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Basic local alignment search tool (BLAST)

Mark Herbert

World Development Institute
39 Main Street, Flushing, Queens, New York 11354, USA, ma708090@gmail.com

Abstract: In bioinformatics, basic local alignment search tool (BLAST) is an algorithm and program for comparing primary biological sequence information, such as the amino-acid sequences of proteins or the nucleotides of DNA and/or RNA sequences. A BLAST search enables a researcher to compare a subject protein or nucleotide sequence (called a query) with a library or database of sequences, and identify database sequences that resemble the query sequence above a certain threshold. For example, following the discovery of a previously unknown gene in the mouse, a scientist will typically perform a BLAST search of the human genome to see if humans carry a similar gene; BLAST will identify sequences in the human genome that resemble the mouse gene based on similarity of sequence.

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Background

BLAST, which *The New York Times* called *the Google of biological research*,[2] is one of the most widely used bioinformatics programs for sequence searching.[3] It addresses a fundamental problem in bioinformatics research. The heuristic algorithm it uses is much faster than other approaches, such as calculating an optimal alignment. This emphasis on speed is vital to making the algorithm practical on the huge genome databases currently available, although subsequent algorithms can be even faster.

Before BLAST, FASTA was developed by David J. Lipman and William R. Pearson in 1985.[4]

Before fast algorithms such as BLAST and FASTA were developed, searching databases for protein or nucleic sequences was very time consuming because a full alignment procedure (e.g., the Smith–Waterman algorithm) was used.

BLAST came from the 1990 stochastic model of Samuel Karlin and Stephen Altschul[5] They proposed "a method for estimating similarities between the known DNA sequence of one organism with that of another",[2] and their work has been described as "the statistical foundation for BLAST."[6] Subsequently, Altschul, along with Warren Gish, Webb Miller, Eugene Myers, and David J. Lipman at the National Institutes of Health designed the BLAST algorithm, which was published in the *Journal of Molecular Biology* in 1990 and cited over 75,000 times.[7]

While BLAST is faster than any Smith-Waterman implementation for most cases, it cannot "guarantee the optimal alignments of the query and database sequences" as Smith-Waterman algorithm does. The optimality of Smith-Waterman "ensured the best performance on accuracy and the most precise results" at the expense of time and computer power.

BLAST is more time-efficient than FASTA by searching only for the more significant patterns in the sequences, yet with comparative sensitivity. This could be further realized by understanding the algorithm of BLAST introduced below.

Examples of other questions that researchers use BLAST to answer are:

- Which bacterial species have a protein that is related in lineage to a certain protein with known amino-acid sequence
- What other genes encode proteins that exhibit structures or motifs such as ones that have just been determined

BLAST is also often used as part of other algorithms that require approximate sequence matching.

BLAST is available on the web on the NCBI website. Different types of BLASTs are available according to the query sequences and the target databases. Alternative implementations include AB-BLAST (formerly known as WU-BLAST), FSA-BLAST (last updated in 2006), and ScalaBLAST.[8][9]

The original paper by Altschul, *et al.*[7] was the most highly cited paper published in the 1990s.[10]

Input

Input sequences (in FASTA or Genbank format), database to search and other optional parameters such as scoring matrix.

Output

BLAST output can be delivered in a variety of formats. These formats include HTML, plain text, and XML formatting. For NCBI's web-page, the default format for output is HTML. When performing a BLAST on NCBI, the results are given in a graphical format showing the hits found, a table showing sequence identifiers for the hits with scoring related data, as well as alignments for the sequence of interest and the hits received with corresponding BLAST scores for these. The easiest to read and most informative of these is probably the table.

If one is attempting to search for a proprietary sequence or simply one that is unavailable in databases available to the general public through sources such as NCBI, there is a BLAST program available for download to any computer, at no cost. This can be found at BLAST+ executables. There are also commercial programs available for purchase. Databases can be found from the NCBI site, as well as from Index of BLAST databases (FTP).

Process

Using a heuristic method, BLAST finds similar sequences, by locating short matches between the two sequences. This process of finding similar sequences is called seeding. It is after this first match that BLAST begins to make local alignments. While attempting to find similarity in sequences, sets of common letters, known as words, are very important. For example, suppose that the sequence contains the following stretch of letters, GLKFA. If a BLAST was being conducted under normal conditions, the word size would be 3 letters. In this case, using the given stretch of letters, the searched words would be GLK, LKF, KFA. The heuristic algorithm of BLAST locates all common three-letter words between the sequence of interest and the hit sequence or sequences from the database. This result will then be used to build an alignment. After making words for the sequence of interest, the rest of the words are also assembled. These words must satisfy a requirement of having a score of at least the threshold *T*, when compared by using a scoring matrix.

One commonly used scoring matrix for BLAST searches is BLOSUM62,[11] although the optimal scoring matrix depends on sequence similarity. Once both words and neighborhood words are assembled and compiled, they are compared to the sequences in the database in order to find matches. The threshold score *T* determines whether or not a particular word will be included in the alignment. Once seeding has been conducted, the alignment which is only 3 residues long, is extended in both directions by the algorithm used by BLAST. Each extension impacts the score of the alignment by either increasing or decreasing it. If this score is higher than a pre-determined *T*, the alignment will be included in the results given by BLAST. However, if this score is lower than this pre-determined *T*, the alignment will cease to extend, preventing the areas of poor alignment from being included in the BLAST results. Note that increasing the *T* score limits the amount of space available to search, decreasing the number of neighborhood words, while at the same time speeding up the process of BLAST

Algorithm

To run the software, BLAST requires a query sequence to search for, and a sequence to search against (also called the target sequence) or a sequence database containing multiple such sequences. BLAST will find sub-sequences in the database which are similar to subsequences in the query. In typical usage, the query sequence is much smaller than the database, e.g., the query may be one thousand nucleotides while the database is several billion nucleotides.

The main idea of BLAST is that there are often High-scoring Segment Pairs (HSP) contained in a statistically significant alignment. BLAST searches for high scoring sequence alignments between the query sequence and the existing sequences in the database using a heuristic approach that approximates the Smith-Waterman algorithm. However, the exhaustive Smith-Waterman approach is too slow for searching large genomic databases such as GenBank. Therefore, the BLAST algorithm uses a heuristic approach that is less accurate than the Smith-Waterman algorithm but over 50 times faster. [8] The speed and relatively good accuracy of BLAST are among the key technical innovations of the BLAST programs.

An overview of the BLAST algorithm (a protein to protein search) is as follows:[12]

1. *Remove low-complexity region or sequence repeats in the query sequence.*
   "Low-complexity region" means a region of a sequence composed of few kinds of elements. These regions might give high scores that confuse the program to find the actual significant sequences in the database, so they should be filtered out. The regions will be marked with an X (protein sequences) or N (nucleic acid sequences) and then be ignored by the BLAST program. To filter out the low-complexity regions, the SEG program is used for protein sequences and the program DUST is used for DNA sequences. On the other

hand, the program XNU is used to mask off the tandem repeats in protein sequences.

2. *Make a* k-*letter word list of the query sequence.*
3. *List the possible matching words.*
   This step is one of the main differences between BLAST and FASTA. FASTA cares about all of the common words in the database and query sequences that are listed in step 2; however, BLAST only cares about the high-scoring words. The scores are created by comparing the word in the list in step 2 with all the 3-letter words. By using the scoring matrix (substitution matrix) to score the comparison of each residue pair, there are 20^3 possible match scores for a 3-letter word. For example, the score obtained by comparing PQG with PEG and PQA is respectively 15 and 12 with the BLOSUM62 weighting scheme. For DNA words, a match is scored as +5 and a mismatch as -4, or as +2 and -3. After that, a neighborhood word score threshold *T* is used to reduce the number of possible matching words. The words whose scores are greater than the threshold *T* will remain in the possible matching words list, while those with lower scores will be discarded. For example, PEG is kept, but PQA is abandoned when T is 13.
4. *Organize the remaining high-scoring words into an efficient search tree.*
   This allows the program to rapidly compare the high-scoring words to the database sequences.
5. *Repeat step 3 to 4 for each* k-*letter word in the query sequence.*
6. *Scan the database sequences for exact matches with the remaining high-scoring words.*
   The BLAST program scans the database sequences for the remaining high-scoring word, such as PEG, of each position. If an exact match is found, this match is used to seed a possible un-gapped alignment between the query and database sequences.
7. *Extend the exact matches to high-scoring segment pair (HSP).*
   - The original version of BLAST stretches a longer alignment between the query and the database sequence in the left and right directions, from the position where the exact match occurred. The extension does not stop until the accumulated total score of the HSP begins to decrease. A simplified example is presented in figure 2.
   - To save more time, a newer version of BLAST, called BLAST2 or gapped BLAST, has been developed. BLAST2 adopts a lower neighborhood word score threshold to maintain the same level of sensitivity for detecting sequence similarity. Therefore, the possible matching words list in step 3 becomes longer. Next, the exact matched regions, within distance A from each other on the same diagonal in figure 3, will be joined as a longer new region. Finally, the new regions are then extended by the same method as in the original version of BLAST, and the HSPs' (High-scoring segment pair) scores of the extended regions are then created by using a substitution matrix as before.
8. *List all of the HSPs in the database whose score is high enough to be considered.*
   We list the HSPs whose scores are greater than the empirically determined cutoff score *S*. By examining the distribution of the alignment scores modeled by comparing random sequences, a cutoff score *S* can be determined such that its value is large enough to guarantee the significance of the remaining HSPs.
9. *Evaluate the significance of the HSP score.*
   BLAST next assesses the statistical significance of each HSP score by exploiting the Gumbel extreme value distribution (EVD). (It is proved that the distribution of Smith-Waterman local alignment scores between two random sequences follows the Gumbel EVD. For local alignments containing gaps it is not proved.). In accordance with the Gumbel EVD, the probability *p* of observing a score *S* equal to or greater than x is given by the equation.
10. *Make two or more HSP regions into a longer alignment.*
    Sometimes, we find two or more HSP regions in one database sequence that can be made into a longer alignment. This provides additional evidence of the relation between the query and database sequence. There are two methods, the Poisson method and the sum-of-scores method, to compare the significance of the newly combined HSP regions. Suppose that there are two combined HSP regions with the pairs of scores (65, 40) and (52, 45), respectively. The Poisson method gives more significance to the set with the maximal lower score (45>40). However, the sum-of-scores method prefers the first set, because 65+40

(105) is greater than 52+45(97). The original BLAST uses the Poisson method; gapped BLAST and the WU-BLAST uses the sum-of scores method.

11. *Show the gapped Smith-Waterman local alignments of the query and each of the matched database sequences.*
    - The original BLAST only generates un-gapped alignments including the initially found HSPs individually, even when there is more than one HSP found in one database sequence.
    - BLAST2 produces a single alignment with gaps that can include all of the initially found HSP regions. Note that the computation of the score and its corresponding *E*-value involves use of adequate gap penalties.
12. *Report every match whose expect score is lower than a threshold parameter* E.

Parallel BLAST

Parallel BLAST versions of split databases are implemented using MPI and Pthreads, and have been ported to various platforms including Windows, Linux, Solaris, Mac OS X, and AIX. Popular approaches to parallelize BLAST include query distribution, hash table segmentation, computation parallelization, and database segmentation (partition). Databases are split into equal sized pieces and stored locally on each node. Each query is run on all nodes in parallel and the resultant BLAST output files from all nodes merged to yield the final output. Specific implementations include MPIblast, ScalaBLAST, DCBLAST and so on.[14]

Program

The BLAST program can either be downloaded and run as a command-line utility "blastall" or accessed for free over the web. The BLAST web server, hosted by the NCBI, allows anyone with a web browser to perform similarity searches against constantly updated databases of proteins and DNA that include most of the newly sequenced organisms.

The BLAST program is based on an open-source format, giving everyone access to it and enabling them to have the ability to change the program code. This has led to the creation of several BLAST "spin-offs".

There are now a handful of different BLAST programs available, which can be used depending on what one is attempting to do and what they are working with. These different programs vary in query sequence input, the database being searched, and what is being compared. These programs and their details are listed below:

BLAST is actually a family of programs (all included in the blastall executable). These include:[15]

Nucleotide-nucleotide BLAST (blastn)

This program, given a DNA query, returns the most similar DNA sequences from the DNA database that the user specifies.

Protein-protein BLAST (blastp)

This program, given a protein query, returns the most similar protein sequences from the protein database that the user specifies.

Position-Specific Iterative BLAST (PSI-BLAST) (blastpgp)

This program is used to find distant relatives of a protein. First, a list of all closely related proteins is created. These proteins are combined into a general "profile" sequence, which summarises significant features present in these sequences. A query against the protein database is then run using this profile, and a larger group of proteins is found. This larger group is used to construct another profile, and the process is repeated.

By including related proteins in the search, PSI-BLAST is much more sensitive in picking up distant evolutionary relationships than a standard protein-protein BLAST.

Nucleotide 6-frame translation-protein (blastx)

This program compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database.

Nucleotide 6-frame translation-nucleotide 6-frame translation (tblastx)

This program is the slowest of the BLAST family. It translates the query nucleotide sequence in all six possible frames and compares it against the six-frame translations of a nucleotide sequence database. The purpose of tblastx is to find very distant relationships between nucleotide sequences.

Protein-nucleotide 6-frame translation (tblastn)

This program compares a protein query against the all six reading frames of a nucleotide sequence database.

Large numbers of query sequences (megablast)

When comparing large numbers of input sequences via the command-line BLAST, "megablast" is much faster than running BLAST multiple times. It concatenates many input sequences together to form a large sequence before searching the BLAST database, then post-analyzes the search results to glean individual alignments and statistical values.

Of these programs, BLASTn and BLASTp are the most commonly used because they use direct comparisons, and do not require translations. However, since protein sequences are better conserved evolutionarily than nucleotide sequences, tBLASTn, tBLASTx, and BLASTx, produce more reliable and accurate results when dealing with coding DNA. They also enable one to be able to directly see the function of the protein sequence, since by translating the sequence of interest before searching often gives you annotated protein hits.

Alternative versions

A version designed for comparing large genomes or DNA is BLASTZ.

CS-BLAST (Context-Specific BLAST) is an extended version of BLAST for searching protein sequences that finds twice as many remotely related sequences as BLAST at the same speed and error rate. In CS-BLAST, the mutation probabilities between amino acids depend not only on the single amino acid, as in BLAST, but also on its local sequence context. Washington University produced an alternative version of NCBI BLAST, called WU-BLAST. The rights have since been acquired to Advanced Biocomputing, LLC.

In 2009, NCBI has released a new set of BLAST executables, the C++ based BLAST+, and has released C versions until 2.2.26.[16] Starting with version 2.2.27 (April 2013), only BLAST+ executables are available. Among the changes is the replacement of the blastall executable with separate executables for the different BLAST programs, and changes in option handling. The formatdb utility (C based) has been replaced by makeblastdb (C++ based) and databases formatted by either one should be compatible for identical blast releases. The algorithms remain similar, however, the number of hits found and their order can vary significantly between the older and the newer version. BLAST+ since

Accelerated versions

TimeLogic offers an FPGA-accelerated implementation of the BLAST algorithm called Tera-BLAST that is hundreds of times faster.

Other formerly supported versions include:

- FPGA-accelerated
  - ○ Prior to their acquisition by Qiagen, CLC bio collaborated with SciEngines GmbH on an FPGA accelerator they claimed will give 188x acceleration of BLAST.
  - ○ The Mitrion-C Open Bio Project was an effort to port BLAST to run on Mitrion FPGAs.
- GPU-accelerated
  - ○ GPU-Blast[17] is an accelerated version of NCBI BLASTP for CUDA which is 3x~4x faster than NCBI Blast.
  - ○ CUDA-BLASTP[18] is a version of BLASTP that is GPU-accelerated and is claimed to run up to 10x faster than NCBI BLAST.
  - ○ G-BLASTN[19] is an accelerated version of NCBI blastn and megablast, whose speedup varies from 4x to 14x (compared to the same runs with 4 CPU threads). Its current limitation is that the database must fit into the GPU memory.
- CPU-accelerated
  - ○ MPIBlast is a parallel implementation of NCBI BLAST using Message Passing Interface. By efficiently utilizing distributed computational resources through database fragmentation, query segmentation, intelligent scheduling, and parallel I/O, mpiBLAST improves NCBI BLAST performance by several orders of magnitude while scaling to hundreds of processors.
  - ○ CaBLAST[20] makes search on large databases orders of magnitude faster by exploiting redundancy in data.
  - ○ Paracel BLAST was a commercial parallel implementation of NCBI BLAST, supporting hundreds of processors.
  - ○ QuickBLAST (kblastp) from NCBI is an implementation accelerated by prefiltering based on Jaccard index estimates with hashed pentameric fragments. The filtering slightly reduces sensitivity, but increases performance by an order of magnitude.[21] NCBI only makes the search available on their non-redundant (nr) protein collection, and does not offer downloads.

Alternatives to BLAST

The predecessor to BLAST, FASTA, can also be used for protein and DNA similarity searching. FASTA provides a similar set of programs for comparing proteins to protein and DNA databases, DNA to DNA and protein databases, and includes additional programs for working with unordered short peptides and DNA sequences. In addition, the FASTA package provides SSEARCH, a vectorized implementation of the rigorous Smith-Waterman algorithm. FASTA is slower than BLAST, but provides a much wider range of scoring matrices, making it easier to tailor a search to a specific evolutionary distance.

An extremely fast but considerably less sensitive alternative to BLAST is BLAT (*B*last *L*ike *A*lignment *T*ool). While BLAST does a linear search, BLAT relies on k-mer indexing the database, and can thus often find seeds faster.[22] Another software alternative similar to BLAT is PatternHunter.

Advances in sequencing technology in the late 2000s has made searching for very similar nucleotide matches an important problem. New alignment programs tailored for this use typically use BWT-indexing of the target database (typically a genome). Input sequences can then be mapped very quickly, and output is typically in the form of a BAM file. Example alignment programs are BWA, SOAP, and Bowtie.

For protein identification, searching for known domains (for instance from Pfam) by matching with Hidden Markov Models is a popular alternative, such as HMMER.

An alternative to BLAST for comparing two banks of sequences is PLAST. PLAST provides a high-performance general purpose bank to bank sequence similarity search tool relying on the PLAST[23] and ORIS[24] algorithms. Results of PLAST are very similar to BLAST, but PLAST is significantly faster and capable of comparing large sets of sequences with a small memory (i.e. RAM) footprint.

For applications in metagenomics, where the task is to compare billions of short DNA reads against tens of millions of protein references, DIAMOND[25] runs at up to 20,000 times as fast as BLASTX, while maintaining a high level of sensitivity.

The open-source software MMseqs is an alternative to BLAST/PSI-BLAST, which improves on current search tools over the full range of speed-sensitivity trade-off, achieving sensitivities better than PSI-BLAST at more than 400 times its speed.[26]

Optical computing approaches have been suggested as promising alternatives to the current electrical implementations. OptCAM is an example of such approaches and is shown to be faster than BLAST.[27]

Comparing BLAST and the Smith-Waterman Process

While both Smith-Waterman and BLAST are used to find homologous sequences by searching and comparing a query sequence with those in the databases, they do have their differences.

Due to the fact that BLAST is based on a heuristic algorithm, the results received through BLAST, in terms of the hits found, may not be the best possible results, as it will not provide you with all the hits within the database. BLAST misses hard to find matches.

A better alternative in order to find the best possible results would be to use the Smith-Waterman algorithm. This method varies from the BLAST method in two areas, accuracy and speed. The Smith-Waterman option provides better accuracy, in that it finds matches that BLAST cannot, because it does not miss any information. Therefore, it is necessary for remote homology. However, when compared to BLAST, it is more time consuming, not to mention that it requires large amounts of computer usage and space. However, technologies to speed up the Smith-Waterman process have been found to improve the time necessary to perform a search dramatically. These technologies include FPGA chips and SIMD technology.

In order to receive better results from BLAST, the settings can be changed from their default settings. However, there is no given or set way of changing these settings in order to receive the best results for a given sequence. The settings available for change are E-Value, gap costs, filters, word size, and substitution matrix. Note, that the algorithm used for BLAST was developed from the algorithm used for Smith-Waterman. BLAST employs an alignment which finds "local alignments between sequences by finding short matches and from these initial matches (local) alignments are created".[28]

BLAST output visualization

To help users interpreting BLAST results, different software is available. According to installation and use, analysis features and technology, here are some available tools:[29]

- NCBI BLAST service
- general BLAST output interpreters, GUI-based: JAMBLAST, Blast Viewer, BLASTGrabber
- integrated BLAST environments: PLAN, BlastStation-Free, SequenceServer
- BLAST output parsers: MuSeqBox, Zerg, BioParser, BLAST-Explorer
- specialized BLAST-related tools: MEGAN, BLAST2GENE, BOV, Circoletto

Example visualisations of BLAST results are shown in Figure 4 and 5.

Uses of BLAST

BLAST can be used for several purposes. These include identifying species, locating domains, establishing phylogeny, DNA mapping, and comparison.

Identifying species

With the use of BLAST, you can possibly correctly identify a species or find homologous species. This can be useful, for example, when you are working with a DNA sequence from an unknown species.

Locating domains

When working with a protein sequence you can input it into BLAST, to locate known domains within the sequence of interest.

Establishing phylogeny

Using the results received through BLAST you can create a phylogenetic tree using the BLAST web-page. Phylogenies based on BLAST alone are less reliable than other purpose-built computational phylogenetic methods, so should only be relied upon for "first pass" phylogenetic analyses.

DNA mapping

When working with a known species, and looking to sequence a gene at an unknown location, BLAST can compare the chromosomal position of the sequence of interest, to relevant sequences in the database(s). NCBI has a "Magic-BLAST" tool built around BLAST for this purpose.[30]

Comparison

When working with genes, BLAST can locate common genes in two related species, and can be used to map annotations from one organism to another.

Almeida, M. F., et al. (2021). "Distinct and dementia-related synaptopathy in the hippocampus after military blast exposures." Brain Pathol: e12936.

Explosive shockwaves, and other types of blast exposures, are linked to injuries commonly associated with military service and to an increased risk for the onset of dementia. Neurological complications following a blast injury, including depression, anxiety, and memory problems, often persist even when brain damage is undetectable. Here, hippocampal explants were exposed to the explosive 1,3,5-trinitro-1,3,5-triazinane (RDX) to identify indicators of blast-induced changes within important neuronal circuitries. Highly controlled detonations of small, 1.7-gram RDX spherical charges reduced synaptic markers known to be downregulated in cognitive disorders, but without causing overt neuronal loss or astroglial responses. In the absence of neuromorphological alterations, levels of synaptophysin, GluA1, and synapsin IIb were significantly diminished within 24 hr, and these synaptic components exhibited progressive reductions following blast exposure as compared to their stable maintenance in control explants. In contrast, labeling of the synapsin IIa isoform remained unaltered, while neuropilar staining of other markers decreased, including synapsin IIb and neural cell adhesion molecule (NCAM) isoforms, along with evidence of NCAM proteolytic breakdown. NCAM180 displayed a distinct decline after the RDX blasts, whereas NCAM140 and NCAM120 exhibited smaller or no deterioration, respectively. Interestingly, the extent of synaptic marker reduction correlated with AT8-positive tau levels, with tau pathology stochastically found in CA1 neurons and their dendrites. The decline in synaptic components was also reflected in the size of evoked postsynaptic currents recorded from CA1 pyramidals, which exhibited a severe and selective reduction. The identified indicators of blast-mediated synaptopathy point to the need for early biomarkers of explosives altering synaptic integrity with links to dementia risk, to advance strategies for both cognitive health and therapeutic monitoring.

Arun, P., et al. (2021). "Blast Exposure Causes Long-Term Degeneration of Neuronal Cytoskeletal Elements in the Cochlear Nucleus: A Potential Mechanism for Chronic Auditory Dysfunctions." Front Neurol **12**: 652190.

Blast-induced auditory dysfunctions including tinnitus are the most prevalent disabilities in service members returning from recent combat operations. Most of the previous studies were focused on the effect of blast exposure on the peripheral auditory system and not much on the central auditory signal-processing regions in the brain. In the current study, we have exposed rats to single and tightly coupled repeated blasts and examined the degeneration of neuronal cytoskeletal elements using silver staining in the central auditory signal-processing regions in the brain at 24 h, 14 days, 1 month, 6 months, and 1 year. The brain regions evaluated include cochlear nucleus, lateral lemniscus, inferior colliculus, medial geniculate nucleus, and auditory cortex. The results obtained indicated that a significant increase in degeneration of neuronal cytoskeletal elements was observed only in the left and right cochlear nucleus. A significant increase in degeneration of neuronal cytoskeletal elements was observed in the cochlear nucleus at 24 h and persisted through 1 year, suggesting acute and chronic neuronal degeneration after blast exposure. No statistically significant differences were observed between single and repeated blasts. The localized degeneration of neuronal cytoskeletal elements in the cochlear nucleus suggests that the damage could be caused by transmission of blast shockwaves/noise through the ear canal and that use of suitable ear protection devices can protect against acute and chronic central auditory signal processing defects including tinnitus after blast exposure.

Behrens, Y. L., et al. (2021). "BCR-ABL1 positive AML or CML in blast crisis? A pediatric case report with inv(3) and t(9;22) in the initial clone." Cancer Genet **254-255**: 70-74.

The co-occurrence of an inversion inv(3)(q21q26)/GATA2-MECOM and a Philadelphia translocation t(9;22)(q34;q11)/BCR-ABL1 in the context of chronic myeloid leukemia (CML) in blast crisis or acute myeloid leukemia (AML) has only rarely been described. To our knowledge, this co-occurrence has been reported in six pediatric patients with CML but not in pediatric patients with AML. Here, we report on a 7-year-old girl, who, presented with a t(9;22) and inv(3) in 14 of 15 metaphases and an additional monosomy 7 was detected in 5 of these metaphases (ISCN: 46,XX,inv(3)(q21q26),t(9;22)(q34q11)[9]/45, idem,-7[5]/46,XX[1]). The p190 BCR-ABL1 fusion transcript was detected by multiplex PCR and targeted RNA sequencing. Due to these results, a clear distinction between a CML in blast crisis and a BCR-ABL1 positive AML was not possible. The patient was treated according to the treatment recommendations of the AML-BFM study group and additionally received tyrosine kinase inhibitor therapy (Dasatinib). The treatment with Dasatinib was successful in eliminating the inv(3)/t(9;22) clone, but the ancestral inv(3) clone persisted. Based upon these findings we diagnosed an AML with inv(3) and a secondary acquisition of t(9;22). This treatment as well as an allogenic transplantation has led to a complete remission of the disease up to this date (21 months post diagnosis).

Belding, J. N., et al. (2021). "Potential Health and Performance Effects of High-Level and Low-Level Blast: A Scoping Review of Two Decades of Research." Front Neurol **12**: 628782.
Although blast exposure has been recognized as a significant source of morbidity and mortality in military populations, our understanding of the effects of blast exposure, particularly low-level blast (LLB) exposure, on health outcomes remains limited. This scoping review provides a comprehensive, accessible review of the peer-reviewed literature that has been published on blast exposure over the past two decades, with specific emphasis on LLB. We conducted a comprehensive scoping review of the scientific literature published between January 2000 and 2019 pertaining to the effects of blast injury and/or exposure on human and animal health. A three-level review process with specific inclusion and exclusion criteria was used. A full-text review of all articles pertaining to LLB exposure was conducted and relevant study characteristics were extracted. The research team identified 3,215 blast-relevant articles, approximately half of which (55.4%) studied live humans, 16% studied animals, and the remainder were non-subjects research (e.g., literature reviews). Nearly all (99.49%) of the included studies were conducted by experts in medicine or epidemiology; approximately half of these articles were categorized into more than one medical specialty. Among the 51 articles identified as pertaining to LLB specifically, 45.1% were conducted on animals and 39.2% focused on human subjects. Animal studies of LLB predominately used shock tubes to induce various blast exposures in rats, assessed a variety of outcomes, and clearly demonstrated that LLB exposure is associated with brain injury. In contrast, the majority of LLB studies on humans were conducted among military and law enforcement personnel in training environments and had remarkable variability in the exposures and outcomes assessed. While findings suggest that there is the potential for LLB to harm human populations, findings are mixed and more research is needed. Although it is clear that more research is needed on this rapidly growing topic, this review highlights the detrimental effects of LLB on the health of both animals and humans. Future research would benefit from multidisciplinary collaboration, larger sample sizes, and standardization of terminology, exposures, and outcomes.

Boggio, F., et al. (2021). "CD34-Positive Blast Count and p53 Expression in Bone Marrow Biopsies of Patients with Low-Risk Myelodysplastic Syndromes: Potential Predictive Tools of Response to Erythropoietin Stimulating Agents." Pathobiology: 1-9.
INTRODUCTION: The first-line therapy for patients with low-risk myelodysplastic syndromes (MDSs) commonly consists of erythropoietin stimulating agents (ESAs), with a response rate ranging from 34 to 62%. For nonresponder patients, outside clinical trials, blood transfusions are the most frequent therapeutic option, with detrimental effect on the quality of life and with risks of iron-overload. Since no studies have been yet conducted on this topic, we investigated the potential predictive role of bone marrow (BM) histological evaluation in patients treated with ESAs. MATERIALS AND METHODS: We performed a morphological and immunohistochemical retrospective analysis of BM biopsies of 96 patients with low-risk MDSs subsequently treated with ESAs. RESULTS: In our series, substantial morphological overlap was found between responder and nonresponder patients. On the contrary, patients with a percentage of CD34-positive blasts >3% or with p53 protein expression <1% responded with a significantly higher frequency to ESAs. CONCLUSIONS: Our study reinforces the role of BM biopsy as diagnostic tool in MDSs, being also able to supply information related to response to ESAs and to its loss over time.

Bosch, K., et al. (2021). "Optimization of Underbody Blast Energy-Attenuating Seat Mechanisms Using Modified MADYMO Human Body Models." J Biomech Eng.
Though energy attenuating (EA) seats for air and spacecraft applications have existed for decades, they have not yet been fully characterized for their energy attenuation capability or resulting effect on occupant protection in vertical underbody blast. EA seats utilize stroking mechanisms to absorb energy and reduce the vertical forces imparted on the occupant's pelvis and lower spine. Using dynamic rigid-body modeling, a tool to determine optimal force and deflection limits was developed to reduce pelvis and lower spine injuries in underbody blast events using a generic seat model.

MAthematical DYnamic MOdels (MADYMO) and modeFRONTIER software were leveraged for this study. This optimizing tool may be shared with EA seat manufacturers and applied to military seat development efforts for EA mechanisms for a given occupant and designated blast severity. To optimally tune the EA seat response, the MADYMO Human Body Model (HBM) was first updated to improve its fidelity in kinematic response data for high rate vertical accelerative loading relative to experimental data from laboratory simulated underbody blast tests using post-mortem human surrogates (PMHS). Subsequently, using available injury criteria for underbody blast, the optimization tool demonstrated the ability to identify successful EA mechanism configurations to reduce forces and accelerations in the pelvis and lower spine HBM to presumed non-injurious levels. This tool could be tailored by varying input pulses, force and deflection limits, and occupant size to evaluate EA mechanism designs.

Burke, K., et al. (2021). "Long term changes to auditory sensitivity following blast trauma in mice." Hear Res **403**: 108201.
Blast trauma is a common acoustic/physical insult occurring in modern warfare. Twenty percent of active duty military come into close proximity to explosions and experience mild to severe sensory deficits. The prevalence of such injuries is high but correlating auditory sensitivity changes with the initial insult is difficult because injury and evaluations are often separated by long time periods. Here, auditory sensitivity was measured before and after a traumatic blast in adult CBA/CaJ mice using auditory brainstem responses, distortion production otoacoustic emissions, and behavioral detection of pure tones. These measurements included baseline auditory sensitivity prior to injury in all mice, and again at 3, 30, and 90 days after the blast in the two physiological groups, and daily for up to 90 days in the behavioral group. Mice in all groups experienced an initial deterioration in auditory sensitivity, though physiological measurements showed evidence of recovery that behavioral measurements did not. Amplitudes and latencies of ABR waves may reflect additional changes beyond the peripheral damage shown by the threshold changes and should be explored further. The present work addresses a major gap in the current acoustic trauma literature both in terms of comparing physiological and behavioral methods, as well as measuring the time course of recovery.

Campo, S., et al. (2021). "A novel Transposable element-derived microRNA participates in plant immunity to rice blast disease." Plant Biotechnol J.
MicroRNAs (miRNAs) are small non-coding RNAs that direct post-transcriptional gene silencing in plant development and stress responses through cleavage or translational repression of target mRNAs. Here, we report the identification and functional characterization of a new member of the miR812 family in rice (named as miR812w) involved in disease resistance. miR812w is present in cultivated Oryza species, both japonica and indica subspecies, and wild rice species within the Oryza genus, but not in dicotyledonous species. miR812w is a 24nt-long that requires DCL3 for its biogenesis and is loaded into AGO4 proteins. Whereas overexpression of miR812w increased resistance to infection by the rice blast fungus Magnaporthe oryzae, CRISPR/Cas9-mediated MIR812w editing enhances disease susceptibility, supporting that miR812w plays a role in blast resistance. We show that miR812w derives from the Stowaway type of rice MITEs (Miniature Inverted-Repeat Transposable Elements). Moreover, miR812w directs DNA methylation in trans at target genes that have integrated a Stowaway MITE copy into their 3' or 5' untranslated region (ACO3, CIPK10, LRR genes), as well as in cis at the MIR812w locus. The target genes of miR812 were found to be hypo-methylated around the miR812 recognition site, their expression being up-regulated in transgene-free CRISPR/Cas9-edited miR812 plants. These findings further support that, in addition to post-transcriptional regulation of gene expression, miRNAs can exert their regulatory function at the transcriptional level. This relationship between miR812w and Stowaway MITEs integrated into multiple coding genes might eventually create a network for miR812w-mediated regulation of gene expression with implications in rice immunity.

Corrigan, F., et al. (2021). "NK1 antagonists attenuate tau phosphorylation after blast and repeated concussive injury." Sci Rep **11**(1): 8861.
Exposure to repeated concussive traumatic brain injury (TBI) and to blast-induced TBI has been associated with the potential development of the neurodegenerative condition known as chronic traumatic encephalopathy (CTE). CTE is characterized by the accumulation of hyperphosphorylated tau protein, with the resultant tau tangles thought to initiate the cognitive and behavioral manifestations that appear as the condition progresses. However, the mechanisms linking concussive and blast TBI with tau hyperphosphorylation are unknown. Here we show that single moderate TBI, repeated concussive TBI and blast-induced mild TBI all result in hyperphosphorylation of tau via a substance P mediated mechanism. Post-injury administration of a substance P, NK1 receptor antagonist attenuated the injury-induced phosphorylation of tau by modulating the activity of several key kinases including Akt,

ERK1/2 and JNK, and was associated with improvement in neurological outcome. We also demonstrate that inhibition of the TRPV1 mechanoreceptor, which is linked to substance P release, attenuated injury-associated tau hyperphosphorylation, but only when it was administered prior to injury. Our results demonstrate that TBI-mediated stimulation of brain mechanoreceptors is associated with substance P release and consequent tau hyperphosphorylation, with administration of an NK1 receptor antagonist attenuating tau phosphorylation and associated neurological deficits. NK1 antagonists may thus represent a pharmacological approach to attenuate the potential development of CTE following concussive and blast TBI.

Dai, Q., et al. (2021). "Combined use of peripheral blood blast count and platelet count during and after induction therapy to predict prognosis in children with acute lymphoblastic leukemia." Medicine (Baltimore) **100**(15): e25548.

ABSTRACT: Several studies have reported an association between the rapidity of reduction in peripheral blood blast count or recovery of normal hematopoiesis and treatment outcome during therapy in children with acute lymphoblastic leukemia (ALL). However, little is known about the impact of both of these aspects on prognosis in pediatric ALL. Accordingly, the purpose of this study was to evaluate whether the combined use of blood blast count and platelet count could predict event-free survival (EFS) and overall survival (OS) when minimal residual disease (MRD) detection was not available.A total of 419 patients aged 0 to 14 years diagnosed and treated for ALL between 2011 and 2015 were enrolled.Patients with a blast count >/=0.1 x 109/L on day 8 exhibited significantly lower survival rates than that in those with blast counts <0.1 x 109/L. The EFS and OS in patients with platelet count >/=100 x 109/L on day 33 were significantly higher than those with platelet counts <100 x 109/L. In univariate and multivariate analyses, patients with low blast count on day 8 and high platelet count on day 33 were significantly associated with better EFS and OS. The combination of blast cell count on day 8 and platelet count on day 33 demonstrated a strong association with MRD-based risk stratification.Complete blood count is an inexpensive, easy to perform, and reliable measurement in children with ALL. The combination of blast count and platelet count during and after induction chemotherapy was a significant and independent prognostic factor for treatment outcome in pediatric ALL.

Dai, Q., et al. (2021). "Clinical features and outcome of pediatric acute lymphoblastic leukemia with low peripheral blood blast cell count at diagnosis." Medicine (Baltimore) **100**(4): e24518.

ABSTRACT: Peripheral blood (PB) blast cell count on day 8 of prednisone therapy has been considered one of the strongest predictors of outcome in children with acute lymphoblastic leukemia (ALL). However, little is known about the clinical features and prognostic impact of PB blast cell count at diagnosis in these patients. The aim of this study was to evaluate the relationship between initial PB blast cell count and clinical prognosis of pediatric ALL.The study comprised 367 patients with ALL, aged 0 to 14 years, enrolled and treated using the Chinese Children's Leukemia Group-ALL 2008 protocol between 2011 and 2015. The majority (91.6%) of patients were B-cell precursor ALL (BCP ALL), and 8.4% were T-cell ALL (T-ALL).Patients with BCP ALL in the low PB blast cell count group (<1 x 109/L) had significantly superior survival rates to those in the high count group (>/=30 x 109/L). In T-ALL, the low count group showed significantly inferior survival rates compared to both the intermediate count group (1-29.9 x 109/L) and high count group. Multivariate analysis revealed that the initial white blood cell count and minimal residual disease at the end of induction therapy were independently predictive of BCP ALL outcome, while risk stratification was shown to be an independent prognostic factor for T-ALL outcome.These results indicated that low blast cell count in PB at diagnosis was associated with different clinical outcomes in patients with BCP ALL and T-ALL, although it was not an independent outcome predictor by multivariate analysis.

Dash, S., et al. (2021). "iBLAST: Incremental BLAST of new sequences via automated e-value correction." PLoS One **16**(4): e0249410.

Search results from local alignment search tools use statistical scores that are sensitive to the size of the database to report the quality of the result. For example, NCBI BLAST reports the best matches using similarity scores and expect values (i.e., e-values) calculated against the database size. Given the astronomical growth in genomics data throughout a genomic research investigation, sequence databases grow as new sequences are continuously being added to these databases. As a consequence, the results (e.g., best hits) and associated statistics (e.g., e-values) for a specific set of queries may change over the course of a genomic investigation. Thus, to update the results of a previously conducted BLAST search to find the best matches on an updated database, scientists must currently rerun the BLAST search against the entire updated database, which translates into irrecoverable and, in turn, wasted execution time, money, and computational resources. To address this issue, we devise a novel and efficient method to redeem past BLAST searches by introducing iBLAST. iBLAST leverages previous BLAST search results to conduct the same query search but only on the incremental (i.e., newly added) part of the database, recomputes the associated critical statistics such as e-values, and combines these results to produce updated search results. Our experimental results and fidelity analyses show that iBLAST delivers search results that are identical to NCBI BLAST at a substantially reduced computational cost, i.e., iBLAST performs (1 + delta)/delta times faster than NCBI BLAST, where delta represents the fraction of database growth. We then present three different use cases to demonstrate that iBLAST can enable efficient biological discovery at a much faster speed with a substantially reduced computational cost.

De la Concepcion, J. C., et al. (2021). "The allelic rice immune receptor Pikh confers extended resistance to strains of the blast fungus through a single polymorphism in the effector binding interface." PLoS Pathog **17**(3): e1009368.

Arms race co-evolution drives rapid adaptive changes in pathogens and in the immune systems of their hosts. Plant intracellular NLR immune receptors detect effectors delivered by pathogens to promote susceptibility, activating an immune response that halts colonization. As a consequence, pathogen effectors evolve to escape immune recognition and are highly variable. In turn, NLR receptors are one of the most diverse protein families in plants, and this variability underpins differential recognition of effector variants. The molecular mechanisms underlying natural variation in effector recognition by NLRs are starting to be elucidated. The rice NLR pair Pik-1/Pik-2 recognizes AVR-Pik effectors from the blast fungus Magnaporthe oryzae, triggering immune responses that limit rice blast infection. Allelic variation in a heavy metal associated (HMA) domain integrated in the receptor Pik-1 confers differential binding to AVR-Pik variants, determining resistance specificity. Previous mechanistic studies uncovered how a Pik allele, Pikm, has extended recognition to effector variants through a specialized HMA/AVR-Pik binding interface. Here, we reveal the mechanistic basis of extended recognition specificity conferred by another Pik allele, Pikh. A single residue in Pikh-HMA increases binding to AVR-Pik variants, leading to an extended effector response in planta. The crystal structure of Pikh-HMA in complex with an AVR-Pik variant confirmed that Pikh and Pikm use a similar molecular mechanism to extend their pathogen recognition profile. This study shows how different NLR receptor alleles functionally converge to extend recognition specificity to pathogen effectors.

de Sousa, T. P., et al. (2021). "Molecular identification of Trichoderma sp. isolates and biochemical characterization of antagonistic interaction against rice blast." Arch Microbiol.

This study aimed to identify four isolates of Trichoderma sp. (Ufra.T06, Ufra.T09, Ufra.T12, and Ufra.T52) and characterize their interaction with Magnaporthe oryzae in vitro and in vivo conditions. The four isolates of Trichoderma sp. were sequenced, investigated as an antagonist against M. oryzae in five Petri plate assays, and as an inhibitor of conidial germination appressoria formation. Finally, were quantified the lytic activity of chitinase (CHI), glucanase (GLU), and protease (PRO) during co-cultivation of Trichoderma sp. and M. oryzae. In vivo, leaf blast suppression was evaluated in two assays: simultaneous and curative application. Both in vitro and in vivo assays were scanned by electron microscopy (SEM). All isolates were identified as Trichoderma asperellum. All in vitro Petri plates assays reduced M. oryzae colony growth (paired-91.18% by Ufra.T09, volatile metabolites-all isolates equally reduced, non-volatile-68.33% by Ufra.T06, thermostability-99.77% by Ufra.T52 and co-cultivate-64.25% by Ufra.T52). The filtrates and conidia suspensions for T. asperellum isolates inhibited the conidia germination and appressoria formation significantly. In co-cultivate (mycelial or cell wall), all enzymes (GLU, CHI, and PRO) and times (24, 48, and 72 h) showed increased activity. In vivo, reduced leaf blast severity until 94.64% (Ufra.T52cs) in a simultaneous and until 85% (Ufra.T09 24 and 48 hasi) in a curative application. T. asperellum isolates showed efficient control of M. oryzae by mycoparasitism, and antibiosis mechanisms were interfered with by the M. oryzae infection process.

Dettori, S., et al. (2021). "A Deep Learning-based approach for forecasting off-gas production and consumption in the blast furnace." Neural Comput Appl: 1-13.

This article presents the application of a recent neural network topology known as the deep echo state network to the prediction and modeling of strongly nonlinear systems typical of the process industry. The article analyzes the results by introducing a comparison with one of the most common and efficient topologies, the long short-term memories, in order to highlight the strengths and weaknesses of a reservoir computing approach compared to one currently considered as a standard of recurrent neural network. As benchmark application, two specific processes common in the integrated steelworks are selected, with the purpose of forecasting the future energy exchanges and transformations. The procedures of training, validation

and test are based on data analysis, outlier detection and reconciliation and variable selection starting from real field industrial data. The analysis of results shows the effectiveness of deep echo state networks and their strong forecasting capabilities with respect to standard recurrent methodologies both in terms of training procedures and accuracy. Supplementary Information: The online version contains supplementary material available at 10.1007/s00521-021-05984-x.

Dong, X. W., et al. (2021). "[Influences of gas explosion on acute blast lung injury and time phase changes of pulmonary function in rats under real roadway environment]." Zhonghua Lao Dong Wei Sheng Zhi Ye Bing Za Zhi **39**(2): 137-142.
Objective: The aims of this study were to investigate the effect of gas explosion on rats and to explore the pulmonary function alterations associated with gas explosion-induced acute blast lung injury (ABLI) in real roadway environment. Methods: In April 2018, the large coal mine gas explosion test roadway and explosion test system were used to simulate the real gas explosion roadway environment, fixed the cage and set the explosion parameters. 72 SD rats, male, SPF grade, were randomly divided into nine groups by completely random grouping method according to their body weight: control group, close range group (160 m) , and long range group (240 m) . In each group, there were wound groups (24 h group and 48h group, 8/group, total 48 in six groups) and no wound groups (8/group, total 24 in three groups) . Except for the control group, the other groups were placed in cages at different distances under anesthesia, the experiment of gas explosion was carried out by placing the rats in a position that could force the lungs. The changes of respiratory function of the rats in the non-invasive group were monitored with pulmonary function instrument at 2 h, 24 h, 48 h, 72 h and 168h after the explosion, and were killed under anesthesia 7 days later; the rats in invasive groups were anesthetized and killed at 24 h, 48 h and 168 h, respectively. Gross observation, lung wet-dry ratio and lung histopathology were performed. Results: Compared with the control group, f (respiratory frequency, f) , MV (minute ventilation, MV) , PEF (peak expiratory flow rate, PEF) , PIF (peak inspiratory flow rate, PIF) and EF50 (1/2 tidal volume expiratory flow, EF50) of rats in the close and long range groups decreased significantly after gas explosion 2 h. PAU (respiration pause, PAU) , Te (expiratory time, Te) , Ti (inspiratory time, Ti) and Tr (relaxation time, Tr) were significantly increased ($P<0.05$) . After 48 h, TV (tidal volume, TV) , Penh (enhanced respiration pause, Penh) , PAU, and PIF of rats in the long range group were significantly increased ($P<0.05$) . After 72 h, MV in the long range group was significantly decreased ($P<0.05$) . Compared with the control group, Penh, PAU, Ti and Te were significantly decreased after 168 h in the close and long range groups, with statistical significance ($P<0.05$) . At the same time, the body weight of rats in different range groups was significantly decreased ($P<0.05$) . In addition, both HE staining and routine observation of lung tissues of rats in different range groups showed that gas explosion caused pulmonary edema, obviously congested pulmonary capillaries, a large number of inflammatory cells and infiltrated red blood cells. Conclusion: Gas explosion in real roadway environment can cause the change of respiratory function phase and lung tissue damage in rats, suggesting that the model of gas explosion-induced ABLI has been initially established successfully, which would provide a basis for further study on the pathogenesis of ABLI.

Dong, Y., et al. (2021). "Isolated Central Nervous System Blast Crisis of Chronic Myeloid Leukemia with Dasatinib Therapy." Clin Lab **67**(2).
BACKGROUND: Isolated central nervous system (CNS) blast crisis was uncommon in chronic myeloid leukemia (CML). METHODS: The present study reported an interesting case of a CML patient administered with dasatinib presenting with headache and seizure unconsciousness. Imaging investigation, immunophenotyping, bone marrow cytology inspection, chromosomal analysis, and polymerase chain reaction (PCR) were performed on a 41-year-old CML patient. RESULTS: Bone marrow examination revealed complete cytogenetic remission and there were no obvious abnormalities in head CT and MR. Cytomorphological examination of cerebrospinal fluid (CSF) showed 50% blasts. Flow cytometry analysis was showed 78.3% CSF cells expressing the specific myeloid antigens. PCR analysis on CSF cells was positive for BCR/ABL P210 fusion gene. All the above CSF findings were suggestive of CNS infiltrating isolated from bone marrow cytogenetic remission. CONCLUSIONS: Isolated CNS blast crisis of CML with dasatinib were rare. The mechanism still remains unclear and the treatment regimen requires further exploration. Flow cytometry showed great value to detect the blast cells in this patient.

Drexler, B., et al. (2021). "Blast counts are lower in the aspirate as compared to trephine biopsy in acute myeloid leukemia and myelodysplastic syndrome expressing CD56." Int J Lab Hematol.
INTRODUCTION: CD56 is aberrantly expressed in myeloid neoplasms including myelodysplastic syndrome (MDS) and acute myeloid leukemia (AML). Considering the adhesion effects of CD56, blast quantification in bone marrow might depend on the technique used to obtain respective diagnostic

specimens. Therefore, the objective of our study was to investigate the impact of CD56-expression on blast counts in myeloid neoplasms comparing bone marrow aspirates to biopsies. METHODS: We retrospectively analyzed 75 patients diagnosed with MDS and AML. We compared patients with (n = 36) and without (n = 39) CD56-expression by flow cytometry with respect to their blast quantities assessed on bone marrow aspirates versus biopsies. RESULTS: The frequency of CD56-expression on blasts correlated with higher blast counts on biopsies vs. aspirate smears (rs = 0.52; P = .001). This difference in blast counts was only significant in the CD56 high expressing subgroup (median 68%, 5.5%-95% in biopsy compared to median 32.5%, 1.5%-90% in aspirate; P < .01). The percentage of CD56-positive blasts among the total blast population was lower in the peripheral blood compared to bone marrow (median 31%, 6%-88% vs. 55%, 14%-98%; P = .016). The discrepancy in the blast count between the aspirate and trephine biopsy would have led to misclassification of four cases as MDS instead of AML, if diagnosis had based on the bone marrow aspirate blast count alone. CONCLUSION: Counting blasts in bone marrow aspirates of CD56-positive AML and MDS may be linked to underestimation, potentially leading to misclassification of these myeloid neoplasms, and should therefore be adjusted considering the results obtained on trephine biopsies for reliable diagnosis.

Eseola, A. B., et al. (2021). "Investigating the cell and developmental biology of plant infection by the rice blast fungus Magnaporthe oryzae." Fungal Genet Biol: 103562.

Magnaporthe oryzae is the causal agent of rice blast disease, the most widespread and serious disease of cultivated rice. Live cell imaging and quantitative 4D image analysis have provided new insight into the mechanisms by which the fungus infects host cells and spreads rapidly in plant tissue. In this video review article, we apply live cell imaging approaches to understanding the cell and developmental biology of rice blast disease. To gain entry to host plants, M. oryzae develops a specialised infection structure called an appressorium, a unicellular dome-shaped cell which generates enormous turgor, translated into mechanical force to rupture the leaf cuticle. Appressorium development is induced by perception of the hydrophobic leaf surface and nutrient deprivation. Cargo-independent autophagy in the three-celled conidium, controlled by cell cycle regulation, is essential for appressorium morphogenesis. Appressorium maturation involves turgor generation and melanin pigment deposition in the appressorial cell wall. Once a threshold of turgor has been reached, this triggers re-polarisation which requires regulated generation of reactive oxygen species, to facilitate septin GTPase-dependent cytoskeletal re-organisation and re-polarisation of the appressorium to form a narrow, rigid penetration peg. Infection of host tissue requires a further morphogenetic transition to a pseudohyphal-type of growth within colonised rice cells. At the same time the fungus secretes an arsenal of effector proteins to suppress plant immunity. Many effectors are secreted into host cells directly, which involves a specific secretory pathway and a specialised structure called the biotrophic interfacial complex. Cell-to-cell spread of the fungus then requires development of a specialised structure, the transpressorium, that is used to traverse pit field sites, allowing the fungus to maintain host cell membrane integrity as new living plant cells are invaded. Thereafter, the fungus rapidly moves through plant tissue and host cells begin to die, as the fungus switches to necrotrophic growth and disease symptoms develop. These morphogenetic transitions are reviewed in the context of live cell imaging studies.

Fawaz, M. and M. Itani (2021). "The psychological experiences of Lebanese ground zero front-line nurses during the most recent COVID-19 outbreak post Beirut blast: A qualitative study." Int J Soc Psychiatry: 207640211004989.

BACKGROUND: For the past 2 months the number of COVID-19 cases in Lebanon has been on the rise, while frontline nurses after the Beirut Blast of August 4th have been practicing through limited resources and a challenging context. AIM: This paper aims at exploring the psychological experiences of Lebanese frontline nurses serving at ground zero hospital during the current COVID-19 outbreak. SETTING: This study was carried out in three main ground-zero hospitals in Beirut which are receiving COVID-19 cases. METHOD: This study have employed a phenomenological exploratory qualitative research design, where virtual interviews were conducted with 18 frontline nurses during the second week of January 2021. RESULTS: Thematic analysis of the data expressed by the frontline nurses working in the approached ground-zero hospitals gave rise to five themes, namely 'helplessness and impending doom', 'increased mortality rates and depressive mood', 'fear of death and obsessive thinking', 'flashbacks, panic, and incompetence', and 'public recklessness, governmental responsibility, and anger'. CONCLUSION: The frontline nurses working at ground zero hospitals in Beirut are facing significant psychological challenges that should be mediated by the government and health policymakers in order to safeguard the quality of care and avoid higher mortality rates.

Fernandez, J., et al. (2021). "Role of Two Metacaspases in Development and Pathogenicity of the Rice Blast Fungus Magnaporthe oryzae." mBio **12**(1).
Rice blast disease caused by Magnaporthe oryzae is a devastating disease of cultivated rice worldwide. Infections by this fungus lead to a significant reduction in rice yields and threats to food security. To gain better insight into growth and cell death in M. oryzae during infection, we characterized two predicted M. oryzae metacaspase proteins, MoMca1 and MoMca2. These proteins appear to be functionally redundant and can complement the yeast Yca1 homologue. Biochemical analysis revealed that M. oryzae metacaspases exhibited Ca(2+)-dependent caspase activity in vitro Deletion of both MoMca1 and MoMca2 in M. oryzae resulted in reduced sporulation, delay in conidial germination, and attenuation of disease severity. In addition, the double DeltaMomca1mca2 mutant strain showed increased radial growth in the presence of oxidative stress. Interestingly, the DeltaMomca1mca2 strain showed an increased accumulation of insoluble aggregates compared to the wild-type strain during vegetative growth. Our findings suggest that MoMca1 and MoMca2 promote the clearance of insoluble aggregates in M. oryzae, demonstrating the important role these metacaspases have in fungal protein homeostasis. Furthermore, these metacaspase proteins may play additional roles, like in regulating stress responses, that would help maintain the fitness of fungal cells required for host infection.IMPORTANCE Magnaporthe oryzae causes rice blast disease that threatens global food security by resulting in the severe loss of rice production every year. A tightly regulated life cycle allows M. oryzae to disarm the host plant immune system during its biotrophic stage before triggering plant cell death in its necrotrophic stage. The ways M. oryzae navigates its complex life cycle remain unclear. This work characterizes two metacaspase proteins with peptidase activity in M. oryzae that are shown to be involved in the regulation of fungal growth and development prior to infection by potentially helping maintain fungal fitness. This study provides new insights into the role of metacaspase proteins in filamentous fungi by illustrating the delays in M. oryzae morphogenesis in the absence of these proteins. Understanding the mechanisms by which M. oryzae morphology and development promote its devastating pathogenicity may lead to the emergence of proper methods for disease control.

Frontini, M., et al. (2021). "Genome-wide association of rice response to blast fungus identifies loci for robust resistance under high nitrogen." BMC Plant Biol **21**(1): 99.
BACKGROUND: Nitrogen fertilization is known to increase disease susceptibility, a phenomenon called Nitrogen-Induced Susceptibility (NIS). In rice, this phenomenon has been observed in infections with the blast fungus Magnaporthe oryzae. A previous classical genetic study revealed a locus (NIS1) that enhances susceptibility to rice blast under high nitrogen fertilization. In order to further address the underlying genetics of plasticity in susceptibility to rice blast after fertilization, we analyzed NIS under greenhouse-controlled conditions in a panel of 139 temperate japonica rice strains. A genome-wide association analysis was conducted to identify loci potentially involved in NIS by comparing susceptibility loci identified under high and low nitrogen conditions, an approach allowing for the identification of loci validated across different nitrogen environments. We also used a novel NIS Index to identify loci potentially contributing to plasticity in susceptibility under different nitrogen fertilization regimes. RESULTS: A global NIS effect was observed in the population, with the density of lesions increasing by 8%, on average, under high nitrogen fertilization. Three new QTL, other than NIS1, were identified. A rare allele of the RRobN1 locus on chromosome 6 provides robust resistance in high and low nitrogen environments. A frequent allele of the NIS2 locus, on chromosome 5, exacerbates blast susceptibility under the high nitrogen condition. Finally, an allele of NIS3, on chromosome 10, buffers the increase of susceptibility arising from nitrogen fertilization but increases global levels of susceptibility. This allele is almost fixed in temperate japonicas, as a probable consequence of genetic hitchhiking with a locus involved in cold stress adaptation. CONCLUSIONS: Our results extend to an entire rice subspecies the initial finding that nitrogen increases rice blast susceptibility. We demonstrate the usefulness of estimating plasticity for the identification of novel loci involved in the response of rice to the blast fungus under different nitrogen regimes.

Galvez, S., et al. (2021). "BLVector: Fast BLAST-Like Algorithm for Manycore CPU With Vectorization." Front Genet **12**: 618659.
New High-Performance Computing architectures have been recently developed for commercial central processing unit (CPU). Yet, that has not improved the execution time of widely used bioinformatics applications, like BLAST+. This is due to a lack of optimization between the bases of the existing algorithms and the internals of the hardware that allows taking full advantage of the available CPU cores. To optimize the new architectures, algorithms must be revised and redesigned; usually rewritten from scratch. BLVector adapts the high-level concepts of BLAST+ to the x86 architectures with AVX-512, to harness their

capabilities. A deep comprehensive study has been carried out to optimize the approach, with a significant reduction in time execution. BLVector reduces the execution time of BLAST+ when aligning up to mid-size protein sequences (approximately 750 amino acids). The gain in real scenario cases is 3.2-fold. When applied to longer proteins, BLVector consumes more time than BLAST+, but retrieves a much larger set of results. BLVector and BLAST+ are fine-tuned heuristics. Therefore, the relevant results returned by both are the same, although they behave differently specially when performing alignments with low scores. Hence, they can be considered complementary bioinformatics tools.

Gangat, N., et al. (2021). "Venetoclax with azacitidine or decitabine in blast-phase myeloproliferative neoplasm: A multicenter series of 32 consecutive cases." Am J Hematol.
Venetoclax (Ven) combined with a hypomethylating agent (HMA) has now emerged as an effective treatment regimen for acute myeloid leukemia, in both de novo and relapsed/refractory setting. The current multicenter study retrospectively examined Ven + HMA treatment outcome among 32 patients (median age 69 years; 59% males) with blast-phase myeloproliferative neoplasm (MPN-BP). Pre-leukemic phenotype included essential thrombocythemia (ET)/post-ET myelofibrosis (34%), polycythemia vera (PV)/post-PV myelofibrosis (38%) and primary myelofibrosis (28%). Twenty-nine study patients were fully annotated cytogenetically and molecularly (NGS): 69% harbored complex karyotype and/or mutations, including TP53 (41%), IDH1/2 (21%), ASXL1 (21%), N/KRAS (14%), SRSF2 (10%), EZH2 (10%) and U2AF1 (7%). All patients received Ven combined with either azacitidine ($n = 12$) or decitabine ($n = 20$); either up front ($n = 23$) or after failing another induction therapy ($n = 9$). Complete remission with (CR) or without (CRi) count recovery was achieved in 14 (44%) patients and was more likely to occur in the absence of pre-leukemic PV/post-PV myelofibrosis phenotype ($p < .01$), complex karyotype ($p < .01$) or K/NRAS ($p = .03$) mutations; seven of eight patients (88%) without vs four of 21 (19%) with complex karyotype or K/NRAS mutation achieved CR/CRi ($p < .01$); all 11 informative patients with pre-leukemic PV/post-PV myelofibrosis phenotype displayed complex karyotype ($p < .01$). In contrast, neither TP53 ($p = .45$) nor IDH1/2 ($p = .63$) mutations affected response. Compared to historical controls treated with HMA alone ($n = 26$), the CR/CRi rate (44% vs 4%) and median survival (8 vs 5.5 months) were more favorable with Ven + HMA, but without significant difference in overall survival. Importantly, six patients with CR/CRi subsequently received allogeneic hematopoietic stem cell transplant (AHSCT). Note, Ven + HMA produces robust CR/CRi rates in MPN-BP, especially in the absence of RAS mutations and complex karyotype, thus enabling AHSCT, in some patients.

Hanifehzadeh, M., et al. (2021). "Structural Response of Steel Jacket-UHPC Retrofitted Reinforced Concrete Columns under Blast Loading." Materials (Basel) **14**(6).
The lateral capacity of exterior concrete columns subjected to a blast load is the key factor in the building collapse probability. Due to potentially severe consequences of the collapse, efforts have been made to improve the blast resistance of existing structures. One of the successful approaches is the use of ultra-high-performance-concrete (UHPC) jacketing for retrofitting a building's columns. The columns on the first floor of a building normally have higher slenderness due to the higher first story. Since an explosion is more likely to take place at the ground level, retrofitting the columns of the lower floors is crucial to improve a building's blast resistance. Casting a UHPC tube around a circular RC column can increase the moment of inertia of the column and improve the flexural strength. In this study, a retrofitting system consisting of a UHPC layer enclosed by a thin steel jacket is proposed to improve the blast resistance of buildings in service. Most of the previous research is focused on design aspects of blast-resistant columns and retrofitting systems are mostly based on fiber reinforced polymers or steel jackets. A validated FE model is used to investigate the effectiveness of this method. The results showed significant improvement both at the component and building system levels against combined gravity and blast loading.

Heyburn, L., et al. (2021). "Repeated Low-Level Blast Acutely Alters Brain Cytokines, Neurovascular Proteins, Mechanotransduction, and Neurodegenerative Markers in a Rat Model." Front Cell Neurosci **15**: 636707.
Exposure to the repeated low-level blast overpressure (BOP) periodically experienced by military personnel in operational and training environments can lead to deficits in behavior and cognition. While these low-intensity blasts do not cause overt changes acutely, repeated exposures may lead to cumulative effects in the brain that include acute inflammation, vascular disruption, and other molecular changes, which may eventually contribute to neurodegenerative processes. To identify these acute changes in the brain following repeated BOP, an advanced blast simulator was used to expose rats to 8.5 or 10 psi BOP once per day for 14 days. At 24 h after the final BOP, brain tissue was

collected and analyzed for inflammatory markers, astrogliosis (GFAP), tight junction proteins (claudin-5 and occludin), and neurodegeneration-related proteins (Abeta40/42, pTau, TDP-43). After repeated exposure to 8.5 psi BOP, the change in cytokine profile was relatively modest compared to the changes observed following 10 psi BOP, which included a significant reduction in several inflammatory markers. Reduction in the tight junction protein occludin was observed in both groups when compared to controls, suggesting cerebrovascular disruption. While repeated exposure to 8.5 psi BOP led to a reduction in the Alzheimer's disease (AD)-related proteins amyloid-beta (Abeta)40 and Abeta42, these changes were not observed in the 10 psi group, which had a significant reduction in phosphorylated tau. Finally, repeated 10 psi BOP exposures led to an increase in GFAP, indicating alterations in astrocytes, and an increase in the mechanosensitive ion channel receptor protein, Piezo2, which may increase brain sensitivity to injury from pressure changes from BOP exposure. Overall, cumulative effects of repeated low-level BOP may increase the vulnerability to injury of the brain by disrupting neurovascular architecture, which may lead to downstream deleterious effects on behavior and cognition.

Hofer, U. (2021). "Blast from the past for coronavirus immunity." Nat Rev Microbiol.

Huang, X., et al. (2021). "Craniocerebral Dynamic Response and Cumulative Effect of Damage Under Repetitive Blast." Ann Biomed Eng.
Soldiers suffer from multiple explosions in complex battlefield environment resulting in aggravated brain injuries. At present, researches mostly focus on the damage to human body caused by single explosion. In the repetitive impact study, small animals are mainly used for related experiments to study brain nerve damage. No in-depth research has been conducted on the dynamic response and damage of human brain under repetitive explosion shock waves. Therefore, this study use the Euler-Lagrange coupling method to construct an explosion shock wave-head fluid-structure coupling model, and numerically simulated the brain dynamic response subjected to single and repetitive blast waves, obtained flow field pressure, skull stress, skull displacement, intracranial pressure to analyze the brain damage. The simulation results of 100 g equivalent of TNT exploding at 1 m in front of the craniocerebral show that repetitive blast increase skull stress, intracranial pressure, skull displacement, and the damage of brain tissue changes from moderate to severe. Repetitive blasts show a certain cumulative damage effect, the severity of damage caused by double blast is 122.5% of single shock, and the severity of damage caused by triple blast is 105.9% of double blast and 131.5% of single blast. The data above shows that it is necessary to reduce soldiers' exposure from repetitive blast waves.

Jain, T. and R. K. Rampal (2021). "Accelerated and Blast Phase Myeloproliferative Neoplasms." Hematol Oncol Clin North Am **35**(2): 325-335.
Accelerated and blast phase myeloproliferative neoplasms are advanced stages of the disease with historically a poor prognosis and little improvement in outcomes thus far. The lack of responses to standard treatments likely results from the more aggressive biology reflected by the higher incidence of complex karyotype and high-risk somatic mutations, which are enriched at the time of transformation. Treatment options include induction chemotherapy (7 + 3) as that used on de novo acute myeloid leukemia or hypomethylating agent-based therapy, which has shown similar outcomes. Allogeneic stem cell transplantation remains the only potential for cure.

Jiang, S., et al. (2021). "Dual-laser measurement of human stapes footplate motion under blast exposure." Hear Res **403**: 108177.
Hearing damage is one of the most frequently observed injuries in Service members and Veterans even though hearing protection devices (HPDs, e.g. earplugs) have been implemented to prevent blast-induced hearing loss. However, the formation and prevention mechanism of the blast-induced hearing damage remains unclear due to the difficulty for conducting biomechanical measurements in ears during blast exposure. Recently, an approach reported by Jiang et al. (2019) used two laser Doppler vibrometers (LDVs) to measure the motion of the tympanic membrane (TM) in human temporal bones during blast exposure. Using the dual laser setup, we further developed the technology to detect the movement of the stapes footplate (SFP) in ears with and without HPDs while under blast exposure. Eight fresh human cadaveric temporal bones (TBs) were involved in this study. The TB was mounted in a "head block" after performing a facial recess surgery to access the SFP, and a pressure sensor was inserted near the TM in the ear canal to measure the pressure reaching the TM (P1). The TB was exposed to a blast overpressure measuring around 7 psi or 48 kPa at the entrance of the ear canal (P0). Two LDVs were used to measure the vibrations of the SFP and TB (as a reference). The exact motion of the SFP was determined by subtracting the TB motion from the SFP data. Results included a measured peak-to-peak SFP displacement of 68.7 +/- 31.6 mum (mean +/- SD) from all eight TBs without HPDs. In five of the TBs, the insertion of a foam earplug reduced the SFP displacement from 48.3 +/- 6.3 mum to 21.8 +/- 10.4

mum. The time-frequency analysis of the SFP velocity signals indicated that most of the energy spectrum was concentrated at frequencies below 4 kHz within the first 2 ms after blast and the energy was reduced after the insertion of HPDs. This study describes a new methodology to quantitatively characterize the response of the middle ear and the energy entering the cochlea during blast exposure. The experimental data are critical for determining the injury of the peripheral auditory system and elucidating the damage formation and prevention mechanism in an ear exposed to blast.

Kapatia, G., et al. (2021). "Myeloid Neoplasm with t(8;22)(p11;q11): A Mimicker of Chronic Myeloid Leukaemia in Blast Crisis." Indian J Hematol Blood Transfus **37**(2): 334-336.

Kawoos, U., et al. (2021). "Blast-induced temporal alterations in blood-brain barrier properties in a rodent model." Sci Rep **11**(1): 5906.
The consequences of blast-induced traumatic brain injury (bTBI) on the blood-brain barrier (BBB) and components of the neurovascular unit are an area of active research. In this study we assessed the time course of BBB integrity in anesthetized rats exposed to a single blast overpressure of 130 kPa (18.9 PSI). BBB permeability was measured in vivo via intravital microscopy by imaging extravasation of fluorescently labeled tracers (40 kDa and 70 kDa molecular weight) through the pial microvasculature into brain parenchyma at 2-3 h, 1, 3, 14, or 28 days after the blast exposure. BBB structural changes were assessed by immunostaining and molecular assays. At 2-3 h and 1 day after blast exposure, significant increases in the extravasation of the 40 kDa but not the 70 kDa tracers were observed, along with differential reductions in the expression of tight junction proteins (occludin, claudin-5, zona occluden-1) and increase in the levels of the astrocytic water channel protein, AQP-4, and matrix metalloprotease, MMP-9. Nearly all of these measures were normalized by day 3 and maintained up to 28 days post exposure. These data demonstrate that blast-induced changes in BBB permeability are closely coupled to structural and functional components of the BBB.

Kazezian, Z., et al. (2021). "Development of a rodent high-energy blast injury model for investigating conditions associated with traumatic amputations." Bone Joint Res **10**(3): 166-172.
AIMS: In recent conflicts, most injuries to the limbs are due to blasts resulting in a large number of lower limb amputations. These lead to heterotopic ossification (HO), phantom limb pain (PLP), and functional deficit. The mechanism of blast loading produces a combined fracture and amputation. Therefore, to study these conditions, in vivo models that replicate this combined effect are required. The aim of this study is to develop a preclinical model of blast-induced lower limb amputation. METHODS: Cadaveric Sprague-Dawley rats' left hindlimbs were exposed to blast waves of 7 to 13 bar burst pressures and 7.76 ms to 12.68 ms positive duration using a shock tube. Radiographs and dissection were used to identify the injuries. RESULTS: Higher burst pressures of 13 and 12 bar caused multiple fractures at the hip, and the right and left limbs. Lowering the pressure to 10 bar eliminated hip fractures; however, the remaining fractures were not isolated to the left limb. Further reducing the pressure to 9 bar resulted in the desired isolated fracture of the left tibia with a dramatic reduction in the fractures to other sites. CONCLUSION: In this paper, a rodent blast injury model has been developed in the hindlimb of cadaveric rats that combines the blast and fracture in one insult, necessitating amputation. Experimental setup with 9 bar burst pressure and 9.13 ms positive duration created a fracture at the tibia with total reduction in non-targeted fractures, rendering 9 bar burst pressure suitable for translation to a survivable model to investigate blast injury-associated diseases. Cite this article: Bone Joint Res 2021;10(3):166-172.

Knapp, P., et al. (2021). "High-Energy Blast Injury Requiring Transradial Amputation with Associated Essex Lopresti and Terrible Triad Injuries of the Elbow: A Rare Presentation." Case Rep Orthop **2021**: 6645082.
Case: Blast injuries to the upper extremity can be devastating and emotionally stressful injuries. We describe a case of a high-energy blast injury to an upper extremity from an explosive. The transfer of energy caused severe soft tissue/bony damage to the hand, but also led to associated Essex Lopresti and terrible triad injuries. The patient required emergent transradial amputation by hand surgery as well as definitive fixation by our orthopaedic team. Conclusion: We describe a unique salvage operation that established forearm pronosupination, elbow flexion, and proper prosthetic fitting. We feel that describing our technique could help others in treating this injury if encountered.

Kumar, V., et al. (2021). "Understanding Rice-Magnaporthe Oryzae Interaction in Resistant and Susceptible Cultivars of Rice under Panicle Blast Infection Using a Time-Course Transcriptome Analysis." Genes (Basel) **12**(2).
Rice blast is a global threat to food security with up to 50% yield losses. Panicle blast is a more severe form of rice blast and the response of rice plant to leaf and panicle blast is distinct in different genotypes. To

understand the specific response of rice in panicle blast, transcriptome analysis of blast resistant cultivar Tetep, and susceptible cultivar HP2216 was carried out using RNA-Seq approach after 48, 72 and 96 h of infection with Magnaporthe oryzae along with mock inoculation. Transcriptome data analysis of infected panicle tissues revealed that 3553 genes differentially expressed in HP2216 and 2491 genes in Tetep, which must be the responsible factor behind the differential disease response. The defense responsive genes are involved mainly in defense pathways namely, hormonal regulation, synthesis of reactive oxygen species, secondary metabolites and cell wall modification. The common differentially expressed genes in both the cultivars were defense responsive transcription factors, NBS-LRR genes, kinases, pathogenesis related genes and peroxidases. In Tetep, cell wall strengthening pathway represented by PMR5, dirigent, tubulin, cell wall proteins, chitinases, and proteases was found to be specifically enriched. Additionally, many novel genes having DOMON, VWF, and PCaP1 domains which are specific to cell membrane were highly expressed only in Tetep post infection, suggesting their role in panicle blast resistance. Thus, our study shows that panicle blast resistance is a complex phenomenon contributed by early defense response through ROS production and detoxification, MAPK and LRR signaling, accumulation of antimicrobial compounds and secondary metabolites, and cell wall strengthening to prevent the entry and spread of the fungi. The present investigation provided valuable candidate genes that can unravel the mechanisms of panicle blast resistance and help in the rice blast breeding program.

Langner, T., et al. (2021). "Genomic rearrangements generate hypervariable mini-chromosomes in host-specific isolates of the blast fungus." PLoS Genet **17**(2): e1009386.

Supernumerary mini-chromosomes-a unique type of genomic structural variation-have been implicated in the emergence of virulence traits in plant pathogenic fungi. However, the mechanisms that facilitate the emergence and maintenance of mini-chromosomes across fungi remain poorly understood. In the blast fungus Magnaporthe oryzae (Syn. Pyricularia oryzae), mini-chromosomes have been first described in the early 1990s but, until very recently, have been overlooked in genomic studies. Here we investigated structural variation in four isolates of the blast fungus M. oryzae from different grass hosts and analyzed the sequences of mini-chromosomes in the rice, foxtail millet and goosegrass isolates. The mini-chromosomes of these isolates turned out to be highly diverse with distinct sequence composition. They are enriched in repetitive elements and have lower gene density than core-chromosomes. We identified several virulence-related genes in the mini-chromosome of the rice isolate, including the virulence-related polyketide synthase Ace1 and two variants of the effector gene AVR-Pik. Macrosynteny analyses around these loci revealed structural rearrangements, including inter-chromosomal translocations between core- and mini-chromosomes. Our findings provide evidence that mini-chromosomes emerge from structural rearrangements and segmental duplication of core-chromosomes and might contribute to adaptive evolution of the blast fungus.

Li, J. S., et al. (2021). "Sustainable stabilization/solidification of arsenic-containing soil by blast slag and cement blends." Chemosphere **271**: 129868.

Arsenic (As) is a naturally occurring trace element that may pose a threat to human health and the ecosystem, while effective remediation and sustainable reuse of As-containing soil is a challenge. This study investigated the geoenvironmental characteristics of a geogenic As-rich soil, and green binders (ground granulated blast slag (GGBS) and cement blends) were employed for the stabilization/solidification (S/S) of the soil under field-relevant conditions. Results indicate that the use of 10% binder could effectively immobilize As and chemical stabilization/physical encapsulation jointly determined the leaching characteristics of the S/S soils. The geogenic As could be effectively immobilized at the pH range of 5.5-6.5. The increasing use of GGBS enhanced the strength of the 28-d cured S/S soils because of long-term pozzolanic reaction, but also slightly improved the As leachability. Besides, the moisture content of the contaminated soils should be suitably adjusted to allow for desirable compaction of S/S soils, which resulted in high compressive strength and low of As leachability. Results show that soil moisture content of 20% was the most appropriate, which resulted in the highest strength and relatively lower As leaching. In summary, this study presents a sustainable S/S binder for recycling As-contaminated soil by using a combination of cement and GGBS.

Li, Y., et al. (2021). "(18)F-FDG PET Combined With MR Spectroscopy Elucidates the Progressive Metabolic Cerebral Alterations After Blast-Induced Mild Traumatic Brain Injury in Rats." Front Neurosci **15**: 593723.

A majority of blast-induced mild traumatic brain injury (mTBI) patients experience persistent neurological dysfunction with no findings on conventional structural MR imaging. It is urgent to develop advanced imaging modalities to detect and understand the pathophysiology of blast-induced mTBI. Fluorine-18 fluorodeoxyglucose positron emission tomography ((18)F-FDG PET) could detect neuronal function and activity of the injured brain, while MR spectroscopy provides complementary information and assesses metabolic irregularities following injury. This study aims to investigate the effectiveness of combining (18)F-FDG PET with MR spectroscopy to evaluate acute and subacute metabolic cerebral alterations caused by blast-induced mTBI. Thirty-two adult male Sprague-Dawley rats were exposed to a single blast (mTBI group) and 32 rats were not exposed to the blast (sham group), followed by (18)F-FDG PET, MRI, and histological evaluation at baseline, 1-3 h, 1 day, and 7 days post-injury in three separate cohorts. (18)F-FDG uptake showed a transient increase in the amygdala and somatosensory cortex, followed by a gradual return to baseline from day 1 to 7 days post-injury and a continuous rise in the motor cortex. In contrast, decreased (18)F-FDG uptake was seen in the midbrain structures (inferior and superior colliculus). Analysis of MR spectroscopy showed that inflammation marker myo-inositol (Ins), oxidative stress marker glutamine + glutamate (Glx), and hypoxia marker lactate (Lac) levels markedly elevated over time in the somatosensory cortex, while the major osmolyte taurine (Tau) level immediately increased at 1-3 h and 1 day, and then returned to sham level on 7 days post-injury, which could be due to the disruption of the blood-brain barrier. Increased (18)F-FDG uptake and elevated Ins and Glx levels over time were confirmed by histology analysis which showed increased microglial activation and gliosis in the frontal cortex. These results suggest that (18)F-FDG PET and MR spectroscopy can be used together to reflect more comprehensive neuropathological alterations in vivo, which could improve our understanding of the complex alterations in the brain after blast-induced mTBI.

Lopez-Moya, F., et al. (2021). "Chitosan inhibits septin-mediated plant infection by the rice blast fungus Magnaporthe oryzae in a protein kinase C and Nox1 NADPH oxidase-dependent manner." New Phytol **230**(4): 1578-1593.
Chitosan is a partially deacetylated linear polysaccharide composed of beta-1,4-linked units of d-glucosamine and N-acetyl glucosamine. As well as a structural component of fungal cell walls, chitosan is a potent antifungal agent. However, the mode of action of chitosan is poorly understood. Here, we report that chitosan is effective for control of rice blast disease. Chitosan application impairs growth of the blast fungus Magnaporthe oryzae and has a pronounced effect on appressorium-mediated plant infection. Chitosan inhibits septin-mediated F-actin remodelling at the appressorium pore, thereby preventing repolarization of the infection cell. Chitosan causes plasma membrane permeabilization of M. oryzae and affects NADPH oxidase-dependent synthesis of reactive oxygen species, essential for septin ring formation and fungal pathogenicity. We further show that toxicity of chitosan to M. oryzae requires the protein kinase C-dependent cell wall integrity pathway, the Mps1 mitogen-activated protein kinase and the Nox1 NADPH oxidase. A conditionally lethal, analogue (PP1)-sensitive mutant of Pkc1 is partially remediated for growth in the presence of chitosan, while nox1 mutants increase their glucan : chitin cell wall ratio, rendering them resistant to chitosan. Taken together, our data show that chitosan is a potent fungicide which requires the cell integrity pathway, disrupts plasma membrane function and inhibits septin-mediated plant infection.

Lovat, F., et al. (2021). "Loss of expression of both miR-15/16 loci in CML transition to blast crisis." Proc Natl Acad Sci U S A **118**(11).
Despite advances that have improved the treatment of chronic myeloid leukemia (CML) patients in chronic phase, the mechanisms of the transition from chronic phase CML to blast crisis (BC) are not fully understood. Considering the key role of miR-15/16 loci in the pathogenesis of myeloid and lymphocytic leukemia, here we aimed to correlate the expression of miR-15a/16 and miR-15b/16 to progression of CML from chronic phase to BC. We analyzed the expression of the two miR-15/16 clusters in 17 CML patients in chronic phase and 22 patients in BC and in 11 paired chronic phase and BC CML patients. BC CMLs show a significant reduction of the expression of miR-15a/-15b/16 compared to CMLs in chronic phase. Moreover, BC CMLs showed an overexpression of miR-15/16 direct targets such as Bmi-1, ROR1, and Bcl-2 compared to CMLs in chronic phase. This study highlights the loss of both miR-15/16 clusters as a potential oncogenic driver in the transition from chronic phase to BC in CML patients.

Lv, Q. Q., et al. (2021). "A study on the characteristics of coke in the hearth of a superlarge blast furnace." PLoS One **16**(3): e0247051.
An in-depth study on the characteristics of coke in the hearths of blast furnaces is of great significance for explaining the mechanism of coke deterioration in blast furnaces. In the present work, the changes in macromorphology, degree of graphitization, and microstructure of the coke taken from different hearth locations of a 5,800 m3 superlarge blast furnace during its intermediate repair period were systematically studied. Significant differences were found between cokes obtained from the edge ("edge coke") and from the center ("center coke") of the hearth in terms of properties and degradation mechanisms. Edge coke

was severely eroded by liquid metal, and only a small amount of slag was detected in the coke porosity, whereas center coke was basically free from erosion by liquid metal, and a large amount of slag was detected in the coke porosity. The degree of graphitization of edge coke was higher than that of center coke. The carburizing effect of liquid metal was the main cause of the degradation of edge coke and made it smaller or even disappear. Center coke was degraded due to the combination of two factors: slag inserted into micropores on the surface of center coke loosened the surface structure; and graphite-like flakes that appeared on the center coke surface lowered the strength and caused cracks in the surface.

MacGregor, A. J., et al. (2021). "The Relationship Between Blast-related Hearing Threshold Shift and Insomnia in U.S. Military Personnel." Mil Med.
INTRODUCTION: Hearing loss and insomnia emerged as preeminent sources of morbidity among military service members and veterans who served in the recent Iraq and Afghanistan conflicts. Significant threshold shift (STS), an early indicator of hearing loss, has not been studied in relation to insomnia. This study's objective was to examine the co-occurrence of STS and insomnia among U.S. military personnel with blast-related injury. MATERIALS AND METHODS: A total of 652 service members who were blast-injured during military operations in Iraq or Afghanistan between 2004 and 2012 were identified from the Blast-Related Auditory Injury Database. Pre- and post-injury audiometric data were used to ascertain new-onset STS, defined as 30 dB or greater increase for the sum of thresholds at 2,000, 3,000, and 4,000 Hz for either ear. Insomnia diagnosed within 2 years post-injury was abstracted from electronic medical records. Multivariable logistic regression analysis examined the relationship between STS and insomnia, while adjusting for age, year of injury, occupation, injury severity, tinnitus and concussion diagnosed in-theater, and PTSD. RESULTS: A majority of the study sample was aged 18-25 years (79.9%) and sustained mild-to-moderate injuries (92.2%). STS was present in 21.1% of service members. Cumulative incidence of diagnosed insomnia was 22.3% and 11.1% for those with and without STS, respectively. After adjusting for covariates, those with STS had nearly 2-times higher odds of insomnia (odds ratio (OR) = 1.91, 95% CI = 1.12-3.24) compared with those without STS. In multivariable modeling, the strongest association was between PTSD and insomnia (OR = 5.57, 95% CI = 3.35-9.26). A secondary finding of note was that military personnel with STS had a significantly higher frequency of PTSD compared with those without STS (28.1% vs. 15.2%). CONCLUSIONS: Hearing threshold shift was associated with insomnia in military personnel with blast-related injury and could be used to identify service members at risk. Multidisciplinary care is needed to manage the co-occurrence of both conditions during the post-deployment rehabilitation phase. Future research should evaluate the specific mechanisms involved in this relationship and further explore the association between hearing threshold shift and PTSD.

Marsh, J. L. and S. A. Bentil (2021). "Cerebrospinal Fluid Cavitation as a Mechanism of Blast-Induced Traumatic Brain Injury: A Review of Current Debates, Methods, and Findings." Front Neurol **12**: 626393.
Cavitation has gained popularity in recent years as a potential mechanism of blast-induced traumatic brain injury (bTBI). This review presents the most prominent debates on cavitation; how bubbles can form or exist within the cerebrospinal fluid (CSF) and brain vasculature, potential mechanisms of cellular, and tissue level damage following the collapse of bubbles in response to local pressure fluctuations, and a survey of experimental and computational models used to address cavitation research questions. Due to the broad and varied nature of cavitation research, this review attempts to provide a necessary synthesis of cavitation findings relevant to bTBI, and identifies key areas where additional work is required. Fundamental questions about the viability and likelihood of CSF cavitation during blast remain, despite a variety of research regarding potential injury pathways. Much of the existing literature on bTBI evaluates cavitation based off its prima facie plausibility, while more rigorous evaluation of its likelihood becomes increasingly necessary. This review assesses the validity of some of the common assumptions in cavitation research, as well as highlighting outstanding questions that are essential in future work.

Martindale, S. L., et al. (2021). "Research Letter: Blast Exposure and Brain Volume." J Head Trauma Rehabil.
OBJECTIVE: To determine whether blast exposure is associated with brain volume beyond posttraumatic stress disorder (PTSD) diagnosis and history of traumatic brain injury (TBI). SETTING: Veterans Affairs Medical Center. PARTICIPANTS: One hundred sixty-three Iraq and Afghanistan combat veterans, 86.5% male, and 68.10% with a history of blast exposure. Individuals with a history of moderate to severe TBI were excluded. MAIN MEASURES: Clinician-Administered PTSD Scale (CAPS-5), Mid-Atlantic MIRECC Assessment of TBI (MMA-TBI), Salisbury Blast Interview (SBI), and magnetic resonance imaging. Maximum blast pressure experienced from a blast event represented blast severity. METHODS: Hierarchical regression analysis evaluated effects of maximum pressure experienced

from a blast event on bilateral volume of hippocampus, anterior cingulate cortex, amygdala, orbitofrontal cortex, precuneus, and insula. All analyses adjusted for effects of current and lifetime PTSD diagnosis, and a history of deployment mild TBI. RESULTS: Maximum blast pressure experienced was significantly associated with lower bilateral hippocampal volume (left: DeltaR2 = 0.032, P < .001; right: DeltaR2 = 0.030, P < .001) beyond PTSD diagnosis and deployment mild TBI history. Other characteristics of blast exposure (time since most recent exposure, distance from closest blast, and frequency of blast events) were not associated with evaluated volumes. CONCLUSION: Exposure to a blast is independently associated with hippocampal volume beyond PTSD and mild TBI; however, these effects are small. These results also demonstrate that blast exposure in and of itself may be less consequential than severity of the exposure as measured by the pressure gradient.

Masarova, L., et al. (2021). "Clinical Significance of Bone Marrow Blast Percentage in Patients With Myelofibrosis and the Effect of Ruxolitinib Therapy." Clin Lymphoma Myeloma Leuk **21**(5): 318-327 e316.
BACKGROUND: The effect of bone marrow (BM) blasts on the outcome of patients with myelofibrosis (MF) is poorly understood, unless they are >/= 10% and represent a more aggressive accelerated phase. Similarly, the role of the JAK inhibitor, ruxolitinib (RUX), has not been assessed in correlation with BM blasts. PATIENTS AND METHODS: Herein, we present clinical characteristics and outcomes of 1412 patients with MF stratified by BM blasts and therapy. RESULTS: Seven percent and 4% of patients had 5% to 9% and >/= 10% BM blasts, respectively. Forty-four percent of patients were treated with RUX throughout their disease course. Overall survival (OS) differed among patients with 0% to 1%, 2% to 4%, and 5% to 9% BM blasts, with median OS of 64, 48, and 22 months, respectively (P < .001). Patients with 5% to 9% BM blasts had similar OS as patients with >/= 10% BM blasts (22 vs. 14 months; P = .73). All patients with < 10% blasts who were treated with RUX showed superior OS to patients who did not receive RUX. CONCLUSIONS: Our results indicate that patients with MF with >/= 5% BM blasts represent a high-risk group with adverse clinical characteristics and inferior outcome. However, they still appear to derive substantial survival benefit from therapy with RUX.

Mendonca, F. B., et al. (2021). "Damage diagram of blast test results for determining reinforced concrete slab response for varying scaled distance, concrete strength and reinforcement ratio." An Acad Bras Cienc **93**(1): e20200511.
Dynamic loads continue to draw the interest of structural engineers. The sources of these loads can be earthquakes, blast effects or transportation loads from railroads or highways. Especially for blast loads, terrorist attacks or military actions have caused many loses of lives and damages in several buildings. The verification of structural behavior is necessary to help designers to plan structures that support these loads and reduce damages. Although computer simulation with, specific software, have helped these designers, full-scale tests can provide valuable information about the real response of the structure. This paper presents damage diagram from ten full-scale field tests using approximately 2.70 kg of non-confined plastic bonded explosive against reinforced concrete slabs with different scaled distance, reinforcement ratio and concrete strength. The damage diagram is expected to be a help tool for designers to understand the effects of blast loads on slabs.

Mondal, D., et al. (2021). "Evaluation of indigenous aromatic rice cultivars from sub-Himalayan Terai region of India for nutritional attributes and blast resistance." Sci Rep **11**(1): 4786.
Indigenous folk rice cultivars often possess remarkable but unrevealed potential in terms of nutritional attributes and biotic stress tolerance. The unique cooking qualities and blissful aroma of many of these landraces make it an attractive low-cost alternative to high priced Basmati rice. Sub-Himalayan Terai region is bestowed with great agrobiodiversity in traditional heirloom rice cultivars. In the present study, ninety-nine folk rice cultivars from these regions were collected, purified and characterized for morphological and yield traits. Based on traditional importance and presence of aroma, thirty-five genotypes were selected and analyzed for genetic diversity using micro-satellite marker system. The genotypes were found to be genetically distinct and of high nutritive value. The resistant starch content, amylose content, glycemic index and antioxidant potential of these genotypes represented wide variability and 'Kataribhog', 'Sadanunia', 'Chakhao' etc. were identified as promising genotypes in terms of different nutritional attributes. These cultivars were screened further for resistance against blast disease in field trials and cultivars like 'Sadanunia', 'T4M-3-5', 'Chakhao Sampark' were found to be highly resistant to the blast disease whereas 'Kalonunia', 'Gobindabhog', 'Konkanijoha' were found to be highly susceptible. Principal Component analysis divided the genotypes in distinct groups for nutritional potential and blast tolerance. The resistant and susceptible genotypes were screened for the presence of the blast resistant pi genes and association analysis was performed with disease tolerance. Finally, a logistic model based on phenotypic traits for prediction

of the blast susceptibility of the genotypes is proposed with more than 80% accuracy.

Nagashima, Y., et al. (2021). "Synthesis of (12R,13S)-pyriculariol and (12R,13S)-dihydropyriculariol revealed that the rice blast fungus, Pyricularia oryzae, produces these phytotoxins as racemates." Biosci Biotechnol Biochem **85**(1): 134-142.
Synthesis of assumed natural (12R,13S)-enantiomers of pyriculariol (1) and dihydropyriculariol (2), phytotoxins isolated from rice blast disease fungus, Pyricularia oryzae, was achieved using Wittig reaction or microwave-assisted Stille coupling reaction as the key step. The synthesis revealed that the natural 1 and 2 are racemates. Foliar application test on a rice leaf indicated that both the salicylaldehyde core and side chain were necessary for phytotoxic activity. The fungus is found to produce optically active phytotoxins when incubated with rotary shaker, but racemic ones when cultured using an aerated jar fermenter.

Nonaka, M., et al. (2021). "Behavioral and Myelin-Related Abnormalities after Blast-Induced Mild Traumatic Brain Injury in Mice." J Neurotrauma.
In civilian and military settings, mild traumatic brain injury (mTBI) is a common consequence of impacts to the head, sudden blows to the body, and exposure to high-energy atmospheric shockwaves from blast. In some cases, mTBI from blast exposure results in long-term emotional and cognitive deficits and an elevated risk for certain neuropsychiatric diseases. Here, we tested the effects of mTBI on various forms of auditory-cued fear learning and other measures of cognition in male C57BL/6J mice after single or repeated blast exposure (blast TBI; bTBI). bTBI produced an abnormality in the temporal organization of cue-induced freezing behavior in a conditioned trace fear test. Spatial working memory, evaluated by the Y-maze task performance, was also deleteriously affected by bTBI. Reverse-transcription quantitative real-time polymerase chain reaction (RT-qPCR) analysis for glial markers indicated an alteration in the expression of myelin-related genes in the hippocampus and corpus callosum 1-8 weeks after bTBI. Immunohistochemical and ultrastructural analyses detected bTBI-related myelin and axonal damage in the hippocampus and corpus callosum. Together, these data suggest a possible link between blast-induced mTBI, myelin/axonal injury, and cognitive dysfunction.

Ohara, T., et al. (2021). "Structural Alternation of Rice Pectin Affects Cell Wall Mechanical Strength and Pathogenicity for the Rice Blast Fungus under Weak Light Conditions." Plant Cell Physiol.
Pectin, a component of the plant cell wall, is involved in cell adhesion and environmental adaptations. We generated OsPG-FOX rice lines with little pectin due to overexpression of the gene encoding a pectin degrading enzyme (OsPG). Overexpression of OsPG2 in rice under weak light conditions increased the activity of PG, which increased the degradation of pectin in the cell wall, thereby reducing adhesion. Under weak light conditions, the overexpression of OsPG decreased the pectin content and cell adhesion, resulting in abnormally large intercellular gaps and facilitating invasion by the rice blast fungus. OsPG2-FOX plants weaker mechanical properties, and greater sensitivity to biotic stresses than WT plants. However, the expression levels of disease resistance genes in non-infected leaf of OsPG2-FOX were more than twice as high as that of WT and intensity of disease symptoms was reduced, compared to the WT. Under normal light conditions, overexpression of OsPG2 decreased the pectin content, but did not affect cell adhesion and sensitivity to biotic stresses. Therefore, PG plays a role in regulating intercellular adhesion and the response to biotic stresses in rice.

Pathak, A., et al. (2021). "Mask blast with a new chemical logic of amino acids for improved protein function prediction." Proteins.
With the exponential increase in protein sequence data, there is an urgency to acquire a knowledge of function of the millions of sequences, using automated methods with high reliability. Conventional methods for annotating a protein sequence transfer the function of a homologous sequence with known functions based on evolutionary information. Here, we present a newer way of classifying amino acids based on chemical measures and demonstrate that, when integrated with mask BLAST, the chemical properties identified outperform current classifications of amino acids as well as evolutionary measures in function detection.

Perez Garcia, G., et al. (2021). "Laterality and region-specific tau phosphorylation correlate with PTSD-related behavioral traits in rats exposed to repetitive low-level blast." Acta Neuropathol Commun **9**(1): 33.
Military veterans who experience blast-related traumatic brain injuries often suffer from chronic cognitive and neurobehavioral syndromes. Reports of abnormal tau processing following blast injury have raised concerns that some cases may have a neurodegenerative basis. Rats exposed to repetitive low-level blast exhibit chronic neurobehavioral traits and accumulate tau phosphorylated at threonine 181 (Thr181). Using data previously reported in separate studies we tested the hypothesis that region-specific patterns of Thr181 phosphorylation correlate with behavioral measures also previously determined and reported in the same animals. Elevated p-tau Thr181 in anterior neocortical regions and right hippocampus

correlated with anxiety as well as fear learning and novel object localization. There were no correlations with levels in amygdala or posterior neocortical regions. Particularly striking were asymmetrical effects on the right and left hippocampus. No systematic variation in head orientation toward the blast wave seems to explain the laterality. Levels did not correlate with behavioral measures of hyperarousal. Results were specific to Thr181 in that no correlations were observed for three other phospho-acceptor sites (threonine 231, serine 396, and serine 404). No consistent correlations were linked with total tau. These correlations are significant in suggesting that p-tau accumulation in anterior neocortical regions and the hippocampus may lead to disinhibited amygdala function without p-tau elevation in the amygdala itself. They also suggest an association linking blast injury with tauopathy, which has implications for understanding the relationship of chronic blast-related neurobehavioral syndromes in humans to neurodegenerative diseases.

Pokhrel, S., et al. (2021). "Transgenic Rice Expressing Isoflavone Synthase Gene from Soybean Shows Resistance against Blast Fungus (Magnaporthe oryzae)." Plant Dis.
The isoflavones are a group of plant secondary metabolites primarily synthesized in legumes and are known for their role in improving human health and plant disease resistance. The isoflavones, especially genistein, act as precursors for the production of phytoalexins, which may induce broad-spectrum disease resistance in plants. In the present study, we screened transgenic rice lines expressing the isoflavone synthase (GmIFS1) gene from soybean for rice blast (Magnaporthe oryzae) resistance. Two homozygous transgenic lines (I2 and I10), based on single copy gene integration, were identified. The expression of GmIFS1 in transgenic lines was confirmed by qRT-PCR. Genistein was detected in the transgenic lines using LC-MS/MS. Subsequently, the transgenic lines were evaluated against the rice blast pathogen, isolate YJ54 (race IB-54). The results indicated that more than 60% of the plants in both the lines (I2 and I10) showed resistance against the blast pathogen. The progenies of one of the resistant transgenic lines (I10) also showed more than 65% resistance against rice blast. The resistance of these transgenic lines against rice blast may be attributed to the synthesis of isoflavone (genistein) in rice.

Qin, P., et al. (2021). "A Procedure for Inducing the Occurrence of Rice Seedling Blast in Paddy Field." Plant Pathol J **37**(2): 200-203.
Rice blast caused by the filamentous fungus Magnaporthe oryzae, is arguably the most devastating rice disease worldwide. Development of a high-throughput and reliable field blast resistance evaluation system is essential for resistant germplasm screening, resistance genes identification and resistant varieties breeding. However, the occurrence of rice blast in paddy field is easily affected by various factors, particularly lack of sufficient inoculum, which always leads to the nonuniform occurrence and reduced disease severity. Here, we described a procedure for adequately inducing the occurrence of rice seedling blast in paddy field, which involves pretreatment of diseased straw, initiation of seedling blast for the first batch of spreader population, inducing the occurrence of the second batch of spreader population and test materials. This procedure enables uniform and consistent infection, which facilitates efficient and accurate assessment of seedling blast resistance for diverse rice materials.

Sadat, M. A., et al. (2021). "The Membrane-Bound Protein, MoAfo1, Is Involved in Sensing Diverse Signals from Different Surfaces in the Rice Blast Fungus." Plant Pathol J **37**(2): 87-98.
To establish an infection, fungal pathogens must recognize diverse signals from host surfaces. The rice blast fungus, Magnaporthe oryzae, is one of the best models studying host-pathogen interactions. This fungus recognizes physical or chemical signals from the host surfaces and initiates the development of an infection structure called appressorium. Here, we found that protein MoAfo1(appressorium formation, MGG_10422) was involved in sensing signal molecules such as cutin monomers and long chain primary alcohols required for appressorium formation. The knockout mutant (DeltaMoafo1) formed a few abnormal appressoria on the onion and rice sheath surfaces. However, it produced normal appressoria on the surface of rice leaves. MoAfo1 localized to the membranes of the cytoplasm and vacuole-like organelles in conidia and appressoria. Additionally, the DeltaMoafo1 mutant showed defects in appressorium morphology, appressorium penetration, invasive growth, and pathogenicity. These multiple defects might be partially due to failure to respond properly to oxidative stress. These findings broaden our understanding of the fungal mechanisms at play in the recognition of the host surface during rice blast infection.

Schindler, A. G., et al. (2021). "Repetitive blast mild traumatic brain injury increases ethanol sensitivity in male mice and risky drinking behavior in male combat veterans." Alcohol Clin Exp Res.
BACKGROUND: Mild traumatic brain injury (mTBI) is common in civilians and highly prevalent among military service members. mTBI can increase health

risk behaviors (e.g., sensation seeking, impulsivity) and addiction risk (e.g., for alcohol use disorder (AUD)), but how mTBI and substance use might interact to promote addiction risk remains poorly understood. Likewise, potential differences in single vs. repetitive mTBI in relation to alcohol use/abuse have not been previously examined. METHODS: Here, we examined how a history of single (1x) or repetitive (3x) blast exposure (blast-mTBI) affects ethanol (EtOH)-induced behavioral and physiological outcomes using an established mouse model of blast-mTBI. To investigate potential translational relevance, we also examined self-report responses to the Alcohol Use Disorders Identification Test-Consumption questions (AUDIT-C), a widely used measure to identify potential hazardous drinking and AUD, and used a novel unsupervised machine learning approach to investigate whether a history of blast-mTBI affected drinking behaviors in Iraq/Afghanistan Veterans. RESULTS: Both single and repetitive blast-mTBI in mice increased the sedative properties of EtOH (with no change in tolerance or metabolism), but only repetitive blast potentiated EtOH-induced locomotor stimulation and shifted EtOH intake patterns. Specifically, mice exposed to repetitive blasts showed increased consumption "front-loading" (e.g., a higher rate of consumption during an initial 2-h acute phase of a 24-h alcohol access period and decreased total daily intake) during an intermittent 2-bottle choice condition. Examination of AUDIT-C scores in Iraq/Afghanistan Veterans revealed an optimal 3-cluster solution: "low" (low intake and low frequency), "frequent" (low intake and high frequency), and "risky" (high intake and high frequency), where Veterans with a history of blast-mTBI displayed a shift in cluster assignment from "frequent" to "risky," as compared to Veterans who were deployed to Iraq/Afghanistan but had no lifetime history of TBI. CONCLUSIONS: Together, these results offer new insight into how blast-mTBI may give increase AUD risk and highlight the increased potential for adverse health risk behaviors following repetitive blast-mTBI.

Schwarz, M., et al. (2021). "rboAnalyzer webserver: web service for non-coding RNA characterization from NCBI BLAST output." Bioinformatics.
SUMMARY: We present a web service for improving characterization of non-coding RNAs (ncRNAs) from NCBI BLAST outputs, based on a command line application rboAnalyzer. Briefly, the application extends subject sequences of selected high scoring pairs (HSPs) in BLAST output to their plausible full length, and predicts their homology and secondary structures. The aim of the application is to aid to characterize subject RNAs in HSPs that come uncharacterized in BLAST output. The main advantages of the web-server are easy use and interactive analysis with search, filtering and data export options. AVAILABILITY AND IMPLEMENTATION: The web server is freely available at rboanalyzer.elixir-czech.cz. The website frontend is implemented in Elm, while backend is implemented in Python and served by Apache.

Sekine, Y., et al. (2021). "Efficacy of Body Armor in Protection Against Blast Injuries Using a Swine Model in a Confined Space with a Blast Tube." Ann Biomed Eng.
The purpose of this study was to clarify whether or not body armor would protect the body of a swine model using a blast tube built at National Defense Medical College, which is the first such blast tube in Japan. Seventeen pigs were divided into two groups: the body armor group and the non-body armor group. Under intravenous anesthesia, the pigs were tightly fixed in the left lateral position on a table and exposed from the back neck to the upper lumbar back to the blast wave and wind with or without body armor, with the driving pressure of the blast tube set to 3.0 MPa. When the surviving and dead pigs were compared, blood gas analyses revealed significant differences in PaO2, PaCO2, and pH in the super-early phase. All pigs injured by the blast wave and wind had lung hemorrhage. All 6 animals in the body armor group and 6 of the 11 animals in the control group survived for 3 hours after injury. Respiratory arrest immediately after exposure to the blast wave was considered to influence the mortality in our pig model. Body armor may have a beneficial effect in protecting against respiratory arrest immediately after an explosion.

Sembill, S., et al. (2021). "Paediatric chronic myeloid leukaemia presenting in de novo or secondary blast phase - a comparison of clinical and genetic characteristics." Br J Haematol **193**(3): 613-618.
Additional data on blast phase (BP) chronic myeloid leukaemia (CML) in children and adolescents is essential for improving diagnostic and therapeutic approaches of this rare but serious condition. Here, we describe distinct clinical and genetic characteristics of 18 paediatric patients with de novo (n = 10) and secondary (n = 8) BP CML enrolled in the CML-PAED-II trial and registry. Our findings suggest that paediatric patients exhibit a diverse cytogenetic profile compared to adults with BP CML. In addition, patients with de novo BP CML in this cohort presented at a younger age, whereas patients with secondary BP CML more often harboured complex karyotypes.

Shah, M. V., et al. (2021). "Allogeneic stem cell transplant for patients with myeloproliferative neoplasms in blast phase: improving outcomes in the recent era." Br J Haematol.

Shen, J. Z., et al. (2021). "A case of extramedullary T-lymphoblastic blast crisis as an initial presentation of chronic myelogenous leukemia." Int J Lab Hematol.

Sherman, D., et al. (2021). "Dynamic Response of the Thoracolumbar and Sacral Spine to Simulated Underbody Blast Loading in Whole Body Post Mortem Human Subject Tests." Ann Biomed Eng.
Fourteen simulated underbody blast impact sled tests were performed using a horizontal deceleration sled with the aim of evaluating the dynamic response of the spine in under various conditions. Conditions were characterized by input (peak velocity and time-to-peak velocity for the seat and floor), seat type (rigid or padded) and the presence of personnel protective equipment (PPE). A 50% (T12) and 30% (T8) reduction in the thoracic spine response for the specimens outfitted with PPE was observed. Longer duration seat pulses (55 ms) resulted in a 68-78% reduction in the magnitude of spine responses and a reduction in the injuries at the pelvis, thoracic and lumbar regions when compared to shorter seat pulses (10 ms). The trend analysis for the peak Z (caudal to cranial) acceleration measured along the spine showed a quadratic fit ($p < 0.05$), rejecting the hypothesis that the magnitude of the acceleration would decrease linearly as the load traveled caudal to cranial through the spine during an Underbody Blast (UBB) event. A UBB event occurs when an explosion beneath a vehicle propels the vehicle and its occupants vertically. Further analysis revealed a relationship ($p < 0.01$) between peak sacrum acceleration and peak spine accelerations measured at all levels. This study provides an initial analysis of the relationship between input conditions and spine response in a simulated underbody blast environment.

Steel, J. J. (2021). "Genome Analysis of SARS-CoV-2 Case Study: An Undergraduate Online Learning Activity To Introduce Bioinformatics, BLAST, and the Power of Genome Databases." J Microbiol Biol Educ **22**(1).

Sun, Q. N., et al. (2021). "[Removal of Oxytetracycline from Water Using Blast Furnace Slag Loaded Sulfide Nanoscale Zero-valent Iron]." Huan Jing Ke Xue **42**(2): 867-873.
Blast furnace slag loaded with sulfide nano zero valent iron (S-nZVI@BFS) was applied to remove oxytetracycline (OTC) from water. S-nZVI@BFS was synthesized via liquid reduction and characterized using scanning electron microscopy (SEM), X-ray diffraction (XRD), and Brunauer, Emmett and Teller (BET) theory. The effect of reaction time, initial concentration of OTC, initial pH, and coexisting hexavalent chromium[Cr()] were investigated. The results show that Fe and S were successfully immobilized on the surface of S-nZVI@BFS, the specific surface area and pore volume of which increased to 141.986 m(2).g(-1) and 0.388 cm(3).g(-1), respectively, following the loading of nZVI and sulfurization. The utilization rate of the surface active sites of S-nZVI@BFS was improved with an increase of the initial concentration of OTC; the removal rate increased from 20.12 mg.g(-1) to 202.74 mg.g(-1) when the initial concentration of OTC was increased from 10 mg.L(-1) to 100 mg.L(-1). The removal rate decreased with pH, declining from 99.78 mg.g(-1) to 41.12 mg.g(-1) when pH was increased from 3 to 11 due to the switch from Fendon oxidation to electrostatic adsorption. There was notable competition between OTC and Cr() meaning that Cr() can inhibit the removal of OTC, which is dose dependent.

Tahtabasi, M., et al. (2021). "Bomb blast: imaging findings, treatment and clinical course of extremity traumas." BMC Emerg Med **21**(1): 28.
BACKGROUND: To describe the severity and types of blast-related extremity injuries and the presence of accompanying vascular injuries (VI) and amputation, and to identify the associated factors affecting the treatment management and clinical course. METHODS: The study included 101 patients with extremity injuries caused by a bomb explosion. The radiographs and computed tomography angiographies of the patients were evaluated in terms of injury patterns, presence of penetrating fragments and fractures, and localization (upper or lower extremity) and type (open or closed) of injury. The Gustilo-Anderson classification was used for open fractures. According to their severity, open fractures classified as types 1 and 2 were included in Group 1 and those classified as type 3A, 3B and 3C in Group 2. RESULTS: As a result of blast exposure, 101 (57.7%) patients had extremity injuries, of which 76 (75.2%) presented with at least one fracture. Of the total of 103 fractures, nine (8.8%) were closed and 94 (91.2%) were open. Thirty-eight (40.4%) of the open fractures were located in the upper extremities, and 56 (59.6%) in the lower extremities and pelvis. Open fractures were most frequently localized in the femur (n = 20; 21.2%), followed by the tibia (n = 18; 19.1%). The majority of patients with open fractures were in Group 1 (71.4%). The duration of hospital stay was longer in Group 2 (12.1 +/- 5.8 vs. 6.3 +/- 6.7 days, $p < 0.0001$, respectively). Mortality among patients in Group 2 (45.0%) was significantly higher than in Group 1 (8.0%) ($p < 0.0001$). Similarly, the injury severity score (ISS) was higher in Group 2 (median 20 vs. 9, p

< 0.0001). VI was present in 13 (12.9%) of all patients, and amputation in seven (7.9%). CONCLUSION: The presence of severe open fractures, VI, and high ISS score can be considered as important factors that increase morbidity and mortality. In extremity traumas, through the secondary blast mechanism, contaminated-fragmented tissue injuries occur. Therefore, we believe that it will be beneficial to apply damage control surgery in places with low socioeconomic level and poor hygienic conditions.

Tavora, F., et al. (2021). "Shotgun proteomics coupled to transient-inducible gene silencing reveal rice susceptibility genes as new sources for blast disease resistance." J Proteomics **241**: 104223.
A comparative proteomic analysis between two near-isogenic rice lines, displaying a resistant and susceptible phenotype upon infection with Magnaporthe oryzae was performed. We identified and validated factors associated with rice disease susceptibility, representing a flourishing source toward a more resolute rice-blast resistance. Proteome profiles were remarkably different during early infection (12 h post-inoculation), revealing several proteins with increased abundance in the compatible interaction. Potential players of rice susceptibility were selected and gene expression was evaluated by RT-qPCR. Gene Ontology analysis disclosed susceptibility gene-encoded proteins claimed to be involved in fungus sustenance and suppression of plant immunity, such as sucrose synthase 4-like, serpin-ZXA-like, nudix hydrolase15, and DjA2 chaperone protein. Two other candidate genes, picked from a previous transcriptome study, were added into our downstream analysis including pyrabactin resistant-like 5 (OsPYL5), and rice ethylene-responsive factor 104 (OsERF104). Further, we validated their role in susceptibility by Transient-Induced Gene Silencing (TIGS) using short antisense oligodeoxyribonucleotides that resulted in a remarkable reduction of foliar disease symptoms in the compatible interaction. Therefore, we successfully employed shotgun proteomics and antisense-based gene silencing to prospect and functionally validate rice potential susceptibility factors, which could be further explored to build rice-blast resistance. SIGNIFICANCE: R gene-mediated disease resistance is race-specific and often not durable in the field. More recently, advancements in new breeding techniques (NBTs) have made plant disease susceptibility genes (S-genes) a new target to build a broad spectrum and more durable resistance, hence an alternative source to R-genes in breeding programs. We successfully coupled shotgun proteomics and gene silencing tools to prospect and validate new rice-bast susceptibility genes that can be further exploited toward a more resolute blast disease resistance.

W, D. L. (2021). "CORR Insights(R): How Common Are Civilian Blast Injuries in the National Trauma Databank, and What Are the Most Common Mechanisms and Characteristics of Associated Injuries?" Clin Orthop Relat Res **479**(4): 692-693.

Wang, H., et al. (2021). "NF-kappaB and FosB mediate inflammation and oxidative stress in the blast lung injury of rats exposed to shock waves." Acta Biochim Biophys Sin (Shanghai) **53**(3): 283-293.
Blast lung injury (BLI) is the major cause of death in explosion-derived shock waves; however, the mechanisms of BLI are not well understood. To identify the time-dependent manner of BLI, a model of lung injury of rats induced by shock waves was established by a fuel air explosive. The model was evaluated by hematoxylin and eosin staining and pathological score. The inflammation and oxidative stress of lung injury were also investigated. The pathological scores of rats' lung injury at 2 h, 24 h, 3 days, and 7 days post-blast were 9.75+/-2.96, 13.00+/-1.85, 8.50+/-1.51, and 4.00+/-1.41, respectively, which were significantly increased compared with those in the control group (1.13+/-0.64; P<0.05). The respiratory frequency and pause were increased significantly, while minute expiratory volume, inspiratory time, and inspiratory peak flow rate were decreased in a time-dependent manner at 2 and 24 h post-blast compared with those in the control group. In addition, the expressions of inflammatory factors such as interleukin (IL)-6, IL-8, FosB, and NF-kappaB were increased significantly at 2 h and peaked at 24 h, which gradually decreased after 3 days and returned to normal in 2 weeks. The levels of total antioxidant capacity, total superoxide dismutase, and glutathione peroxidase were significantly decreased 24 h after the shock wave blast. Conversely, the malondialdehyde level reached the peak at 24 h. These results indicated that inflammatory and oxidative stress induced by shock waves changed significantly in a time-dependent manner, which may be the important factors and novel therapeutic targets for the treatment of BLI.

Wang, X., et al. (2021). "A Multiobjective Evolutionary Nonlinear Ensemble Learning With Evolutionary Feature Selection for Silicon Prediction in Blast Furnace." IEEE Trans Neural Netw Learn Syst **PP**.
In the blast furnace ironmaking process, accurate prediction of silicon content in molten iron is of great significance for maintaining stable furnace conditions, improving hot metal quality, and reducing energy consumption. However, most of the current research works employ linear correlation coefficient methods to select input features in modeling, which may not fully

take the nonlinear and coupling relationships between features into account. Therefore, this article considers the input feature selection issue of silicon content prediction model from a new perspective and proposes a multiobjective evolutionary nonlinear ensemble learning model with evolutionary feature selection mechanism (MOENE-EFS), in which extreme learning machine is adopted as the base learner. MOENE-EFS takes the input feature scheme of each base learner as well as their network structure and parameters as decision variables and proposes a modified nondominated sorting differential evolution algorithm to optimize two conflicting objectives, i.e., accuracy and diversity of base learners, simultaneously. Through the optimization, a set of Pareto optimal base learners with high accuracy and strong diversity can be obtained. Moreover, different from the linear ensemble methods commonly used in classical evolutionary ensemble learning, this article proposes a nonlinear ensemble method to combine the obtained base learners based on differential evolution. Experimental results indicate that the two proposed strategies, i.e., evolutionary feature selection and nonlinear ensemble, are very effective in improving the accuracy and stability of the prediction model. MOENE-EFS also outperforms the other prediction models in both benchmark data and practical industrial data. Furthermore, analysis on the input features of all Pareto optimal base learners shows that the evolutionary feature selection is capable of selecting essential features and is consistent with human experience, which indicates it is a promising method to deal with the input feature selection issue in silicon content prediction.

Xu, S., et al. (2020). "Helmet chinstrap protective role in maxillofacial blast injury." Technol Health Care.
BACKGROUND: The protective role of helmet accessories in moderating stress load generated by explosion shock waves of explosive devices is usually neglected. OBJECTIVE: In the presented study, the protective role of the helmet chinstrap against the impulse and overpressure experienced by the maxillofacial region were examined. METHODS: The explosion shock wave and skull interaction were investigated under three different configurations: (1) unprotected skull, (2) skull with helmet (3) skull with helmet and chinstrap. For this purpose, a 3D finite element model (FEM) was constructed to mimic the investigated biomechanics module. Three working conditions were set according to different explosive charges and distances to represent different load conditions. Case 1: 500 mg explosive trinitrotoluene (TNT), 3 cm, case 2: 1000 mg TNT, 3 cm, and case 3: 1000 mg TNT and 6 cm distance to the studied object. The explosion effect was discussed by examining the shock wave stress flow pattern. Three points were selected on the skull and the stress curve of each point position were illustrated for each case study. RESULTS: The results showed that the helmet chinstrap can reduce the explosive injuries and plays a protective role in the maxillofacial region, especially for the mandible.

Yang, C. F., et al. (2021). "Clinical significance of blast percentage assessed by bone marrow trephine biopsy and aspirate smear of myeloid malignancies." Pathology.
The blast percentage in bone marrow (BM) can be evaluated through biopsy and aspiration, which is essential for diagnosing myeloid neoplasms especially for dividing myelodysplastic syndrome (MDS)/acute myeloid leukaemia (AML). However, methods for integrating the results of biopsy and smear have yet to be developed, particularly for cases in which the results fall on both sides of the cut-off value (10% or 20%). We studied 188 cases of MDS/AML initially diagnosed during 2011-2015 by using concomitant BM biopsy and aspiration and used different methods to compare the estimated blast percentages. A linear relationship was noted between the blast percentages estimated through biopsy and smear (R(2)=0.765). When the blast percentage was classified into four relevant clinical categories (<5%, 5-9%, 10-19%, and >/=20%), the total concordance between the results of the biopsy and smear was 76.1%. Although the prognostic values obtained through biopsy and smear were not significantly different, using the higher blast percentage estimation by biopsy and smear fared better in classifying patients into categories of 10-19% and >/=20% and demonstrated survival significance in both univariate and multivariate analyses. Subgroup analyses demonstrated that BM blast percentages had no prognostic significance when patients underwent intensive chemotherapy. However, blast percentages of >/=10% indicated poor prognosis for patients receiving only supportive care. In conclusion, most of the clinically relevant categories of blast percentages estimated through concomitant BM biopsy and smear were concordant. When the categories were different, the best prognostic prediction method was to select the higher blast percentage determined through biopsy and smear to diagnose MDS/AML.

Yang, E., et al. (2021). "Evaluation of acute myeloid leukemia blast percentage on MethylC-Capture Sequencing results." Exp Hematol Oncol **10**(1): 26.
Aberrant DNA methylation is often related to the diagnosis, prognosis, and therapeutic response of acute myeloid leukemia (AML); however, relevant studies on the relationship between bone marrow myeloblast percentage and the DNA methylation level in AML

have not been reported. We evaluated the effects of AML blast percentage on DNA methylation level using the MethylC-capture sequencing (MCC-Seq) approach based on next-generation sequencing (NGS) and found that the methylation level of both genome-wide and promoter regions significantly increased when the percentage of AML blasts reached >/= 40%, indicating that an accurate DNA methylation level in cancer cells can be obtained when the bone marrow samples of AML patients have more than 40% myeloblasts.

Zhang, X., et al. (2021). "The Redox Proteome of Thiol Proteins in the Rice Blast Fungus Magnaporthe oryzae." Front Microbiol **12**: 648894.

Redox modification, a post-translational modification, has been demonstrated to be significant for many physiological pathways and biological processes in both eukaryotes and prokaryotes. However, little is known about the global profile of protein redox modification in fungi. To explore the roles of redox modification in the plant pathogenic fungi, a global thiol proteome survey was performed in the model fungal pathogen Magnaporthe oryzae. A total of 3713 redox modification sites from 1899 proteins were identified through a mix sample containing mycelia with or without oxidative stress, conidia, appressoria, and invasive hyphae of M. oryzae. The identified thiol-modified proteins were performed with protein domain, subcellular localization, functional classification, metabolic pathways, and protein-protein interaction network analyses, indicating that redox modification is associated with a wide range of biological and cellular functions. These results suggested that redox modification plays important roles in fungal growth, conidium formation, appressorium formation, as well as invasive growth. Interestingly, a large number of pathogenesis-related proteins were redox modification targets, suggesting the significant roles of redox modification in pathogenicity of M. oryzae. This work provides a global insight into the redox proteome of the pathogenic fungi, which built a groundwork and valuable resource for future studies of redox modification in fungi.

Zhou, M., et al. (2021). "miR-181d/RBP2/NF-kappaB p65 Feedback Regulation Promotes Chronic Myeloid Leukemia Blast Crisis." Front Oncol **11**: 654411.

Background: Chronic myeloid leukemia (CML) is a malignant clonal proliferative disease. Once it progresses into the phase of blast crisis (CML-BP), the curative effect is poor, and the fatality rate is extremely high. Therefore, it is urgent to explore the molecular mechanisms of blast crisis and identify new therapeutic targets. Methods: The expression levels of miR-181d, RBP2 and NF-kappaB p65 were assessed in 42 newly diagnosed CML-CP patients and 15 CML-BP patients. Quantitative real-time PCR, Western blots, and cell proliferation assay were used to characterize the changes induced by overexpression or inhibition of miR-181d, RBP2 or p65. Luciferase reporter assay and ChIP assay was conducted to establish functional association between miR-181d, RBP2 and p65. Inhibition of miR-181d expression and its consequences in tumor growth was demonstrated in vivo models. Results: We found that miR-181d was overexpressed in CML-BP, which promoted leukemia cell proliferation. Histone demethylase RBP2 was identified as a direct target of miR-181d which downregulated RBP2 expression. Moreover, RBP2 inhibited transcriptional expression of NF-kappaB subunit, p65 by binding to its promoter and demethylating the tri/dimethylated H3K4 region in the p65 promoter locus. In turn, p65 directly bound to miR-181d promoter and upregulated its expression. Therefore, RBP2 inhibition resulting from miR-181d overexpression led to p65 upregulation which further forwarded miR-181d expression. This miR-181d/RBP2/p65 feedback regulation caused sustained NF-kappaB activation, which contributed to the development of CML-BP. Conclusions: Taken together, the miR-181d/RBP2/p65 feedback regulation promoted CML-BP and miR-181d may serve as a potential therapeutic target of CML-BP.

Zhou, X., et al. (2021). "Complete nucleotide sequence of a novel botourmiavirus from the rice blast fungus Magnaporthe oryzae isolate SH05." Arch Virol.

A novel mycovirus with the proposed name "Magnaporthe oryzae botourmiavirus 9" (MoBV9) was found in the rice blast fungus Magnaporthe oryzae isolate SH05. The virus has a positive single-stranded RNA genome of 2,812 nucleotides and contains a single open reading frame predicted to encode an RNA-dependent RNA polymerase that is closely related to those of some unclassified viruses of the family Botourmiaviridae, including Plasmopara viticola lesion associated ourmia-like virus 44, Plasmopara viticola lesion associated ourmia-like virus 47, and Cladosporium uredinicola ourmiavirus 1. Genome sequence comparisons and phylogenetic analysis supported the notion that MoBV9 is a new member of the family Botourmiaviridae.

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