

Genetic Divergence over Environments in Rice Germplasm Adapted to Temperate Conditions

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Abstract

Genetic divergence over environment was studied in rice (*O. sativa* L.) to assess its magnitude. Fifty rice genotypes along with two checks viz. SKAU-27 and SKAU-23 were evaluated during *kharif* of 2004 across two random locations in randomized block design with three replications. Analysis of divergence using Mahalanobis D^2 statistics revealed high significance (5182.37) and grouped into 12 clusters. Cluster-I having 37 genotypes while VI and VII had two each, and rest were monogenotypic. The check was grouped into one cluster. Inter cluster distance was maximum between cluster VI and cluster VIII (119, 06). The maximum combination of divergence came from head rice recovery (18.67%) followed by grain yield/plant (18.43%) for loose grain weight (18.36%).

Key words : *Oryza sativa* L., Genetic divergence, D^2 statistics, Environment.

Rice (*Oryza sativa* L.) is one of the most important staple food crop for the world's population and a major source of calories for more than two billion people of Asia. Rice occupies one third of world's total area among cereals and provides 35—60% of the calories consumed by 2.7 billion people (1). In India rice is cultivated on 42.84 million hectares under four major ecosystems, viz. irrigated (19 m ha), rainfed lowlands (14 m ha), flood prone (3 m ha) and rainfed upland (6 m ha). Rice ecosystems in India represent 24% of irrigated areas, 34% of rainfed lowlands, 26% of flood prone and 37% of rainfed uplands of cultivated rice in entire world (2). In the Kashmir valley rice is cultivated in an area of 1.40 lakh hectares with a production of 24.60 lakh tones and productivity of only 17.40 q/ha. This scenario leaves a wide gap between supply and demand and this gap need to be narrowed down through adoption of recent technologies for yield enhancement. Major increases in the area planted for rice in the valley are unlikely because of pressure on rice lands from urbanization and industrialization. Since the land resources are shrinking and water is becoming a limiting factor, the previously achieved productive gains in rice are not only to be sustained but increasing yield productivity to feed the increasing population is a challenge for future. Efforts to close the yield gap in rice, to overcome productivity decline, and to reach

new yield plateau has to be linked with new approaches. These approaches facilitate the development of improved varieties with greater stability for increase the production level needed to meet the projected demand. Currently there are two strategic approaches being followed vigorously to enhance the productivity at global level one conventional approach based on new plant type to obtain higher yield potential. Second, exploiting the phenomenon of hybrid vigor which has been successfully utilized in China with yield advantage of 20 to 25 percent over the best purelines. Both these approaches capitalize on the existence of genetic diversity. For identifying appropriate genotypes as parents with their long term potentialities, analysis of genetic make-up in the purposeful management of genetic variability has been of paramount importance. Mahalanobis D^2 statistics is a powerful tool in quantifying the degree of divergence at genotypic level with regard to characters which need to be improved and provides an opportunity to identify parents for executing an effective breeding strategy.

Methods

The present investigation was carried out at two random location viz. Rice Research and Regional Station, Khudwani, and Experimental Farm of Divi-

Table 1. Distribution of different rice (*Oryza sativa* L.) genotypes into clusters based on D² statistics (pooled over environment).

Cluster	Number of genotypes in the cluster	Variety/accession number of the genotypes
I	37	K 696-84-1, K 696-71-6, K 681-33-1, K 680-70-2-1-1-2, K 696-9-7-2-2-1, K 696-80-8-1-1-1, K 696-7-9-3-2-2-1, K 696-10-2-1-2-2, K 696-36-1-1-1-1, K 696-62-1-2-2-2, K 696-70-3-1-1-1, K 696-115-2-2-2-1, K 696-30-2-3-2-1, K 717-1-1-1, SKAU-343, SKAU-23, SKAU-345, SKAU-344, SKAU-5, SKAU-350, SKAU-353, SKAU-354, SKAU-353, SKAU-360, SKAU-105, SKAU-338, CH-1007, CH-968, SKAU-27, CH-1039, CH-977, VLD-81, K 450-3-2-2, IRTON 2001 (107), IRTON 522 (077)
II	1	K 680-123
III	1	K 696-3-2-3-1
IV	1	K 680-5-1-1-2-1
V	1	K-116
VI	2	IRTON 2001 (09), SKAU-358
VII	1	SKAU-98
VIII	2	K 696-2-1-2-8, SKAU-355
IX	1	SKAU-364
X	1	SKAU-349
XI	1	IRTON 508 (084)
XII	1	SKAU-363
Checks		Jhelum Chenab

sion of Plant Breeding and Genetic (SKUAST-K), Shalimar during *kharif* of 2004. The experimental material consisted of 50 rice genotypes including two standard high yield varieties of rice viz. SKAU-27 and SKAU-23. The experimental material was grown in randomized block design with three replications. Each experiment consisted of two rows of 4 m length spaced 20 cm apart. Recommended package of practices was adopted to raise a good crop. List of genotypes used is given in Table 1. Observation was recorded on various morphological, maturity, quality, yield and yield component traits to study the level of genetic divergence in the material. The competitive plants were selected at random from each experimental plot and tagged for recording bio-metrical observation. The analysis of genetic divergence using Mahalanobis D²-statistics was carried out as described by Rao (3). On the basis of magnitude of D² values the varieties were grouped into clusters according to Tochers method following the procedure given by Singh and Chowdhary (4).

Results and Discussion

Genetic divergence was estimated in 50 rice geno-

types along with two standard checks viz. SKAU-27 and SKAU-23 over the two environments (pooled data). Analysis of variance of dispersion revealed that the genotypes tested expressed significant variability for morphological, maturity, quality, yield and yield component traits in the pooled analysis over environments. The V-statistic, which is a measure of Wilk's creations was significant and its value was 5183.37, revealing that genotypes possessed significant diversity and thus could be studies for divergence studies.

Pooling the performance of genotypes across the locations 50 genotypes (including checks) were grouped into (12) clusters (Tables 1 and 2). Cluster 1 expressed maximum (37) genotypes followed by cluster VI and cluster VIII with (2) genotypes each. Rest of the clusters were monogenotypic. Here the checks got grouped in the same cluster i.e. cluster 1.

The clustering pattern suggested that geographical diversity was not an essential factor to group the genotypes from a particular source of origin into one particular cluster. This means that geographical diversity though important, was not the only factor in

Table 2. Average inter-cluster (above diagonal) and intra-cluster (diagonal) D^2 values among different rice (*Oryza sativa* L.) genotypes under temperate climatic conditions of Kashmir (pooled over environments).

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII
I	24.746	32.296	32.427	38.927	39.627	71.637	41.240	54.500	38.174	53.563	44.229	60.299
II		0.0000	32.521	55.669	38.574	64.872	42.933	69.483	39.693	68.116	55.235	44.636
III			0.0000	53.904	29.670	49.818	23.217	75.815	38.438	67.998	47.123	46.827
IV				0.0000	67.845	100.032	68.350	35.110	56.196	26.626	45.818	91.908
V					0.0000	39.206	19.590	83.710	32.832	82.927	52.408	31.209
VI						18.531	38.675	119.066	62.009	113.942	80.276	33.098
VII							0.0000	84.147	44.472	81.139	57.906	37.427
VIII								23.300	74.787	38.453	68.250	105.427
IX									0.0000	76.825	28.360	54.033
X										0.0000	64.96	104.536
XI											0.0000	77.149
XII												0.0000

determining the genetic divergence (5). Genetic diversity is the outcome of several factors, including geographical diversification. Therefore, selection of genotype for hybridization should be based on genetic diversity rather than geographic diversity and statistical distance (D^2) presented the index of genetic diversity among these cluster. The various genotypes shift their position from one cluster to another cluster across the location because changes in location alter the clustering pattern due to $G \times E$ interaction.

Estimation of mean intra and inter cluster distances among the genotype, grouped on the basis of pooled performance across the environments (Tables 2 and 3).

The maximum intercluster distance (D^2) value of 119.06 was observed between cluster VI and cluster VIII following by 113.94 between cluster VI and cluster X and 105.42 between cluster VIII and cluster XII.

Cluster means for pooled analysis revealed that mean days to 50% following ranged from 85.50 in cluster IX to 108.00 in cluster X. For days to maturity it ranged from 128.50 in cluster IX to 145.50 in cluster X. Maximum mean plant height (115.97 cm) was exhibited by cluster VIII and minimum (69.50) by cluster XI. The mean value of effective tillers/plant was maximum (10.91) for cluster IX and minimum (7.83) for cluster III. Maximum mean value for tillers/m (418.33) was expressed by cluster VIII and minimum by cluster III (313.50). Highest mean panicle length (22.90 cm) was expressed by cluster V and minimum (20.07) by cluster XII. The lowest grains/panicle (67.89) were ex-

pressed by cluster IX and highest (105.89) by cluster III. The highest mean value for grain yield/plant (26.05 g) was for cluster VI and lowest (7.856 g) for cluster X. Mean value for 1,000 grain weight was maximum (34.04 g) for cluster VI and minimum (13.13 g) for cluster VIII. Mean harvest index was lowest (24.82%) for cluster X and highest (41.70%) for cluster VI and Kernal L : B ratio was lowest (1.68) for cluster V and highest (2.42) for cluster III. The mean head rice recover was minimum (48.14%) for cluster II and maximum (66.90%) for cluster VII. These cluster means help in identifying the characters to be chosen for hybridization. Sardana et al. (6) suggested that cluster mean and coefficient of variation are an interacting picture of diversity.

Pooling analysis over environment revealed that head rice recovery contributed to a maximum of 18.67% towards total divergence followed by grain yield/plant (18.43%) and 1,000-grain weight (18.36%). The minimum contribution was from harvest index (1.55%) followed by days to 50% flowering (2.82%). For rest of the traits the percent contribution ranged from (3.24%) for days to maturity to (8.64%) for grains/panicle (Table 3).

Characters contributing to divergence are reported to vary from crop to crop (7). The percent contribution of trait toward's total divergence revealed that head rice recovery was the main factor contributing to divergence in the present study according for 18.67% followed by grain yield of 18.43% and 1,000-grain weight of 18.36%. De et al. (8) proposed that traits contributing maximum towards D^2 value need

Table 3. Cluster means for morphological, maturity, quality, grain yield and yield component traits of rice (*Oryza sativa* L.) under temperate climatic conditions of Kashmir (pooled over environments).

Clus- ters	Days to 50% flowering	Dry to maturity	Plant height (cm)	Effective tillers/ plant	Tillers/ m	Panicle length (cm)	Grains/ panicle	Grain yield/ plant (g)	1000- grain wt (g)	Harvest index (%)	Kernel L : B. ratio (mm)	Head rice recovery (%)
I	95.40	136.03	107.58	9.65	378.79	21.79	88.32	17.17	21.95	35.64	2.14	59.97
II	98.00	140.00	109.11	9.69	380.50	21.77	79.76	19.01	24.66	36.93	2.21	48.14
III	96.00	137.50	103.12	7.83	313.50	22.54	105.89	20.81	25.06	39.88	2.42	59.52
IV	93.33	135.50	99.59	8.37	332.66	22.54	77.21	10.37	16.06	32.41	2.39	61.43
V	90.66	131.00	106.73	10.32	394.66	22.90	80.33	20.47	28.26	38.60	1.68	64.97
VI	88.25	130.25	105.23	8.85	350.75	22.60	85.96	26.05	34.04	41.70	2.11	64.49
VII	97.00	138.00	112.42	9.32	364.50	22.41	90.83	23.43	27.57	40.96	2.04	66.90
VIII	100.00	139.00	115.97	10.80	418.33	21.76	88.88	12.77	13.13	32.49	2.00	62.42
IX	85.50	128.50	85.53	10.91	408.66	22.53	67.89	18.47	24.82	41.05	1.98	60.48
X	108.00	146.50	104.72	7.69	308.33	20.65	69.66	7.85	14.68	24.82	2.32	60.70
XI	93.00	135.00	69.56	9.68	388.50	21.24	82.81	17.00	21.14	39.56	2.01	63.85
XII	94.50	134.00	115.42	10.57	395.00	20.07	72.23	24.70	32.44	40.52	1.75	55.21

to be given greater emphasis for deciding on cluster to be chosen for the purpose of further selection and choice of parent for hybridization.

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