

Genetic divergence in traditional rice accessions in Chhattisgarh

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SUMMARY

The D² analysis allowed the 96 genotypes of rice to be identified into nine distinct clusters. Among the different clusters, cluster VII contained maximum of 20 genotypes and cluster V contained a minimum of 6 genotypes. The cluster IV was characterized by highest mean value for days to 50 per cent flowering, plant height, number of filled grains per panicle and grain yield per plant. The clusters VI and II had highest mean value for panicle length and head rice recovery percentage, respectively. The cluster IX was characterized by highest mean value for number of effective tillers per plant, kernel length and milling percentage. The highest inter cluster distance was observed between cluster IV and VIII while the lowest between III and VI. The lowest and highest intra cluster distance was observed in cluster III and VI, respectively. There is good scope to bring about improvement through hybridization and selection by crossing accessions from different clusters.

Key Words : Genetic divergence, D² technique, Cluster, Rice germplasm

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Crop improvement basically depends on the extent of diversity present in the genotypes. The success of any breeding programme depends upon the selection of the parents for hybridization. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for breeding programme. The available diversity in the germplasm serves as an insurance against unknown future needs. The more diverse the parents, the greater are the chances of obtaining higher amount of heterotic expression in F₁s and broad spectrum of variability in segregating generations (Maurya and Singh, 1977). Careful

selection of parents for hybridization programme will decide the extent of possible improvement in the genotypes under consideration. Improvement is primarily depends on the diversity of the parents. Multivariate analysis developed by Mahalanobis (1936) is an appropriate method for selection of parents (Vivekanandan and Subramanian, 1993; Mishra *et al.*, 1994). In the present study, an attempt was made to classify and understand the nature and magnitude of genetic diversity by using Mahalanobis D² statistics.

MATERIAL AND METHODS

The experimental material consisted of 96 rice germplasm including 6 checks namely IR-64, Poornima, Mahamaya, Swarna, Samleshwari and Chandrahasini. Rice germplasm collected from Bastar region of Chhattisgarh. The experiment was conducted in a Complete Randomized Block Design with two replications during the wet season, 2006. Twenty five days old seedlings were transplanted with a spacing of 20 cm and 15 cm between rows and between plants, respectively. Observations were recorded on five randomly selected plants for 18 morphological and quality characters *viz.*, leaf length, leaf width, days to 50 per cent flowering, number of effective tillers per plant, plant height, panicle length, number of filled grains per panicle, spikelet sterility percentage, 100 seed

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weight, paddy length, paddy breadth, brown rice length, brown rice breadth, kernel length, kernel breadth, milling percentage, head rice recovery percentage and grain yield per plant. The analysis of genetic divergence using Mahalanobis (1936) D^2 statistics was done as described by Spark (1973) and the material has grouped into different clusters.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all characters indicating existence of variability among the genotypes for the characters studied. Based on the relative magnitude of D^2 values, 96 genotypes were grouped into 9 clusters. Among the different clusters (Table 1) cluster VII contained maximum of 20 genotypes and cluster V contained a minimum of 6 genotypes. The 11 genotypes each were assigned to cluster I, II and III. The 12

genotypes included in cluster VIII and 9 genotypes included in cluster IV. The cluster VI and IX contained 8 genotypes each. The clustering pattern of genotypes (cluster II and IX) revealed that the genotypes released / recommended for state were clubbed together in one group (cluster IX). The other genotypes clubbed together with cluster II and IX might be the valuable sources for further improvement of well adapted varieties of state. The clustering distribution of some other clusters indicated that the genetic diversity found among the genotypes belong to same geographic origin (Bastar region) might be due to differences in adaptation, selection criteria, selection pressure and environmental condition (Vivekanandan and Subramanian, 1993; Nayak *et al.*, 2004).

A wide range of variation was observed in cluster means for all the characters studied (Table 2). The cluster IV was characterized by highest mean values for leaf width, days to

Table 1: Clustering pattern of 96 rice genotypes

Cluster number	Number of genotypes	Genotype name
I	11	PSR-11127, PSR-11208, PSR-11210, PSR-11211, PSR-11213, PSRSK-11128, PSRSK-11129, PSRSK-11133, PSRSK-11147, ND-9-3, ND-17
II	11	PSR-11126, PSRSK-11135, PSRSK-11152, PSRSK-11154, PSRSK-11158, PSRSK-11159, PSRSK-11162, PSRSK-11166, PSRSK-11188, PSRSK-11189, Swarna
III	11	PSRSK-11139, PSRSK-11146, PSRSK-11182, ND-4, ND-9-2, ND-13, ND-15, ND-18-2, IGD-79, ND-82, ND-104
IV	9	PSR-11195, PSR-11198, PSR-11202, PSR-11203, PSR-11206, PSR-11207, PSRSK-11156, PSRSK-11165, ND-8
V	6	PSR-11216, PSR-11220, PSRSK-11148, PSRSK-11150, PSRSK-11191, ND-2
VI	8	PSR-11125, PSR-11194, PSR-11218, PSRSK-11132, PSRSK-11185, PSRSK-11186, PSRSK-11190, PSRSK-11193
VII	20	PSR-11196, PSR-11209, PSR-11212, PSRSK-11137, PSRSK-11141, PSRSK-11145, PSRSK-11157, PSRSK-11163, ND-1, ND-11, ND-12, IGD-23, IGD-5, IGD-22, IGD-25, IGD-40, ND-49, ND-20, Mascatia Dhan, Chaina Dhan
VIII	12	PSR-11199, PSR-11200, PSR-11215, PSR-11221, PSRSK-11130, PSRSK-11140, PSRSK-11151, PSRSK-11160, PSRSK-11161, PSRSK-11181, PSRSK-11183, PSRSK-11187
IX	8	PSRSK-11131, PSRSK-11167, PSRSK-11192, Poornima, IR-64, Mahamaya, Samleshwari, Chandrahasani

Table 2: Cluster mean for morphological and quality characters in 96 rice genotypes

Characters cluster	LL (cm)	LW (cm)	DF	FG/Pa	PH (cm)	PaL (cm)	ET/P	SPS %	TW (g)	PL (mm)	PB (mm)	BRL (mm)	BRB (mm)	KL (mm)	KB (mm)	Mill %	HRR %	GY/P (g)
I	46.76	1.15	97.18	9.32	138.84	26.63	155.50	8.60	2.49	8.98	2.94	6.52	2.46	5.85	2.30	71.14	56.61	26.41
II	49.88	1.15	99.23	10.59	137.31	23.80	160.09	13.04	1.87	7.93	2.53	6.00	2.25	5.25	2.05	72.63	63.81	22.30
III	39.40	0.96	83.77	14.32	118.43	21.95	103.82	6.06	2.47	8.30	2.99	6.15	2.51	5.52	2.33	70.62	35.26	19.38
IV	50.62	1.37	100.94	8.72	151.05	27.30	163.28	11.83	2.45	8.22	3.06	6.16	2.62	5.49	2.44	72.97	61.20	30.21
V	40.43	1.06	90.33	10.42	116.00	25.65	98.58	11.88	2.44	8.77	3.10	6.49	2.32	5.92	2.17	71.11	53.55	16.79
VI	50.97	1.14	98.19	9.69	145.88	28.87	153.50	9.71	2.19	9.73	2.44	7.01	2.09	6.36	1.94	72.03	57.02	27.94
VII	42.60	1.13	84.62	11.52	129.58	25.08	129.48	7.47	2.55	8.31	3.04	6.25	2.60	5.59	2.42	71.54	40.74	26.12
VIII	49.35	1.23	97.25	9.67	139.70	25.75	157.79	16.16	2.82	9.03	3.26	6.34	2.73	5.80	2.67	73.00	54.52	28.33
IX	37.76	1.14	90.81	14.75	97.32	26.15	142.06	15.12	2.43	9.43	2.52	7.21	2.21	6.47	2.06	73.28	58.94	27.47

Note :- LL - Leaf length, LW - Leaf width, DF - Days to 50% flowering, FG/Pa - Number of filled grains per panicle, PH - Plant height, PaL - Panicle length, ET/Pa - Number of effective tillers per plant, SPS% - Spikelet sterility percentage, TW - 100 seed weight, PL - Paddy length, PB - Paddy breadth, BRL - Brown rice length, BRB - Brown rice breadth, KL - Kernel length, KB - Kernel breadth, Mill% - Milling percentage, HRR% - Head rice recovery percentage, GY/P - Grain yield per plant

50 per cent flowering, plant height, number of filled grains per panicle and grain yield per plant. The highest value for leaf length, panicle length and paddy length was observed for clusters VI. The highest mean value for spikelet sterility percentage, 100 seed weight, paddy breadth, brown rice breadth and kernel breadth was observed for cluster VIII. The cluster IX was characterized by highest mean value for number of effective tillers per plant, brown rice length, kernel length and milling percentage. The cluster III had lowest mean value for days to 50 per cent flowering, panicle length, spikelet sterility percentage, milling percentage and head rice recovery percentage. The highest mean value for head rice recovery percentage was observed for cluster II.

The average intra and inter cluster D^2 values are presented in Table 3. An intra cluster distance was maximum in cluster III (8.421) followed by cluster V (5.212), cluster I (5.026) and cluster II (4.182). High intra cluster distance indicates wide genetic divergence among the constituent genotypes. The inter cluster distance was maximum between cluster I and cluster IV (70.879) followed by cluster II and IV (60.031) and cluster III and cluster IV (36.747) suggesting that these groups of genotypes were highly divergent from each

other. The genotypes in above clusters revealed substantial differences in the means for important yield contributing characters, suggesting that the genotypes belonging to these clusters form ideal parents for initiating hybridization. The minimum inter cluster was found between cluster I and cluster II (5.784) indicating that the genotypes of these clusters were genetically very close to each other. To realize much variability and high heterotic effect, Mishra *et al.* (2004) and Chaturvedi and Maurya (2005) recommended that parents should be selected from two clusters having wider inter cluster distance. In the present study the genotypes from cluster IV (ND-8, PSR-11203, PSRSK-11181, PSR-11215, PSRSK-11183) having desired mean value for number of filled grains per panicle and grain yield per plant (Table 4); cluster IX (IR-64, Chandrahasini, Mahamaya, PSRSK-11167) having high value for number of effective tillers per plant, kernel length and milling percentage; cluster II (PSRSK-11189, PSRSK-11188, PSRSK-11154) having high value for head rice recovery percentage and cluster III (ND-104, ND-82 and PSRSK-11182) having low value for days to 50 per cent flowering. These may be used in hybridization programme to achieve desired segregants for good grain quality with higher yield.

Table 3: Intra- and inter- cluster distances based on D^2 statistics

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	3.295								
II	4.024	3.274							
III	4.698	5.610	2.370						
IV	3.243	4.060	6.389	2.650					
V	3.474	4.826	3.157	5.363	2.857				
VI	3.439	4.608	6.674	5.078	4.951	3.628			
VII	3.017	4.712	2.672	4.121	3.078	5.405	2.719		
VIII	3.451	5.233	5.767	2.666	4.840	5.527	3.715	2.832	
IX	4.798	5.558	5.773	6.211	4.307	4.283	5.120	5.695	3.003

Table 4: Desirable rice genotypes from best clusters for different traits

Character	Rank		
	I	II	III
Days to 50% flowering	ND-104	ND-82	PSRSK-11182
Number of effective tillers per plant	IR-64, Mahamaya	Chandrahasini	Poornima
Panicle length (cm)	PSRSK-11190	PSRSK-11193	PSR-11194
Plant height (cm)	Samleshwari	PSRSK-11192	Poornima
Number of filled grains per panicle	PSR-11203	ND-8	PSRSK-11165
Spikelet sterility percentage	PSRSK-11146	ND-18-2	ND-82
100 seed weight (g)	PSRSK-11181	PSR-11215, PSRSK-11183	PSRSK-11160
Grain yield per plant (g)	PSR-11195	PSR-11202, PSR-11203	PSR-11207
Paddy length (mm)	PSRSK-11190	PSRSK-11132, PSRSK-11185, PSRSK-11193	PSR-11194
Kernel length (mm)	PSRSK-11167	IR-64	Chandrahasini
Milling percentage	Chandrahasini	IR-64	PSRSK-11167
Head rice recovery percentage	PSRSK-11189	PSRSK-11188	PSRSK-11154

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