Variability, heritability and genetic divergence in lowland rice genotypes under the mid-hills of Sikkim

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ABSTRACT

Twenty seven genotypes of lowland rice were evaluated under organic conditions in the mid-hills of Sikkim in during the wet season of 2007-08 for 11 quantitative traits namely days to 50% flowering, days to maturity, plant height, tiller number, productive tillers, panicle length, number of grains panicle $^{-1}$, grain length, grain breadth, length breadth ratio and yield hectare $^{-1}$. Analysis of variance revealed significant differences among the genotypes for all the traits studied. Heritability in broad sense was high for all the traits, highest being recorded for plant height, grain breadth and length breadth ratio. Number of tillers, grain yield ha $^{-1}$ and length breadth ratio were having high genetic advance coupled with high heritability. The genetic divergence among the genotypes was estimated through Mahalanobis D^2 statistics. The 27 genotypes were grouped into 4 clusters. Yield ha^{-1} (20.80 %) contributed maximum towards divergence followed by plant height (16.81 %), grain breadth (16.52 %) and grain length (15.10%).

Key words: lowland rice, genetic divergence, mid-hill, Sikkim

The North-Eastern region is seen to be the richest source of genetic variability in agricultural and horticultural crops. Nearly 90% of the total population of the region depends on agriculture where rice is the principal food crop, cultivated (72% of the total cultivated area) in upland, lowland and deep water conditions (Singh *et al*. 2006). In Sikkim, it is one of the staple crop as inferred from the epithet "Denzong" meaning the "valley of rice". It is grown in an area of 12.27(000'ha) with an annual production of 20.93(000' tones) and the productivity of 1750.79 Kg/ha (FSADD, 2009-10). It is prerogative to undertake location specific rice breeding program to mainly focus on breeding semi dwarf, short duration and high yielding traits which are lacking in local cultivars.

Genetic diversity is measured by determining the proportion of polymorphic loci across the genome, or by the number of heterozygous individuals in a population or by calculating the Mahalanobis distance (D^2 statistics) of different genotypes which takes into account the correlations among the quantitative traits. From the evolutionary point of view, genetic diversity serves as a way for a genotype to adapt to changing environments, including new pests and diseases and new climatic conditions. With more variation, it is more likely that some genotypes or individuals in a species or population will possess variations of alleles that are suited for the environment and the genotypes or individuals that bear that alleles or gene are more likely to survive and likely to give higher yield. From the crop improvement point of view, knowledge on genetic diversity in the germplasm of a species or among the parental line or variety of crop is a prerequisite in the hybridization programmes either for combining desirable genes in new recombination or to obtain heterotic crosses. Therefore, an assessment of genetic diversity among the parents or germplasm is paramount important to a breeder. Twenty seven genotypes, including improved varieties of rice were evaluated in the mid-hills of Sikkim during 2007-08. The genetic divergence among these rice genotypes was assessed in this report

along with the relative importance of different traits in the total divergence through Mahalanobis D^2 statistics.

The material for the present investigation consisted of twenty seven lowland rice genotypes comprises local cultivars, improved and released varieties. The experiment was conducted at research farm of ICAR, Sikkim Centre, Tadong, Gangtok which represent the midhills of Sikkim (1350 m amsl). The experiment was laid out in a randomized block design with three replications during wet season 2007-08. Row

Grain breadth(GB) and length breadth ratio(LB). The analysis of variance was performed as per the standard statistical procedures (Singh and Chaudhary, 1985). Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation was estimated as per the procedure given by Johnson *et al.* (1955), broad sense heritability (h^2) by Burton and de-Vane (1953) and expected genetic advance by Singh and Chaudhary (1985). The Mahalanobis D^2 distance was calculated to estimate the genetic divergence (Mahalanobis, 1936). The genotypes were

Table 1. Analysis of variance among the genotypes studied.

Source of variation	df	DF	DM	PH	TN	PT	PL	GN	GL	GB	L/B	GY
Replication	2	0.36	17.22	40.04	0.46	0.56	6.82	329.92	0.16	0.01	0.14	12.58
Treatment	26	24.18**	228.11**	1161.55**	16.10**	6.66**	31.95**	2401.58**	5.67**	0.42**	2.18**	203.83**
Error	52	10.33	36.24	31.85	2.08	0.85	4.58	299.69	0.18	0.01	0.04	13.47

*, ** refers to significant at 1% and 5% probability level.
DF-days to 50% flowering, DM - days to maturity, PH-plant height, TN - tiller number, PT-productive tillers, PL-panicle length, GN-number of grains panicle^{-1}, GL- grain length, GB-Grain breadth, LB-length breadth ratio

to row and plant to plant spacing were maintained at 20 x 15 cm. All the recommended organic agronomic practices were followed to raise a good crop as the state is declared as organic. Observations were recorded on five randomly selected plants for grain yield ha^{-1} and other traits *viz*., days to 50% flowering (DF), days to maturity(DM), plant height(PH), tiller number (TN), productive tillers (PT), panicle length(PL), number of grains panicle^{-1} (GN), grain length (GL),

grouped into different clusters on the basis of D^2 values, as suggested by Tocher (Rao, 1952). The intra and inter cluster distance was calculated as per Singh and Chaudhary (1985). Statistical software INDOSTAT was used for analysis.

The analysis of variance indicated highly significant differences among the genotypes for all the eleven traits under study (Table 1). Significant differences were found between the means in respect

Table 2. Variability parameters for 11 traits in 27 genotypes of rice

Parameters	DF	DM	PH	TN	PT	PL	GN	GL	GB	L/B	GY
Range: Min	68.33	125.33	40.33	4.66	4.33	13.83	90.33	5.66	2.15	1.99	14.77
Max	105.00	168.66	141.66	13.00	10.00	26.66	220.66	11.21	3.56	4.94	52.16
Mean	90.30	142.21	94.00	8.06	6.49	21.85	130.03	8.83	2.62	3.49	33.23
SEm(±)	1.82	3.41	3.19	0.81	0.52	1.21	9.80	0.24	0.06	0.12	2.07
PCV(%)	10.10	6.13	20.93	28.72	22.93	14.93	21.75	15.57	14.40	24.43	24.80
GCV(%)	9.89	5.62	20.64	26.79	21.42	13.81	20.35	15.31	14.19	24.16	23.97
Heritability (%) bs	0.95	0.84	0.97	0.87	0.87	0.85	0.87	0.96	0.97	0.97	0.93
Genetic advance	118.02	15.10	39.42	4.15	2.67	5.75	51.01	2.74	0.75	1.72	15.85
Genetic advance (% of mean)	19.95	10.62	41.93	51.51	41.21	26.34	39.23	31.03	28.79	49.23	47.72
CV(%)	3.56	4.23	6.00	17.89	14.20	9.79	13.31	4.89	4.29	6.22	11.04
CD(P=0.05)	5.26	9.86	9.24	2.36	1.51	3.50	28.36	0.71	0.18	0.36	6.01

DF-days to 50% flowering, DM - days to maturity, PH-plant height, TN - tiller number, PT-productive tillers, PL-panicle length, GN-number of grains panicle^{-1}, GL- grain length, GB-Grain breadth, LB-length breadth ratio

of the pooled effect of 11 characters among 27 rice genotypes, using Wilk's criteria calculatd 'V' stat. The characters which contributed maximum towards the diversity were yield ha^{-1} (20.80 %), plant height (16.81 %), grain breadth (16.52 %) and grain length (15.10%).

The height of the plant varied from 40.33 cm in WB local to 141.66 in Attey. The mean height of 27 genotypes was 94.01 cm. The days to 50% flowering in the mid-hills of Sikkim was seen at 68th day in VL Dhan-61 whereas, the flowering was delayed till 105th day in genotypes like Ranjit and Ketaki Joha. Genotypes RCPL-1-16 and TRC-87-251 were significantly earlier in maturity than the general mean. Number of grains per panicle varied from 90.33 in Taraori Basmati to 220.66 in Kanchi Attey. The yield was calculated on per hectare basis and was highest in VL Dhan 61 (52.16 q ha^{-1}) followed by Satyaranjan (49.78 q ha^{-1}) and RCPL-1-87-251 (45.06 q ha^{-1}).

The estimates of variability parameters for 11 yield related characters of 27 rice genotypes grown in the midhills of Sikkim is presented in Table 2. The narrow differences between PCV and GCV values is suggestive of the fact that phenotypic variation was determined by and large by genotype with negligible influence of extraneous factors and therefore, selection for such traits will be rewarding. Heritability in broad sense was high for all the traits studied, highest being recorded for plant height, grain breadth and length breadth ratio (97% each). The traits like tiller number, grain yield and length breadth ratio were having high

All the 27 genotypes were grouped in to 4 clusters, in such a way that the genotypes within cluster had smaller D^2 values among themselves than those belonging to different clusters. Out of the 4 clusters, two clusters (Cluster III and IV) were solitary (containing only one genotype in each cluster) while cluster I comprised of 17 genotypes, cluster II encompasses 8 genotypes. The mean of each character in each cluster are presented in Table 3. Murty and Arunachalam (1966) has opined that hybridization programmes should be formulated in such a way that the parents belonging to different clusters with maximum divergence could be utilized so as to get desirable transgressive segregants. The maximum inter-cluster distance(30.91) was observed between cluster III and IV followed by cluster I and IV (26.11) and cluster II and IV (18.49)(Table 4). The genotypes grouped in a same cluster would display the lowest degree of divergence from one another, and therefore, crosses made between genotypes belonging to a same cluster may not give heterotic progenies or transgressive segregants as also reported by earlier workers (Mishra *et al*.,2003; Chaturvedi and Maurya, 2005).

As evidenced from the clustering pattern, group III and IV are most diverse for the eleven morphological traits studied in the rice genotypes. Hybridization between them may be expected to produce desirable segregants. Apart from it genotypes of cluster I and IV i.e genotype Attey of group IV and 17 genotypes of group I could be utilized in hybridization

Table 3. Cluster mean values for eleven traits of 27 rice genotypes

Cluster	DF	DM	PH	TN	PT	PL	GN	GL	GB	L/B	GY
I	92.63	142.44	92.08	8.69	6.69	22.49	126.97	9.49	2.40	3.99	29.99
II	87.38	142.67	98.83	7.00	6.00	21.01	141.63	7.64	2.91	2.65	39.79
III	73.33	135.33	40.33	8.33	8.00	13.83	109.00	8.52	2.57	3.32	31.15
IV	91.00	141.67	141.67	5.67	5.67	26.00	110.33	7.47	3.57	2.10	37.82

DF-days to 50% flowering, DM - days to maturity, PH-plant height, TN - tiller number, PT-productive tillers, PL-panicle length, GN-number of grains panicle^{-1}, GL- grain length, GB-Grain breadth, LB-length breadth ratio

genetic advance coupled with high heritability whereas plant height, productive tillers and grain number were having moderate genetic advance and high heritability. Therefore, direct selection based on phenotypic observations may be effective for improvement of these traits.

programme for getting desirable segregants and high heterotic response. The genetic distance between the parents largely govern the variability spectrum generated the segregating populations and also heterosis in the F1's. Therefore, identification of genetically diverse genotypes helps in selecting desirable parents

Table 4. Inter and intra-cluster values among four clusters
of 27 rice genotypes

Cluster	I	II	III	IV
I	9.29	14.38	13.59	26.11
II		11.58	17.68	18.49
III			0.00	30.91
IV				0.00

for hybridization programmes. Based on the mean performance and their inter-cluster distances the promising genotypes identified were VL Dhan61 for days to 50% flowering and yield ha^{-1}, TRC-87-251 for earliness and WB local for dwarfness. These genotypes can be used for improvement of the respective traits.

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