

Genetic diversity for grain quality parameters in traditional rice (*Oryza sativa* L.) accessions from Madhya Pradesh, India

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ABSTRACT

Genetic divergence as measured by D^2 technique was studied for 18 grain quality traits in 132 rice genotypes (128 traditional cultivars and 4 standard genotypes). The analysis of variance revealed significant differences among the genotypes for each character indicating genotypes for characters studied. The genotypes were grouped into 10 clusters and the maximum intra-cluster distance was observed in cluster VIII comprising of a single traditional rice cultivar Gonda jhul. Clusters VI and VIII were identified as genetically divergent. Considering the cluster means and cluster distances, Bakal-B and Jondhera dhan of cluster VI, Gonda jhul of cluster VIII, Poorva and IR-36 of cluster VII, Kranchi, X-12, Moti bakiya and Assam chudi of cluster V and Kranti of cluster X were the most promising varieties. These may be utilized in future breeding programme to obtain high heterotic effect or evolve desirable recombinants.

Key words: Cluster analysis, genetic diversity, grain quality, *Oryza sativa*, rice.

INTRODUCTION

Genetic improvement mainly depends upon the amount of genetic variability present in a population. In any crop germplasm serves as a valuable source of base population and provides scope for wide variability. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right type of parents for breeding programme (Vivekanandan and Subramanian 1993).

In respect of the rice germplasm, Chhattisgarh region of Madhya Pradesh, India can be considered as a centre of divergence where approximately at every 250 ha the germplasm pattern changes (Richharia 1979). With increase in rice production, greater emphasis is being given to grain quality and has been of major concern to rice breeding programmes in recent years. The development of improved germplasm with superior grain qualities is one of the most important objectives.

The spectrum of variability in segregating generations for grain quality parameters depends on the genetic diversity of the combining parents. Hence, estimation of genetic diversity for quality parameters among genotypes is important for planning the future crossing programmes. Mahalanobis D^2 statistic is a potent tool for estimating it, as has been emphasized by many workers (Murty and Arunachalam 1966, Anand and Murty 1968, Arunachalam 1981, Rahaman *et al.* 1997). Understanding the genetic diversity for grain quality parameters in traditional rice accessions and its utilization for selection of desirable parents/donors, either for exploitation of hybrid

vigour or to get desirable recombinants is important for improving rice quality. Therefore, an attempt was made to classify and to understand the nature and magnitude of genetic diversity present in available rice germplasm for quality traits.

MATERIALS AND METHODS

The material for the study consisted of 128 rice germplasm accessions of Madhya Pradesh, India along with four improved cultivars namely Poorva, IR-36, Kranti and R 296-260. The material was grown in a randomized complete block design with three replications. Each accession was grown in plots of three rows of 3 m length at a spacing of 20 cm between rows and 15 cm between plants in a row. The nutrients (N: P: K) were applied at the rate of 80, 50 and 30 kg ha⁻¹ as urea, super phosphate and muriate of potash, respectively. No plant protection measures were applied. Observations were recorded on five randomly selected plants of each accession per replication for eighteen quality traits viz. Milled grain length, milled grain breadth, milled grain thickness, hundred milled grain weight, length: breadth ratio, length: thickness ratio, breadth: thickness ratio, length: breadth/breadth: thickness ratio, normalized grain weight, lengthwise elongation percentage, breadthwise expansion percentage, lengthwise elongation : breadthwise expansion, elongation ratio, elongation index, water absorption percentage, proportionate change, gel consistency and gelatinization temperature. The data were subjected to the Mahalanobis D^2 statistic (1936) to measure the genetic divergence. The varieties

were grouped into a number of clusters by Tocher's method as described by Rao (1952). The criterion was that any two varieties on an average showing lower D^2 values were grouped into the same cluster while those showing high D^2 values were grouped into different clusters.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for each character, indicating the existence of variability among the genotypes for the characters studied (Table 1). Based on the relative magnitude of D^2 values 132 genotypes were grouped into ten clusters (Table 2). Maximum number of 78 cultivars were accommodated in cluster I followed by 22 in cluster

III, 17 in cluster II, 4 each in clusters IV and V, 2 each in clusters VI and VII and 1 genotype each in clusters VIII, IX and X. The intra-cluster distance scored for clusters VIII, IX and X was '0' comprising of single genotype for each cluster. The maximum intra-cluster distance ($D=14.19$) was observed in cluster VII followed by cluster VI ($D=12.57$) and IV ($D=11.58$). The cluster VII consisted of two improved varieties Poorva and IR-36, cluster VI of two accessions Bakal-B and Jondhera dhan and cluster IV of four accessions Badal Phool, X-4, Laxmibhog and Anijan. The above grouping indicates existence of wide genetic divergence among constituent genotypes. Such high degree of divergence was found in local collections (Rahaman *et al.* 1997; Sardana *et al.* 1997) as well as in international collections (Usha Kumari and

Table 1. Analysis of variance of quality characters in rice accessions from Madhya Pradesh, India.

Source of Variation	D.F.	Characters								
Replications	2	1	2	3	4	5	6	7	8	9
Genotypes	131	0.000229	0.000013	0.000007	0.027893	0.002808	1.358887	0.009491	0.019348	0.00511
Error	262	0.005335**	0.000997**	0.000234**	0.158763**	0.262011**	1.801309	0.015166**	0.238860**	0.003127**
		0.000128	0.000049	0.000015	0.014858	0.005872	1.510572	0.005782	0.013273	0.000101

Source of Variation	D.F.	Characters								
Replications	2	10	11	12	13	14	15	16	17	18
Genotypes	131	15.421875	0.261719	0.163483	0.002533	0.001343	210.085940	0.000606	0.164063	0.015137
Error	262	3.247480	7.217989**	0.239640	0.000393**	0.000944**	16.788466	0.000960**	10.828185**	0.403195
		2.718213	4.830003	0.188544	0.000293	0.000616	14.463562	0.000624	0.276926	0.018815

1. Milled grain length	7. Breadth:thickness ratio	13. Elongation ratio
2. Milled grain breadth	8. Length:breadth:thickness ratio	14. Elongation index
3. Milled grain thickness	9. Normalized grain weight	15. Water absorption percentage
4. Hundred milled grain weight	10. Lengthwise elongation percentage	16. Proportionate change
5. Length:breadth ratio	11. Breadthwise expansion percentage	17. Gel consistency
6. Length:thickness ratio	12. Lengthwise elongation:breadthwise expansion	18. Gelatinization temperature

Table 2. Clustering of 132 rice genotypes based on D^2 statistics.

Cluster	No. of genotypes included	Genotypes
I	78	J.S. 5, Nankoo, Motijhira, Lallo 14, Lallu, Davar, Laloo, Byora, Lalna Kanka, Granji, Khairabasant, Bakal (A), Laloo-14, Chipada, Sonkharchi, Jhina local, Antraved, Sathiva, Laloo-14, Bhadokenkar, Cuvery, Shikiya, Byora, Baikoni, Hhumariya, Uraibut, Dhour, Nungi, Nungi, Niwari, E-B-17, No. 17, Lawa dewar, Thumsi, Kajalibunda, Bhulru, Mundariya, Dhor, Nungi Dhaur, Nau Mohar, X-2, X-1, Nungi, Bhatha Luchai, Baikoni, X-5, Uraibuta, Newari, Jagannath Prasad, Sulti, Bangala, Bhata Safri, Sumatia, Barji, Peelec-luchai, Makado, al sunghawala, Koilari, Nirguni, Nungi, Nunga, Kala Kardhana, Chiniakkar, Katasari, Basant, Choroungi, Raghunath-I, Raghunath-II, Khuraban, Newari (N/358).
II	17	Lallu-14, Nungi, Gadursela, Chingi, T.D.-d, Gada Khuta, Sindur singa, Surja, Dar Banko, Bhado Kankar, Luchai, Khetudisal Safed, X-5, Pyagi, Mani gurmata, Anjan, Luchai.
III	22	Lallu, Bhata Makdo, Sohan dhan, Nilam dhan, Lakhaua, Koram, Barik, Baikoni-B, Sota, Chhatri, Luchai, Benikath, Deshi, Anjan, Rajim-1, Munchhwali, Assamchudi-82, Tulsi Prasad, R-29a6-260.
IV	4	Badal Phool, X-4, Laxmibhog, Anjan.
V	4	Kranchi, X-12, Moti Bakiya, Assamchudi.
VI	2	Bakal-B, Jondhara Dhan.
VII	2	Poorva, IR-36
VIII	1	Gonda Jhul
IX	1	Halso
X	1	Kranti

Rangaswamy 1997). The minimum intra-cluster value (D=9.50) exhibited by cluster I indicated limited genetic diversity among the constituent genotypes. The unidirectional selection practiced in the past might have resulted in uniform features with less divergence between these genotypes (Table 3).

The relative divergence of each cluster from other clusters (inter-cluster distances) indicated greater divergence between clusters VI and VIII (D=36.24) followed by clusters VII and VIII (D=33.19) and clusters V and X (D=32.99). The selection of divergent genotypes from above clusters would produce a broad spectrum of variability for quality traits studied which may enable further selection and improvement of quality traits. The hybrids developed from the selected genotypes within the limits of compatibility of these clusters may produce high magnitude of heterosis or desirable transgressive segregants which would be rewarding in a rice quality breeding programme. Bhatt (1973), Roy and Panwar (1993), Vivekanandan and Subramanian (1993) and Rahaman *et al.* (1997) also found similar degree of diversity in rice. The inter-cluster distance (Table 3) analysis revealed the maximum divergence between clusters VI and VIII (D=36.24) followed by clusters

VII and VIII (D=33.19). Due emphasis for breeding programme should be given to Bakal-B and Jondhera dhan of cluster VI, Gonda jhul of cluster VIII, Poorva and IR-36 of cluster VII.

The cluster mean values for all the 18 characters are furnished in Table 4. There was a wide range of variation in the cluster mean values for most of the characters under study. However, characters like breadth:thickness ratio, Elongation ratio, elongation index and proportionate change did not vary to a great extent among the different clusters.

The average clusterwise mean for different characters showed that the genotypes included in cluster V, such as Kranchi, X-12, Moti bakiya and Assam chudi had maximum length:breadth ratio, length:thickness ratio and length:breadth/breadth:thickness ratio. The genotype Gonda Jhul forming a separate cluster (VIII) had maximum lengthwise elongation percentage, elongation ratio, elongation index and lengthwise elongation percentage: breadthwise expansion percentage. The genotypes Bakal-B and Jondhara Dhan forming a separate cluster (VI) had maximum milled grain length and hundred grain weight while Poorva and IR-36 in cluster VII and Kranti in cluster X had intermediate gelatinization temperature.

Table 3. Mean intra-cluster (diagonal and bold) and inter-cluster distances among ten clusters.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	90.29 (9.50)	230.25 (15.17)	251.20 (15.85)	284.36 (16.86)	445.41 (21.10)	386.31 (19.65)	635.91 (25.22)	531.77 (23.06)	334.42 (18.29)	430.62 (20.75)
II		117.22 (10.83)	286.13 (16.92)	415.22 (20.38)	270.13 (16.44)	502.95 (22.43)	575.34 (23.99)	398.45 (19.96)	254.78 (15.96)	644.31 (25.38)
III			127.10 (11.27)	544.74 (23.34)	271.86 (16.49)	342.46 (18.51)	605.95 (24.62)	648.99 (25.48)	604.58 (24.59)	872.36 (29.54)
IV				134.14 (11.58)	918.28 (30.30)	981.36 (31.33)	1041.01 (32.26)	241.03 (15.53)	317.92 (17.83)	515.61 (22.71)
V					122.30 (11.06)	319.15 (17.86)	579.98 (24.08)	914.95 (30.25)	614.02 (24.78)	1088.16 (32.99)
VI						158.02 (12.57)	745.56 (27.30)	1313.52 (36.24)	895.02 (29.97)	1057.09 (32.51)
VII							201.40 (14.19)	1101.81 (33.19)	899.70 (30.00)	591.35 (24.32)
VIII								-	404.96 (20.12)	892.55 (29.88)
IX									-	466.24 (21.59)
X										-

Note: D values given below in parenthesis and D² values above in the diagonal and non-diagonal.

Table 4. Cluster means for different characters.

Cluster	No. of genotypes included	Milled grain length	Milled grain breadth	Milled grain thickness	Hundred milled grain weight	Length: breadth ratio	Length: thickness ratio	Breadth: thickness ratio	Length: breadth: thickness ratio	Normalized grain weight	Lengthwise elongation percentage	Breadthwise expansion percentage	Length elongation: breadth expansion	Elongation ratio	Elongation index	Water absorption percentage	Proportionate change	Gel consistency	Gel T°
I	78	0.61	0.25	0.18	1.90	2.33	3.54	1.41	1.73	0.32	5.59	6.08	1.09	1.06	0.99	16.39	-0.01	9.46	2.13
II	17	0.61	0.24	0.17	1.79	3.02	3.53	1.39	1.85	0.29	5.77	5.71	1.14	1.06	1.00	15.91	0.00	4.39	2.25
III	22	0.63	0.21	0.16	1.48	3.01	3.85	1.29	2.35	0.24	5.44	7.49	0.83	1.05	0.98	17.38	-0.02	9.30	2.18
IV	4	0.49	0.26	0.18	1.46	1.87	2.68	1.46	1.27	0.30	6.48	6.96	0.89	1.06	1.00	16.01	0.00	9.29	2.06
V	4	0.71	0.22	0.16	1.90	3.27	4.29	1.31	2.51	0.27	4.57	6.92	0.71	1.05	0.98	13.94	-0.02	7.93	2.25
VI	2	0.76	0.25	0.18	2.43	3.09	4.27	1.39	2.23	0.28	5.25	7.08	0.82	1.05	0.99	16.48	-0.01	9.48	2.00
VII	2	0.69	0.23	0.17	1.94	3.06	4.12	1.35	2.27	0.28	5.80	5.65	1.19	1.06	1.00	17.91	0.30	7.30	4.80
VIII	1	0.43	0.23	0.16	1.09	1.87	2.65	1.42	1.32	0.25	8.17	6.52	1.33	1.08	1.01	14.35	0.01	4.80	2.20
IX	1	0.56	0.27	0.18	2.01	2.20	3.01	1.47	1.50	0.37	5.40	7.41	0.73	1.05	0.98	10.66	-0.02	3.40	2.00
X	1	0.58	0.28	0.20	2.33	2.05	2.93	1.42	1.44	0.40	4.26	3.51	1.21	1.04	1.00	13.35	0.00	9.65	4.00

Thus, these genotypes hold great promise as parents to obtain promising hybrids and create further variability for these characters.

Crosses among parents having genetic divergence are likely to yield desirable combinations. Therefore, a crossing programme should be initiated between the genotypes belonging to different clusters. Two important factors to be considered are:

- (i) Choice of particular clusters from which genotypes are to be used as parents in crossing scheme, and
- (ii) Selection of particular genotypes from selected groups.

In the present investigation, hybridization among the genotypes Kranchi,, X-12, Moti bakiya, Assam chudi from cluster V (for length:breadth ratio, length:thickness ratio, length:breadth:thickness ratio), Bakal-B and Jondhara dhan of cluster VI (for milled grain length and 100-grain weight), Poorva and IR-36 of cluster VII (for intermediate gelatinization temperature), Gonda jhul of cluster VIII (for lengthwise elongation percentage, elongation ratio, elongation index and lengthwise elongation percentage:breadthwise expansion percentage) and Kranti from cluster X (for intermediate gelatinization temperature) are expected to give promising and desirable recombinants in segregating generations, because they possessed the desirable features as seen from their cluster means.

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