

Studies on Genetic Divergence Analysis in Soft Rice (*Oryza sativa* L.) Genotypes

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ABSTRACT

In the present investigation, seventy five speciality rices called soft rice genotypes collected from different parts of North-East India (especially Assam) were evaluated to study the genetic diversity present in the experimental material for selection of the diverse parents, to estimate the genetic parameters among the genotypes for yield and component traits. The experiment was laid out in a randomized block design with three replications at Directorate of Rice Research Farm, ICRISAT Campus, Patancheru, Hyderabad, India. Based on the relative magnitude of D^2 values, the genotypes were grouped into seven clusters. Cluster I was the largest comprising of 62 genotypes followed by cluster II with eight genotypes, cluster III, IV, V, VI and VII with one genotype each. Based on the inter-cluster distances, crossing between the genotypes of cluster IV and cluster VII, cluster III and cluster VII, cluster I with cluster VII and cluster III and cluster VI is suggested to generate diversified breeding material. The data on character means for seven clusters indicated that, the cluster III is having highest mean value for per cent filled grains per panicle, cluster V for seed yield per plant and cluster I for test weight (1000-grain weight) and cluster II for number of productive tillers per plant and cluster IV for panicle length. The characters per cent filled grains per panicle, plant height, seed yield per plant contributed maximum to the genetic divergence. Hence these characters could be given due importance for selection of genotypes for further crop improvement programme.

Key words: Genetic diversity, D^2 analysis, Soft rice.

INTRODUCTION

Rice (*Oryza sativa* L. 2n : 2X : 24) is the most important cereal crop cultivated widely in many parts of the world. Over two billion people in Asia alone derive 80% of their energy needs from rice which contains 80% carbohydrates, 7-8% protein and also fat and

dietary fibre². Out of the 24 species of rice, 22 species are wild and only 2 species are cultivated i.e., *O. sativa* and *O. glaberrima*. It is one of the very few crop species endowed with rich genetic diversity which account over one lakh landraces and improved cultivars⁸.

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The outstanding genetic diversity that exists for rice in the Indian sub continent has been brought forth not only by natural processes, the conscious human selection due to socio-economic compulsions, socio-economic traditions also played a dominant role in adding variations to its characters. Genetic variability is the basic requirement for making progress in crop breeding. Inclusion of genetically divergent parents in any breeding programme is essential to create new genetic stocks. Genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization programme.

India has a rich source of genetic diversity for rice. The north-east region of India is a veritable natural gene bank representing wide spectrum of rice genetic resources. Among the different classes of rice available, glutinous / waxy rice is an important class, in the sense of being glue-like or sticky. The waxy rice of Assam has been classified in two groups viz., *Bora* (glutinous) and *Chokuwa* (Semi-glutinous) based on amylose content⁹. *Bora* rice of Assam has significance in social and religious ceremonies and forms a popular daily breakfast diet in rural Assam. *Chokuwa* (soft rice), is another class of rice used for instant preparations. This class of rice is not known in any other parts of the world. Its preparations are very popular in community feasts and festivals in Assam. “Soft rice (komal chawl)” are prepared from this class of rice by soaking the rice either in cold or hot water for a brief period of time and then consumed with sugar or molasses, milk or curd and even with salts and oils and pickles. These preparations seem to be useful for sailors, travelers, space researchers, mountaineers, defense personal etc. Thus this class of rice is metaphorically termed as “magical rice” as it becomes ready to use just by soaking with no fuel requirement and hence it has a great demand in the domestic as well as foreign market. The multiplicities of uses make the glutinous rice very popular among farmers. In spite of the advent of modern high yielding rice varieties, these soft rices being mostly

landraces are highly valuable and possess traits that are most preferred by farmers.

Rice contains significant diversity in plant architecture and growing habits and in grain phenotypes such as width, weight, cooking properties, aroma and texture. The extensive phenotypic and genotypic variation within the *Oryza sativa* makes these varieties a powerful tool to study rice genetic diversity, such that methods can be developed to enhance health promoting qualities of rice grain. Hence, to study the nature and magnitude of genetic divergence and characters contributing to it should be based on sound scientific procedures such as D^2 analysis to measure the genetic divergence among the test entries and their grouping into different clusters.

So far no work has been done on genetic diversity studies of these soft rice genotypes. The systemic study of genetic variability analysis in the material is meagre. Hence, keeping in view the importance of soft rices and scanty literature on these aspects, the present investigation was undertaken as a first attempt in the state of Andhra Pradesh with the objective to study the genetic divergence among the soft rices through D^2 analysis.

MATERIAL AND METHODS

Present investigations were conducted at the Directorate of Rice Research Farm, ICRI SAT Campus, Patancheru, Hyderabad, India. Seventy five (75) soft rice genotypes were used for genetic diversity study. The experiment was laid out in a Randomized Block Design with three replications during the season. Thirty days old seedlings were transplanted at the rate of one seedling per hill in three rows of five metre length with plant to plant distance of 15 cm and row to row distance of 20 cm. The standard cultivation practices prescribed for rice under irrigated conditions were followed precisely.

Five random plants were selected from central rows and the data was recorded in each replication on these five plants for diversity studies. Nine yield components were recorded for genetic diversity analysis and the mean

values were considered for statistical analysis. Genetic diversity between genotypes can be better estimated using D^2 statistics given by Mahalanobis³. Grouping of genotypes into different clusters was done by using Tocher's method⁷.

The experimental material consist of seventy five soft rice genotypes obtained from the germplasm collections maintained at Directorate of Rice Research, Rajendranagar, Hyderabad and these genotypes were primarily collected from the north eastern region of

Assam. The soft rice lines were given notation as SR and the names of these soft rices were mentioned in Table 1.

For recording observations on yield components like Days to fifty per cent flowering, Plant height, Number of tillers per plant, Number of productive tillers per plant, Panicle length, Percent filled grains per panicle, Days to maturity, Seed yield per plant (g) and Test weight (g), panicles from five labeled plants were harvested separately from each replication.

Table 1: Details of soft rice genotypes used in the study

S.No.	Soft rice line number	Local name of the genotype during collection
1	SR-1	Joha bora
2	SR-2	Ranga bora
3	SR-3	Sungal bora
4	SR-4	Noldong bora
5	SR-5	Tegori bora
6	SR-6	Bongari bora
7	SR-7	Kola ampaki bora
8	SR-8	Bora-1
9	SR-9	Dadhora bora
10	SR-10	Chokura bora
11	SR-11	Sakoibhanu bora
12	SR-12	Kola bora
13	SR-13	Misiri chakua
14	SR-14	Boka chakua
15	SR-15	Ch-5 bora chakua
16	SR-16	Kagori chakura
17	SR-17	Kola boka chakura
18	SR-18	Haru chakua
19	SR-19	Boga chakua
20	SR-20	Lahi chakua
21	SR-21	Sam chakua
22	SR-22	Maju chakua
23	SR-23	Ham chakua
24	SR-24	Hampori chakua
25	SR-25	Malbhog
26	SR-26	Helochi
27	SR-27	Kalamdani
28	SR-28	Dadhora
29	SR-29	Aghoni bora
30	SR-30	Bhogali bora
31	SR-31	Abor bora
32	SR-32	Beji bora l
33	SR-33	Begun bora
34	SR-34	Boga bora l

35	SR-35	Boga bora 3
36	SR-36	Bhat bora
37	SR-37	Bora 1
38	SR-38	Bora 3
39	SR-39	Bora 5
40	SR-40	Botia bora
41	SR-41	Bor malbhog
42	SR-42	Chakkua bora 1
43	SR-43	Chansep bora
44	SR-44	Chandra bora
45	SR-45	Danbori bora
46	SR-46	Fakkai bora
47	SR-47	Gela bora
48	SR-48	Ghew bora 1
49	SR-49	Garu chakua bora 2
50	SR-50	Gomiri bora
51	SR-51	Naldang bora
52	SR-52	Helochi bora 1
53	SR-53	Helochi bora 2
54	SR-54	Aghoni
55	SR-55	Bhogali
56	SR-56	KMJ bora 56
57	SR-57	KMJ bora 53
58	SR-58	KMJ bora 51
59	SR-59	KMJ bora 41
60	SR-60	KMJ bora 36
61	SR-61	KMJ bora49
62	SR-62	KMJ bora 74
63	SR-63	KMJ bora 5
64	SR-64	KMJ bora 13
65	SR-65	KMJ bora 21
66	SR-66	KMJ bora 25
67	SR-67	Boka chakua 1
68	SR-68	Boka chakua 2
69	SR-69	Kajoli chakua
70	SR-70	Kalamdani chakua
71	SR-71	Lahi chakua 1
72	SR-72	Maju chakua 1
73	SR-73	Maju chakua 2
74	SR-74	Misiri chakua
75	SR-75	Sam chakura

RESULTS AND DISCUSSION

The seventy five soft rice genotypes were grouped into nine clusters using Tocher's method such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters is presented in Table 2. Out of seven clusters,

cluster I was the largest comprising of 62 genotypes followed by cluster II with eight genotypes, and cluster III, IV, V, VI and VII with only one genotype each. The pattern of distribution of genotypes into various clusters was at random indicating that geographical and genetic diversity were not related. The cluster diagram (dendrogram) is given in

Figure 1. The clusters III, IV, V, VI and VII were represented by single genotypes namely SR-55, SR-12, SR-29, SR-68 and SR-38 respectively indicating high degree of heterogeneity among the genotypes.

The average intra and inter cluster D^2 values are presented in Table 3. Intra cluster D^2 values ranged from 0.000 (cluster III, IV, V, VI and VII) to 157.08 (cluster II). Maximum intra cluster distance was observed in cluster II (157.08), followed by cluster I (104.95) indicating that some genetic divergence still existed among the genotypes. From the inter cluster D^2 values of seven clusters, it can be seen that the highest divergence occurred between cluster IV and cluster VII (1817.85) followed by cluster III and cluster VII (1795.23), cluster I and cluster VII (1425.51) and cluster III and cluster VI (1286.81), suggesting that the crosses involving lines from these clusters would give wider and desirable recombinations. The lowest divergence was noticed between cluster VI and cluster VII (186.32) followed by cluster I and cluster IV (192.07) and cluster I and cluster III (195.12) and cluster II and V (236.14). Statistical representation of cluster distances was shown in fig 1.

It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. The greater the distance between two clusters, the wider the genetic diversity between the genotypes. Keeping this in view, it is indicated that hybridization between the genotypes (SR-12) of cluster IV and cluster VII (SR-38), cluster III (SR-55) and cluster VII (SR-38), cluster I with cluster VII (SR-38) and cluster III (SR-55) and cluster VI (SR-68) would produce encouraging results. The genotypes of these clusters may be used as parents in the crossing programme to generate breeding material with high diversity.

Cluster means of the characters

The cluster means for each of nine characters are presented in Table 4. From the data it can be seen that considerable differences exist for all the traits studied. It indicated that the

cluster mean for days to 50% flowering was highest in cluster VII (130.33) and the lowest in cluster II (113.88). Plant height was highest in cluster IV (142.27 cm) and lowest in cluster III (70.00 cm). Cluster II recorded the highest number of tillers per plant (17.08) and the lowest number of tillers per plant was in cluster VII (12.33). Cluster II recorded the highest number of productive tillers per plant (15.21) and the lowest number of productive tillers per plant was in cluster VI (11.00).

Cluster IV recorded the highest panicle length (27.53 cm) and the lowest was recorded in cluster III (21.47 cm). The percent filled grains per panicle were highest in cluster III (95.40) and the lowest in cluster VII (35.40). Days to maturity was highest in cluster VII (159.67) lowest in cluster VI (142.33). Cluster V recorded the highest seed yield per plant (29.83 g) while, in cluster IV it was low (11.00 g). Highest test weight (1000-grain weight) was recorded in cluster I (24.98 g) and the lowest in cluster IV and cluster VII (21.00 g).

The cluster III is having highest mean value for percent filled grains per panicle, cluster V for seed yield per plant and cluster I for test weight (1000-grain weight) and cluster II for number of productive tillers per plant and cluster IV for panicle length. The genotypes from these clusters having high mean values may be directly used for adaptation or may be used as parents in future hybridization programme.

Relative contribution of characters towards genetic divergence

The number of times that each of the nine characters appeared in first rank and its respective per cent contribution towards genetic divergence is presented in Table 5. The results showed that the contribution of per cent filled grains per panicle was highest towards genetic divergence (5181.98%) by ranking 1438 times first, followed by plant height (2237.84%) by 621 times, seed yield per plant (g) (1441.44%) by 400 times, days to maturity (403.6%) by 112 times, test weight (371.17%) by 103 times, number of tillers per plant (252.25%) by 70 times, days to 50% flowering (50.45%) by 14 times, panicle length (cm)

(46.85%) by 13 times, number of productive tillers per plant (14.41%) by 4 times respectively to the genetic divergence in decreasing order. The results were in conformity with Mani⁴ for plant height, Nayak *et al.*⁵ for panicle length, Patil and Sarawgi⁶ 1000-grain weight, grain yield per plant and

Chandra *et al.*¹ for plant height. The traits, per cent filled grains per panicle, plant height and seed yield per plant contributed maximum towards total divergence, these characters should be taken into consideration while selecting parents for hybridization.

Table 2: Clustering pattern among 75 soft rice genotypes (D² analysis)

Cluster No	No. of genotypes	Names of the Genotypes
I	62	SR-2, SR-3, SR-4, SR-5, SR-6, SR-7, SR-9, SR-10, SR-11, SR-13, SR-14, SR-15, SR-16, SR-17, SR-18, SR-19, SR-20, SR-21, SR-22, SR-24, SR-25, SR-27, SR-28, SR-30, SR-31, SR-32, SR-33, SR-34, SR-35, SR-36, SR-37, SR-39, SR-40, SR-41, SR-42, SR-43, SR-44, SR-45, SR-46, SR-47, SR-48, SR-49, SR-50, SR-51, SR-53, SR-54, SR-56, SR-57, SR-58, SR-59, SR-61, SR-62, SR-63, SR-64, SR-67, SR-69, SR-70, SR-71, SR-72, SR-73, SR-74 and SR-75.
II	8	SR-1, SR-8, SR-23, SR-26, SR-52, SR-60, SR-65, SR-66.
III	1	SR-55.
IV	1	SR-12.
V	1	SR-29.
VI	1	SR-68.
VII	1	SR-38.

Table 3: Intra (diagonal) and Inter cluster average of D² values of soft rice genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	104.95	284.18	195.12	192.07	311.65	861.07	1425.51
Cluster II		157.08	491.23	473.68	236.14	341.21	743.29
Cluster III			0.00	361.54	318.15	1286.81	1795.23
Cluster IV				0.00	676.12	1199.44	1817.85
Cluster V					0.00	474.78	693.97
Cluster VI						0.00	186.32
Cluster VII							0.00

Table 4: Cluster means for yield components and quality traits (D^2 analysis) in soft rice genotypes

Cluster No.	Days to 50% flowering	Plant height (cm)	Number of tillers per plant	Number of Productive tillers per plant	Panicle length (cm)	Per cent filled grains per panicle	Days to maturity	seed yield per plant (g)	Test weight (1000 grain) (g)
Cluster I	115.07	112.63	16.42	14.28	27.10	87.24	144.36	19.32	24.98
Cluster II	113.88	110.69	17.08	15.21	27.51	68.20	144.04	15.10	22.09
Cluster III	119.67	70.00	16.33	15.00	21.47	95.40	149.00	18.07	23.00
Cluster IV	123.00	142.27	15.00	14.00	27.53	91.71	152.33	11.00	21.00
Cluster V	119.67	75.73	17.00	14.67	26.27	73.72	151.00	29.83	23.00
Cluster VI	115.00	122.60	15.33	11.00	25.07	45.31	142.33	19.91	24.13
Cluster VII	130.33	105.33	12.33	12.33	25.40	35.40	159.67	25.57	21.00

Table 5: Relative contribution of different traits towards total genetic divergence

S. No.	Character	No. of times ranked first	Contribution (%)
1	Days to 50% flowering	14	50.45
2	Plant height (cm)	621	2237.84
3	Number of tillars per plant	70	252.25
4	Number of productive tillers per plant	4	14.41
5	Panicle length (cm)	13	46.85
6	Per cent filled grains per panicle	1438	5181.98
7	Days to maturity	112	403.6
8	Seed yield per plant (g)	400	1441.44
9	Test weight (g)	103	371.17

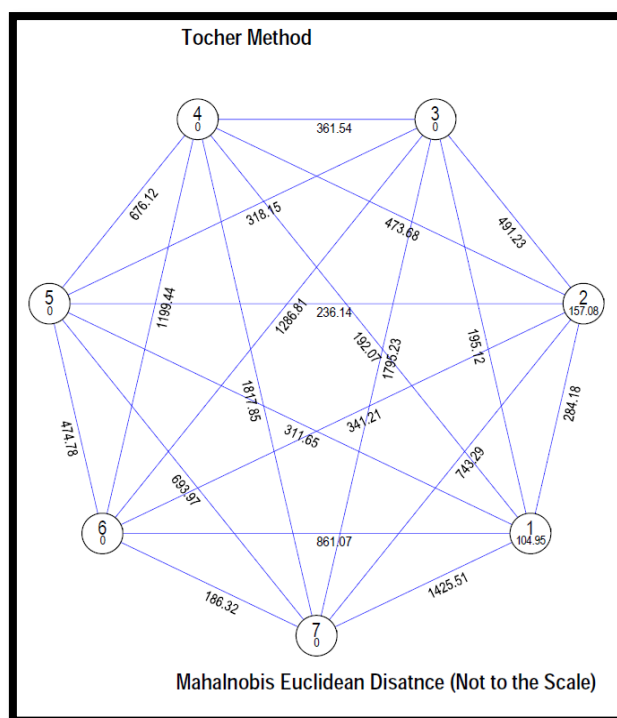


Fig. 1: Intra and inter cluster statistical distances of various clusters

SUMMARY AND CONCLUSIONS

Divergence studies through D^2 statistic indicated the presence of substantial diversity by forming large number of clusters with wide range of inter-cluster distances. The diversity

was more for per cent filled grains per panicle, plant height, seed yield per plant, days to maturity and test weight indicating their importance in contribution towards genetic diversity. The multivariate analysis revealed

that 75 genotypes were distributed into seven clusters. The clusters III is having highest mean value for per cent filled grains per panicle, cluster V for seed yield per plant and cluster I for test weight (1000-grain weight) and cluster II for number of productive tillers per plant and cluster IV for panicle length and also they were highly divergent from each other. Hence, crosses between genotypes selected from these clusters may be used to generate soft rice varieties with good grain yield and quality traits. It is observed that no cluster contained at least one genotype with all the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

The 75 genotypes of soft rice were randomly grouped into seven divergent clusters indicating that geographical distribution and genetic diversity were not related. The pattern of group constellations indicated significant variability among the genotypes. The higher amount of divergence was observed between cluster IV and cluster VII (1817.85) followed by cluster III and cluster VII (1795.23), cluster I and cluster VII (1425.51) and cluster III and cluster VI (1286.81). The greater the distance between two clusters, the wider the genetic diversity between the genotypes. Keeping this in view, it is indicated that hybridization between the genotypes (SR-12) of cluster IV and cluster VII (SR-38), cluster III (SR-55) and cluster VII (SR-38), cluster I with cluster VII (SR-38) and cluster III (SR-55) and cluster VI (SR-68) would produce encouraging results and promising segregants for grain yield. The maximum genetic divergence was contributed by per cent filled grains per panicle (5181.98%), plant height (2237.84%), seed yield per plant (1441.44%).

The conclusion drawn from the cluster analysis is that in the studied population high variability was observed between the genotypes in different clusters for different

traits. Recombination breeding among genotypes belonging to cluster II having maximum intra-cluster distance can improve the yield potential. As maximum inter-cluster distance was noticed between cluster IV and VII, cluster III and VII, crosses involving genotypes from these clusters would give wider and desirable recombination.

REFERENCES

1. Chandra, B.S., Reddy, T.D. and Ansari. Genetic divergence in rice. *Research on crops*. **8(3)**: 600-603 (2007).
2. Juliano, B.O., Rice: chemistry and technology. American Association of Cereal Chemists. **2(4)**: 774 pp (1985).
3. Mahalanobis, P.C., On the generalized distance in statistics. *Proceedings of National Institute of Sciences, India* **12**: 49-55 (1936).
4. Mani, S.D.S.C., Genetic divergence in elite genotypes of basmati rice. *Indian Journal of Genetics and Plant Breeding*. **63(1)**: 73-74 (2003).
5. Nayak, A.R., Chaudhary, D. and Reddy, J.N., Genetic divergence in scented rice. *Oryza*. **41(3&4)**: 79-82 (2004).
6. Patil, P.V. and Sarawgi, A.K., Studies on genetic variability, correlation and path analysis in traditional aromatic rice accessions. *Annals of Plant Physiology*. **19(1)**: 92-95 (2005).
7. Rao, C.R., Advanced statistical methods in biometric research. Wiley, Oxford, England. **17**: 390 (1952).
8. Samal, K.C., Meti, N., Bastia, D.N., Rout, G.R., Genetic diversity analysis of traditional aromatic rice using molecular markers. *BMR*, **1(2)**: 1-14 (2014).
9. Shaptadvipa, B., Sarma, R.N., Study on apparent amylose content in context of polymorphism information content along with indices of genetic relationship derived through SSR markers in Birain, Bora and Chakuwa groups of traditional glutinous rice of Assam. *Asian Journal of Biochemistry*. **4(2)**: 45-54 (2009).