Short Communication

Genetic divergence in rice (*Oryza sativa* L.) genotypes grown in Kumaun Himalaya

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Classification of germplasm collection is a prerequisite for distinguishing genetically close and divergent types for various plant breeding programmes. By using advanced biometric techniques such as multivariate analysis based on Mahalanobis's D^2 statistic [1] it has now become possible to quantify the degree of genetic divergence amongst biological populations and assessing of relative contribution of various desirable attributes of breeding and agronomic value to the total divergence. Information on this aspect in rice, barring a few reports from different parts of the country [2-6] is still lacking on rice genotypes grown in Kumaun region of north-west Himalayas.

The experimental material consisted of a collection of 55 rice genotypes grown in Kumaun Himalaya (Table 1). Field trials were conducted in a randomized block design with three replications having a plot size of 4.5 × 0.6 m at three different locations. Each plot comprised three rows with a spacing of 20 × 15 cm. Randomly selected five plants were used from the central row of each plot for recording of data. Statistical analyses were carried out using the pooled mean data over locations. All possible D^2 values between the 55 cultivars were computed utilizing the genotypes means, variance and covariance in respect of fifteen characters and the constellation of distinct clusters was done following Tocher's method [7].

Highly significant variations were found amongst the rice genotypes with regard to all the fifteen characters studied. On the basis of D^2 values for the 1485 possible pairs of genotypes, the 55 genotypes were grouped into twelve clusters (Table 1). A maximum of 15 genotypes were included in cluster III, followed by clusters II and IV with 9 genotypes each. Dispersion pattern of genotypes over a large number of clusters with a maximum of 15 genotypes in cluster III to five single genotype clusters from VIII to XII indicated the presence of high degree of genetic divergence and genetic heterogeneity among the genotypes.

Intra-cluster divergence was maximum (D = 11.88) in cluster VII which is not significantly different from other clusters, excluding solitary ones (Table 2). All inter-cluster distances were found more than the intra-cluster distances. High order of inter-cluster distance was recorded between cluster XII and the remaining clusters, excluding clusters I and II. The highest inter-cluster distance was noticed between cluster XII and VII (D = 31.0), followed by cluster IX (D = 30.7) and cluster VIII (D = 30.3). Inter-cluster distances amongst the remaining clusters were recorded low, except between cluster VII and clusters I and XI (D = 22.9 each).

High mean values (Table 3) for grain yield/plant, shoot height, panicle length and panicle weight, straw yield/plant, total and fertile grains/panicle, days to 50% flowering and days to maturity were observed in cluster VII which included two genotypes ('Munakoti' and 'Ratdhan') and their minimum values were recorded in cluster XII, followed by cluster XI. Maximum mean values for grain yield/plant, fertile tillers/plant, 1000-grain

Table 1. Cluster composition of different rice genotypes grown in Kumaun Himalaya

Cluster No.	Name of genotypes in each cluster	No. of genotypes
CI	Almora dhan, Basmati-type, Dhur basmati, Ghundaya basmati, Nandhan	5
CII	Borrani, Kashmira, Khairna-local, Matyai dudh, Mukhmal, Rajmati, Thapachini, VL-8, VL-16	9
CIII	Banderpuchha, Bhujan-local, Boran, Dalbadal, Dhundhan, Dhyari-local, Gazziya, Lal Sangrati, Mail Magran, Malkhai, Peelya, Radmati, Shakuntala, Thal-local, VLK-39	15
CIV	Chinthapa, Dhania, Dudhia, Goldhan, Jhulaghat-local, Jhussia, Kuturi, Suntola	9
CV	Chaupadhan, Chunkuli, Dudh, Gaudhan, Mangraat, Thapuli	6
CVI	Hawalbaghia, Jaulia-safed, Lal Jaulia, Lambisa	4
CVII	Munakoti, Ratdhan	2
CVIII	Bermi	1
CIX	Motadhan	1
CX	Basmati	1
CXI	Banpasa	1
CXII	Pahari basmati	1
	Total	55

Table 2. Average intra-cluster (diagonal) and inter-cluster distance (D) in rice genotypes

Cluster No.	CI	CII	CIII	CIV	CV	CVI	CVII	CVIII	CIX	CX	CXI	CXII
CI	10.3	14.0	17.6	19.5	20.6	19.5	22.9	19.4	20.2	14.7	15.9	15.5
CII		10.3	14.2	14.5	15.7	15.2	16.4	15.9	14.9	16.3	16.4	20.3
CIII			10.4	13.0	15.9	12.5	15.7	11.1	12.0	14.9	14.0	28.6
CIV				10.9	15.4	15.5	13.1	12.9	15.3	17.6	19.7	28.4
CV					11.2	16.8	14.4	13.2	17.2	21.4	18.2	29.0
CVI						11.5	16.1	14.1	11.7	15.4	15.9	29.6
CVII							11.9	15.5	17.6	19.4	22.9	31.0
CVIII								0.0	13.0	17.3	14.0	30.3
CIX									0.0	17.3	15.5	30.7
CX										0.0	17.3	24.6
CXI											0.0	26.9
CXII												0.0

Table 3. Cluster means and general mean for different characters in rice

Sl. No.	Characters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	Mean	% cont. towards diverg.
1.	Grain yield/plant (g)	7.5	10.6	7.9	9.3	13.8	8.4	13.6	7.8	7.1	8.4	7.2	8.5	9.2	5.9
2.	Shoot height (cm)	91.0	108.0	119.0	130.0	124.0	125.0	139.0	114.0	125.0	113.0	85.0	77.0	113.0	7.2
3.	Fertile tillers/plant	6.5	5.4	3.1	3.2	5.4	3.5	3.7	2.6	3.2	3.9	4.4	9.8	4.6	5.1
4.	Panicle length (cm)	19.2	22.2	21.7	20.5	20.9	21.2	26.2	20.9	19.5	23.8	18.3	20.1	21.2	4.5
5.	Panicle weight (g)	1.8	2.9	3.2	3.5	4.1	3.1	4.6	4.1	2.5	2.7	2.7	1.1	3.0	10.1
6.	Straw yield/plant (g)	10.9	15.3	12.8	15.5	18.0	15.2	23.0	11.1	12.3	11.5	8.5	12.4	13.9	5.6
7.	Total grains/panicle	87.0	114.0	128.0	145.0	172.0	122.0	194.0	167.0	89.0	140.0	109.0	56.0	127.0	22.6
8.	Fertile grains/panicle	63.0	90.0	101.0	121.0	132.0	102.0	146.0	117.0	66.0	104.0	84.0	41.0	97.0	13.4
9.	1000-grain weight (g)	21.0	25.0	27.0	25.0	26.0	28.0	25.0	25.0	33.0	24.0	31.0	17.0	26.0	5.2
10.	Grain length (mm)	6.6	6.2	6.4	5.7	5.8	7.3	6.5	5.7	6.0	7.8	6.3	6.4	6.4	2.7
11.	Grain breadth (mm)	2.1	2.8	2.7	2.7	2.9	2.8	2.6	2.8	3.5	2.0	2.6	2.0	2.6	0.5
12.	Grain fineness	3.2	2.2	2.4	2.1	2.0	2.7	2.6	2.0	1.7	3.8	2.5	3.3	2.5	2.4
13.	Days to 50% flowering	82.0	92.0	91.0	96.0	93.0	90.0	101.0	89.0	96.0	81.0	80.0	78.0	89.0	7.6
14.	Days to maturity	116.0	129.0	127.0	133.0	130.0	128.0	137.0	126.0	135.0	115.0	113.0	114.0	125.0	5.8
15.	Seed protein %	8.7	6.7	9.1	7.1	7.3	6.8	6.4	6.9	6.7	8.4	9.6	6.5	7.5	1.4

weight, grain fineness and seed protein(%) were noticed in clusters V, XII, IX, X and XI respectively. The highest contribution towards total divergence was rendered by total grains/panicle (22.6%), followed by fertile grains/panicle (13.4%), panicle weight (10.1%), days to 50% flowering (7.6%) and shoot height (7.2%). Contribution made by other characters towards total divergence was comparatively low ranging from 0.5% for grain breadth to 5.9% for grain yield/plant (Table 3).

Rice genotypes of Kumaun Himalayan region exhibited a distinct and wide spread clustering pattern, and high inter-cluster distances thereby indicating a huge amount of genetic divergence and heterogeneity. The determinants such as gene frequencies, mutations, male sterility, introgressive hybridization, random genetic drift, preferential selection pressures, and distantly exchange of germplasm by the people, microclimates and erratic changes in the environmental conditions are likely to be the predominant factors responsible for infusing such a high degree of genetic divergence and heterogeneity. The greater the distance between two clusters, the wider the genetic diversity amongst the genotypes of the two clusters. Based on mean performance, genetic distance and clustering pattern a

hybridization programme may be initiated involving genotypes 'Pahari basmati' (cluster XII) × 'Munakoti' and 'Ratdhan' (cluster VIII), × 'Motadhan' (cluster IX), × 'Bermi' (cluster VIII); 'Mangraat' and 'Thapuli' (cluster V) × 'Basmati' (cluster X), × 'Banpasa' (cluster XI); 'Munakoti' and 'Ratdhan' (cluster VII) × 'Banpasa' (cluster XI) for combining high yielding traits which are likely to produce superior segregants for high grain yield.

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