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A BRIEF REVIEW ON GENETIC DIVERGENCE IN RICE FOR YIELD CONTRIBUTING TRAITS AND QUALITY PARAMETERS

^{*}M.Sudharani¹ A.Prasanna Rajesh² V.Jayalakshmi³ and K.Rajyalakshmi⁴

¹Corresponding Author, Scientist (Genetics & Plant Breeding) Seed Research and Technology Centre, Rajendranagar,Hyderabad-30 . E.Mail: <u>madugula.sudharani@yahoo.com</u>

²Scientist (Plant Breeding), Agricultural Research Station, Kadiri

³Senior Scientist (Plant Breeding), Regional Agricultural Research Station, Nandyal

⁴Senior Research Fellow, Seed Research and Technology Centre, Rajendranagar, Hyderabad- 30

Breeding rice varieties with preferred grain quality features has become second most important objective next to yield. The grain quality features are important for all people involved in production, processing and consumption. The significance of grain quality varies depending upon the requisites established by the international market, ethnic customs, uses *etc*. A given community may demand a certain rice quality that would be unacceptable to another. The preferences and tastes of one country differ from those of another country and even within the same country, distinct appreciations of quality may exist.

Different characteristics of grain quality in rice largely determine the products market price and acceptability. If the consumer does not like the flavor, texture, aroma, appearance or ease of cooking in a new variety, whatever the other outstanding traits it may possesses loses its value. With the improvement of rural infra structure, economic globalization and changes in acquisitive power, dietary patterns and working conditions, consumers have become more demanding with respect to grain quality and is willing to pay higher prices for a given quality and type of rice. For the rice market, appearance, translucence and degree of whiteness are very important. Industries and mills pay special attention to the percentage of whole grains, and food processors emphasize characteristics associated with food processing. For nutritionists, nutritional quality is the most relevant attribute and finally consumers demand a diversity of rice types. Despite the development of varieties with good grain quality having been an important objective of improvement programmes today, its relevance is much greater, because varieties with good grain quality hampers the acceptance and spread of the modern high yielding varieties, quality improvement needs special emphasis since last decades.

Rice quality comes from a polygenic group of traits that are affected by environmental factors, crop management and the resulting interactions among these. Grain quality can be considered as physical, chemical, cooking and nutritional quality groups. Physical quality includes grain length, grain breadth and length/breadth ratio, chemical quality includes gel consistency, alkali value and amylose content, cooking characters are kernel length and kernel breadth after cooking, kernel elongation ratio, volume expansion ratio and water uptake, whereas nutritional quality includes protein and other micronutrients like iron and zinc.

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In order to develop better or good quality varieties with high yield potential, information regarding the type of parents to be used for crossing purpose is essential. The extent of variation among the available germplasm gives an indication about the variability for different yield and quality traits. Genetic divergence of various yield components and quality traits were studied by several investigators. The literature pertaining to previous research efforts for yield and quality characters are presented as under.

Genetic improvement mainly depends upon the amount of genetic variability present in the population. The estimation of genetic diversity between different genotypes in the crop of interest is the first and foremost process in any plant breeding programme. The D^2 technique based on multivariate analysis developed by Mahalanobis (1928) is the most potent technique for quantifying the degree of genetic diversity among the genotypes, which in turn is much helpful in selecting parents for hybridization. Several workers studied genetic divergence previously. A brief review of work done is given below.

Many of the workers in their studies on genetic divergence found that there was no association between geographical distribution of genotypes and genetic divergence. Selvakumar *et.al.* (1989), Vivekanandan and Subramanian (1993), Murthy and Arunachalam (1996), Patil *et.al.* (2005), Raju *et.al.* (2004), Rajesh *et.al.* (2010) *etc.*

Chuahan and Chauhan (1994) studied genetic divergence among 44 breeding lines of rainfed upland rice employing Mahalanobis D^2 analysis. Based on eleven characters, the genotypes were grouped into twelve clusters. The characters *viz.*, 1000 grain weight followed by days to fifty percent flowering, panicle weight and spikelets per panicle contributed maximum towards genetic divergence.

Singh *et.al.* (1996) estimated genetic diversity in 40 genotypes of scented and fine rice varieties based on ten characters. A total of six clusters were observed and the character grain yield followed by plant height contributed major portion of genetic divergence. Bansal *et.al.* (1999) studied genetic diversity in 34 rice stocks and reported that there was no parallelism between genetic diversity and geographic diversity. All the entries were differentiated into 15 clusters based on morphological and quality characters.

According to Kole (2000), grain length, panicle number, 500 grain weight, flag area and days to 50per cent flowering contributed to the total diversity. Based on genetic divergence, twenty aromatic rice genotypes were clustered into four based on fifteen yield and quality traits. Roy and Das (2000) estimated genetic distance among 28 hill rice genotypes and divided into 6 clusters. The traits number of grains per panicle, effective panicles per plant and grain yield per plant contributed maximum towards total genetic divergence.

Shanmugasundaram *et.al.* (2000) conducted an experiment to study genetic distances among 38 rice cultivars and grouped them into 4 clusters based on ten morphological traits. The characters *viz.* plant height, panicle length, grain yield and tiller number were the major contributors to the total genetic divergence. According to Babu *et.al.* (2003), the trait days to 50 per cent flowering, followed by plant height, panicle length and 100 grain weight contributed more towards genetic divergence. The thirty three rice genotypes were grouped into ten clusters based on eight characters.

Vanaja *et.al.* (2003) conducted an experiment with 56 rice genotypes and grouped them into nine clusters based on genetic distance and concluded that there was no relationship between clustering pattern and geographic distribution and at the same time the relationship between genetic divergence and geographic distribution also exists to some extent. Cheema *et.al.* (2004) studied genetic divergence in 30 rice collections of Pakistan. According to Anderson's Metroglyph technique the genotypes were grouped into 11 groups based on 7 characters. They suggested that hybridization between group-II would give better rice varieties. Nayak *et.al.* (2004) assessed nature and magnitude of genetic divergence in 200 scented rice genotypes for 10 morphological characters. This investigation revealed that there was no relationship between clustering pattern and geographic distribution. The characters grain length (31.5%) followed by days to 50 per cent flowering (31.2%) contributed maximum towards total genetic diversity.

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A total of 124 accessions of rice collected from various parts of Pakistan were evaluated for seven quantitative and eight qualitative characters by Zafar *et.al.* (2004) and the results revealed that a wide agro-ecological range exhibited significant variation for quantitative and qualitative traits through out Pakistan. A total of six accessions (Pak 2950, Pak 3311, Pak 3169, Pak 3291, Pak 3310 and Pak 2958) were selected based on their performance and suggested for exploitation in breeding programs.

Awasthi *et.al.* (2005) evaluated twenty one aromatic rice genotypes for nineteen characters and grouped them into six clusters. The traits number of grains per panicle, grain yield per plant, days to 50per cent flowering, leaf length and leaf breadth showed high percent of contribution towards genetic divergence.

Chand *et.al.* (2005) evaluated nineteen genotypes of Aman rice and observed considerable diversity both within and between clusters. Out of 12 characters studied, 1000 grain weight followed by plant height, panicle length and grain length were the major traits contributing to divergence. In a study conducted by Deepa Sankar *et.al.* (2005), 34 genotypes were grouped into seven clusters based on eight characters. The characters contributed towards genetic diversity were days to 50 per cent flowering, single plant yield and grains per panicle.

Patil *et.al.* (2005) conducted a study on genetic divergence with 135 aromatic traditional rice accessions and grouped into ten clusters based on genetic distances. Pradhan and Mani (2005) estimated genetic divergence among 38 bastmati lines for 12 characters by using Mahalanobis D^2 analysis. The genotypes grouped into ten clusters. They found that none of the clusters was superior with respect to all the characters studied. Days to 50 per cent flowering alone contributed 67.85% to the total divergence.

Forty tall *indica* rice genotypes were studied by Senapati and Sarkar (2005) and results revealed that majority of genotypes (30) were included in cluster I only. The characters namely panicle number per hill, panicle length, sterility parentage, yield per plot and 1000 grain weight were the chief contributors towards genetic divergence and they suggested that these characters must be given importance while selecting parents in crossing pogramme as well as selection of seggregants in succeeding generations.

Deepak Naik *et.al.* (2006) found appreciable amount of genetic diversity in the 50 genotypes studied. The fifty genotypes were grouped into seven clusters. The cluster VI had the highest mean for grain yield per plant and for biological yield per plant.

Ravindra Babu *et.al.* (2006) studied genetic divergence using quality characters and found that the characters water uptake, gel consistency and head rice recovery percentage contributed maximum towards genetic divergence. Shukla *et.al.* (2006) reported that harvest index contributed highest to genetic divergence followed by biological yield per plant, grain number per panicle and 100 grain weight whereas panicle length had not contributed towards genetic divergence.

Ramesh Chandra *et.al.* (2007) assessed nature and magnitude of genetic divergence in 57 genotypes of rice germplasm lines, based on 14 agro morphological traits. The grouping by Tocher's method showed three multi genotypic and two mono-genotypic clusters. The clustering patterns of genotypes were quite at random indicating that the geographical origin and genetic diversity were not related .The characters such as grain Length/breadth ratio, 1000 grain weight, grain length and grain yield and biological yield contributed more towards genetic divergence.

Vimla Bisht (2007) studied genetic divergence among the land races of Uttarakhand and found that the characters like ear bearing tillers (33.36%), plant height (21.62%), panicle length (18.61) and spikelet number per panicle (9.19%) prominently contributed to total genetic divergence.

Arun Sharma *et.al.* (2008) revealed that there is no relationship between clustering pattern and geographical distribution of genotypes. On the basis of divergence the crosses between kaojaohawn, basmati safaid-187, KCN - 80152, aborbora and hara was suggested.

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A collection of 200 salt tolerance rice landraces was assessed for genetic diversity using 11 quantitative agromorphological characters by Nguyen Thi Lang et.al. (2008). Cluster analysis generated by UPGMA grouped the 200 rice landraces into six clusters. Although they were collected from different areas, they were grouped together suggesting that they may have probably originated from the same population.

Fifty-two traditional aromatic rice genotypes of India were studied by Prasad and Agarwal (2009) for genetic divergence and reported that characters namely grain maturity duration, plant height and panicle weight contributed maximum towards divergence. On the basis of D^2 inter cluster distance the cross namely; Lalmati (cluster VI) / HUR-BL-6AR (cluster VII) exhibiting contrasting differences for a large number of traits is expected to result in desirable segregants on hybridization.

Sabesan et.al. (2009) calculated percentage contribution of each character towards genetic divergence. With 42.71 per cent contribution, the number of grains per panicle followed by days to first flower (25.62%) were the major force of discrimination among the genotypes tested.

Shahidullah et.al. (2009) grouped 40 genotypes composed of 32 local aromatic, 5 exotic aromatic and three nonaromatic rice cultivars into 6 clusters based on 10 phenological characters using multivariate analysis. They found wider genetic diversity among the genotypes of different groups than those in the same group. Forty one promising rice varieties of eastern India were evaluated for physico- chemical and cooking characters to study the diversity pattern among the genotypes by Subudhi et.al. (2009) and reported that the characters alkali spreading value, kernel length after cooking, amylose content and kernel breadth together accounted for 83.78 per cent to the total divergence Iftekharuddaula et.al. (2010) found that the characters grains per panicle, spikelets per panicle, flag leaf area, 1000 grain weight and plant height were the potential contributors to genetic divergence. Rajesh et.al. (2010) studied genetic divergence in 29 genotypes of rice and found that the mode of distribution of genotypes from different geographic regions into various clusters was at random indicating that the geographic diversity and genetic diversity were not related. The characters days to 50per cent flowering (25.61%), grain yield per plant (25.12%) and plant height (11.57%) contributed maximum towards genetic divergence.

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