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Genetic divergence in rice for physiological and quality attributes

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Abstract: Genetic divergence study of 42 genotypes of rice for 20 agronomic, physiological and quality traits led to their grouping into 12 clusters. Grouping of the genotypes from different eco-geographical regions into one cluster and from the same location into different clusters indicated non-parallelism between geographical distribution and genetic diversity. Highest contribution to the genetic diversity was through 100 grain weight followed by volume expansion ratio, kernel length, days to 50% flowering and plant height. The clusters XI and XII were highly divergent. The other clusters with moderate divergence and having single genotypes were VI, VII, VIII, and IX. Based on the inter-cluster distance, mean performance and clustering pattern, hybridization between Tellahamsa, Shiva, WGL-NDL2, Erramallelu, Lunisree, RDR763 and IR20 is likely to give recombinants having high yield potential and high grain quality.

Keywords: Rice, Genetic divergence, Quality.

Introduction

Genetic variability is the basic requirement for making progress in crop breeding. Inclusion of genetically diverse parents in any breeding programme is essential to create new genetic stock. Earlier workers showed the importance of study of genetic divergence for yield and yield attributes. In rice, low priority is accorded to evaluation of germplasm for physiological and quality traits. The development of high yielding, long duration varieties using *Javanicas* shows the great potential still remaining unutilised in germplasm. Therefore, the information on genetic divergence for physiological characters would help the plant breeder in choosing right parents for breeding programme aimed at yield improvement. Similarly, with growing demand for non-Basmati quality rices, germplasm studies for quality characters would be 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 physiological, agronomical and quality traits for use in hybridization programme to improve yield and quality.

Materials and Methods

Forty two rice genotypes were grown in a randomised block design with three replications during *Kharif* 1998. Each genotype was raised in 2 rows of 3m length at a spacing of 20 x 15 cm and the recommended doses of fertilizers at the rate of 100 Kg N, 60 Kg P_2O_5 and 40 Kg K_2O ha^{-1} was followed. Observations were recorded on 10 randomly, selected plants for yield components and 5 randomly selected plants for physiological traits. The mean values were subjected to analysis of variance and then to Mahalanobis (1936) D^2 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 twenty characters studied. Out of the 12 clusters obtained by grouping 42 genotypes based on relative magnitude of D^2 values, cluster I was the largest one with 19 genotypes. Cluster III, II and X had 8, 5 and 2 genotypes respectively, while the remaining 8 Clusters (IV to IX, XI and XII) were single genotype clusters (Table 1). The clustering pattern indicated existence of significant amount of variability, which was confirmatory with the findings of JawaharRam and Panwar (1970), Vairavan *et al.* (1979), Palanichamy and Siddiq (1979), Mahajan *et al.* (1981), Soni *et al.* (1999) and Jha *et al.* (1999).

Maximum intra-cluster distance (Table 2) was observed in cluster X (20.42), followed by III (15.47) and 1 (15.25). Thus, selection of genotypes based on high *per se* and other desirable traits from cluster I which had maximum number of genotypes (19) might be fruitful to generate the breeding material.

Based on the inter-cluster distance, cluster XII and XI having single genotypes, Chittimutyalu and MTU 1006 respectively were observed to

Table 1. Clustering pattern of 42 rice genotypes on D^2 statistics

Cluster	No. of genotypes	Name of genotypes included
I	19	MTU 9993, Rasi, Sasyasri, WGL 18011-15, Kalinga 1, Pothana, MTU 1003, MTU 1010, Tellahamsa, MTU 6203, Keshava, RDR 536, Himalaya 2, WGL 16388, WGL 9209, Divya, WGL 9335, Shiva, MTU 2400
II	5	Bhadrakali, WGL-16348, WGL-9380, Surekha, Himalaya -741
III	8	CTH 1, WGL-NDL 2, RNR-M7, Mudhol Thellalu, Kavya, RDR-836i WGL 16383, WGL 3929
IV	1	WGL 3938
V	1	Annada
VI	1	Erramallelu
VII	1	Lunisree
VIII	1	RDR 763
IX	1	IR 20
X	2	Gadengipatnam, RDR 831
XI	1	MTU 1006
XII	1	Chittimutyalu

Table 2. Mean intra (bold) and. inter-cluster distances among 12 clusters

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**15.25**	20.11	23.70	18.10	21.09	18.22	22.16	23.84	25.75	31.03	32.58	42.82
II		**12.38**	27.42	18.24	27.93	20.98	20.45	24.25	22.09	32.66	34.72	46.96
III			**15.47**	24.94	21.01	22.16	30.27	24.61	25.90	27.41	33.44	29.18
IV				**0.00**	18.88	21.89	1.6.05	28.84	28.05	28.51	37.15	45.76
V					**0.00**	27.30	25.81	30.92	25.45	24.32	40.65	37.09
VI						**0.00**	27.81	15.16	26.07	34.01	21.12	42.34
VII							**0.00**	35.28	30.60	27.27	38.80	45.79
VIII								**0.00**	24.37	37.70	25.82	40.23
IX									**0.00**	26.51	35.59	37.01
X										**20.42**	39.81	31.14
XI											**0.00**	43.62
XII												**0.00**

be highly divergent as compared to others. Cluster X with 2 genotypes (Gadengipatnam and RDR-831) was separated by higher genetic distance from clusters VI and VIII. Another cluster (VII) in which only one genotype (Lunisree) was included was divergent from the clusters III, VIII and IX. Hence, hybridization between genotypes from these clusters should result expression of hybrid vigour in higher magnitudes and production of large number of desirable recombinants for yield and quality. Hybridization between genetically distant genotypes to generate promising breeding material was suggested frequently (Viveknanadan and Subramanian, 1993; Roy and Panwar, 1993) by many workers.

A wide range of variation was registered in the cluster means for most of the characters

Table 3. Cluster means for 20 different characters

Clusters	Days to 50% flowering	Productive tillers plant^{-1}	Plant height (cm)	Panicle length (cm)	Filled grains panicle^{-1}	100 grain weight (g)	Leaf area index at tillering	Leaf area index at heading	Crop growth rate (T-H)	Net assimilation rate (T-H)
I	90.61	6.86	89.93	23.76	124	2.43	1.76	3.44	15.29	0.062
II	95.40	6.82	88.97	23.48	136	2.51	1.68	3.72	15.45	0.060
III	98.66	6.97	92.29	22.68	181	1.65	1.76	4.03	14.42	0.053
IV	104.66	6.73	91.13	21.60	126	2.64	1.61	4.40	14.60	0.052
V	105.66	7.86	86.33	21.20	166	2.28	1.91	5.00	16.52	0.052
VI	88.00	6.90	84.66	23.06	100	1.99	1.92	3.86	13.77	0.049
VII	101.33	6.33	124.76	23.13	141	3.08	2.10	4.11	21.05	0.070
VIII	84.66	8.53	79.60	22.73	143	1.60	2.29	3.28	14.14	0.051
IX	103.00	7.46	88.13	27.06	144	1.92	2.06	3.67	14.91	0.052
X	108.60	6.43	132.03	28.53	217	2.22	1.99	5.94	15.11	0.045
XI	79.00	6.13	112.46	24.13	120	1.54	1.20	2.45	15.81	0.071
XII	98.00	6.86	138.06	25.53	274	1.12	1.81	3.58	16.83	0.06

Table 3. (Contd..)

Clusters	Biological yield plant^{-1}	Crop growth rate(H-R)	Kernel length (mm)	Kernel breadth (mm)	Length/ breadth ratio	Hulling recovery (%)	Kernel elongation ratio	Volume expansion ratio	Harvest index	Grain yield plant^{-1} (g)
I	26.28	20.45	6.79	2.09	3.25	78.98	1.54	3.90	50.30	13.14
II	31.36	21.99	7.10	2.11	3.35	79.12	1.71	4.98	51.09	15.97
III	30.88	20.19	5.75	1.85	3.09	79.42	1.56	4.37	46.67	14.55
IV	29.70	16.92	7.39	2.08	3.55	78.06	1.50	3.86	41.40	12.30
V	36.76	25.20	6.16	2.21	2.78	77.21	1.60	3.73	48.03	17.66
VI	21.90	18.45	6.44	1.71	3.75	79.06	1.56	4.63	47.83	10.50
VII	44.88	28.25	7.65	2.20	3.46	79.58	1.54	3.80	48.13	21.58
VIII	19.24	25.19	5.8-1	1.76	3.29	76.62	1.78	5.26	49.53	9.54
IX	34.02	29.23	5.81	2.20	2.63	78.17	1.89	5.46	41.66	14.22
X	47.58	32.33	6.35	2.13	2.97	77.30	1.64	4.10	42.40	20.00
XI	12.87	8.01	6.41	1.56	4.09	76.84	1.58	4.73	45.20	5.79
XII	36.78	24.19	4.41	1.88	2.34	77.54	1.7,3	4.66	41.60	15.3

studied (Table 3). Higher differences were observed in respect of days to 50% flowering, plant height, filled grains per panicle, 100-grain weight, biological yield per plant, crop growth rate (heading to ripening), kernel length, volume expansion ratio and grain yield per plant, whereas for productive tillers per plant, leaf area at tillering, hulling recovery and harvest index, the variation was low. The genotypes included in the cluster I exhibited average performance for most of the characters and were mostly characterised by early flowering and high harvest index. The genotypes (CTH 1, WGL-NDL 2, RNR-M7, Mudholthellalu; Kavya and WGL 3929) of cluster III possessed higher number of grain per panicle. Cluster VI had only one genotype (Erramallelu), which was highly adoptable with highest grain L/B ratio. The genotype, Lunisree forming a separate cluster (VII) had highest 100 grain weight, kernel length and high crop growth rate (heading to

Table 4. Contribution of each character to the diversity in percentage.

S.No.	Character	Times ranked 1st	Contribution in percentage
1.	Day to 50% flowering	102	11.85
2.	Productive tillers per plant	1	0.12
3.	Plant height	88	10.22
4.	Panicle length	7	0.81
5.	Filled grain per panicle	12	1.39
6.	100-grain weight	168	19.51
7.	LAI at-tillering	0	0.00
8.	LAI at heading	0	0.00
9.	CGR (tillering to heading)	4	0.46
10.	NAR (tillering to heading)	0	0.00
11.	Biological yield	0	0.00
12.	CGR (Heading to ripening)	35	4.07
13.	Kernel length	107	12.43
14.	Kernel breadth	87	10.10
15.	L/B ratio	19	2.21
16.	Hulling percentage	21	2.44
17.	Kernel elongation ratio	7	8.25
18.	Volume expansion ratio	128	14.87
19.	Harvest index	6	0.70
20.	Grain yield per plant	5	0.58

ripening), biological yield and grain yield per plant. Such type of parent having many desirable traits might be considered as good parent to create further variability for these traits. The other promising genotype, IR 20 of single genotype cluster (IX) had high *per se* for biological yield, CGR and volume expansion ratio. The cluster XI had one genotype (MTU 1006) with lowest *per se* for all the traits except L/B ratio. The cluster XII containing Chittimutyalu was characterised by most undesirable traits like tallness, lowest 100 grain weight and grain L/B ratio.

Grouping of the genotypes indicated non-parallelism between geographical distribution and genetic diversity, since genotypes from different geographic origins were included in same cluster and those from same location were included in different clusters. Singh *et al.* (1979), Singh (1981), Rao and Gomatinayagam (1997) and Ahmed and Borah (1999) also reported similar findings.

Consideration of relative contribution of individual characters to the genetic divergence revealed that 100 grain weight (Das and Borthakur, 1973), volume expansion ratio, kernel length (Ratho, 1984), days to 50% flowering, plant height (Kanwal *et al.* 1983), kernel elongation ratio and post flowering CGR contributed maximum, and less contribution to the diversity was through physiological traits (Table 4).

Crossing among divergent parents having desirable traits is most likely to produce better hybrids and desirable recombinants. The greater distance between two clusters indicate higher genetic diversity between them.

Based on the inter-cluster distances and high *per se* for other desirable attributes associated, the parents Tellahamsa and Shiva of cluster I, WGL-NDL 2 of cluster III Lunisree of cluster VII and IR 20 of cluster IX and RDR 831 of cluster X are expected to give promising segregants for grain yield and quality in segregating generations.

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