional similarities with the mesoglea of jellyfish. CJ not only represents a filler substance, facilitating end-systolic occlusion of the embryonic heart lumen. Its elastic components antagonize the systolic deformations of the heart wall and thereby power the refilling phase of the ventricular tube. Non-uniform spatial distribution of CJ generates non-circular cross sections of the opened endocardial tube (initially elliptic, later deltoid), which seem to be advantageous for valveless pumping. Endocardial cushions/ridges are cellularized remnants of non-removed CJ.

Mansfield, K. M. and T. D. Gilmore (2019). "Innate immunity and cnidarian-Symbiodiniaceae mutualism." Dev Comp Immunol **90**: 199-209.

The phylum Cnidaria (sea anemones, corals, hydra, jellyfish) is one the most distantly related animal phyla to humans, and yet cnidarians harbor many of the same cellular pathways involved in innate immunity in mammals. In addition to its role in pathogen recognition, the innate immune system has a role in managing beneficial microbes and supporting mutualistic microbial symbioses. Some corals and sea anemones undergo mutualistic symbioses with photosynthetic algae in the family Symbiodiniaceae. These symbioses can be disrupted by anthropogenic disturbances of ocean environments, which can have devastating consequences for the health of coral reef ecosystems. Several studies of cnidarian-Symbiodiniaceae symbiosis have implicated proteins in the host immune system as playing a role in both symbiont tolerance and loss of symbiosis (i.e., bleaching). In this review, we critically evaluate current knowledge about the role of host immunity in the regulation of symbiosis in cnidarians.

Mansson, T., et al. (1985). "Recurrent cutaneous jellyfish eruptions without envenomation." Acta Derm Venereol **65**(1): 72-75.

Three patients exhibiting recurrent cutaneous eruptions induced by contact with jellyfish tentacles are presented. The recurrent eruptions appeared several days after the primary exposure without contact with any offending coelenterate. The principal species involved include Pelagia noctiluca, Physalia physalis and probably Lychnorhiza lucerna. These three cases, combined with an earlier similar report of recurrent lesions induced by Physalia physalis suggest that this phenomenon may be widespread. In two of the three cases, the secondary eruption was more severe than that occurring after the primary envenomation.

Mao, C., et al. (2016). "Ocular Jellyfish Stings: Report of 2 Cases and Literature Review." Wilderness Environ Med **27**(3): 421-424.

An ocular jellyfish sting is an ophthalmic emergency and is rarely reported in the medical literature. With the evolution of aquatic activities and entertainment in recent decades, we anticipate that more patients with ocular jellyfish stings may be taken to the emergency department. However, most physicians are unaware of the typical presentations, suitable treatments, prognosis, and possible complications of ocular jellyfish stings. We reported 2 cases with ocular jellyfish stings and collected cases series from literature review. The most common clinical features of ocular jellyfish stings were pain, conjunctival injection, corneal lesion, and photophobia. All patients who sustained ocular stings did so during aquatic activities, and the best management at the scene was proper analgesics and copious irrigation of affected eyes with seawater or saline. The ocular lesions were treated with topical cycloplegics, topical steroids, topical antibiotics, topical antihistamines, and removal of nematocysts. The prognosis was good, and

all patients recovered without any permanent sequelae. However, symptoms in some patients may last longer than 1 week. Reported complications included iritis, increased intraocular pressures, mydriasis, decreased accommodation, and peripheral anterior synechiae.

Marcais, G. and C. Kingsford (2011). "A fast, lock-free approach for efficient parallel counting of occurrences of k-mers." Bioinformatics **27**(6): 764-770.

MOTIVATION: Counting the number of occurrences of every k-mer (substring of length k) in a long string is a central subproblem in many applications, including genome assembly, error correction of sequencing reads, fast multiple sequence alignment and repeat detection. Recently, the deep sequence coverage generated by next-generation sequencing technologies has caused the amount of sequence to be processed during a genome project to grow rapidly, and has rendered current k-mer counting tools too slow and memory intensive. At the same time, large multicore computers have become commonplace in research facilities allowing for a new parallel computational paradigm. RESULTS: We propose a new k-mer counting algorithm and associated implementation, called Jellyfish, which is fast and memory efficient. It is based on a multithreaded, lock-free hash table optimized for counting k-mers up to 31 bases in length. Due to their flexibility, suffix arrays have been the data structure of choice for solving many string problems. For the task of k-mer counting, important in many biological applications, Jellyfish offers a much faster and more memory-efficient solution. AVAILABILITY: The Jellyfish software is written in C++ and is GPL licensed. It is available for download at http://www.cbcb.umd.edu/software/jellyfish.

Marchini, B., et al. (2004). "A fast centrifuge method for nematocyst isolation from Pelagia noctiluca Forskal (Cnidaria: Scyphozoa)." Riv Biol **97**(3): 505-515.

Nematocyst isolation from surrounding tissue is an important step to characterize Cnidarian venom. Although several protocols have been used to extract venoms from cnidarian tissues, the complete isolation of nematocysts from tissue is still difficult. The goal of the present work was to evaluate the effectiveness of three different media, Percoll, Ficoll and Methylcellulose in isolating nematocysts from Pelagia noctiluca tentacles by centrifugation. The complete sedimentation of nematocysts and tissue fragments to the bottom of the test tubes was observed in Ficoll and Methylcellulose suspensions. The best result was obtained using a discontinuous density gradient of Percoll: three types of nematocysts were concentrated in three different fractions along the density gradient. Protein assay and preliminary chromatographic analyses confirmed these results.

Marino, A., et al. (2007). "The unusual toxicity and stability properties of crude venom from isolated nematocysts of Pelagia noctiluca (Cnidaria, Scyphozoa)." Cell Mol Biol (Noisy-le-grand) **53 Suppl**: OL994-1002.

We have firstly investigated the toxicological activity by hemolytic assay of crude extract obtained by sonication of holotrichous isorhiza isolated nematocysts of the Scyphozoan Pelagia noctiluca, collected in the Strait of Messina. The hemolytic activity was both time- and dose-dependent on fish, rabbit, chicken and human red blood cells. At lowest doses rabbit and chicken erythrocytes were the most sensitive, whereas those of eel were the most resistant to the crude extract. Different storage conditions, such as -20 degrees C, -80 degrees C for up to 6 months and lyophilization, did not affect the stability of crude venom. Moreover, neither treatment at 4 degrees C, 20 degrees C and 37 degrees C for different time periods ranging between 30 min and 24 h, nor harsh thermal treatment at 80 degrees C and 100 degrees C affected the hemolytic power. The crude venom resulted even stable towards proteolysis and alkaline pH values.

Marino, A., et al. (2009). "Protective effect of melatonin against the inflammatory response elicited by crude venom from isolated nematocysts of Pelagia noctiluca (Cnidaria, Scyphozoa)." J Pineal Res **47**(1): 56-69.

Melatonin (N-acetyl-5-methoxytryptamine) is an efficient free radical scavenger and antioxidant, both in vitro and in vivo. The role of melatonin as an immunomodulator is, in some cases, contradictory. In this study we have investigated the therapeutic efficacy of melatonin in rats subjected to Pelagia noctiluca crude venom (of the familia Pelaguiidae; and genus Pelagia) induced acute paw inflammation. In particular, injection of the venom into the paw of rats elicited an acute inflammatory response characterized by accumulation of fluid containing a large number of polymorphonuclear neutrophils in the paw and subsequent lipid peroxidation. Furthermore, the venom promoted an expression of iNOS, nitrotyrosine and the activation of the nuclear enzyme poly (ADP-ribose) polymerase as determined by immunohistochemical analysis of paw tissues. Administration of melatonin 30 min, 1 and 6 hr after the challenge with the venom, caused a significant reduction in all the parameters of inflammation measured. Thus, based on these findings we propose that melatonin may be useful a treatment of local acute inflammation induced by P. noctiluca crude venom.

Marino, A., et al. (2011). "Evidence for aquaporin-mediated water transport in nematocytes of the jellyfish Pelagia noctiluca." Cell Physiol Biochem **28**(6): 1211-1218.

Nematocytes, the stinging cells of Cnidarians, have a cytoplasm confined to a thin rim. The main cell body is occupied by an organoid, the nematocyst, containing the stinging tubule and venom. Exposed to hypotonic shock, nematocytes initially swell during an osmotic phase (OP) and then undergo regulatory volume decrease (RVD) driven by K (+), Cl (-) and obligatory water extrusion mechanisms. The purpose of this report is to characterize the OP. Nematocytes were isolated by the NaSCN/Ca (2+) method from tentacles of the jellyfish Pelagia noctiluca, collected in the Strait of Messina, Italy. Isolated nematocytes were subjected to hyposmotic shock in 65% artificial seawater (ASW) for 15 min. The selective aquaporin water channel inhibitor HgCl (2) (0.1-25 muM) applied prior to osmotic shock prevented the OP and thus RVD. These effects were attenuated in the presence of 1mM dithiothreitol (DTT), a mercaptide bond reducing agent. AgNO (3) (1 muM) and TEA (tetraethylammonium, 100 muM), also reported to inhibit water transport, did not alter the OP but significantly diminished RVD, suggesting different modes of action for the inhibitors tested. Based on estimates of the nematocyte surface area and volume, and OP duration, a relative water permeability of ~10(-7) cm/sec was calculated and the number of putative aquaporin molecules mediating the OP was estimated. This water permeability is 3-4 orders of magnitude lower in comparison to higher order animals and may constitute an evolutionary advantage for Cnidarian survival.

Marino, A., et al. (2008). "Effect of various factors on Pelagia noctiluca (Cnidaria, Scyphozoa) crude venom-induced haemolysis." Comp Biochem Physiol A Mol Integr Physiol **151**(1): 144-149.

The haemolytic power of isolated nematocysts from the scyphozoan Pelagia noctiluca was studied with attention to the effect of osmotic protectants as carbohydrates at different MW, cations as Mg2+, Ca2+, Ba2+,Cu2+, K+; proteases as collagenase, trypsin, alpha-chymotrypsin, papain; and antioxidants. Crude venom was at first obtained by sonication of holotrichous-isorhiza nematocysts previously isolated from oral arms of P. noctiluca and then haemolytically tested upon human erythrocytes. Osmotic protectants were effective in inhibiting the haemolytic power depending on their molecular weight so that total inhibition of crude venom-induced haemolysis was observed after PEG treatment (polyethyleneglycol 6000Da). Amongst divalent cations only Ba2+ and Cu2+ significantly inhibited the haemolytic power of crude venom. Proteases seem not to alter the haemolytic activity while antioxidant compounds only slightly reduced the haemolytic power. Such findings may suggest a pore-forming mechanism for P. noctiluca crude venom rather than an oxidative damage to the cell membrane.

Mariottini, G. L. (2014). "Hemolytic venoms from marine cnidarian jellyfish - an overview." J Venom Res **5**: 22-32.

Cnidarian jellyfish are viewed as an emergent problem in several coastal zones throughout the world. Recurrent outbreaks pose a serious threat to tourists and bathers, as well as to sea-workers, involving health and economical aspects. As a rule, cnidarian stinging as a consequence of nematocyst firing induces merely local symptoms but cardiovascular or neurological complications can also occur. Hemolysis is a frequent effect of cnidarian stinging; this dangerous condition is known to be caused by several venoms and can sometimes be lethal. At present, the bulk of data concerning hemolytic cnidarian venoms comes from the study of benthic species, such as sea anemones and soft corals, but hemolytic factors were found in venoms of several siphonophore, cubozoan and scyphozoan jellyfish, which are mainly involved in the envenomation of bathers and sea-workers. Therefore, the aim of this paper is to review the scientific literature concerning the hemolytic venoms from cnidarian jellyfish taking into consideration their importance in human pathology as well as health implications and possible therapeutic measures.

Mariottini, G. L. and A. Carli (2001). "Variations of ATP content in V79 cells treated with crude toxins of--Aequorea aequorea (Cnidaria: Hydrozoa) and Rhizostoma pulmo (Cnidaria: Scyphozoa). A preliminary study." Boll Soc Ital Biol Sper **77**(4-6): 27-34.

The toxicity of Cnidaria exerts a noticeable influence on some human activities, such as fishery and bathing, and on public health. As toxins of Mediterranean Cnidaria are located in nematocysts and in tissues, in this study the influence of crude toxins (nematocyst and surrounding tissue venom) extracted from the jellyfish Aequorea aequorea and Rhizostoma pulmo on ATP content of cultured V79 cells was assessed. Using the crude toxin of A. aequorea an increase of ATP levels in treated cells was noted; highest values (41.2 10(-7) mM/ml after 180 min treatment) were reached using the highest dose. Otherwise, a generalized decrease of ATP levels was observed treating cells with crude toxin of R. pulmo; recorded values showed the complete depletion of cell ATP at 115 min treatment with the highest dose. A statistical significance was recorded between treatment

times and between doses using crude toxin of R. pulmo, and only between treatment times for A. aequorea.

Mariottini, G. L., et al. (2008). "The mauve stinger Pelagia noctiluca (Forsskal, 1775). Distribution, ecology, toxicity and epidemiology of stings. A review." Mar Drugs **6**(3): 496-513.

The toxicity of Cnidaria is a subject of concern due to its influence on humans. In particular, jellyfish blooms can highly affect human economical activities, such as bathing, fishery, tourism, etc., as well as the public health. Stinging structures of Cnidaria (nematocysts) produce remarkable effects on human skin, such as erythema, swelling, burning and vesicles, and at times further severe dermonecrotic, cardio- and neurotoxic effects, which are particularly dangerous in sensitive subjects. In several zones the toxicity of jellyfish is a very important health problem, thus it has stimulated the research on these organisms; to date toxicological research on Cnidarian venoms in the Mediterranean region is not well developed due to the weak poisonousness of venoms of jellyfish and anemones living in this area. In spite of this, during last decades several problems were also caused in the Mediterranean by stinging consequent to Cnidarian blooms mainly caused by Pelagia noctiluca (Forsskal, 1775) which is known to be the most venomous Mediterranean jellyfish. This paper reviews the knowledge on this jellyfish species, particularly considering its occurrence and toxicity.

Mariottini, G. L. and I. D. Grice (2019). "Natural Compounds and Drug Discovery: Can Cnidarian Venom Play a Role?" Cent Nerv Syst Agents Med Chem **19**(2): 114-118.

Natural compounds extracted from organisms and microorganisms are an important resource for the development of drugs and bioactive molecules. Many such compounds have made valuable contributions in diverse fields such as human health, pharmaceutics and industrial applications. Presently, however, research on investigating natural compounds from marine organisms is scarce. This is somewhat surprising considering that the marine environment makes a major contribution to Earth's ecosystems and consequently possesses a vast storehouse of diverse marine species. Interestingly, of the marine bioactive natural compounds identified to date, many are venoms, coming from Cnidarians (jellyfish, sea anemones, corals). Cnidarians are therefore particularly interesting marine species, producing important biological compounds that warrant further investigation for their development as possible therapeutic agents. From an experimental aspect, this review aims to emphasize and update the current scientific knowledge reported on selected biological activity (antiinflammatory, antimicrobial, antitumoral, anticoagulant, along with several less studied effects) of Cnidarian venoms/extracts, highlighting potential aspects for ongoing research towards their utilization in human therapeutic approaches.

Mariottini, G. L. and L. Pane (2010). "Mediterranean jellyfish venoms: a review on scyphomedusae." Mar Drugs **8**(4): 1122-1152.

The production of natural toxins is an interesting aspect, which characterizes the physiology and the ecology of a number of marine species that use them for defence/offence purposes. Cnidarians are of particular concern from this point of view; their venoms are contained in specialized structures--the nematocysts--which, after mechanical or chemical stimulation, inject the venom in the prey or in the attacker. Cnidarian stinging is a serious health problem for humans in the zones where extremely venomous jellyfish or anemones are common, such as in temperate and tropical oceanic waters and particularly along several Pacific coasts, and severe cases of envenomation, including also lethal cases mainly induced by cubomedusae, were reported. On the contrary, in the Mediterranean region the problem of jellyfish stings is quite modest, even though they can have anyhow an impact on public health and be of importance from the ecological and economic point of view owing to the implications on ecosystems and on some human activities such as tourism, bathing and fishing. This paper reviews the knowledge about the various aspects related to the occurrence and the stinging of the Mediterranean scyphozoan jellyfish as well as the activity of their venoms.

Mariottini, G. L., et al. (2002). "Cytotoxicity of the venom of Pelagia noctiluca forskal (Cnidaria: Scyphozoa)." Toxicon **40**(6): 695-698.

The activity of Pelagia noctiluca venom was never assessed on cultured cells; therefore, we have evaluated on V79 cells the cytotoxicity, genotoxicity and ATP depletion induced after treatment. Venom did not cause alteration on cell DNA, but showed remarkable cytotoxic properties. With the highest nematocyst concentration (150,000 nematocyst/ml) 74 and 39% cells survived after 1 and 3 h, respectively, when evaluated by Trypan blue. Treated cells showed increased ATP levels during the same time. Preliminary HPLC analyses have showed the occurrence of a protein containing peak.

Markova, S. V., et al. (2010). "Green-fluorescent protein from the bioluminescent jellyfish Clytia gregaria: cDNA cloning, expression, and characterization of novel recombinant protein."

Photochem Photobiol Sci **9**(6): 757-765.

The bioluminescent systems of many marine organisms are comprised of two proteins--the Ca (2+)-regulated photoprotein and green-fluorescent protein (GFP). This work reports the cloning of the full-size cDNA encoding GFP (cgreGFP) from jellyfish Clytia gregaria, its expression and properties of the recombinant protein. The overall degree of identity between the amino acid sequence of the novel cgreGFP and the sequence of GFP (avGFP) from Aequorea victoria is 42% (similarity--64%) despite these GFPs originating from jellyfish that both belong to the same class, Hydrozoa. However although the degree of identity is low, three residues, Ser-Tyr-Gly, which form the chromophore are identical in both GFPs. The cgreGFP displayed two absorption peaks at 278 and 485 nm, and the fluorescence maximum at 500 nm. The fluorescence quantum yield was determined to be 0.86, the brightness to be 54 mM (-1) cm (-1). For the first time we have also demonstrated an efficient radiationless energy transfer in vitro between clytin and cgreGFP in solution at micromolar concentrations. The cgreGFP may be a useful intracellular fluorescent marker, as it was able to be expressed in mammalian cells.

Markova, S. V., et al. (2012). "The light-sensitive photoprotein berovin from the bioluminescent ctenophore Beroe abyssicola: a novel type of Ca (2+) -regulated photoprotein." FEBS J **279**(5): 856-870.

Light-sensitive Ca (2+) -regulated photoproteins are responsible for the bright bioluminescence of ctenophores. Using functional screening, four full-size cDNA genes encoding the same 208-amino-acid polypeptide were isolated from two independent cDNA libraries prepared from two Beroe abyssicola specimens. Sequence analysis revealed three canonical EF-hand calcium-binding sites characteristic of Ca (2+) -regulated photoproteins, but a very low degree of sequence identity (27-29%) with aequorin-type photoproteins, despite functional similarities. Recombinant berovin was expressed in Escherichia coli cells, purified, converted to active photoprotein and characterized. Active berovin has absorption maxima at 280 and 437 nm. The Ca (2+) -discharged protein loses visible absorption, but exhibits a new absorption maximum at 335 nm. The berovin bioluminescence is blue (lambda (max) = 491 nm) and a change in pH over the range 6.0-9.5 has no significant effect on the light emission spectrum. By contrast, the fluorescence of Ca (2+) -discharged protein (lambda (ex) = 350 nm) is pH sensitive: at neutral pH the maximum is at 420 nm and at alkaline pH there are two maxima at 410 and 485 nm. Like native ctenophore photoproteins, recombinant berovin is also inactivated by light. The Ca (2+) concentration-effect curve is a sigmoid with a slope on a log-log plot of approximately 2.5. Although this curve for berovin is very similar to those obtained for obelin and aequorin, there are evident distinctions: berovin responds to calcium changes at lower concentrations than jellyfish photoproteins and its Ca (2+) -independent luminescence is low. Recombinant berovin was successfully expressed in mammalian cells, thereby demonstrating potential for monitoring intracellular calcium. Database The nucleotide sequences have been deposited in the GenBankTM/EBI Data Bank with accession numbers: apoberovin cDNA genes, JN673813 (BA1), JN673814 (BA2), JN673815 (BA3), JN673816 (BA4); fragment 18S rRNA, JN673817 (BA-rRNA5).

Marques, R., et al. (2019). "Molecular approach indicates consumption of jellyfish by commercially important fish species in a coastal Mediterranean lagoon." Mar Environ Res **152**: 104787.

Until recently, jellyfish have been ignored as an important source of food, due to their low nutritional value. Here, quantitative PCR was used to detect and quantify the DNA of the jellyfish Aurelia coerulea in the gut contents of commercially important fish species from the Thau Lagoon. Individuals from five fish species were collected during two different periods: the bloom period, when the pelagic stages of A. coerulea are abundant, and the post-bloom period, when only the benthic stage - polyps - is present in the lagoon. The DNA of A. coerulea was detected in the guts of 41.9% of the fish analysed, belonging to four different species. The eel Anguilla anguilla and the seabream Sparus aurata were important jellyfish consumers during the bloom and post-bloom periods, respectively. These results provide new insights on the potential control of jellyfish populations and on jellyfish importance as a food source for exploited fishes.

Marshall, J., et al. (1995). "The jellyfish green fluorescent protein: a new tool for studying ion channel expression and function." Neuron **14**(2): 211-215.

Two methods are described for using the jellyfish green fluorescent protein (GFP) as a reporter gene for ion channel expression. GFP fluorescence can be used to identify the transfected cells, and to estimate the relative levels of ion channel expression, in cotransfection experiments. A GFP-NMDAR1 chimera can be constructed that produces a functional, fluorescent receptor subunit. These methods should facilitate studies of ion channel expression, localization, and processing.

Martellos, S., et al. (2016). "JellyWeb: an

interactive information system on Scyphozoa, Cubozoa and Staurozoa." Zookeys (554): 1-25.

Identification of organisms is traditionally based on the use of "classic" identification keys, normally printed on paper. These keys have several drawbacks: they are mainly based on the systematics, requiring identification of orders, families and genera at first; they are written by experts for other experts, in a specific scientific jargon; they have a "frozen" structure (sequence of theses/antitheses); once published, they cannot be changed or updated without printing a new edition. Due to the use of computers, it is now possible to build new digital identification tools, which: 1) can be produced automatically, if the characters are stored in a database; 2) can be freed from the traditional systematics, giving priority to easy-to-observe characters, incl. those usually uncommon to the classical keys, such as ecology and distribution; 3) can be updated in real time once published on-line; 4) can be available on different media, and on mobile devices. An important feature of these new digital tools is their "collaborative" nature. They can be enriched by the contribution of several researchers, which can cooperate while maintaining rights and property of the resources and data they contribute to the system. JellyWeb, the information system on Scyphozoa, Cubozoa and Staurozoa has been developed in Trieste since 2010. The system was created with the aim of - potentially - becoming a starting point for a wide collaborative effort in developing a user-friendly worldwide digital identification system for jellyfishes.

Martin, J. C. and I. Audley (1990). "Cardiac failure following Irukandji envenomation." Med J Aust **153**(3): 164-166.

This paper presents a case of Irukandji syndrome (envenomation by the jellyfish, Carukia barnesi) with pulmonary oedema and hypokinetic cardiac failure. This case highlights the need for victims (and operators of tours venturing into the waters of North Queensland) to treat even apparently innocuous stings with vinegar and to avoid freshwater bathing and rubbing of stings immediately after such incidents. It also reinforces the use of phentolamine to treat the symptoms of catecholamine release associated with the syndrome. This patient required inotropic support and further underlines the need for practitioners to be aware that the syndrome can have severe sequelae and that central venous monitoring and inotropic management should be available when treating Irukandji stings.

Martin, J. W., et al. (1997). "Chrysaora achlyos, a Remarkable New Species of Scyphozoan from the Eastern Pacific." Biol Bull **193**(1): 8-13.

An enormous new species of scyphozoan jellyfish, Chrysaora achlyos, is described from the eastern Pacific. The description is based primarily on color photographs and video footage of living animals and the morphology of four specimens collected in 1989. The natural history, life cycle, and sporadic appearance of the species all are unknown. The species appeared most recently in large numbers in 1989 but has appeared at least twice previously in this century; published photographs (unlabeled or incorrectly identified) appeared in 1926 and 1965. The species is easily distinguished by its size and coloration from other known species in the genus, all of which are considerably smaller. Morphological characters are described, and limited data on nematocyst types are presented. Because of the size of the new species and the known potency of the sting of congeners, we mention briefly the possible consequences of human contact.

Martin, L. E., et al. (2006). "Marine lake ecosystem dynamics illustrate ENSO variation in the tropical western Pacific." Biol Lett **2**(1): 144-147.

Understanding El Nino/Southern Oscillation (ENSO) and its biological consequences is hindered by a lack of high-resolution, long-term data from the tropical western Pacific. We describe a preliminary, 6 year dataset that shows tightly coupled ENSO-related bio-physical dynamics in a seawater lake in Palau, Micronesia. The lake is more strongly stratified during La Nina than El Nino conditions, temperature anomalies in the lake co-vary strongly with the Nino 3.4 climate index, and the abundance of the dominant member of the pelagic community, an endemic subspecies of zooxanthellate jellyfish, is temperature associated. These results have broad relevance because the lake: (i) illustrates an ENSO signal that is partly obscured in surrounding semi-enclosed lagoon waters and, therefore, (ii) may provide a model system for studying the effects of climate change on community evolution and cnidarian-zooxanthellae symbioses, which (iii) should be traceable throughout the Holocene because the lake harbours a high quality sediment record; the sediment record should (iv) provide a sensitive and regionally unique record of Holocene climate relevant to predicting ENSO responses to future global climate change and, finally, (v) seawater lake ecosystems elsewhere in the Pacific may hold similar potential for past, present, and predictive measurements of climate variation and ecosystem response.

Martindale, M. Q., et al. (2004). "Investigating the origins of triploblasty: 'mesodermal' gene expression in a diploblastic animal, the sea anemone Nematostella vectensis (phylum, Cnidaria; class,

Anthozoa)." Development **131**(10): 2463-2474.

Mesoderm played a crucial role in the radiation of the triploblastic Bilateria, permitting the evolution of larger and more complex body plans than in the diploblastic, non-bilaterian animals. The sea anemone Nematostella is a non-bilaterian animal, a member of the phylum Cnidaria. The phylum Cnidaria (sea anemones, corals, hydras and jellyfish) is the likely sister group of the triploblastic Bilateria. Cnidarians are generally regarded as diploblastic animals, possessing endoderm and ectoderm, but lacking mesoderm. To investigate the origin of triploblasty, we studied the developmental expression of seven genes from Nematostella whose bilaterian homologs are implicated in mesodermal specification and the differentiation of mesodermal cell types (twist, snailA, snailB, forkhead, mef2, a GATA transcription factor and a LIM transcription factor). Except for mef2, the expression of these genes is largely restricted to the endodermal layer, the gastrodermis. mef2 is restricted to the ectoderm. The temporal and spatial expression of these 'mesoderm' genes suggests that they may play a role in germ layer specification. Furthermore, the predominantly endodermal expression of these genes reinforces the hypothesis that the mesoderm and endoderm of triploblastic animals could be derived from the endoderm of a diploblastic ancestor. Alternatively, we consider the possibility that the diploblastic condition of cnidarians is a secondary simplification, derived from an ancestral condition of triploblasty.

Martini, S. and S. H. Haddock (2017). "Quantification of bioluminescence from the surface to the deep sea demonstrates its predominance as an ecological trait." Sci Rep **7**: 45750.

The capability of animals to emit light, called bioluminescence, is considered to be a major factor in ecological interactions. Because it occurs across diverse taxa, measurements of bioluminescence can be powerful to detect and quantify organisms in the ocean. In this study, 17 years of video observations were recorded by remotely operated vehicles during surveys off the California Coast, from the surface down to 3,900 m depth. More than 350,000 observations are classified for their bioluminescence capability based on literature descriptions. The organisms represented 553 phylogenetic concepts (species, genera or families, at the most precise taxonomic level defined from the images), distributed within 13 broader taxonomic categories. The importance of bioluminescent marine taxa is highlighted in the water column, as we showed that 76% of the observed individuals have bioluminescence capability. More than 97% of Cnidarians were bioluminescent, and 9 of the 13 taxonomic categories were found to be bioluminescent dominant. The percentage of bioluminescent animals is remarkably uniform over depth. Moreover, the proportion of bioluminescent and non-bioluminescent animals within taxonomic groups changes with depth for Ctenophora, Scyphozoa, Chaetognatha, and Crustacea. Given these results, bioluminescence has to be considered an important ecological trait from the surface to the deep-sea.

Martorelli, S. R. (1996). "First record of encysted metacercariae in hydrozoan jellyfishes and ctenophores of the southern Atlantic." J Parasitol **82**(2): 352-353.

Three species of pelagic coelenterates and ctenophores captured in Mar del Plata port, Buenos Aires, Argentina, were examined for digenean parasites. Encysted metacercariae were observed and collected. Cysts were found in the mesoglea of the hydromedusae Phialidium sp. and Liriope tetraphylla, and in the ectenophore Mnemiopsis macradyi. The morphology of the worms resembles that of the lepocreadiid digeneans. This is the first record for a metacercaria encysted in hydromedusae or ctenophores.

Martynov, V. I., et al. (2001). "Alternative cyclization in GFP-like proteins family. The formation and structure of the chromophore of a purple chromoprotein from Anemonia sulcata." J Biol Chem **276**(24): 21012-21016.

Anemonia sulcata purple protein (asFP595) belongs to a family of green fluorescent protein (GFP)-like proteins from the Anthozoa species. Similar to GFP, asFP595 apparently forms its chromophore by modifying amino acids within its polypeptide chain. Until now, the GFP-like proteins from Anthozoa were thought to contain chromophores with the same imidazolidinone core as GFP. Mass spectral analysis of a chromophore-containing tryptic pentapeptide from asFP595 demonstrates that chromophore formation in asFP595 is stoichiometrically the same as that in GFP: one H (2)O and two H (+) are released while a Schiff base and dehydrotyrosine are formed. However, structural studies of this asFP595 chromopeptide show that in contrast to GFP, the other peptide bond nitrogen and carbonyl carbon are required for chromophore cyclization, a reaction that yields the six-membered heterocycle 2-(4-hydroxybenzylidene)-6-hydroxy-2,5-dihydropyrazine. Spectrophotometric titration reveals three pH-dependent forms of the asFP595 chromopeptide: yellow (absorption maximum = 430 nm) at pH 3.0; red (absorption maximum = 535 nm) at pH 8.0; and colorless (absorption maximum = 380 nm) at pH 14.0. The pK (a) values for these spectral transitions (6.8 and 10.9) are consistent with the

ionization of the phenolic group of dehydrotyrosine and deprotonation of the amidinium cation in the chromophore heterocycle, respectively. The amidinium group in asFP595 accounts for the unique absorption spectrum of the protein, which is substantially red-shifted relative to that of GFP. When the asFP595 chromophore cyclizes, the Cys-Met bond adjacent to the chromophore hydrolyzes, splitting the chromoprotein into 8- and 20-kDa fragments. High performance liquid chromatography analysis of a tryptic digest of denatured asFP595 shows that a pentapeptide with the cleaved Cys-Met bond is the only fragment associated with the red-shifted absorbance. These results imply that fragmentation of asFP595 is a critical step in protein maturation.

Masuda, A., et al. (2007). "Mucin (qniumucin), a glycoprotein from jellyfish, and determination of its main chain structure." J Nat Prod **70**(7): 1089-1092.

We extracted a novel glycoprotein, a member of the mucin family, from five species of jellyfish with high yields (1%-3% dry weight, 0.02%-0.1% wet weight) and determined its main chain structure and molecular mass. The glycoprotein contains unique tandem repeats of eight amino acids, of which two threonine residues are probably glycosylated by N-acetyl-d-galactosamine (GalNAc). We named this substance, which is common in jellyfish and similar to the human mucin MUC5AC, "qniumucin" and suggested the utilization of this compound as a new marine resource.

Masuda, M., et al. (1999). "Analysis of receptor usage by ecotropic murine retroviruses, using green fluorescent protein-tagged cationic amino acid transporters." J Virol **73**(10): 8623-8629.

Entry of ecotropic murine leukemia virus (MuLV) into host cells is initiated by interaction between the receptor-binding domain of the viral SU protein and the third extracellular domain (TED) of the receptor, cationic amino acid transporter 1 (CAT1). To study the molecular basis for the retrovirus-receptor interaction, mouse CAT1 (mCAT1) was expressed in human 293 cells as a fusion protein with jellyfish green fluorescent protein (GFP). Easily detected by fluorescence microscopy and immunoblot analysis with anti-GFP antibodies, the mCAT1-GFP fusion protein was expressed in an N-glycosylated form on the cell surface and in the Golgi apparatus, retaining the ecotropic receptor function. The system was applied to compare Friend MuLV (F-MuLV) and its neuropathogenic variant, PVC-211 MuLV, which exhibits a unique cellular tropism and host range, for the ability to use various CAT family members as a receptor. The results indicated that F-MuLV and PVC-211 MuLV could infect the cells expressing wild-type mCAT1 at comparable efficiencies and that rat CAT3, but not mCAT2, conferred a low but detectable level of susceptibility to F-MuLV and PVC-211 MuLV. The data also suggested that CAT proteins might be expressed in an oligomeric form. Further application of the system developed in this study may provide useful insights into the entry mechanism of ecotropic MuLV.

Masuda, R. (2011). "Ontogeny of swimming speed, schooling behaviour and jellyfish avoidance by Japanese anchovy Engraulis japonicus." J Fish Biol **78**(5): 1323-1335.

The ontogeny of swimming speed, schooling behaviour and jellyfish avoidance was studied in hatchery-reared Japanese anchovy Engraulis japonicus to compare its life-history strategy with two other common pelagic fishes, jack mackerel Trachurus japonicus and chub mackerel Scomber japonicus. Cruise swimming speed of E. japonicus increased allometrically from 1.4 to 3.9 standard length (L (S)) per s (L (S) s (-1)) from early larval to metamorphosing stage. Burst swimming speed also increased from 6.1 to 28 L (S) s (-1) in these stages. Cruise speed was inferior to that of S. japonicus, as was burst speed to that of T. japonicus. Engraulis japonicus larvae were highly vulnerable to predation by moon jellyfish Aurelia aurita and were readily eaten until they reached 23 mm L (S), but not at 26 mm L (S). Schooling behaviour (indicated by parallel swimming) started at c. 17 mm L (S). Average distance to the nearest neighbour was shorter than values reported in other pelagic fishes. The relatively low predator avoidance capability of E. japonicus may be compensated for by their transparent and thus less conspicuous body, in addition to their early maturation and high fecundity.

Masuda, R., et al. (2016). "Recovery of Coastal Fauna after the 2011 Tsunami in Japan as Determined by Bimonthly Underwater Visual Censuses Conducted over Five Years." PLoS One **11**(12): e0168261.

Massive tsunamis induce catastrophic disturbance in marine ecosystems, yet they can provide unique opportunities to observe the process of regeneration. Here, we report the recovery of fauna after the 2011 tsunami in northeast Japan based on underwater visual censuses performed every two months over five years. Both total fish abundance and species richness increased from the first to the second year after the tsunami followed by stabilization in the following years. Short-lived fish, such as the banded goby Pterogobius elapoides, were relatively abundant in the first two years, whereas long-lived species, such as the black rockfish Sebastes cheni, increased in the latter half of the survey period. Tropical fish species

were recorded only in the second and third years after the tsunami. The body size of long-lived fish increased during the survey period resulting in a gradual increase of total fish biomass. The recovery of fish assemblages was slow at one site located in the inner bay, where the impact of the tsunami was the strongest. Apart from fish, blooms of the moon jellyfish Aurelia sp. occurred only in the first two years after the tsunami, whereas the abundances of sea cucumber Apostichopus japonicus and abalone Haliotis discus hannai increased after the second year. Although we lack quantitative data prior to the tsunami, we conclude that it takes approximately three years for coastal reef fish assemblages to recover from a heavy disturbance such as a tsunami and that the recovery is dependent on species-specific life span and habitat.

Masuda-Nakagawa, L. M., et al. (2000). "The HOX-like gene Cnox2-Pc is expressed at the anterior region in all life cycle stages of the jellyfish Podocoryne carnea." Dev Genes Evol **210**(3): 151-156.

The marine jellyfish Podocoryne carnea (Cnidaria, Hydrozoa) has a metagenic life cycle consisting of a larva, a colonial polyp and a free-swimming jellyfish (medusa). To study the function of HOX genes in primitive diploblastic animals we screened a library of P. carnea cDNA using PCR primers derived from the most conserved regions in helix 1 and helix 3 of the homeobox. A novel gene, Cnox2-Pc, has been isolated and characterized. Cnox2-Pc is a HOX cluster-like gene, and its homeodomain shows similarity to the Deformed subfamily of HOM-C/HOX genes. In situ hybridization revealed that Cnox2-Pc is expressed in the anterior region of the larva, the polyp head, and the most apical ectoderm of the differentiating bud during medusa development. In adult medusa expression is restricted to the gastrovascular entoderm. The results suggest that Cnox2-Pc is involved in establishment of an anterior-posterior axis during development in primitive metazoans.

Matveev, I. V., et al. (2007). "A novel Aurelia aurita protein mesoglein contains DSL and ZP domains." Gene **399**(1): 20-25.

Body of the scyphoid jellyfish Aurelia aurita consists of 2 epithelia -- epidermis and gastroderm. The layers are separated by a thick layer of extracellular matrix -- mesoglea. A. aurita has a lot of cells in the mesoglea unlike many other Cnidarians. The major protein of the mesoglea with apparent molecular mass of 47 kDa was detected by SDS-PAGE. A partial mRNA of the protein 1421 bp long was cloned and sequenced. The search for homologous nucleotide and protein sequences shows that the mRNA sequence is novel. Deduced amino acid sequence of 416 aa contains zona pellucida (ZP) domain and Delta/Serrate/Lag-2 (DSL) domain. The protein was named mesoglein. According to reverse transcription PCR analysis it is expressed in the mature medusa exclusively in the mesogleal cells. Mesoglein belongs to the lowest phyla among ZP domain-containing proteins. The protein is supposed to be a structural element of the mesoglea extracellular matrix.

Matz, M. V., et al. (2002). "Family of the green fluorescent protein: journey to the end of the rainbow." Bioessays **24**(10): 953-959.

Members of the family of the Green Fluorescent Protein (GFP) are the only known type of natural pigments that are essentially encoded by a single gene, since both the substrate for pigment biosynthesis and the necessary catalytic moieties are provided within a single polypeptide chain. In sharp contrast to the state of knowledge just three years ago when GFP was the only known protein of its kind, a whole family of related proteins, exhibiting striking diversity of features have now been identified. This provides new possibilities for a variety of studies ranging from applied biotechnology to evolutionary ecology.

Mazzei, M., et al. (1994). "HPLC separation of toxic fraction components extracted from planktonic and benthic Cnidaria." Boll Soc Ital Biol Sper **70**(5-6): 143-151.

HPLC separation of crude extract components derived from nematocysts and extranematocystic tissues of macroplanktonic jellyfish Aequorea aequorea and Rhizostoma pulmo and benthic sea-anemones Actinia equina and Anemonia sulcata was carried out by different columns. A satisfactory peak separation was obtained analyzing the toxin of Rhizostoma pulmo by cationic and C18 columns. Low molecular weight fragments were separated by C18 column and U.V. monitored varying pH values and obtaining the displacement of significant peaks. Clear differences between chromatographic plots concerning planktonic and benthic species was evidenced by anionic column; this result can point out a clear ecological analogy between species living in the same environment and a similar toxin biosynthesis, due to selective actions related to both the environment and the phylogenetic relationships; these organisms could have developed similar mechanisms useful to tackle the environment.

Mc, D. T. D., et al. (2002). "A sting from an unknown jellyfish species associated with persistent symptoms and raised troponin I levels." Emerg Med (Fremantle) **14**(2): 175-180.

We describe a patient stung by an unknown

jellyfish species offshore in Far North Queensland. The sting caused immediate and severe pain, multiple whip-like skin lesions and constitutional symptoms. The jellyfish tentacular nematocysyts were similar to, but distinct from, those of Carukia barnesi, a cause of the 'Irukandji' syndrome. The patients symptoms largely resolved over seven months and were associated with elevated cardiac troponin levels, in the absence of other evidence of cardiac disease. This case highlights the envenomation risks associated with marine recreation, and the need for critical evaluation of cardiac troponin assays and for further research in marine toxicology.

McAfee, J. S., et al. (2015). "Jellyfish model for ototoxicity." Otol Neurotol **36**(2): 329-335.

OBJECTIVE: Pharmacologic ototoxicity is well described in the medical literature, yet efficient screening models are lacking. Aurelia aurita ephyrae, transparent jellyfish with identifiable hair cells, could be an effective model. Structural changes readily manifest behaviorally, and hair cells are easily stained and observed. We treated ephyrae with various gentamicin concentrations, evaluated its motility, and quantified its hair cell loss. STUDY DESIGN: Baseline pulsing per minute (P), swimming (S), and orientation (O) values were recorded from cultured ephyrae. Ephyrae were transferred into test tubes containing artificial seawater (ASW), gentamicin, or penicillin. P, S, and O were scored at 0, 24, and 48 hours. Ephyrae were formalin fixed, phalloidin stained, and imaged with confocal microscopy, and hair cells were then counted. RESULTS: P was impaired by gentamicin in a dose-dependent fashion, whereas ASW controls maintained baseline P, S, and O values. Impairment of S and O occurred with 3.5 mmol/L gentamicin at 24 hours. For six experiments each using 40 ephyrae, at 24 hours, average P was reduced from 75.2 in ASW to 28.8, 12.3, and 1.9 for 1, 2, and 3.5 mmol/L gentamicin, respectively ($p < 0.05$ for all cases). Hair cell loss at 24 and 48 hours was significant (32% and 48% reduction compared with control, $p < 0.05$) and correlated with motility deficits. Deficits from penicillin exposure were not statistically significant. CONCLUSION: The ephyra model demonstrated functional and histologic gentamicin-mediated impairments, showing promise as a screening tool for ototoxic agents. The changes in ephyra motility after gentamicin exposure correlated significantly with hair cell loss.

McCann, J. (2001). "Jellyfish protein gives new glow to tumor imaging." J Natl Cancer Inst **93**(13): 976-977.

McCormick, D. P. and A. L. Davis (1988). "Injuries in sailboard enthusiasts." Br J Sports Med **22**(3): 95-97.

This study was carried out to determine the rate and types of injuries experienced by boardsailors. Results derive from: (a) a review of hospital medical records for water sports injuries, and (b) a questionnaire-interview of 73 athletes windsurfing on waters in the Galveston area during a hurricane and in moderate and light wind conditions. Windsurfers reported 0.22 injuries per 1,000 participant hours. Seventy-six per cent of athletes reported injuries while boardsailing, but only 15 per cent reported significant injuries. The most common reported injuries included lacerations, jellyfish stings, abrasions, muscle strain, sunburn, contusions, and blisters. A small number of athletes reported ligament sprain, ear infection, knee injury, eye injury, and splinters. The large majority of injuries reported are preventable by wearing protective gear, applying sunscreen, avoiding overpowering winds, and selecting safe sailing areas. Four per cent of water-sport injuries requiring hospitalisation resulted when epileptic water-sports participants had a seizure in or near the water.

McGeown, J. G. (2010). "Seeing is believing! Imaging Ca2+-signalling events in living cells." Exp Physiol **95**(11): 1049-1060.

Ever since it was shown that maintenance of muscle contraction required the presence of extracellular Ca (2+), evidence has accumulated that Ca (2+) plays a crucial role in excitation-contraction coupling. This culminated in the use of the photoprotein aequorin to demonstrate that [Ca (2+)] (i) increased after depolarization but before contraction in barnacle muscle. Green fluorescent protein was extracted from the same jellyfish as aequorin, so this work also has important historical links to the use of fluorescent proteins as markers in living cells. The subsequent development of cell-permeant Ca (2+) indicators resulted in a dramatic increase in related research, revealing Ca (2+) to be a ubiquitous cell signal. High-speed, confocal Ca (2+) imaging has now revealed subcellular detail not previously apparent, with the identification of Ca (2+) sparks. These act as building blocks for larger transients during excitation-contraction coupling in cardiac muscle, but their function in smooth muscle appears more diverse, with evidence suggesting both 'excitatory' and 'inhibitory' roles. Sparks can activate Ca (2+)-sensitive Cl () and K (+) currents, which exert positive and negative feedback, respectively, on global Ca (2+) signalling, through changes in membrane potential and activation of voltage-operated Ca (2+) channels. Calcium imaging has also demonstrated that agonists that appear to evoke relatively tonic increases in average [Ca (2+)] (i) at the whole tissue level often stimulate

much higher frequency phasic Ca (2+) oscillations at the cellular level. These findings may require re-evaluation of some of our models of Ca (2+) signalling to account for newly revealed cellular and subcellular detail. Future research in the field is likely to make increasing use of genetically coded Ca (2+) indicators expressed in an organelle- or tissue-specific manner.

Meech, R. W. and G. O. Mackie (1995). "Synaptic potentials and threshold currents underlying spike production in motor giant axons of Aglantha digitale." J Neurophysiol **74**(4): 1662-1670.

1. Motor giant axons that excite swimming muscles in the jelly-fish Aglantha digitale interface with units of the inner and outer nerve rings in the margin at the base of the bell. External recording electrodes were used to monitor electrical activity at different sites within the nerve ring while events in the motor giant axon were recorded with intracellular micropipettes placed within 100 microns of the synaptic area. In some experiments, 4- to 6-micron-diam patch pipettes were used to record in situ from ion channel clusters at different locations along the axon. 2. Independently propagating calcium and sodium spikes in the motor giant axon were found to arise from different excitatory postsynaptic potentials (EPSPs). Two separate inputs were identified; one EPSP class represented an input from the pacemaker system in the inner nerve ring, whereas another represented an input from the giant axon in the outer nerve ring. EPSPs from the two nerve rings had significantly different time courses and amplitudes. EPSPs from the ring giant axon reached a peak in little more than 1 ms, whereas EPSPs from the pacemaker system reached a maximum in approximately 7 ms. These slower EPSPs may be compound events composed of postsynaptic potentials from multiple synapses excited in series by the passage of the pacemaker neuron signal. 3. The threshold for the production of calcium spikes by the slow EPSPs of the pacemaker system (-51 +/- 2.2 mV, mean +/- SD; n = 5) corresponded well with the voltage at which a net inward "T"-type calcium current first appeared in recordings from axon membrane patches (-55 to -50 mV); the threshold for the initiation of the sodium spike by the fast EPSPs of the ring giant system (-32 +/- 1.2 mV, mean +/- SD; n = 6) corresponded well with the voltage at which a net inward sodium current first appeared (-35 to -30 mV). 4. Inward currents were rarely observed in membrane patches formed using pipettes with tips of < 1 micron OD. Even with 4-micron pipettes, patches of membrane were sometimes obtained with a channel population consisting exclusively of potassium channels; calcium and sodium currents were found in highly discrete areas ("hot spots"). Preliminary findings on the undersurface of the axon, which makes synaptic contact with the myoepithelium, are consistent with a similar distribution. 5. The pathway by which the ring giant excites the motor giant axon is not definitely known. The synaptic delay between the peak of the ring giant action potential (monitored externally) and the initial rise of the fast EPSP (1.64 +/- 0.15 ms, mean +/- SD; n = 21) would allow for transmission at two synapses, because single synaptic delays at neuromuscular junctions in Aglantha are approximately 0.7 ms at 12 degrees C. The mean synaptic delay at the slow EPSP synapse was 0.88 +/- 0.09 (SD) ms (n = 12). 6. The delay between the impulse in the ring giant axon and the subsequent excitation of the motor giant axon may permit the animal to withdraw its tentacles and so lower the drag that would otherwise reduce the effectiveness of any escape swim and might induce tentacle autotomy.

Siemering, K. R., et al. (1996). "Mutations that suppress the thermosensitivity of green fluorescent protein." Curr Biol **6**(12): 1653-1663.

BACKGROUND: The green fluorescent protein (GFP) of the jellyfish Aequorea victoria has recently attracted great interest as the first example of a cloned reporter protein that is intrinsically fluorescent. Although successful in some organisms, heterologous expression of GFP has not always been straight forward. In particular, expression of GFP in cells that require incubation temperatures around 37 degrees C has been problematic. RESULTS: We have carried out a screen for mutant forms of GFP that fluoresce more intensely than the wild-type protein when expressed in E. coli at 37 degrees C. We have characterized a bright mutant (GFPA) with reduced sensitivity to temperature in both bacteria and yeast, and have shown that the amino acids substituted in GFPA act by preventing temperature-dependent misfolding of the GFP apoprotein. We have shown that the excitation and emission spectra of GFPA can be manipulated by site-directed mutagenesis without disturbing its improved folding characteristics, and have produced a thermostable folding mutant (GFP5) that can be efficiently excited using either long-wavelength ultraviolet or blue light. Expression of GFP5 results in greatly improved levels of fluorescence in both microbial and mammalian cells cultured at 37 degrees C. CONCLUSIONS: The thermotolerant mutants of GFP greatly improve the sensitivity of the protein as a visible reporter molecule in bacterial, yeast and mammalian cells. The fluorescence spectra of these mutants can be manipulated by further mutagenesis without deleteriously affecting their improved folding characteristics, so it may be possible to engineer a range of spectral variants with improved tolerance to temperature. Such a range of sensitive reporter

proteins will greatly improve the prospects for GFP-based applications in cells that require relatively high incubation temperatures.

Winter, K. L., et al. (2009). "An in vivo comparison of the efficacy of CSL box jellyfish antivenom with antibodies raised against nematocyst-derived Chironex fleckeri venom." Toxicol Lett **187**(2): 94-98.

Although CSL box jellyfish antivenom (AV) remains the primary treatment for Chironex fleckeri envenoming, there has been considerable debate regarding its clinical effectiveness. Animal studies have shown that AV is largely ineffective in preventing C. fleckeri-induced cardiovascular collapse. This study examined the effectiveness of CSL box jellyfish AV (ovine IgG), raised against 'milked' venom, and polyclonal rabbit IgG antibodies (Ab) raised against nematocyst-derived venom. A venom dose of 30microg/kg, i.v., which causes an initial presser response (34+/-5mmHg; n=7) followed by cardiovascular collapse, was used in all experiments. A bolus dose of AV (3000U/kg, i.v.) or Ab (12mg; i.e. an equivalent protein 'load' to 3000U/kg AV), administered 15min prior to a bolus dose of venom, did not significantly attenuate the effects of venom. The venom response was also not significantly attenuated when AV (3000U/kg) was given as a bolus dose 10-60min prior to venom infusion. However, when the venom was incubated with either AV (3000U/kg) or Ab (12mg) for 3h prior to infusion, the effect of the venom was almost abolished. The results of this study demonstrate that antibodies raised against both 'milked' and nematocyst-derived venom are able to neutralise the cardiovascular collapse produced by the venom. However, large amounts of AV are required and must be preincubated with the venom to be protective. This indicates a very rapid action of the toxin (s) and that AV is unlikely to be clinically effective because it cannot be administered early enough.

Winter, K. L., et al. (2010). "A pharmacological and biochemical examination of the geographical variation of Chironex fleckeri venom." Toxicol Lett **192**(3): 419-424.

Chironex fleckeri (box jellyfish) are found in the northern tropical waters of Australia. Although C. fleckeri have a wide geographical distribution and are able to swim large distances, adults tend to stay in small restricted areas. Clinical data shows that deaths from envenoming have not been recorded in Western Australia, yet numerous fatalities have occurred in Northern Territory and Queensland waters. One explanation for this discrepancy is a geographical variation in venom composition. This study examined the pharmacological and biochemical profiles of C. fleckeri venom from different geographical locations and seasons. Venoms were screened for cytotoxicity using a rat aortic smooth muscle cell line (A7r5). While all venoms caused concentration-dependent cytotoxicity, differences were seen in the potency of venoms from Mission Beach and Weipa, when collected in different seasons, as indicated by IC (50) values. Similarly venoms collected within the same season, from different locations around Australia, displayed marked differences in venom composition as shown by size exclusion HPLC and SDS-PAGE profiles which indicated the absence or reduced quantity of 'peaks' in some venoms. Based on IC (50) data obtained from the cell assay, the effects of the most potent (i.e. from Weipa in 2006) and the least potent (i.e. from Broome in 2007) venoms were examined in anesthetised rats. Both venoms at 10 microg/kg (i.v.) caused a transient hypertensive phase followed by cardiovascular collapse. However, at 4 microg/kg (i.v.) venom from Weipa 2006 caused a transient hypertensive phase followed by a transient decrease in MAP while venom from Broome 2007 only caused a small transient increase in MAP. This study demonstrates that there is considerable geographical variation in the composition of C. fleckeri venoms which is most distinct between specimens from western and eastern Australia and may explain the geographical variation in reported deaths.

Winter, K. L., et al. (2008). "An examination of the cardiovascular effects of an 'Irukandji' jellyfish, Alatina nr mordens." Toxicol Lett **179**(3): 118-123.

Irukandji syndrome is usually characterized by delayed severe abdominal, back and chest pain associated with autonomic effects including diaphoresis, hypertension and, in severe cases, myocardial injury and pulmonary oedema. It is most often associated with envenoming by the jellyfish Carukia barnesi, but a number of other jellyfish, including Alatina mordens, are now known to produce Irukandji syndrome. In the present study, nematocyst-derived venom from A. nr mordens (150-250 microg/kg, i.v.) produced a long-lasting pressor effect in anaesthetised rats. This pressor response (250 microg/kg, i.v.) was significantly inhibited by prior administration of the alpha-adrenoceptor antagonist prazosin (200 microg/kg, i.v.) but not by CSL box jellyfish antivenom (300 U/kg, i.v.). A. nr mordens venom 250 microg/kg (i.v.) caused marked increases in plasma adrenaline and noradrenaline concentrations following administration in anaesthetised rats. The venom did not contain appreciable amounts of either adrenaline or noradrenaline. A. nr mordens venom (25 microg/ml) produced a contractile response in rat electrically stimulated vas deferens which was

markedly reduced in tissues pre-treated with reserpine (0.1mM) or guanethidine (0.1mM). Sodium dodecyl sulphate (SDS)-PAGE analysis showed that A. nr mordens venom is comprised of multiple protein bands ranging from 10 to 200 kDa. Western blot analysis using CSL box jellyfish antivenom indicated several antigenic proteins in A. nr mordens venom, however, it did not detect all proteins present in the venom. This study characterizes the in vitro and in vivo effects of A. nr mordens venom and indicates that the cardiovascular effects are at least partially mediated by endogenous catecholamine release.

Winter, K. L., et al. (2007). "An in vivo examination of the stability of venom from the Australian box jellyfish Chironex fleckeri." Toxicon **49**(6): 804-809.

We have previously characterised the pharmacological activity of a number of jellyfish venoms with a particular emphasis on the profound cardiovascular effects. It has been suggested that jellyfish venoms are difficult to work with and are sensitive to pH, temperature and chemical changes. The current study aimed to examine the working parameters of the venom of the Australian box jellyfish Chironex fleckeri to enable fractionation and isolation of the toxins with cardiovascular activity. C. fleckeri venom was made up fresh each day and subjected to a number of different environments (i.e. a pH range of 5-9 and a temperature range of 4-30 degrees C). In addition, the effect of freeze drying and reconstituting the venom was investigated. Venom (50 microg/kg, i.v.) produced a transient hypertensive response followed by cardiovascular collapse in anaesthetised rats. This biphasic response was not significantly effected by preparation of the venom at a pH of 5, 7 or 9. Similarly, venom (50 microg/kg, i.v.) did not display a loss of activity when exposed to temperatures of 4, 20 or 30 degrees C for 1.5h. However, the cardiovascular activity was abolished by boiling the venom. Freeze drying, and then reconstituting, the venom did not significantly affect its cardiovascular activity. However, repeated freeze drying and reconstituting of extracted venom resulted in a significantly loss of activity. This study provides a more detailed knowledge of the parameters in which C. fleckeri venom can be used and, while supporting some previous studies, contradicts some of the perceived problems of working with the venom.

Wit, A. L. and P. F. Cranefield (1978). "Reentrant excitation as a cause of cardiac arrhythmias." Am J Physiol **235**(1): H1-17.

Mechanisms that cause reentry were defined in rings of tissue cut from jellyfish as early as 1906 by Mayer. The concepts were developed by Mines and Garrey during the next 10 years. Lewis then tried to demonstrate that reentry caused atrial flutter. Lewis, Garrey, and later Moe also proposed that atrial fibrillation was caused by reentry. Rosenblueth provided additional experimental evidence that reentry could cause atrial arrhythmias after crushing the intercaval bridge of atrial muscle. Recent studies by Allessie using microelectrodes have provided detailed evidence for reentry in atrial tissue. Mines in 1913 also proposed that reentry could occur in the AV node. Scherf then introduced the concept of functional longitudinal dissociation as a cause of return extrasystoles and this was later shown to happen in the node by Moe and his colleagues. Reentry can also occur between atria and ventricles utilizing accessory connecting pathways. Schmitt and Erlanger in 1913 were the first to do experiments which indicated that reentry can also occur in the ventricles. Subsequently it was shown that reentry can occur in Purkinje fiber bundles. Reentry in ventricular muscle may also cause some of the arrhythmias that occur after myocardial infarction.

Wodarz, D., et al. (2012). "Complex spatial dynamics of oncolytic viruses in vitro: mathematical and experimental approaches." PLoS Comput Biol **8**(6): e1002547.

Oncolytic viruses replicate selectively in tumor cells and can serve as targeted treatment agents. While promising results have been observed in clinical trials, consistent success of therapy remains elusive. The dynamics of virus spread through tumor cell populations has been studied both experimentally and computationally. However, a basic understanding of the principles underlying virus spread in spatially structured target cell populations has yet to be obtained. This paper studies such dynamics, using a newly constructed recombinant adenovirus type-5 (Ad5) that expresses enhanced jellyfish green fluorescent protein (EGFP), AdEGFPuci, and grows on human 293 embryonic kidney epithelial cells, allowing us to track cell numbers and spatial patterns over time. The cells are arranged in a two-dimensional setting and allow virus spread to occur only to target cells within the local neighborhood. Despite the simplicity of the setup, complex dynamics are observed. Experiments gave rise to three spatial patterns that we call "hollow ring structure", "filled ring structure", and "disperse pattern". An agent-based, stochastic computational model is used to simulate and interpret the experiments. The model can reproduce the experimentally observed patterns, and identifies key parameters that determine which pattern of virus growth arises. The model is further used to study the long-term outcome of the dynamics for the different growth patterns, and to investigate conditions under

which the virus population eliminates the target cells. We find that both the filled ring structure and disperse pattern of initial expansion are indicative of treatment failure, where target cells persist in the long run. The hollow ring structure is associated with either target cell extinction or low-level persistence, both of which can be viewed as treatment success. Interestingly, it is found that equilibrium properties of ordinary differential equations describing the dynamics in local neighborhoods in the agent-based model can predict the outcome of the spatial virus-cell dynamics, which has important practical implications. This analysis provides a first step towards understanding spatial oncolytic virus dynamics, upon which more detailed investigations and further complexity can be built.

Wolenski, F. S., et al. (2011). "Characterization of the core elements of the NF-kappaB signaling pathway of the sea anemone Nematostella vectensis." Mol Cell Biol **31**(5): 1076-1087.

The sea anemone Nematostella vectensis is the leading developmental and genomic model for the phylum Cnidaria, which includes anemones, hydras, jellyfish, and corals. In insects and vertebrates, the NF-kappaB pathway is required for cellular and organismal responses to various stresses, including pathogens and chemicals, as well as for several developmental processes. Herein, we have characterized proteins that comprise the core NF-kappaB pathway in Nematostella, including homologs of NF-kappaB, IkappaB, Bcl-3, and IkappaB kinase (IKK). We show that N. vectensis NF-kappaB (Nv-NF-kappaB) can bind to kappaB sites and activate transcription of reporter genes containing multimeric kappaB sites or the Nv-IkappaB promoter. Both Nv-IkappaB and Nv-Bcl-3 interact with Nv-NF-kappaB and block its ability to activate reporter gene expression. Nv-IKK is most similar to human IKKepsilon/TBK kinases and, in vitro, can phosphorylate Ser47 of Nv-IkappaB. Nv-NF-kappaB is expressed in a subset of ectodermal cells in juvenile and adult Nematostella anemones. A bioinformatic analysis suggests that homologs of many mammalian NF-kappaB target genes are targets for Nv-NF-kappaB, including genes involved in apoptosis and responses to organic compounds and endogenous stimuli. These results indicate that NF-kappaB pathway proteins in Nematostella are similar to their vertebrate homologs, and these results also provide a framework for understanding the evolutionary origins of NF-kappaB signaling.

Wong, D. E., et al. (1994). "Seabather's eruption. Clinical, histologic, and immunologic features." J Am Acad Dermatol **30**(3): 399-406.

BACKGROUND: Seabather's eruption (SE) is a highly pruritic eruption under swimwear that occurs after bathing in the ocean. Its cause has been unknown. Few data have been collected since the classic description by Sams in 1949. OBJECTIVE: Our purpose was to describe the clinical and histopathologic findings in SE and to confirm the cause. METHODS: Patients with a pruritic eruption that developed after swimming were seen within 1 week of onset. Skin biopsy specimens and sera were obtained in selected cases. Water samples taken from areas of active SE outbreaks were examined for a causative organism. Sera were tested by enzyme-linked immunosorbent assay for reactivity to this organism. RESULTS: In southeast Florida, during a 4-month period, 70 patients with SE were seen. Inflammatory papules and pruritus were noted within hours of exposure. Eruptions were maximal in areas covered by a bathing suit. Children were more likely than adults to have systemic symptoms. The average duration of the eruption and pruritus was 12.5 days, with recurrences in 4.3% of patients. Histopathologic examination revealed a superficial and deep perivascular and interstitial infiltrate consisting of lymphocytes, neutrophils, and eosinophils. Water samples contained many cnidarian larvae, later grown to maturity and identified as Linuche unguiculata (thimble jellyfish). Enzyme-linked immunosorbent assay demonstrated in patients' sera high IgG levels specific for L. unguiculata. CONCLUSION: SE is a severely pruritic marine dermatosis that resolves spontaneously within 2 weeks. Therapy is symptomatic but often ineffective. Sera from affected persons showed specific reactivity to L. unguiculata.

Zhang, Q., et al. (2018). "Separation and Characterization of Antioxidative and Angiotensin Converting Enzyme Inhibitory Peptide from Jellyfish Gonad Hydrolysate." Molecules **23**(1).

The gonad of jellyfish (RhopilemaesculentumKishinouye), containing high protein content with a rich amino acid composition, is suitable for the preparation of bioactive peptides. Jellyfish gonad was hydrolysed with neutral protease to obtain jellyfish gonad protein hydrolysate (JGPH), which was then purified sequentially by ultrafiltration, gel filtration chromatography, and RP-HPLC. The peptides were characterized with HPLC-MS/MS. One peptide with amino acid sequence Ser-Tyr (SY) was identified and synthesized, which showed good ACE inhibitory and antioxidant activity. The IC50 of this peptide on DPPH,.OH, super oxygen anion scavenging activities, and ACE inhibitory activity are 84.623 muM, 1177.632 muM, 456.663 muM, and 1164.179 muM, respectively. The anchor in the binding site of SY and ACE C-domain (ACE-C) was obtained by molecular simulations. The results showed that the

dipeptide purified from jellyfish gonad protein hydrolysates can be used as functional food material and is helpful in the study of antioxidant and inhibition of ACE.

Zhang, X., et al. (2019). "Bubble-Propelled Jellyfish-like Micromotors for DNA Sensing." ACS Appl Mater Interfaces **11**(14): 13581-13588.

A chemically powered jellyfish-like micromotor was proposed by using a multimetallic shell and a DNA assembly with catalase decorations modified on the concave surface to simulate the umbrella-shaped body and the muscle fibers on the inner umbrella of jellyfish. Relying on the catalytic generation of oxygen gas by catalase in H2O2 fuel, the jellyfish-like micromotor showed good bubble-propelled motion in different biomedia with speed exceeding 209 mum s (-1) in 1.5% H2O2. The jellyfish-like micromotors could also be applied for motion detection of DNA based on a displacement hybridization-triggered catalase release. The proposed jellyfish-like micromotors showed advantages of easy fabrication, good motion ability, sensitive motion detection of DNA, and good stability and reproducibility, indicating considerable promise for biological application.

Zhang, Y., et al. (2017). "Dual-Mode Electronic Skin with Integrated Tactile Sensing and Visualized Injury Warning." ACS Appl Mater Interfaces **9**(42): 37493-37500.

Mimicking the pressure-sensing behavior of biological skins using electronic devices has profound implications for prosthetics and medicine. The developed electronic skins based on single response mode for pressure sensing suffer from a rapid decrease in sensitivity with the increase of pressure. Their highly sensitive range covers a narrow part of tolerable pressure range of the human skin and has a weak response to the injurious high pressures. Herein, inspired by a bioluminescent jellyfish, we develop an electronic skin with dual-mode response characteristics, which is able to quantify and map the static and dynamic pressures by combining electrical and optical responses. The electronic skin shows notable changes in capacitance in the low-pressure regime and can emit bright luminescence in the high-pressure regime, which, respectively, imitates the functions of the mechanoreceptors and nociceptors in the biological skin, enabling it to sense gentle tactile and injurious pressure with sensitivities up to 0.66 and 0.044 kPa (-1), respectively. The complementary highly sensitive sensing ranges of the electronic skin realize a reliable perception to different levels of pressure, and its mechanically robust and stretchable properties may find a wide range of applications in intelligent robots.

Zhao, F., et al. (2016). "Development of tobacco ringspot virus-based vectors for foreign gene expression and virus-induced gene silencing in a variety of plants." Virology **492**: 166-178.

We report here the development of tobacco ringspot virus (TRSV)-based vectors for the transient expression of foreign genes and for the analysis of endogenous gene function in plants using virus-induced gene silencing. The jellyfish green fluorescent protein (GFP) gene was inserted between the TRSV movement protein (MP) and coat protein (CP) regions, resulting in high in-frame expression of the RNA2-encoded viral polyprotein. GFP was released from the polyprotein via an N-terminal homologous MP-CP cleavage site and a C-terminal foot-and-mouth disease virus (FMDV) 2 A catalytic peptide in Nicotiana benthamiana. The VIGS target gene was introduced in the sense and antisense orientations into a SnaBI site, which was created by mutating the sequence following the CP stop codon. VIGS of phytoene desaturase (PDS) in N. benthamiana, Arabidopsis ecotype Col-0, cucurbits and legumes led to obvious photo-bleaching phenotypes. A significant reduction in PDS mRNA levels in silenced plants was confirmed by semi-quantitative RT-PCR.

Zhao, L. and J. Wang (2016). "Uncovering the mechanisms of Caenorhabditis elegans ageing from global quantification of the underlying landscape." J R Soc Interface **13**(124).

Recent studies on Caenorhabditis elegans reveal that gene manipulations can extend its lifespan several fold. However, how the genes work together to determine longevity is still an open question. Here we construct a gene regulatory network for worm ageing and quantify its underlying potential and flux landscape. We found ageing and rejuvenation states can emerge as basins of attraction at certain gene expression levels. The system state can switch from one attractor to another driven by the intrinsic or external perturbations through genetics or the environment. Furthermore, we simulated gene silencing experiments and found that the silencing of longevity-promoting or lifespan-limiting genes leads to ageing or rejuvenation domination, respectively. This indicates that the difference in depths between ageing and the rejuvenation attractor is highly correlated with worm longevity. We further uncovered some key genes and regulations which have a strong influence on landscape basin stability. A dynamic landscape model is proposed to describe the whole process of ageing: the ageing attractor dominates when senescence progresses. We also uncovered the oscillation dynamics, and a similar behaviour was

observed in the long-lived creature Turritopsis dohrnii Our landscape theory provides a global and physical approach to explore the underlying mechanisms of ageing.

Zuryn, S., et al. (2014). "Transdifferentiation. Sequential histone-modifying activities determine the robustness of transdifferentiation." Science **345**(6198): 826-829.

Natural interconversions between distinct somatic cell types have been reported in species as diverse as jellyfish and mice. The efficiency and reproducibility of some reprogramming events represent unexploited avenues in which to probe mechanisms that ensure robust cell conversion. We report that a conserved H3K27me3/me2 demethylase, JMJD-3.1, and the H3K4 methyltransferase Set1 complex cooperate to ensure invariant transdifferentiation (Td) of postmitotic Caenorhabditis elegans hindgut cells into motor neurons. At single-cell resolution, robust conversion requires stepwise histone-modifying activities, functionally partitioned into discrete phases of Td through nuclear degradation of JMJD-3.1 and phase-specific interactions with transcription factors that have conserved roles in cell plasticity and terminal fate selection. Our results draw parallels between epigenetic mechanisms underlying robust Td in nature and efficient cell reprogramming in vitro.

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