

Genetic diversity studies in promising lowland rice varieties

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ABSTRACT

Genetic diversity of 42 rain fed lowland rice varieties of different states of India were studied through Mahalanobis D^2 statistic. The genotypes were grouped into 11 clusters. The cluster II contained highest number of genotypes (9) followed by cluster III (7), cluster IV (7). The cluster VII to XI contained one genotype each. The intra cluster distance was highest in cluster VI (13.42), followed by cluster II (9.95), cluster I (7.13), and lowest was 0.00 from cluster VII to XI. Highest inter cluster distance was noticed in cluster VII and VI ($D=40.07$), followed by cluster XI and VI ($D=37.020$), cluster IX and VI ($D=35.00$) and cluster VI and III ($D=33.74$). The genotypes of the cluster II and VIII, cluster II and IX, and cluster VI and XI will exhibit high level of production as well as earliness. Plant height, Days to 50% flowering, 1000 grain weight, together accounted for 87.11 percent to the total divergence indicating their importance in choice of parents for hybridization programme. The genotypes of these clusters should be selected for future breeding programme to enhance the yield in lowland.

Key words: Genetic diversity, D^2 analysis, lowland rice

Rice is the staple food for the world in general and eastern India in particular. Lowlands are predominant in eastern India. The production is very low in lowlands of eastern India due to erratic climatic condition coupled with non-availability of high yielding varieties. To meet the food requirement, the productivity in lowlands should be increased, which will be achieved only by developing high yielding varieties through hybridization. For hybridization programme, classification of germplasm is the prerequisite for determining the genetically close or divergent types. Genetic divergence study is a useful tool for efficient choice of parents for hybridization to develop high yield potential cultivars. Such study also select the genetically divergent parents to obtain desirable recombinants in the segregating generations. The understanding of association of characters is of prime importance in developing efficient breeding programme. Genetic improvement mainly depend on the amount of genetic variability present in the population. With development of advanced biometric technique, such as multivariate analysis based on Mahalanobis (1936) D^2 statistics, it is now possible to quantify the degree of divergence among the biological population and assessing the relative contribution of different component to total divergence. More diverse parents are believed to increase the chances of obtaining

stronger heterosis and give broad spectrum of variability in segregating population. Islam *et al.*, (2003) and Bisht *et al.*, (2007) have reported some information about genetic diversity studies in lowland rice. The present study was undertaken to study further genetic diversity in promising lowland rice varieties.

MATERIALS AND METHODS

Forty two promising lowland rice varieties of different states were evaluated at Central Rice Research Institute, Cuttack in a randomized block design with three replications. The spacing was 15 x 20 cm. The recommended agronomic practices were followed to raise good crop. Observation on plant height, panicle length, a EBT hill⁻¹, grains panicle⁻¹, sterile spikelets panicle⁻¹, yield hill⁻¹, 1000 grain weight, grain length and grain breadth were recorded on randomly selected plant from each plot, where as days to 50% flowering was recorded on plot basis. Multivariate analysis of genetic divergence among varieties was done using Mahalanobis D^2 statistics and grouping of varieties into clusters by Tochers method (Rao, 1952)

RESULTS AND DISCUSSION

Analysis of variance showed significant differences for

all 12 characters studied among the genotypes. Based on the D² values, 42 genotypes were grouped into eleven clusters (Table 1). Maximum 9 genotypes were grouped in cluster-II, followed by 7 genotypes each in cluster III and cluster IV. The cluster from VII to XI were monogenotypic cluster having only one genotype. The clustering pattern also corroborated with the dendrogram, presented in Fig. 1. Clustering pattern revealed that the varieties representing from same state were grouped in to different clusters indicating genetic heterogeneity among the genotypes.

The intra and inter cluster distance were presented in Table 2. Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among genotypes. The maximum intra cluster distance was recorded in cluster VI (D=13.42), which was significantly different from cluster II (9.95) and I (7.13). The inter cluster distance was higher in cluster all clusters except I and II. Highest inter cluster distance was noticed between cluster VII and cluster VI followed by cluster XI and VI, cluster IX and VI and cluster VI and III indicating wide diversity among these. (Saini and Kaiker, 1987). Minimum inter cluster distance was observed in cluster X and IX, followed by cluster

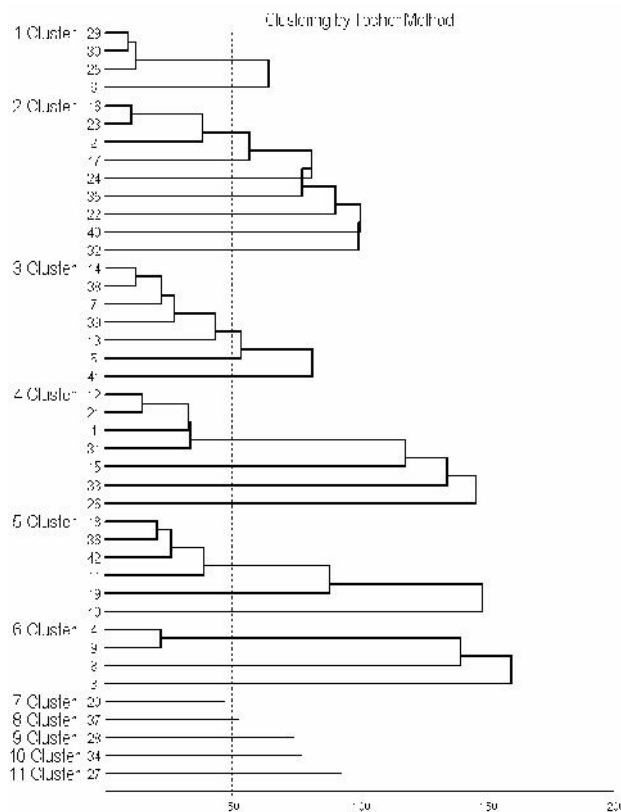


Fig. 1. Clustering of 42 genotypes by Tocher method

Table 1 Clustering pattern of 42 rice genotypes based on D² statistics

Clusters	Number of genotypes	Name of genotypes and serial number	State
I	4	Bhagirathi(25)Matangini(29),Hanseswari(30) Mahalaxmi(6)	West Bengal Orissa
II	9	Saraswati(40), Nalini(23), Sashi(17), Dinesh(24), Golak(35), Sonamani(32). Utkalprava(2), Kanchan(16) FR-13A(22),	West Bengal Orissa Orissa
III	7	Padmini(7), Dhusura(39), Ketekijoha(5), Dubraj(14) Ranjit.(41) Mahsuri(38) Mandyavijay(13),	Orissa Assam AndhraPradesh Karnataka
IV	7	Dharitri(12), Gayatri(1), Savitri(31), Sarala(15), Panidhan(26) Neerja(33),. Salivahana(21)	Orissa West Bengal AndhraPradesh
V	6	Moti(10),Lunishree(36), Sabita(18), Sudhir(42),Suresh(11) Rajshree(19)	Orissa West Bengal Bihar
VI	4	Durga(4),Tulsi(9), Varshadhan(3) Purnendu(8),	Orissa West Bengal
VII	1	Sambhamahsuri(20)	AndhraPradesh
VIII	1	CR1014(37)	Orissa
IX	1	Swarna(28)	AndhraPradesh
X	1	Pooja(34)	Orissa
XI	1	Jogen(27)	West Bengal

Table 2. Intra and inter cluster average D² in 42 rice genotypes

Group	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	(7.13)	13.94	16.06	21.64	13.85	28.63	24.11	20.86	18.73	19.02	21.34
II		(9.95)	20.74	14.70	15.03	19.06	28.54	16.25	23.06	18.52	25.65
III			(7.87)	24.64	20.11	33.74	14.23	16.70	13.46	14.76	21.96
IV				(11.28)	18.70	17.18	28.31	17.09	23.19	16.12	26.03
V					(10.28)	26.19	24.91	22.22	18.73	16.56	16.11
VI						(13.42)	40.07	22.61	35.00	27.94	37.02
VII							(0.00)	23.64	9.01	13.89	18.84
VIII								(0.00)	21.97	15.85	29.65
IX									(0.00)	9.54	14.27
X										(0.00)	16.50
XI											(0.00)

Table 3. Cluster mean for different quantitative characters in 42 rice varieties

Clusters	PH (cm)	EBT hill ⁻¹	PL (cm)	PW (gms)	Grains panicle ⁻¹	Sterile spikelets panicle ⁻¹	DDF (days)	1000 grwt (gms)	GL (mm)	GB (mm)	L/B	SPY (gms)
I	167.24*	11.70	23.43	4.10*	151.92	18.00	126.92	23.92	8.03	3.05*	2.65**	13.65**
II	156.09	11.16	25.41	3.47	142.70	18.30	135.26	23.39	8.22	2.83	2.98	15.99
III	138.82	11.45	25.94	2.51**	137.71	19.00	126.52	15.53	7.70**	2.22	3.48	13.83
IV	111.79	11.04	24.67	3.56	147.71	17.24	138.33	22.52	7.91	2.71	2.96	16.69
V	139.32	10.33	26.13	3.50	143.86	18.28	130.06	28.11	9.75	2.43	4.01	15.41
VI	144.98	12.91	25.32	3.97	171.83*	15.92	146.75*	23.75	8.53	2.48	3.43	14.74
VII	81.83	12.93	21.33**	3.37	119.33	22.67	122.33**	14.50	7.83	2.10	3.75	14.20
VIII	134.33	10.00	27.50*	2.73	146.67	16.00	138.00	14.00**	7.97	1.90**	4.19*	14.57
IX	96.17	20.23*	24.20	3.37	157.00	15.33**	123.67	19.00	7.73	2.50	3.09	18.97*
X	91.90	10.17	27.20	2.77	145.33	16.00	130.33	19.33	7.90	2.37	3.35	18.83
XI	91.67**	9.23**	23.00	2.60	100.67**	27.67*	122.33	28.33*	9.93*	2.50	3.98	13.70
Mean	136.66	11.44	25.18	3.37	145.46	18.12	132.92	22.17	8.31	2.57	3.30	15.32
CV(%)	2.12	13.64	4.62	9.53	10.16	16.66	0.36	2.25	3.10	3.91	4.32	16.20
SEM+ ₋	1.67	0.90	0.67	0.18	8.53	1.74	0.27	0.28	0.14	0.05	0.09	1.43
CD(5%)	4.72	2.53	1.89	0.52	24.01	4.90	0.77	0.81	0.41	0.16	0.25	4.05

*,** represents maximum and minimum values, respectively. PH:Plant height, EBT:Ear bearing tiller, PL:Panicle length, DDF:Days to 50% flowering, GL:Grain length, GB:Grain breadth, SPY:Single plant yield.

IX and VII, cluster V and I and cluster X and IV. These clusters were genetically closed. Inter cluster distance of the remaining clusters were comparatively low. The magnitude of heterosis mainly depends on the genetic distance. Greater distance between the clusters indicate wider genetic diversity between the genotypes. The genotypes in these clusters could be used as parents in hybridization programme for getting transgressive segregates.

The cluster mean and coefficient of variation was presented in Table 3. It provided considerable difference in the cluster mean for different characters. The single genotype from cluster VII to XI justified

their separation in to different clusters. The genotypes in these clusters were quite different from others by having highest or lowest value for different characters. The coefficient of variation was very distinct. The characters like EBT hill⁻¹, grains panicle⁻¹, sterile spikelets panicle⁻¹, single plant yield, are having maximum coefficient of variation. Similar result was reported by Maurya and Singh (1977), Singh *et al.* (1987). The cluster mean was highest for plant height, grain breadth and panicle weight in cluster I and lowest in L/B ratio. Maximum cluster mean value for grains panicle⁻¹ and Days to 50% flowering, was observed in cluster VI. Mean value was highest for panicle length and L/B ratio in cluster VIII. Highest cluster mean for

Table 4. Relative contribution of 12 characters to total genetic divergence

Characters	Time ranked first	Contribution (%)
Plant height	146	16.96
Ear bearing tillers hill ⁻¹	0	0.00
Panicle length	2	0.23
Panicle weight	0	0.00
No of grain panicle ⁻¹	4	0.46
No of sterile spikelets panicle ⁻¹	0	0.00
Days to 50% flowering	397	46.11
grain weight		
1000 grain weight	207	24.04
Grain length	26	3.02
Grain breadth	78	9.06
Length Breadth ratio	0	0.00
Single plant yield	1	0.12

ear bearing tiller hill⁻¹ and single plant yield was reported in cluster IX and for sterile spikelets panicle⁻¹, 1000 grain weight and grain length in cluster XI. Similarly minimum cluster mean value was observed in cluster III for panicle weight and grain length. Minimum cluster mean for 1000 grain weight and grain breadth, was reported in cluster VIII. Mean value for sterile spikelets panicle⁻¹ was reported in cluster IX and for plant height, EBT panicle⁻¹, grains panicle⁻¹ in cluster XI. The percentage of contribution of different characters to total divergence is presented in Table 4. The contribution is highest in days to 50% flowering (46.11) followed by 1000 grain wt(24.04), plant height (16.96) and grain breadth (9.06). Madhabilata and Suneetha (2005) reported similar result.

It is assumed that maximum amount heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. But for a plant breeder, the objective is not only high heterosis but also reduction of duration. The greater the distance

between two clusters, the wider the genetic diversity between their genotypes. Mian and Bhal (1989) reported that parents separated by D² value of medium magnitude generally showed higher heterosis. Keeping this in view, it appeared that genotypes of the cluster II and VIII (Sambhamahsuri), cluster II and IX, (Swarna) and cluster VI and XI will exhibit high level of production as well as earliness. Because cluster IX was having high mean value for EBT Hill⁻¹, and yield. Cluster XI was highest for 1000grain weight. and lowest for DFF. Cluster VI was for no of grains panicle⁻¹. The genotypes of these clusters may be selected as parents for future breeding programme.

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