



Genetic Divergence in Rice

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ABSTRACT

Genetic divergence study of 72 genotypes of rice for 10 agronomic and grain quality traits led to their grouping into 9 clusters. Grouping of the genotypes evolved from the same location into different clusters indicated the presence of good amount of genetic diversity. Highest contribution to the genetic diversity was through 100-grain weight followed by Kernel length and grains per panicle. The clusters VII and IX were highly divergent. The other clusters with moderate divergence and having few genotypes were III and VI. Based on the inter-cluster distance, mean performance and clustering pattern, hybridization between, JGL 1806, JGL 384, JGL 3947, JGL 1881, INRC - 1711, JGL 2984 and JGL 2948 is likely to give recombinants having high yield potential and high grain quality

Key words : Genetic divergence, Quality, Rice.

Genetic variability is the prerequisite for making the progress in crop improvement. As such, inclusion of genetically divergent parents in the breeding programmes is essential to create new genetic variability in any crop. Earlier workers showed the importance of study of genetic divergence for yield and yield attributes in the germplasm lines acquired from other places, which generally have lesser adaptability to new location. Studies in the germplasm lines developed locally by using new introductions are meagre. Therefore, the information on genetic divergence for yield characters would help the plant breeder in choosing right parents for breeding programme aimed at yield improvement of highly adaptable varieties. Similarly, with growing demand for non-Basmati quality rices, germplasm studies for quality characters would be of immense value to aid in selection of parents to create further variability. In the present investigation, an attempt was made to classify and to know the genetic diversity for certain yield and quality traits for use in hybridization programme to improve yield and quality of locally adaptable varieties.

MATERIAL AND METHODS

Seventy-two rice genotypes evolved at jagtial were grown in a randomized block design with two replications during kharif 2003. Each genotype was raised in 1 row of 4.5m length at a spacing of 20 X 15 cm and the recommended doses of fertilizers at the rate of 100 kg N, 60 kg P₂O₅ and 40 kg K₂O ha⁻¹ was followed. Observations were recorded on days to 50% flowering, plant height, productive fillers per plant, panicle length filled grains

per panicle, 100 grain weight, kernel length (L), Kernel breadth (B), kernel L/B, ratio and grain yield per plant. The mean values were subjected to analysis of variance and then to Mahalanobis, (1936) D² statistic to measure genetic distance. The genotypes were grouped using Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

Analysis of variance revealed significant genotypic difference for all the ten characters studied. Out of the 9 clusters obtained by grouping 72 genotypes based on relative magnitude of D² values, cluster I was the largest one with 25 genotypes. Cluster V, VI and II had 11, 9 and 8 genotypes respectively, while the clusters III and VII were two-genotype clusters (Table 1). The clustering pattern indicated existence of significant amount of variability, which was confirmatory with the findings of Vairavan et al. (1979), Mahajan et al. (1979), Soni et al. (1999) and Jha et al. (1999).

Maximum intra-cluster distance (Table 2) was observed in cluster VI (71.96), followed by II (57.23) and VII (48.94). Thus, selection of genotypes based on high per se and other desirable traits from cluster I which had maximum number of genotypes (25) might be fruitful to generate the breeding material.

Based on the inter-cluster distance, clusters IX and VII having four and two genotypes respectively were observed to be highly divergent as compared to others. Cluster VII with 2 genotypes (JGL 3947 and INRC 1711) was separated by higher genetic distance from all the clusters except from

Table 3. Cluster means for 10 different character in 72 rice genotypes

Cluster	Days to 50% flowering	Plant height (cm)	Productive tillers plant ⁻¹	Panicle length (cm)	Filled grains panicle ⁻¹	100 grain weight (g)	Kernel length (mm)	Kernel breadth (mm)	Length / breadth ratio	Grain yield plant ⁻¹
I	110.60	89.56	8.94	21.96	241.28	1.52	5.54	1.55	3.57	21.37
II	107.18	93.37	10.18	21.78	195.87	1.67	6.00	1.63	3.68	18.23
III	106.00	78.25	9.00	20.15	92.25	2.04	5.49	1.72	3.19	12.15
IV	100.25	93.25	7.75	20.36	207.25	1.53	5.36	1.58	3.39	15.70
V	118.27	93.00	9.59	22.90	174.22	1.72	5.56	1.56	3.57	18.31
VI	115.56	98.61	9.16	22.45	177.38	1.98	6.26	1.61	3.89	21.60
VII	116.25	147.00	9.75	24.60	190.25	2.13	6.41	1.71	3.73	30.25
VIII	101.07	106.64	9.21	23.55	134.92	2.10	6.44	1.67	3.86	18.32
IX	101.37	88.62	8.75	24.56	104.62	2.42	7.24	1.64	4.13	10.30

VI. Another cluster IX in which four genotypes (JGL 2683, JGL 2984, JGL 2948 and JGL 3144) were included was divergent from the clusters VII, IV, I and V. Hence, hybridization between genotypes selected from these two clusters (VII and IX) with genotypes of other clusters should result in expression of hybrid vigour in higher magnitudes and production of large number of desirable recombinants for both yield and quality. Hybridization between genetically distant genotypes to generate promising breeding material was suggested frequently by many workers (Vivekanandan and Subramanian, 1993 and Roy and Panwar, 1993).

A wide range of variation was registered in the cluster means for most of the characters studied except for productive tillers per plant (Table 3). Higher genetic differences were observed in case of days to 50% flowering, plant height, filled grains per panicle, 100-grain weight, Kernel length and grain yield per plant, whereas for productive tillers per plant, the variation was low. Similar results were also earlier reported by Raju *et al.* (2002). The genotypes included in the cluster I exhibited average performance for most of the characters and were characterized by higher number of filled grains per panicle. The genotypes (JGL 326, JGL 1806 and JGL 384) of cluster I possessed higher number of grains per panicle. Cluster IX contained genotypes (JGL 2984, JGL 2948) of higher kernel length, kernel L/B ratio and 100 grain weight. The genotype, INRC 1711 of cluster VII had highest productive tillers per plant and grain yield per plant. Parents having many

desirable traits might be considered as good parents to create further variability for the traits under studies. Hence promising genotypes selected from distant clusters viz., JGL 326, JGL 1806 and JGL 384 with higher number of grains per panicle of cluster I, JGL 3947 and INRC 1711 with higher grain yield per plant and productive tillers per plant of cluster VII, JGL 2948 and JGL 2984 with higher Kernel length, grain yield per plant and 100 grain weight of cluster IX can be considered as better parents for hybridization and to create variability in desired direction. Similarly, the entries viz., JGL 1799 and JGL 1881 are also of better choice for improvement grain characters.

The study indicated presence of sufficient amount of genetic diversity though they were developed at Jagtial.

Consideration of relative contribution of individual traits to the genetic divergence revealed that 100 grain weight (Das and Borthakur, 1973), followed by kernel length (Ratho, 1984), contributed maximum, and less contribution to the diversity was through productive tillers per plant.

Crossing among divergent parents having desirable traits is most likely to produce better hybrids and desirable recombinants. The greater distance between the clusters (VII, IX and I) indicates higher genetic diversity between them.

Based on the inter-cluster distance and high per se for other desirable attributes associated, the parents as indicated in the discussion are expected to give promising segregants for grain yield and quality in segregating generations.

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