

Genetic Divergence Studies for Yield and Quality Attributes in Rice

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ABSTRACT

Genetic divergence was assessed among twenty five genotypes of molakolukulu rice using D^2 statistic. Based on the genetic distance the twenty five genotypes were grouped into six clusters. Of the six clusters formed, cluster III had maximum number of genotypes (9) followed by cluster I with seven entries. Maximum intra cluster distance (924.46) was observed in cluster III and minimum in Cluster IV (2922). Gel consistency (64.33%) followed by amylose content (28.67%), kernel elongation ratio (3.67) and water uptake (1.33%) together contribute around 98% to total divergence. The highest inter cluster distance was observed between cluster IV and cluster VI (39317.76) followed by cluster I and cluster VI (20556.42) indicating wide genetic diversity among the genotypes of these clusters and their use in rice hybridization programme for improving grain yield.

Key words: Rice, quality attributes, divergence

Rice is the staple food for half of the world's population, providing over 21% of the calorific intake of the population of South East Asia. In India there is a vast diversity of rice varieties due to the preferences of the people in different parts of the country. Particularly in Andhra Pradesh, the traditional molakolukulu rice is very popular in Nellore district which are of long duration (160-170 days) rice with golden yellow to dark brown husk on the grain and having good cooking and keeping quality. They are of long duration cultures having lodging nature and susceptibility to pests and diseases and research efforts are being made to develop non lodging types having a duration of 150 days, tolerance to pests and diseases, medium slender grain without losing its cooking and keeping quality properties. Keeping this in view, a study was conducted with 25 molakolukulu genotypes with respect to yield and quality traits to know the extent of variability in the molakolukulu genotypes of the traditional to recent past.

A meaningful classification of experimental material depending upon different characters helps to distinguish genetically close and diverse genotypes which is a pre-requisite for any genetic study. Several workers *viz.*, Subudhi *et al* (2009) proposed to choose diverse parents for quality traits such as head rice recovery, kernel length after cooking, gel consistency, kernel elongation ratio and amylose content from the most divergent clusters so that they may produce larger variability and desirable segregants. Similarly, Senapathi and Sarkar (2005) studied the traits like productive tillers per plant and panicle length. While Ramesh Chandra *et al* (2007) and Iftekharuddaula *et al* (2010) studied the traits like test weight contribution towards total divergence.

MATERIAL AND METHODS

Twenty four molakolukulu genotypes developed at Agricultural Research Station, Nellore and one genotype *viz.*, Swarna (MTU 7029) were transplanted in randomized block design with two replications during *kharif* 2017 season at Agricultural Research Station, Nellore, Andhra Pradesh. In each replication single seedling was transplanted per hill in 5 rows of 3 meters length with 20 x 15 cm spacing. Recommended package of practices were followed to obtain a normal crop. The observations were recorded on five randomly taken plants from each plot for days to 50% flowering, plant height (cm), number of productive tillers, panicle length (cm), flag leaf length (cm), flag leaf breadth (cm), filled grains per panicle, test weight (g), grain yield per plant (g), kernel length (mm), kernel breadth (mm), kernel L/B ratio, hulling percentage, milling percentage, head rice recovery (%), gel consistency, water uptake, volume expansion, kernel elongation ratio, alkali spreading value, amylose content, protein content, iron content, zinc content and oil content. The analysis of genetic divergence was done using Mahalanobis D^2 (1936) statistic. The genotypes were grouped into different clusters by Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters studied. Based on D^2 analysis all the 25 genotypes were grouped into six clusters using Tocher's method (Singh and Chaudhary, 1977). However, with variable number of entries in each cluster revealing considerable amount of genetic diversity in the material studied (Table 1). It was observed that the cluster III had maximum number of 9 genotypes followed by cluster I with 7 genotypes

Table 1. Clustering pattern of 25 genotypes of molakolukulu rice (*Oryza sativa* L.) by Tocher's method.

Cluster No.	Number of genotypes	Name of the genotypes
I	7	NLR 33892, NLR 33891, NLR 27999, NLR 33365, NLR 20128, Bulk H/9 and NLR 28600.
II	6	BCP-4, BCP-6, BCP-2, BCP-3, BCP-5 and NLR 28523
III	9	NLR 9672, NLR 9674, NLR 9672-96, POMBAL, NLR 33810, NLR 33641, BCP-1, NLR 20084 and NLR 3337.
IV	1	NLR 3186
V	1	NLR 3115
VI	1	MTU 7029

Table 2. Average intra-and inter –cluster D² values among six clusters in 25 molakolukulu rice (*Oryza sativa* L.).

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
1 Cluster	2552.92	2791.65	6114.17	8055.52	7420.19	20556.42
2 Cluster		1223.53	3133.94	5785.86	6738.47	20280.21
3 Cluster			924.46	7097.45	5792.68	16406.35
4 Cluster				1866.84	1908.46	39317.76
5 Cluster					2099.94	5610.00
6 Cluster						2922.04

and cluster II with six genotypes. Whereas, Cluster IV, V and VI had one genotype in each cluster. The pattern of distribution of genotypes into various clusters was at random, indicating that the genotypes developed at ARS, Nellore fell in different clusters due to genetic drift caused by genetic drift and artificial selection. (Bhatt, 1970 and Raut *et al.*, 1985).

Average intra and inter cluster distance values among six clusters are presented in Table 2 and it revealed that the intra cluster D² values were ranged from 924.46 (cluster III) to 2922 (cluster VI) while the high intra cluster distance was recorded in cluster VI followed by cluster I (2552.92). The cluster VI was a solitary cluster and the cluster I had seven genotypes indicating the presence of wide genetic diversity among the genotypes of this cluster. It could be due to heterogeneity, genetic architecture of the population, past history of the selection in development of traits and degree of combining ability (Dikshit and Swain, 2000). Cluster mean values showed wide range indicating the presence of variation among the genotypes studied.

From the inter cluster D² values of six clusters, it can be seen that the highest divergence occurred between cluster IV and cluster VI (39317.76) followed by cluster I and cluster VI (20556.42), cluster II and cluster VI (20280.2) and cluster III and cluster VI

(16406.35) which indicated that the parents selected from these clusters in crossing programme would give high heterotic response and thus desirable combinations. The lowest divergence was noticed between cluster V and cluster IV (1908.46) followed by cluster I and cluster II (2791.66) and cluster III and cluster VI (3113.94). Parents selected from these clusters in crossing programme may not result in desirable combination as they are closely related without much divergence. These results in accordance with the findings of Chaturvedi and Maurya (2005).

It was observed that cluster IV comprises of only one genotype NLR 3186 and has recorded highest mean values for most of the characters *viz.*, panicle length, flag leaf breadth, grain yield, kernel length, kernel L/B ratio, hulling%, milling% and gel consistency. Hence, selection of this genotype for direct use may be beneficial. Whereas cluster I had highest mean values for days to 50% flowering, plant height and productive tillers per plant. Cluster II recorded highest values for flag leaf length, kernel breadth, water uptake, volume expansion ratio, kernel elongation ratio, moderate amylose content and high zinc content and cluster III for high head rice recovery, more alkali spreading value, oil % and protein content. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

Table 3. Contribution of different characters towards genetic divergence among 25 genotypes of Molakolukulu rice (*Oryza sativa* L.).

S.No.	Characters	Contribution (%)
1	Days to 50% flowering	0
2	Plant height (cm)	0
3	Panicle length (cm)	0
4	Flag leaf length (cm)	0
5	Flag leaf breadth (cm)	0
6	Productive tillers per plant	0
7	Filled grains per panicle	0
8	Test weight (g)	0
9	Grain yield (g)	0.33
10	Kernel length (mm)	0
11	Kernel length (mm)	0
12	Kernel L/B ratio	0
13	Hulling %	0.67
14	Milling %	0
15	Head rice recovery	0.67
16	Water uptake	1.33
17	Volume expansion ratio	0.33
18	Kernel elongation ratio	3.67
19	Gel consistency (mm)	64.33
20	Alkali Spreading Value	0.67
21	Amylose	28.67
22	Iron (ppm)	0
23	Zinc (ppm)	0
24	Oil (%)	0
25	Protein (%)	0

The lowest cluster mean value was observed in cluster VI for number of days to 50% flowering, plant height, panicle length, flag leaf length, flag leaf breadth, grain yield, head rice recovery, water uptake, volume expansion ratio, oil content and kernel elongation ratio, cluster I for filled grains per panicle, hulling %, milling% and gel consistency, cluster IV for low productive tillers per plant, kernel breadth and iron content, cluster V for test weight, kernel length and iron content. cluster II for kernel L/B ratio, alkali spreading value and amylose content and cluster III for low zinc content.

CONCLUSION

It can be concluded that, contribution of each character towards genetic divergence has been estimated from the number of times that each character appeared in the rank first. Percentage contribution of each character towards total divergence is presented in table 3. The data revealed that maximum percentage of contribution came from the trait gel consistency

(64.33%) followed by amylose content (28.67%), kernel elongation ratio (3.67), and water uptake (1.33%). Since, gel consistency and amylose content contributed maximum towards the genetic divergence, direct selection for these traits will give good results. Hence, gel consistency, amylose content, kernel elongation ratio and water uptake may be used as selection parameters in the segregating generations. The other traits had very low contribution to total divergence. The traits which had low or zero contribution towards divergence were of less importance as per the material studied in the experiment.

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