

GENETIC DIVERSITY FOR MORPHOLOGICAL AND QUALITY TRAITS IN RICE (*ORYZA SATIVA* L.)

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ABSTRACT

Nature and magnitude of genetic diversity among 23 genotypes of rice was assessed in the present study by using Mahalanobis D^2 statistics. Significant variation for all the traits revealed presence of notable genetic variability among genotypes. Estimates of components of variance indicated that genotypic variance contributed maximum to phenotypic variance which suggested that available genetic variability can be exploited through selection and hybridization. Based on D^2 analysis, 23 genotypes of rice were grouped into five clusters. Among the five clusters cluster III consists of 7 genotypes (IARI 1460, PB-1, Basmati 564, Pusa 1121, SJR-129, Basmati 1509 and Pusa Sugandh) forming the largest cluster followed by cluster I and IV with 5 genotypes each (K-343, K-448, K-39, SJR-51, Gizza-14 and Saanwal Basmati, RR 600, Ranbir Basmati, Basmati 370, CSR 30) cluster II with 4 genotypes (PC 19, Ratna, IET 1410, SJR 5) and cluster V with 2 genotypes (Jaya, RR 8585). Inter cluster distances were found to be higher than intra cluster distances which depicted wide genetic diversity among the rice genotypes. The contribution of various characters towards the expression of total genetic diversity indicated that 1000 grain weight contributed maximum (54.55%) followed by plant height (13.44%) and kernel breadth (11.86%). Clustering of the cultivars did not show any pattern of association between the morphological characters and the origin of the cultivars. The variability present in the material can be exploited through selection and hybridization for evolving superior rice cultivars.

INTRODUCTION

Rice (*Oryza sativa* L.) occupies a premier place in Indian Agriculture and plays a major role in Indian economy being the staple food of two thirds of the population. With increasing human population its demand is increasing day by day and shall continue to play a vital role in the national food and livelihood security. In hilly and sub-mountainous state of Jammu and Kashmir, rice is grown over an area of 261.66 thousand hectare with production and productivity of 5456 thousand quintals and 20.95 quintals per hectare respectively (Anonymous, 2013) while Basmati the premier rice known for quality is grown over an area of about 38 t ha with production and productivity of approximately 900 t q and 24 q/ha. Being the staple food improving the productivity of rice is of paramount importance and for improving productivity knowledge on the nature and magnitude of the genetic variation governing the inheritance of quantitative characters is essential. In addition improvement in grain quality has significance because of the increase in acreage under basmati rice which benefits farmers due to its premium price.

Genetically diverse parents belonging to different genetic backgrounds when brought together in a hybrid union provide an opportunity for bringing together gene constellations of diverse nature, would offer promising segregant derivatives which often result due to complementary interaction of divergent genes in parents. Several workers have emphasized the importance of genetic divergence for the selection of

desirable parents (Murthy and Arunachalam, 1996 and Rahman, 1997). The use of Mahalanobis D^2 statistics for estimating genetic divergence has been emphasized by many workers (Roy and Panwar, 1993; Ramya and Senthilkumar, 2008).

Keeping this in view, the present study was envisaged to estimate genetic diversity in 23 rice genotypes using Mahalanobis D^2 statistics for efficient selection of the diverse parents for their potential use in the rice breeding programme for development of improved rice cultivars with enhanced productivity.

MATERIALS AND METHODS

23 genotypes of rice comprising locally adapted/improved Basmati as well as non-basmati constitute the basic material for the present study. Among these 12 genotypes belong to Basmati group viz., Basmati 370, IARI 1460, PB-1, Pusa Sugandh, Pusa 1121, CSR 30, Basmati 1509, Basmati-564, Ranbir Basmati, SJR 129, Saanwal Basmati and RR 600 while 11 genotypes belong to non-basmati group viz., K-39, K-343, K-448, Gizza 14, PC 19, IET 1410, Jaya, RR 8585, Ratna, SJR-5 and SJR-51. During *khari* 2013, 23 genotypes of rice were grown in a replicated trial in Randomized Block Design (RBD) at the experimental area of Division of Plant Breeding and Genetics, Sher-e-Kashmir University of Agricultural Sciences and Technology Main Campus, Chatha Jammu. Each plot consisted of 15 rows of 5 m length with inter and intra row

distance of 20 and 15 cm, respectively. Recommended management practices were followed to raise the crop. Observations were recorded on five randomly selected plants in each replication for days to 50 per cent flowering, plant height (cm), number of effective tillers per hill, days to maturity, grain yield (kg/plot), 1000 grain weight, panicle length (cm), kernel length (cm), kernel breadth (cm) and length breadth ratio. Observations on days to 50 per cent flowering and days to maturity were recorded on plot basis. After harvesting the seeds of each genotype were dehulled for evaluation of the grain quality viz. kernel size (kernel length), kernel shape (kernel length-breadth ratio) based on their dimension according to Digimatic Caliper (Mitutoyo) Model CD-8/CSX having range 0-200mm/0-8inch. Analysis of variance was done following the procedure described by Panse and Sukhatme (1978). Genotypic and phenotypic coefficient of variation, heritability (broad sense), genetic advance was calculated following the procedure described by Burton and Devane (1953). The statistical analysis was carried by Mahalanobis D² statistics (Rao, 1952) to quantify the genetic diversity for various grain yield and quality traits.

RESULTS AND DISCUSSION

Variance analysis for all the characters revealed reasonable amount of differences among the genotypes under study

indicating the presence of sufficient variability. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense h² (bs), genetic advance and genetic advance as percentage of mean estimated for yield and quality traits are presented in Table 1 and Fig 1. The phenotypic coefficient of variation (PCV) was in general higher than the genotypic coefficient of variation (GCV) indicating influence of environment on the manifestation of these characters (Sreeparvathy *et al.*, 2010, Dhurai *et al.*, 2014). The difference between PCV and GCV were found to be less for the traits, kernel length, kernel breadth, kernel L/B ratio, days to 50 per cent flowering, plant height, 1000-grain weight and days to maturity (Dhanwani *et al.*, 2013).

High estimates of heritability in broad sense were recorded for all the characters, which ranged from 73.00 (no. of effective tillers per hill) to 99.90 (L/B ratio). Johnson (1955) reported that high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion. A perusal of genetic advance for all the yield and quality characters under study ranged from 0.90 (kernel breadth) to 99.87 (days to maturity). High heritability coupled with high genetic advance was registered for days to maturity, plant height and days to 50 per cent flowering suggesting predominance of additive gene action in the expression of these traits.

The wide range of variation noticed in all the characters had

Table 1: Estimates of genetic parameters for yield and quality characters

S.no.	Character	GCV	PCV	h ² (bs) %	GA	GA as % of mean
1.	Days to 50% flowering	10.55	10.59	99.10	21.83	21.63
2.	Plant height	17.92	17.96	99.50	40.82	36.81
3.	No. of effective tillers per hill	11.35	13.28	73.00	1.57	19.97
4.	Days to maturity	7.43	7.49	98.50	99.87	15.19
5.	Grain yield (kg per plot)	11.57	11.64	89.90	1.53	23.71
6.	1000 grain weight	13.16	13.20	99.50	6.34	27.05
7.	Panicle length	13.45	13.64	97.30	7.32	27.33
8.	Kernel length	13.09	13.11	99.60	1.79	26.91
9.	Kernel breadth	21.15	21.17	98.80	0.90	43.53
10	L/B ratio	29.01	29.02	99.90	2.01	59.73

Table 2: Distribution of 23 varieties of rice in 5 clusters (I-V)

Cluster	Total entries	Name
I	5	K-343, K-448, K-39, SJR-51, Gizza-14
II	4	PC 19, Ratna, IET 1410, SJR 5
III	7	IARI 1460, PB-1, Basmati 564, Pusa 1121, SJR-129, Basmati 1509, Pusa Sugandh,
IV	5	Saanwal Basmati, RR 600, Ranbir Basmati, Basmati 370, CSR 30
V	2	Jaya, RR 8585

Table 3: Cluster means for ten characters under study and their contribution to total divergence

Cluster/ character	I	II	III	IV	V	Contribution (%)
Days to 50% flowering	98.40	104.50	110.53	86.93	107.33	3.56
Plant height	98.86	112.05	142.26	94.13	100.83	13.44
No. of effective tillers/hill	8.20	8.33	7.06	7.73	8.00	4.00
Days to maturity	126.53	133.77	139.26	120.53	136.66	3.16
Grain yield (Kg/plot)	6.74	6.28	5.40	7.19	7.23	1.58
1000-grain weight	24.73	21.94	19.59	26.86	25.78	54.55
Panicle length	26.00	30.44	28.93	22.13	24.00	1.19
Kernel length	6.65	7.67	7.03	5.53	5.64	9.09
Kernel breadth	1.95	1.72	1.79	2.80	2.47	11.86
L/B ratio	3.40	4.44	3.92	1.97	2.28	1.19

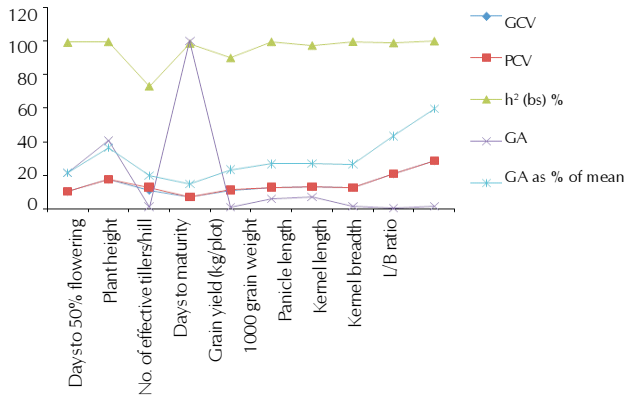


Figure 1: Estimates of genetic parameters for yield and quality characters

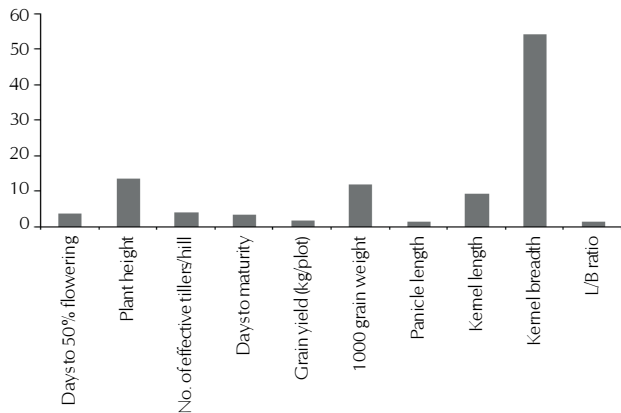


Figure 2: Contribution of different characters to total genetic divergence

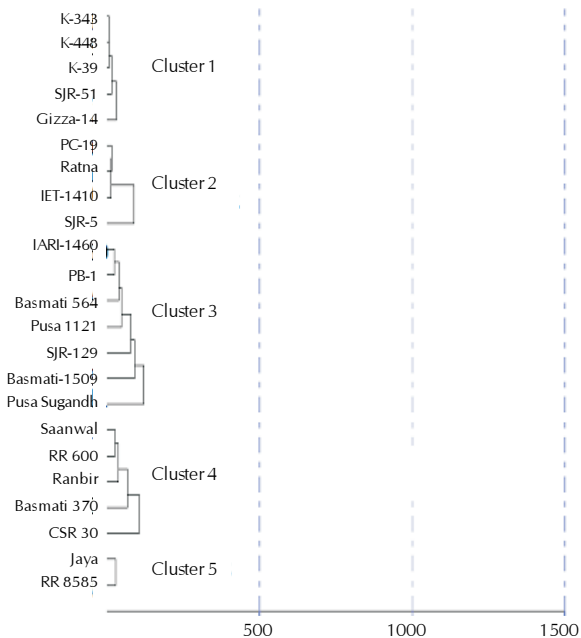


Figure 3: Dendrogram depicting various clusters among 23 rice cultivars

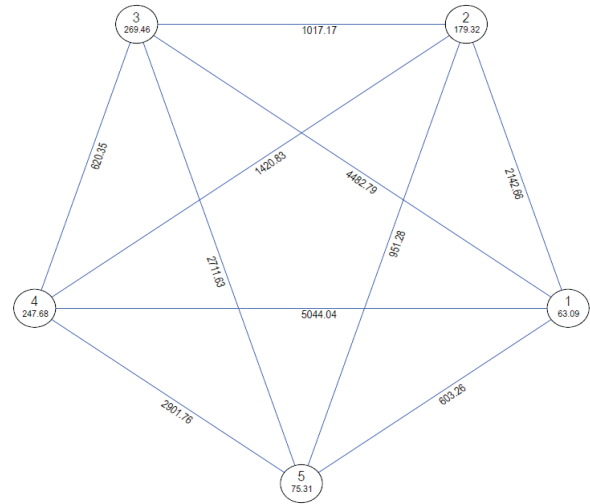


Figure 4: Mahalanobis Euclidean² distances

offered good scope of selection for the development of desirable types. The presence of large amount of variability might be due to diverse source of materials as well as environmental influence affecting the phenotypes. Similar findings were reported by Mishra *et al.* (2003). Estimates of components of variance and genetic parameters revealed that the genotypic variations contributed maximum to phenotypic variations for most of the characters. This suggested that available genetic variability can be successfully exploited through selection and hybridization among desirable lines for the development of superior rice genotypes.

The results of D² statistic indicated that the 23 genotypes differed significantly with regard to traits when studied individually. Based on D² values all the 23 genotypes of rice were grouped by Tocher's method into five clusters. The data relating to number of clusters formed and number of genotypes included in each cluster are given in table 2 and fig. 3. Among the five clusters cluster III had 7 genotypes, forming the largest cluster followed by cluster I and IV (5 genotypes each), cluster II (4 genotypes) and clusters V (2 genotypes).

A perusal of the table 3 on cluster means revealed that cluster IV could be characterized by genotypes having minimum days taken to 50 per cent flowering (86.93), medium plant height (94.13), early maturity (120.53), maximum 1000 grain weight (26.86) with short bold grains. Cluster III was found to have maximum plant height (142.26), maximum days to maturity (139.26), minimum number of effective tillers/hill (7.06) and long slender grain type. Cluster II exhibited maximum panicle length (30.44), maximum number of effective tillers per hill (8.33), maximum kernel length (7.67) and maximum L/B ratio

Table 4: Intra and inter cluster average D values of five clusters (I-V)

Cluster	I	II	III	IV	V
I	63.09	2142.66	4482.79	5044.04	603.26
II		179.32	1017.17	1420.83	951.28
III			269.46	620.35	2711.63
IV				247.68	2901.76
V					75.31

(4.44) with long slender grain type, cluster V exhibited medium plant height (100.83) and maximum grain yield kg/plot (7.23) with short bold grains while cluster I exhibited medium plant height (98.86), medium maturity (126.53) with long slender grain. A dendrogram illustrating the various clusters is depicted in Fig. 3. A critical appraisal of the observations indicated that none of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. Interestingly, all the maximum and minimum cluster mean values were distributed in relatively different clusters. The pattern of group constellation proved the existence of significant amount of variability. The clustering pattern of the genotypes revealed that the clustering did not follow any particular patterning clustering with respect to the origin (Ushakumari and Rangaswamy, 1997).

The inter and intra average distances among five clusters were computed and are presented in table 4 and fig. IV. Inter cluster distances were higher than intra cluster distances indicating wider genetic diversity among the rice genotypes. Intra cluster distance ranged from 63.09 to 269.46 and the maximum intra cluster distance was recorded in cluster III ($D = 269.46$) which was different from other clusters. The inter cluster distance was maximum between cluster I and IV (5044.04) and minimum inter cluster distance was observed between cluster I and V (603.26). To realize sufficient variability and high heterotic effect, Mishra *et al.* (2003) and Chaturvedi and Maurya (2005) recommended that parents should be selected from two clusters having wider inter cluster distance. Therefore, these genotypes are suggested to provide a broad spectrum of variability in segregating generations and would also yield higher amount of heterotic expression in hybrid combinations.

The utility of D^2 statistics as a potent tool to quantify the extent of divergence in biological populations at genetic level is further enhanced by its applicability to estimate the relative contribution of various plant characters to total genetic divergence. The contribution of various characters towards the expression of total genetic divergence (table 3 and fig II) indicated that 1000 grain weight contributed a maximum level (54.55%). It was followed by plant height (13.44), kernel breadth (11.86) and kernel length (9.09). It is well known that crosses between divergent parents usually produce greater heterotic effect than crosses between closely related ones. Considering the importance of genetic distance and relative contribution of characters towards total divergence, the present study indicated that genotypes in cluster IV can be selected for early maturity, medium plant height, maximum 1000 grain weight with short bold grains while genotypes in cluster I can be selected for medium plant height, medium maturity with long slender grain type, genotypes of cluster V for medium

plant height, good grain yield with short bold grain type and cluster III for long maturity and long slender grain type can be used in crossing programmes to identify desirable segregants for isolating improved rice cultures with enhanced productivity.

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