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GENETIC DIVERGENCE IN HIMALAYAN RICE

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Fifty genotypes of rice (*Oryza sativa* L.) from the Himalayan belt were studied for their genetic divergence for a set of ten characters using Mahalanobis D^2 statistics. The genotypes were grouped into 11 clusters. The genetic diversity was not related to geographic diversity. Based on divergence and superior cluster means, crosses between genotypes from cluster IX and I, II, VI, XI may result in superior types.

Key words : Rice, genotype, genetic divergence, heterosis

Genetic diversity in a population provides the basis of any crop improvement programme. The use of diverse parents gives better opportunities to a breeder for selection and development of a superior variety. Estimation of genetic divergence through the use of Mahalanobis D^2 statistics has been emphasized by many workers (Murty and Arunachalam, 1966; Singh and Bains, 1968; Singh and Gupta, 1968), because of its usefulness in forming parental combinations before effecting actual crosses.

MATERIALS AND METHODS

The experimental material consisted of 50 germplasm lines from Himachal Pradesh (11), Jammu & Kashmir (3), Uttar Pradesh (1), Bihar (7), Assam (7), Arunachal Pradesh (3), Meghalaya (14), Nagaland (3), Manipur (1). All the 50 lines were grown in complete randomised block design with two replications under low land conditions at Barapani (900m), Meghalaya during *Kharif* 1992 and 1993. One month old seedlings from the nursery were transplanted under the recommended levels of fertilizers with a spacing of 30cm × 15 cm. Each plot consisted of two meter long, three rows. Observations were recorded on well guarded randomly chosen ten plants per replication for each entry for ten characters. The mean values were subjected to Mahalanobis D^2 statistics to measure genetic divergence as suggested by Rao (1952) and the clusters were formed by Tocher's method (Rao, 1952).

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RESULTS AND DISCUSSION

The analysis of variance exhibited highly significant differences among the genotypes for all the ten characters. On the basis of D^2 values, all the 50 genotypes were grouped into 11 clusters (Table 1). The maximum number of genotypes were in cluster I (19 genotypes) whereas cluster VIII to XI contained only single genotype each. Since the cluster I included genotypes from different areas along the long stretch of Himalaya from west to east, this indicated that there is no association between clustering pattern and eco-geographical distribution of the genotypes. Many rice workers (De and Rao 1987; Mishra and Dash, 1997) have revealed that geographical diversity is not necessarily related to genetic diversity.

The clustering of genotypes from different eco-geographical locations into one cluster could be attributed to possible free exchange of breeding materials or even varieties from one place to another (Verma and Mehta, 1976). This may also be due to the fact that the unidirectional selection practiced for a particular trait in several places produced similar phenotypes which were aggregated in one cluster irrespective of their distant geographic origin (Singh and Bains, 1968). On the other hand many genotypes originating from one place were scattered over different clusters (Table 1). Such genetic diversity among the

Table 1. Distribution of 50 genotypes of rice in different clusters

Cluster No.	No. of genotype	Genotypes/Germplasm lines	Origin/source
I	19	BD18, BD133, BDS 7/378, BDS 7/383, BDJ 1253, C 1003, C 1630, C 1926, C 1946, C 1999, DKH 74, Gnoba, IC 81400, IC 81396, NG 6/42, NKG 1160, NKG 1154, NKG 1211, P 532.	Assam (3) Arunachal Pradesh (2) Bihar (3) Himachal (4) J & K (2) Meghalaya (2) Nagaland (2) U.P. (1)
II	9	BD 10, BD 19, BD 38, BD 71, BD 77, BD 93, BD 99, BD 101, Manipuri	Meghalaya (8) Manipur (1)
III	5	C 1981, DKH 60, NKG 1046, NKG 1047, NKG 1161	Assam (1) Bihar (1) Himachal (3)
IV	4	C 1800,C 1875,NKG 1120,NKG 1209	Bihar (1) Himachal (3)
V	3	BD , BD 2, DKH 89	Assam (1) Meghalaya (2)
VI	3	BD 118, C 1947, C 1964	Bihar (2) Meghalaya (1)
VII	3	C 1645, MMH 6/6, MMH 6/26	Assam (2) J & K (1)
VIII	1	BD 57	Meghalaya (1)
IX	1	BDS 7/376	Arunachal (1)
X	1	NH 6/27	Nagaland (1)
XI	1	NKG 1192	Himachal (1)

genotypes of common geographic origin could be due to factors like heterogeneity, genetic architecture of the populations, past history of selection, developmental traits and degree of general combining ability (Murty and Arunachalam, 1966). The intra-and inter-cluster divergence among the genotypes was of varying magnitude (Table 2). The intra-cluster D^2 values have been found to be zero for clusters VIII to XI as they included only single genotype whereas it was maximum in cluster VII (8.90). The maximum inter-cluster distance was obtained between clusters VI and VIII (35.97) while the minimum inter-cluster distance has been observed between clusters III and VII (12.18) indicating close relationship between these clusters. The greater the distance between clusters, wider the genetic diversity between the genotypes.

Table 2. Intra (bold) and inter-cluster distance among 11 clusters in rice

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**8.47**	16.70	16.34	12.31	17.38	19.14	13.83	22.26	16.60	15.50	23.40
II		**7.92**	22.15	14.31	25.39	31.99	22.44	14.55	28.88	14.21	31.59
III			**6.18**	14.61	15.22	15.25	12.18	24.56	19.09	16.73	25.26
IV				**8.09**	15.77	23.01	13.36	17.76	22.44	12.53	26.15
V					**7.11**	18.02	12.19	26.40	21.73	20.08	21.98
VI						**7.54**	16.10	35.97	12.88	27.68	19.68
VII							**8.90**	26.24	19.97	17.96	24.94
VIII								**0.00**	34.49	16.36	34.76
IX									**0.00**	27.34	17.19
X										**0.00**	29.92
XI											**0.00**

The cluster means for each character are presented in Table 3. The single genotype, BDS 7/736, in the cluster IX showed the highest grain yield performance accompanied by the highest means for panicle weight, grains per panicle, and maximum days to maturity as well as the lowest number of tillers and panicles. NKG 1192 in cluster XI possessed the highest number of tillers and panicles and the heaviest 100-grain weight. The genotypes (BDS 118, C 1947, C 1964) of cluster VI were characterised by the longest duration for days to flower and days to maturity. The maximum plant height was found in genotypes of cluster III but these had the lowest 100-seed weight. Cluster II means showed maximum panicle length for the genotypes it contained. BD 57 in cluster VIII possessed the lowest mean values for days to flower, days to maturity, panicle weight and grain yield per plant. The genotypes in

Table 3. Cluster means for ten characters in 50 genotypes of rice

Cluster number	Plant height (cm)	Tiller number	Days to flower	Panicles per plant	Panicle length (cm)	Days to maturity	Panicle weight (g)	Grains per panicle	100-seed weight (g)	Yield per plant (g)
I	105.17	8.01	138.73	7.81	23.20	161.49	2.53	110.97	2.40	17.11
II	100.42	7.55	118.00	7.31	24.00**	150.00	2.46	95.38	2.59	16.35
III	121.37**	8.01	141.80	7.76	23.37	173.00	1.80	107.68	1.74*	11.29
IV	82.41	9.63	130.25	9.08	21.19	161.50	2.29	93.90	2.41	12.99
V	94.15	7.90	142.00	7.73	20.40	175.70	1.69	92.77	2.62	6.87
VI	117.35	9.10	154.70**	8.73	21.87	194.00**	1.99	105.83	1.98	15.62
VII	83.92	10.10	141.67	8.80	21.58	173.00	1.70	79.60	2.17	11.87
VIII	110.00	7.90	113.00*	7.80	23.50	145.00*	1.59*	109.10	2.15	4.25*
IX	85.95	7.50*	154.00	6.50*	22.35	194.00**	3.28**	128.60**	2.50	21.35**
X	81.65*	9.10	116.00	6.50*	19.00*	151.00	2.12	104.30	2.00	8.55
XI	111.30	10.30**	138.00	10.00**	22.70	159.00	2.56	104.90	2.95**	11.20
Grand mean	102.47	8.27	135.29	7.92	22.75	168.36	2.30	103.25	2.34	14.54
CV(%)	16.34	15.11	1.49	14.52	4.44	1.06	6.68	5.45	3.98	7.63

*, ** lowest and highest means respectively.

clusters I, IV, V possessed medium mean values for all the characters. The coefficient of variation for different characters indicated that major forces of discrimination were plant height, tiller and panicle number and grain yield, which is in agreement with the findings of Mishra and Dash (1997). It is noteworthy that cluster IX consisting of a single genotype (BDS 7/736) from Arunachal Pradesh had superior mean values for grain yield, grain number/panicle, panicle weight combined with the longest maturity duration.

On the basis of divergence and grain yield and components of grain yield, it is suggested that maximum heterosis and good recombinants could be obtained in crosses between genotypes of clusters IX and cluster I, II, VI as well as cluster XI. This information may be useful to the breeders engage in varietal improvement programmes in the Himalayan belt.

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