

Genetic divergence in traditional rice accessions of Chhattisgarh

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ABSTRACT

Based on D^2 analysis, Ninety six genotypes of rice collected from Bastar region of Chhattisgarh were grouped. The genotypes from cluster IV (ND-8, PSR-11203, PSRSK-11181, PSR-11215, PSRSK-11183) having desired mean value for number of filled grains panicle⁻¹ and grain yield plant⁻¹, cluster IX (IR-64, Chandrahasini, Mahamaya, PSRSK-11167) having high value for number of effective tillers plant⁻¹, 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) having low value for days to 50% flowering.

Key words: rice germplasm, genetic diversity, variability, Chhattisgarh

Crop improvement basically depends on the extent of diversity present in the genotypes. The success of any breeding programme depends on 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. Multivariate analysis developed by Mahalanobis (1936) is an appropriate method for selection of parents (Mishra *et al.*, 1994). Therefore, in the present study traditional rice accessions of Chhattisgarh were evaluated to assess the genetic diversity among these genotypes.

The experimental material consisted of 96 rice germplasm lines including 6 checks namely IR-64, Poornima, Mahamaya, Swarna, Samleshwari and Chandrahasini. Rice germplasm were collected from Bastar region of Chhattisgarh. The experiment was conducted in a Complete Randomized Block Design with two replications during the wet season, 2007. 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% flowering, number of effective tillers plant⁻¹, plant height, panicle length, number of filled grains panicle⁻¹, spikelet sterility percentage, 100 seed weight, paddy length, paddy breadth, brown rice

length, brown rice breadth, kernel length, kernel breadth, milling percentage, head rice recovery percentage and grain yield plant⁻¹. The analysis of genetic divergence using Mahalanobis D^2 (1936) statistics was done as described by Spark (1973) and the material has grouped into different clusters.

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 consisted 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

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, Chandrahasini

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 exhibited highest mean value for days to 50% flowering, plant height, number of filled grains per panicle and grain yield plant⁻¹. The cluster VI and II having highest value for panicle length and head rice recovery percentage, respectively. The cluster IX

showed highest mean value for number of effective tillers plant⁻¹, kernel length and milling percentage.

The cluster III exhibited lowest mean value for days to 50% flowering, panicle length, spikelet sterility percentage, milling percentage and head rice recovery percentage. The highest mean value for 100 seed weight has recorded by cluster VIII.

The inter cluster distance (Table 3) ranged from 2.666 to 6.674 between cluster IV and VIII and III

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)	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	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	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	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	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	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	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	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	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	6.47	2.06	73.28	58.94	27.47

LL - Leaf length, LW - Leaf width, DF - Days to 50% flowering, FG/Pa - Number of filled grains panicle⁻¹, PH - Plant height, PaL - Panicle length, ET/Pa - Number of effective tillers plant⁻¹, SPS% - Spikelet sterility percentage, TW - 100 seed weight, KL - Kernel length, KB - Kernel breadth, Mill% - Milling percentage, HRR% - Head rice recovery percentage, GY/P - Grain yield plant⁻¹

Table 3. Intra- and intercluster distances based on D² 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

and VI, respectively. The lowest and highest intracluster distance was observed in cluster III and VI respectively. To realize much variability and high heterotic effect, Mishra *et al.* (2003) 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; 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) having low value for days to 50% flowering. These may be used in hybridization programme to achieve

desired segregants for good grain quality with higher yield.

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