



GENETIC CHARACTERIZATION AND POPULATION STRUCTURE OF INDIAN RICE CULTIVARS

*Dr. Komal Lata Nagpal and **Showkeen Ahmad Gulzar

*Associate Professor, Department of Botany, SunRise University, Alwar, Rajasthan (India)

**Research Scholar, Department of Botany, SunRise University, Alwar, Rajasthan (India)

**e-mail- gulshowkeen838@gmail.com

Abstract: Using genetic engineering techniques rice can produce beta-carotene (pro-Vitamin A) in the seed endosperm tissue as for example in Golden Rice (has a gene that produces vitamin A). Although the precise amount of beta-carotene that Golden Rice variety can produce is not clear, the fact remains that it could still be beneficial to millions of people with Vitamin-A deficiency that could possibly lead to blindness. Similarly research is underway to fortify rice with iron using molecular assisted breeding techniques as it could help reduce anemia in women. These efforts are particularly important, as rice being a staple food is the best mechanism to deliver nutrients to the needy, but nevertheless should not be seen as a substitute to an otherwise balanced diet. Rice milk, rice flour and rice grain cereals, are specially benefited with the emphasis on nutritional fortification of rice.

[Nagpal, K.L. and Guljar, S.A. **GENETIC CHARACTERIZATION AND POPULATION STRUCTURE OF INDIAN RICE CULTIVARS**. *N Y Sci J* 2022;15(5):1-4]. ISSN 1554-0200(print);ISSN 2375-723X (online) <http://www.sciencepub.net/newyork>. I. doi:10.7537/marsnys150522.01.

Keywords: Rice, India, Genetic, Character.

India:

Biotechnology plays an important role in the field of agriculture. Biotechnology in modern parlance especially with regard to plants and crops means understanding genetic nuances at the DNA level which is a kind of genetic engineering. Crops are bred by pollination, cross pollination and molecular techniques. Molecular techniques genetically modify the crops. Rice is the first food crop which has genome sequence readily available, and so from a biotech point of view it is possible to identify the genes in rice that are responsible for productivity, environmental adaptation and resistance to stress. In the 1980s, tissue culture techniques were adopted for producing better rice varieties. Then Agro bacterium tumefactions was used to implant foreign DNA in rice plants, which helped not only in improving the genetic make-up of different varieties of rice, but also helped to study the molecular biology of rice.

There are several ways to alter presently existing rice varieties. Now, marker-assisted methods can be used to select the wanted genes within a species or in transgenic alien genes can be used to get particular traits. Before molecular markers came on the scene, the evaluation of genetic factors associated with dominant traits was done using biometrical methods. The advantage with rice is that, since rice whole genome sequence is readily available it can be

used to identify genes that are responsible for significant phenotypic variation.

Super rice Scientists at the International Rice Research Institute in the Philippines have developed "Super Rice" a high-yielding rice of the future which increases harvests by 25 percent. It is far less bushy as each plant consists of only 10 stems or so in comparison with 20 to 25 of the traditional rice plant. Besides that, a single super rice plant can produce 2,500 grains of rice compared to 1,500 grains from conventional plant.

Herbicide Tolerance Rice: Repeated use of herbicides in rice fields often leads to the growth of herbicide resistant weeds. There are hundreds of these weeds and especially *Oryza rufipogon* and *Echinochloa crus-galli* cause the maximum problems. This means that, the rice farmer has to alternatively use several herbicides or mixtures of different herbicides and there was no guarantee that these herbicides would be harmful to the rice plant as well. As herbicide tolerance was often due to a single gene, the idea has been to create rice plants with the mammalian P450 enzyme that could detoxify several of these herbicides and make these rice plants tolerant to herbicides. Now, a transgenic rice plant with human gene CYP2B6 not only give good yields but also shows high herbicide tolerance capacity. They could detoxify several herbicides such as thiocarbamates, oxyacetamides and

2, 6-dinitroanilines. To the farmer this is extremely beneficial in terms of labor costs saved.

Insecticides resistance rice variety: Insects are another cause of worry in rice fields. Bt proteins have been successful against some insect varieties but significantly have failed against building resistance to larvae of *Scirpophaga incertulans* that very much affects Asian rice fields. To solve this problem of *S. incertulans* the introduction Bt genes into rice is reckoned as a possibility so that they can produce toxins that combat the insects. Like all proteins, Bt toxins are coded for by genes (stretches of DNA found in the cells) and only a single gene encodes each Bt toxin. Other pests that need to be countered are yellow stem border caterpillar, and *Chilo suppressalis* (found in temperate areas). So bio-technology helps in avoiding the use of insecticides that harm both the environment and the farmer.

Rice (*Oryza sativa* L.) is one of the most extensively cultivated cereal crops in the world spreading across a wide range of geographical, ecological and climatic regions. High genotypic and phenotypic diversity exists, and about 1,20,000 different accessions are reported in rice as a consequence of varied adaptations (Das et al. 2013). Large collections of rice germplasm consisting of cultivars of indica, japonica and javanica sub-species along with landraces are conserved in global gene banks (Khush 1997; Tanksley and McCouch 1997; Lu et al. 2005; Garris et al. 2005). Wild accessions of rice are potential reservoir of valuable genes that could be exploited for crop improvement programs (Brar and Khush 1997). There was a significant reduction in genetic diversity during the course of domestication from wild relatives to cultivated rice (Brar and Khush 2003; Sun et al. 2001). In spite of the richness of genetic resources, only a small proportion has been utilized in breeding programs, resulting in high genetic similarity in commercial rice cultivars (Das et al. 2013). To meet the future requirements of food, the yield potential of the varieties has to be improved, but it is difficult due to narrow genetic base of the popular varieties. To break the yield plateau, it is essential to broaden the genetic base of the varieties by introgressions from distant or newer gene pools. Assessment and introgression of the available genetic diversity in germplasm resources is required for detection of novel genes or QTLs for agronomically important traits.

Knowledge of the genetic diversity and genetic relationships between germplasm accessions is the basic foundation for crop improvement programs (Thomson et al. 2008). Domestication and artificial selection pressure changed the genome compositions and population structure of the available germplasm resources (Huang et al. 2012; Yadong et al. 2012). In

depth analysis of population structure is required before initiating any breeding program to get targeted improvement in the traits. There are several ways for estimation of diversity in germplasm viz, evaluation of phenotypic variation, biochemical and DNA polymorphisms. However, both phenotypic and biochemical characterizations are not much reliable because they are environmentally influenced, labor demanding, numerically and phenologically limited, but DNA-based molecular markers are ubiquitous, repeatable, stable and highly reliable (Virk et al. 2000; Song et al. 2003). Among the several classes of available DNA markers, microsatellite or simple sequence repeat (SSR) markers are considered the most suitable due to their multi-allelic nature, high reproducibility, codominant inheritance, abundance and extensive genome coverage (Orjuela et al. 2010). In rice, high-density SSR map with genome coverage of approximately 2 SSRs per centimorgan (cM) (McCouch et al. 2002) and a universal core genetic map (UCGM) (Orjuela et al. 2010) were reported. These maps can help in accurately assessing genomewide diversity. Many researchers evaluated genetic diversity of Indian rice germplasm using other SSRs, but SSRs from UCGM have not been used for studying diversity previously (Saini et al. 2004; Jain et al. 2004; Ram et al. 2007; Sundaram et al. 2008; Kumar et al. 2010; Sivaranjani et al. 2010; Vanniarajan et al. 2012; Yadav et al. 2013). Studies were also conducted globally on classifying rice genotypes based on their genetic diversity and population structure using molecular markers (Garris et al. 2005; Zhao et al. 2010; Jin et al. 2010; Li et al. 2010; Zhang et al. 2011; Wang et al. 2014; Raimondi et al. 2014; Shinada et al. 2014). Most of the diversity studies in rice mainly focused on clustering within cultivated rice group and only few studies were reported using accessions from wild rice species in diversity analysis (Ni et al. 2002; Ravi et al. 2003; Caicedo et al. 2007; Ram et al. 2007). The present study was aimed at investigating the diversity and relationship among selected wild rice accessions and cultivars using SSR markers for the identification of diverse genotypes and polymorphic markers for further utilization in inter-specific breeding programs, and for the development CSSL population from elite/wild crosses.

Genetically Modified Rice

In the long run, biotechnology aims to increase the productivity of rice farming through introduction of transgenic traits and help the developing world prepare adequately for food security. In this regard agronomists use the genetic make up of rice to plan its future evolutionary course. Although advances in plant genetic engineering may

offer even better opportunities for the rice plant, the pace of development of new technologies in rice farming will depend on how the new traits in the rice will be commercially beneficial to the farming community.

Natural rice also known as *Oryza sativa* when introduced with foreign gene is known as genetically modified rice. It's the transgenic variety of rice better in many ways as compared to the natural rice. Different varieties of GM rice have been produced. Rice is the staple food of Asia which includes countries like Bangladesh i.e. the largest producer of rice; half of the world's population feeds on rice. Genes are inserted in edible parts of rice to produce beta-carotene which further produces pro-vitamin A. The advancement in the field of biotechnology another variety of transgenic rice was produced known as golden rice 2, having 23 times more beta-carotene than the original golden rice. It was a breakthrough in the field of biotechnology.

Salinity stress responsive mechanism in rice

Salt tolerance is an important constrain for rice, which is generally categorized as a typical glycophyte. Soil salinity is one of the major constraints affecting rice production worldwide, especially in the coastal areas. Susceptibility or tolerance of rice plants to high salinity is a coordinated action of multiple stress responsive genes, which also interacts with other components of stress signal transduction pathways. Salt tolerant varieties can be produced by marker-assisted selection or genetic engineering by introducing salt-tolerance genes. In this review, we have updated on mechanisms and genes which can help in transferring of the salt tolerance into high-yielding rice varieties. We have focused on the need for integrating phenotyping, genomics, metabolic profiling and phenomics into transgenic and breeding approaches to develop high-yielding as well as salt tolerant rice varieties.

World population is increasing rapidly by every passing year and there will be a need to produce 87% more of what we are producing today especially food crops such as rice, wheat, soy and maize by 2050 (Kromdijk and Long, 2016). However, abiotic stress, which includes salinity, drought, heat and cold, critically threatens crop production and causes significant yield loss in large areas (Pareek et al., 2010, Mantri et al., 2012). Among these, soil salinity is one of the major environmental constraints to crop production and is expected to increase due to global climate changes and as a consequence of many irrigation practices. Salinity can be termed as severe abiotic stress which includes all the problems due to salts primarily by an abundance of sodium chloride from natural accumulation or irrigation (Flowers and

Flowers, 2005). More than 8×10^8 hm² land throughout the world is affected by salinity (FAO, 2008). An average of 2 000 hm² irrigated land across 75 countries has been degraded by salt every year according to a study by Economics of Salt-Induced Land Degradation and Restoration (unu.edu/media-relations/releases). Salinity can be associated with higher sea levels as it brings saline water further inland and exposes more rice growing areas to salty condition (irri.org/news/hot-topics/rice-and-climate-change). Floodwater with the electric conductivity level more than 2 dS/m leads to yield loss up to 1 t/hm² in rice (Asch and Wopereis, 2001). Millions of hectares in South and Southeast Asia, which are well suited for rice production, are left uncultivated or grown with very low yields because of salinity (knowledgebank.irri). Accretion of salts in the soil surface is caused by different factors in different geological and climatic regions (Reynolds et al., 2001).

References:

- [1]. Adem, G. D., Roy, S. J., Zhou, M., Bowman, J. P., & Shabala, S. (2014). Evaluating contribution of ionic, osmotic and oxidative stress components towards salinity tolerance in barley. *BMC plant biology*, 14, 113. <https://doi.org/10.1186/1471-2229-14-113>
- [2]. Aebi, H. (1983). Catalase In: Methods of enzymatic analysis (Ed. H.U. Bergmeyer). Verlag Chemie. 2: 673-684.
- [3]. Ahmadikhah A., Nasrollanejad S., Alishah O. Quantitative studies for investigating variation and its effect on heterosis of rice. *Int. J. Plant Prod.* 2008;2:297–308. [[Google Scholar](#)]
- [4]. Ahmadizadeh, M., Vispo, N. A., Calapit-Palao, C. D. O., Pangaan, I. D., Viña, C. D., & Singh, R. K. (2016). Reproductive stage salinity tolerance in rice: a complex trait to phenotype. *Indian Journal of Plant Physiology*, 21(4), 528-536.
- [5]. Akbar M, Yabuno T, Nakao S. Breeding for Salineresistant Varieties of Rice: I. Variability for Salt Tolerance among Some Rice Varieties. *Jpn J Breed.* 1972; 22:277-284.
- [6]. Akbar M, Yabuno T. Breeding for saline-resistant varieties of rice. III. Response of F1 hybrids to salinity in reciprocal crosses between Jhona 349 and Magnolia. *Jpn J Breed.* 1975; 25:215-220.

- [7]. Akita S, Cabuslay G. Physiological basis of differential response to salinity in rice cultivars. *Plant and Soil* 123 pp: 277-294.
- [8]. Akita, S., & Cabuslay, G. (2004). Physiological basis of differential response to salinity in rice cultivars. *Plant and Soil*, 123, 277-294.
- [9]. Akita, S., & Cabuslay, G. S. (1990). Physiological basis of differential response to salinity in rice cultivars. In *Genetic Aspects of Plant Mineral Nutrition* (pp. 431-448). Springer, Dordrecht.
- [10]. Akita, S. and Cabuslay, G. 1990. Physiological basis of differential response to salinity in rice cultivare. *Plant and Soil*, 123: 277-294.
- [11]. Al Kharusi, L., Al Yahyai, R., & Yaish, M. W. (2019). Antioxidant response to salinity in salt-tolerant and salt-susceptible cultivars of date palm. *Agriculture*, 9(1), 8.
- [12]. Ali G, Srivastava PS, Iqbal M. Proline accumulation, protein pattern and photosynthesis in regenerants grown under NaCl stress. *Biol Plant*. 1999; 42:89-95.
- [13]. Ali MN, Ghosh B, Gantait S, Chakraborty S. Selection of rice genotypes for salinity tolerance through morphobiochemical assessment. *Rice Sci*. 2014a; 21:288-298.
- [14]. Ali MN, Yeasmin L, Gantait S, Goswami R, Chakraborty S. Screening of rice landraces for salinity tolerance at seedling stage through morphological and molecular markers. *Physiol. Mol. Biol. Plants*. 2014b; 12(3):1-10.

5/12/2022