Genetic Diversity among Indigenous Landraces of Rice for Certain Quality Traits

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One hundred twenty indigenous rice genotypes collected from Jharkhand were evaluated for twelve quality characters to study genetic divergence by employing D^2 analysis. The genotypes were grouped into nine diverse clusters. The highest genetic divergence was observed between cluster I and cluster III, whereas cluster IV and VIII were the closest one. Hence, genotypes belonging to cluster I and III can be used as parents for hybridization programme for the development of high yielding rice genotypes.

Key Words: Rice, L/B ratio, Landraces, Quality traits, Genetic diversity

Introduction

The success of any crop breeding programme depends on the nature and amount of genetic variability available in the germplasm collections. Germplasm collected from different states/countries serves as the most valuable natural resource in providing needed attributes for developing successful varieties (Hawkes, 1981). The classification or grouping of germplasm collection is a pre-requisite for distinguishing genetically close and divergent types for various plant breeding programmes. Genetically diverse parents are likely to produce high heterotic effects and desirable segregants. By using advance biometrical techniques such as multivariate analysis based on Mahalanobis's D^2 statistics (Mahalanobis, 1936), it has now become possible to quantify the degree of genetic divergence amongst biological populations. Therefore, the present investigation is aimed at ascertaining the nature and magnitude of genetic diversity among one hundred twenty landraces of rice from Jharkhand State for quality characters.

Materials and Methods

The experimental material comprised of one hundred twenty traditional germplasm lines obtained from Jharkhand State through the NGO Gene Campaign, Ranchi, and were evaluated in a randomized block design experiment with three replications at Research Farm of Kisan P.G. College, Simbhaoli (Ghaziabad) during *kharif* 2005. Each genotype was assigned to two row plots of 3 m length with inter and intra-row spacing of 40 cm and 15 cm, respectively. Recommended agronomic practices were followed to raise a good crop. Data were recorded on five randomly selected competitive plants from each plot on twelve characters, namely, hulling (%), milling (%), head rice recovery (%), kernel length (mm), kernel breadth (mm), length/breadth ratio, kernel length after cooking (KLAC), kernel breadth after cooking (KBAC), kernel elongation ratio (ER), alkali spreading value (ASV), aroma and 1000 grain weight (g). The data recorded on above characters were subjected to D^2 analysis (Mahalanobis, 1936; Rao, 1952).

Result and Discussion

Analysis of variance (Table 1) revealed the significant differences among the genotypes for all the characters studied indicating thereby the existence of genetic variability among the genotypes to identify desirable genotypes. Based on D^2 statistics, 120 genotypes were grouped into nine clusters of which cluster VII had maximum 25 genotypes, followed by cluster IV, V and VIII having 24, 22 and 18 genotypes, respectively (Table 2). The genotypes falling in the same cluster are more closely related and hence the clusters having the maximum number of genotypes, reflected narrow genetic diversity.

Results of cluster analysis indicated that the highest intra-cluster distance was observed for cluster VI followed by cluster III, cluster V, cluster II, cluster VIII, cluster IX, cluster IV, cluster VII and cluster I (Table 3). This suggested that the genotypes in cluster VI were relatively more diverse among themselves, however, in all cases, the inter-cluster distances were greater than the intra-cluster distances implying presence of greater degree of genetic diversity between the genotypes of two clusters than the genotypes present within the cluster.

From the inter-cluster distances for nine clusters (Table 3), it can be seen that the highest divergence occurred between cluster I and III (8.611) followed by cluster II and III (7.923) and cluster I and VI (7.507)

Table 1. Analysis of variance (ANOVA) for quality characters

Sources of variation	df	Mean squares											
		Hulling %	Milling %	HRR %	KL mm	KB mm	L/B ratio	KLAC mm	KBAC mm	ER	Aroma	ASV	1000 GW g
		1	2	3	4	5	6	7	8	9	10	11	12
Replication	2	27.62	15.43	13.12	0.014	3.65	0.111	0.036	0.0008	0.0006	0.019	3.80	0.03
Genotypes	199	38.74**	66.33**	77.25*	0.782**	15.34*	0.033*	4.655**	0.1735**	0.0277**	1.077**	12.77**	100.43**
Error	238	0.52	0.30	1.80	0.003	1.78	0.075	0.003	0.0017	0.0003	0.027	0.20	0.07

** Significant at P=0.05; * P=0.01 levels, respectively
df = Degree of freedom
KLAC= Kernel length after cooking, KBAC= Kernel breadth after cooking, L/B ratio= Length/Breadth ratio, ER= Elongation ratio, ASV= Alkali spreading values, HRR+ head rice recovery, KL= Kernel length, KB= Kernel breadth, GW= Grain weight

Table 2 . Distribution of 120 genotypes of rice in different clusters

No. of cluster	No. of genotypes	Name of genotypes
I	3	Badya(B), U.L-4, Barka-Tilasar
II	8	Garib-Saal, Kanke-Saal, Anjani, Mehra-Dhan, Boka-Dhan, Ejaan, Asamia, U.L-2
III	7	Ujla Basmati1, Basmati 370, Pusa Basmati 1, Banphool(A), Choota-Dahia, Kalam-Dani, U.L-3
IV	24	Mehra-Dhan, Khir-Bhojni, Suga-Thor, Sonagoti, Bhadwa-Kalamdani, Tulsi-Ketki, Karhaini, Maina-Thori, KalamDani, Sitwa, Has-Kalma, Sir Hatti, Doodh-Kandhar(A), Lahi, Bara-Sitwa, Burah-Dhan, Sarna, Karijiri(A), Khutuwa, Karhaim-Chhota, Barah-Saal, Kherka, Rani-Kesar
V	22	Bagh-Panjar, Mehsuri-Nata, Amma-Dhoka, Ramdilal, Kanaschapar, U.L-1, Sanam-Dhan, Mirmitti, Kala-Zira, Makar Kalma, Khir-Bhat(B), Yes-Kalma, Badya(A), Thubka, Konhra-Phool, Nanhiya, Barka-Swarna, Raz-Bhokta, Daani-Gora, Sihul, Kherka–kuchi, Karhaini (B)
VI	4	Barkhadhan, Mirmitti, Panchsala, Kalam-Kathi (B)
VII	25	Katika, Sirhanthi, Chaaina-Gora, Dahiya-2, Barka-Kalma, Rani-Kajjar, Charka-Khairkakuchi, Charka-Nardha, TilaSaar, RupSari, Kalam-Katni(A), Chhotka-Suman, Dehati-Gora, Guda, Maiya-Dulari, Hans-Kalma, BanPhool(B), Budhnu-Nanhi, Karijiri(A), Makar Kalma, Khir-Bhat(B), Miri-Mitti, Ghuthia, Kala-Basmati, Sugandha
VIII	18	Sugandha, Ujla Basmati2, Ketki, Dehati-Gora, Nambri-Dhan, Barka-Dhusri, Lal-Mugdi, Type-III , Chhotka-Sitwa, Kodowa, Budhnu-Nanhi, Barka-Dhan, Kohra-Phool, Charka-Raes, Bihar-Dhan, Barka-Mansuri, Jhilli, Raz-Bhokta
IX	9	Raz-Bhokta, Sitwa-Dhan, Tulsi-Ketki, Kala-Zira, Yes-Kalma, Kalam-Kathi(B), Son-Piya, Dudh-Kandhar, Hardi Muri Lal

Table 3. Average inter and intra-cluster (bold values) distances involving 120 genotypes of rice

	Cluster								
	I	II	III	IV	V	VI	VII	VIII	IX
I	1.750								
II	6.978	2.427							
III	8.611	7.923	2.900						
IV	7.005	4.188	6.981	2.003					
V	7.196	4.258	6.650	2.618	2.477				
VI	7.507	6.052	6.361	4.876	2.203	3.274			
VII	6.441	3.548	5.755	2.280	2.738	4.363	1.956		
VIII	6.915	4.371	5.346	2.061	2.279	4.338	2.131	2.211	
IX	6.962	4.818	5.104	3.994	3.093	4.623	2.574	3.291	2.138

Table 4. Cluster mean value for quality character

Characters	Cluster								
	I	II	III	IV	V	VI	VII	VIII	IX
Hulling (%)	75.93	74.35	80.49	78.37	75.00	79.15	75.71	80.41	77.14
Milling (%)	63.18	54.12	70.93	67.73	64.62	66.50	65.53	68.71	65.23
Head rice recovery (%)	53.29	45.32	62.44	59.78	58.36	61.84	58.31	57.00	58.51
Kernel length (mm)	5.02	4.88	6.49	4.62	4.79	4.17	5.07	5.03	5.18
Kernel breadth (mm)	16.00	2.06	1.61	2.13	1.88	1.93	1.98	1.96	1.72
L/B ratio	2.53	2.37	3.98	2.21	2.56	2.16	2.58	2.68	3.24
Kernel length after cooking	8.69	8.27	11.66	7.40	7.45	9.30	8.65	8.54	9.16
Kernel breadth after cooking	2.80	2.78	2.35	2.70	2.27	2.52	2.71	2.44	2.56
Elongation ratio	1.73	1.69	1.79	1.60	1.56	2.25	1.71	1.69	1.78
Aroma	0.67	0.00	1.76	0.04	0.14	1.33	0.04	0.31	0.11
Alkali spreads value	7.00	3.25	5.86	2.35	3.71	5.83	5.17	3.15	6.81
1000 grain weight	19.97	21.11	19.80	18.30	8.68	16.77	19.86	20.41	5.17

indicating the presence of greater diversity between genotypes of these groups. Hence, crossing between genotypes belonging to these clusters may result in high heterosis, which could be exploited in crop improvement. The least inter-cluster distance was noticed between cluster IV and VIII (2.061) followed by cluster VII and VIII (2.131) and cluster V and VI (2.203) indicating the close relationship and similarity for most of the characters of the genotypes in these clusters.

The cluster III showed the highest cluster means for hulling and milling (%), head rice recovery (%), kernel length, L/B ratio, kernel breadth after cooking (KBAC) and alkali spreading value (ASV). 1000 grain weight exhibited highest mean in cluster II whereas kernel breadth and elongation ratio exhibited highest mean values in cluster IV and cluster VI, respectively (Table 4). The percent contribution of the characters studied towards genetic divergence showed that 1000 grain weight contributed maximum (20.25%) followed by KLAC (17.56%), ASV (13.15) and HRR (6.83%). The results of the present study are in agreement with the findings of several earlier workers (Ratho, 1984; Pradhan and Roy, 1990; Singh, 2005 and Chand *et al*., 2005).

The data on inter-cluster distance and performance of the genotypes was used to select genetically diverse and agronomically superior genotypes among 120 genotypes. As cluster I showed the maximum inter-cluster distances with other cluster hence, the three genotypes (UL-4, Badya and Barka-Jilasar) belonging to cluster I could be utilized as parents in future breeding programme with the desirable genotypes belonging to cluster II, III and VI. Inter-crossing between genotypes belonging to cluster I, II, III and VI may generate large variability and can be expected to produce desired genotypic combinations and transgressive segregants and form a good source material in further crop improvement programme.

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