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Nature and magnitude of genetic diversity among locally adapted rice (*Oryza sativa* L.) genotypes

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Abstract
Present study was carried out during *kharif* 2015 at Experimental Area of Division of Plant Breeding and Genetics to assess nature and magnitude of genetic diversity among 32 locally adapted rice genotypes using Mahalanobis D^2 statistics. Analysis of variance indicated presence of notable genetic variability for yield, its components and quality traits. Estimates of components of variance indicated that genotypic variance contributed maximum to the phenotypic variance, suggesting that available genetic variability can be exploited through selection and hybridization. Based on D^2 analysis 32 rice genotypes were grouped into six clusters. Among these clusters cluster VI consists of 8 genotypes (SJR 51, Jaya, Giza 14, RR 8585, Shalimar rice 2, Shalimar rice 3, SJR 41 and SJR 45) forming the largest cluster followed by cluster II with seven genotypes (Pusa Basmati 1, Pusa sugandh 2, IARI 1460, RR 600, CSR 30, Pusa Basmati 1121 and Jammu Basmati 129), cluster I with six genotypes (Basmati 370, SJR 80, Basmati 564, SJR 81, Saanwal Basmati and Ranbir Basmati) cluster IIIrd and Vth with four genotypes each (Basmati 1509, SJR 5, Pusa Sugandh 5, Taroari Basmati and K-332, K-39, K-343, K-448) and cluster IV with three genotypes (Ratna, IET 1410 and PC 19). Inter cluster distances were found to be higher than intra cluster distances indicating wide genetic diversity among the genotypes. Contribution of various characters towards expression of total genetic divergence indicated that 1000 grain weight contributed a maximum (38.25%), followed by plant height (20.16%) and grain yield per plot (14.92%). The variation present among rice genotypes under study can be exploited through selection and hybridization among identified genotypes.

Keywords: Genetic diversity, D^2 statistics, *Oryza sativa*

Introduction
Rice (*Oryza sativa* L.) plays a major role in Indian economy being the staple food of two thirds of the population and occupies a significant place in Indian agriculture. Its demand is increasing day by day with the increasing population and shall continue to play a vital role in the national food and livelihood security. In India, rice was cultivated over an area of 44.0 m ha with production and productivity of 108.8 m tones and 2.47 tones/ha respectively (Anonymous, 2016) [1]. In J&K during 2016-17 rice was grown over an area of 283.44 thousand hectare with production and productivity of 5725 thousand quintals and 20.20 quintals per hectare respectively (Anonymous, 2016) [2]. In Jammu division in addition to various coarse, semi fine, fine early and medium maturing cultivars Basmati the premier rice known for quality was also grown over an area of about of 62.25 thousand hectare with production of 129.04 metric ton (Anonymous, 2016) [3] thereby, augmenting the income of farmers. Improvement in production and productivity of rice is of paramount importance and for that knowledge on the nature and the magnitude of the genetic variation governing the inheritance of quantitative characters is essential. In addition improvement in grain quality has significance because of the increasing acreage under basmati rice which benefits farmers due to its premium price. Since plant breeding programme solely depends on the genetic variability within the germplasm closely related to the crop of interest but, the success of crop improvement programme is highly reliant on power and efficiency with which this genetic variability can be manipulated (Crouch and Ortiz, 2004) [7]. Based on the objective, the divergent parents are crossed to develop promising breeding lines having sufficient diversity. Therefore, in addition to mean performance the evaluation of material for genetic divergence among various yield and quality traits would be more useful to plant breeders. Similarly, estimates of heritability and genetic advance will be of immense help to the breeder in selecting superior individuals for a desired trait and successfully utilizing them in breeding programme. Keeping this in view, the present study was envisaged to estimate genetic diversity in 32 rice genotypes using Mahalanobis D^2 statistics for efficient selection of the diverse parents.

Materials and methods

32 locally adapted cultivars of Jammu region constitute the material for present investigation. Among these 18 genotypes viz., Shalimar rice 2, Shalimar rice 3, PC 19, IET 1410, RR 8585, Jaya, K 39, K 343, K 448, K 332, Giza 14, SJR 5, SJR 81, SJR 39, SJR 51, Ratna, SJR 41 and SJR 45 belong to non-basmati group and 14 genotypes viz., SJ R 80, Basmati 370, Basmati 564, Ranbir Basmati, Saanwal Basmati, RR 600, CSR 30 Pusa Basmati 1121, Pusa 1460, Pusa Basmati 1, Pusa Sugandh 5, Taroari Basmati, Pusa Sugandh 2 and Jammu Basmati 129 belong to basmati group. During *kharif* 2015 25 days old seedlings of these genotypes were transplanted in Randomized Block Design with three replications having a plot size of $5m^2$/replication/genotype (5 rows each of 5.0 m length) maintained with row to row spacing of 20 cm. Single plant per hill was planted maintaining hill to hill spacing of 15 cm. Recommended package of practice were followed for raising a good crop. Observations were recorded on various morpho-physiological and yield attributing traits in order to study the magnitude and level of genetic diversity in the material under study. Five plants per plot were randomly selected and tagged for recording the observations, while, observations on days to 50 per cent flowering, days to maturity and grain yield 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 and breadth), 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) [11]. Genotypic and phenotypic coefficient of variation, heritability (broad sense), and genetic advance was calculated following the procedure described by Burton and Devane (1953) [5]. The statistical analysis was carried by Mahalanobis D^2 statistics (Rao, 1952) [12] to quantify the genetic diversity for various grain yield and quality traits.

Results and discussion

Analysis of variance revealed highly significant differences among the genotypes for all the traits studied. Wide range of variation exhibited by the genotypes indicated ample scope for selection of superior and desirable genotypes for further exploitation as parents. High magnitude of phenotypic and genotypic coefficient of variation (Table 1and Fig. 1) was observed for days to 50% flowering, plant height, number of effective tillers per plant, peduncle length, panicle length, days to maturity (no.), grain yield per plot (kg), 1000 grain weight, grain length, grain width, grain length/width ratio, dry matter content, total dry mater content indicating high scope of obtaining high selection response. Similar findings were reported by Kumar *et al.,* (2014) [9]. Moderate estimates of coefficient of variability at phenotypic and genotypic level were observed for days to 50% flowering, plant height, peduncle length, panicle length, dry matter content and grain length. Therefore, these characters are likely to allow reasonable scope for improvement through selection. Low estimates of phenotypic and genotypic coefficient of variation were observed for days to maturity, grain yield per plot and total dry matter content indicating that selection directly based on these traits would not be much rewarding. The estimates of PCV were slightly higher than corresponding GCV for all the characters under study. Similar findings were also recorded by Kumar *et al.,* (2014) [9] in their respective studies. High estimates of heritability in broad sense with high genetic advance in per cent of mean were observed for plant height, days to 50% flowering, dry matter content, total dry matter content, no. of effective tillers per

Table 1: Estimates of components of variance and genetic parameters for various traits

S. No.	Character	Range	GCV (%)	PCV (%)	h^2 (bs) %	GA (%)	GA as % of mean
1.	Days to 50% flowering	85.16-124.00	10.27	11.13	85.20	20.49	19.54
2.	Plant height	72.00-152.43	20.23	20.30	99.38	45.59	41.56
3.	No. of effective tillers per plant	6.16-13.00	25.57	26.90	90.36	4.35	50.08
4.	Peduncle length	30.12-45.00	10.94	12.46	77.09	7.83	19.79
5.	Panicle length	18.21-33.10	17.48	18.29	91.28	9.05	34.40
6.	Days to maturity	121.43-151.43	6.38	7.49	72.63	14.81	11.21
7.	Grain yield per plot	1.40-2.60	4.26	9.63	19.65	0.24	3.89
8.	1000 grain weight	17.64-27.00	9.26	12.01	59.47	3.35	14.71
9.	Grain length	5.06-8.73	13.20	14	88.87	1.74	25.64
10.	Grain breadth	1.41-3.00	23.89	24.07	98.52	1.10	48.86
11.	Grain length/breadth ratio	2.18-4.59	27.29	27.78	96.50	1.74	55.24
12.	Dry matter content	14.46-29.58	16.51	16.59	97.75	6.92	33.62
13.	Total dry matter content	24.43-35.51	9.49	9.78	94.20	5.72	18.98

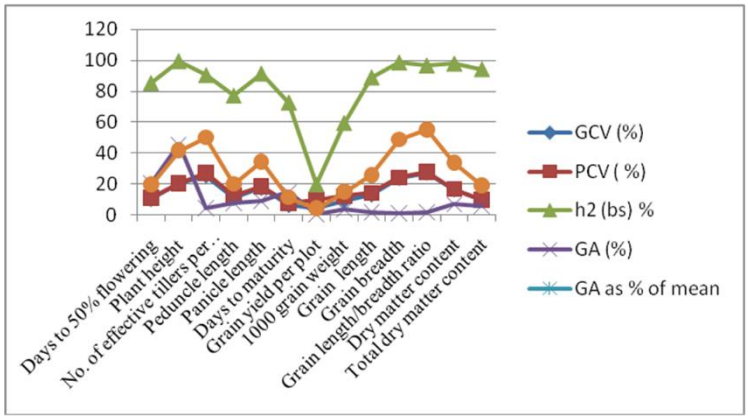

Fig 1: Components of variance and genetic parameters for various traits

Plant, peduncle length, days to maturity, grain length and grain breadth. Similar results were reported for plant height and grain yield by Das *et al.*, (2001) [8]. Mahalanobis's D^2 (1936) [10] statistics is the most widely used measure of genetic diversity and it compares all possible pairs of a population precisely before attempting actual cross combination. In addition a method suggested by Tocher (Rao, 1952) [12] is used for clustering utilizing D^2 values. In present study thirty two rice genotypes were categorized into six clusters (Table 2 and Fig 2).Maximum intra cluster distance was observed in cluster I (514.44), followed by cluster III (363.5), cluster VI (356.99), cluster II (211.97), cluster V (49.74), cluster V (44.44), thereby, indicating that some

Table 2: Distribution of genotypes in various clusters (I-VI)

Cluster No.	No. of genotypes	Name of genotypes
I	6	Basmati 370, SJR 80, Basmati 564, SJR 81, Saanwal Basmati, Ranbir Basmati
II	7	Pusa Basmati 1, Pusa sugandh 2, IARI 1460, RR600, CSR 30, Pusa 1121, Jammu Basmati 129
III	4	Basmati 1509, SJR 5, Pusa sugandh 5, Tarori Basmati
IV	3	Ratna, IET 1410, PC 19
V	4	K 332, K 39, K 343, K 448
VI	8	SJR 51, Jaya, Gizza 14, RR 8585, Shalimar Rice 2, Shalimar Rice 3, SJR -41, SJR -45

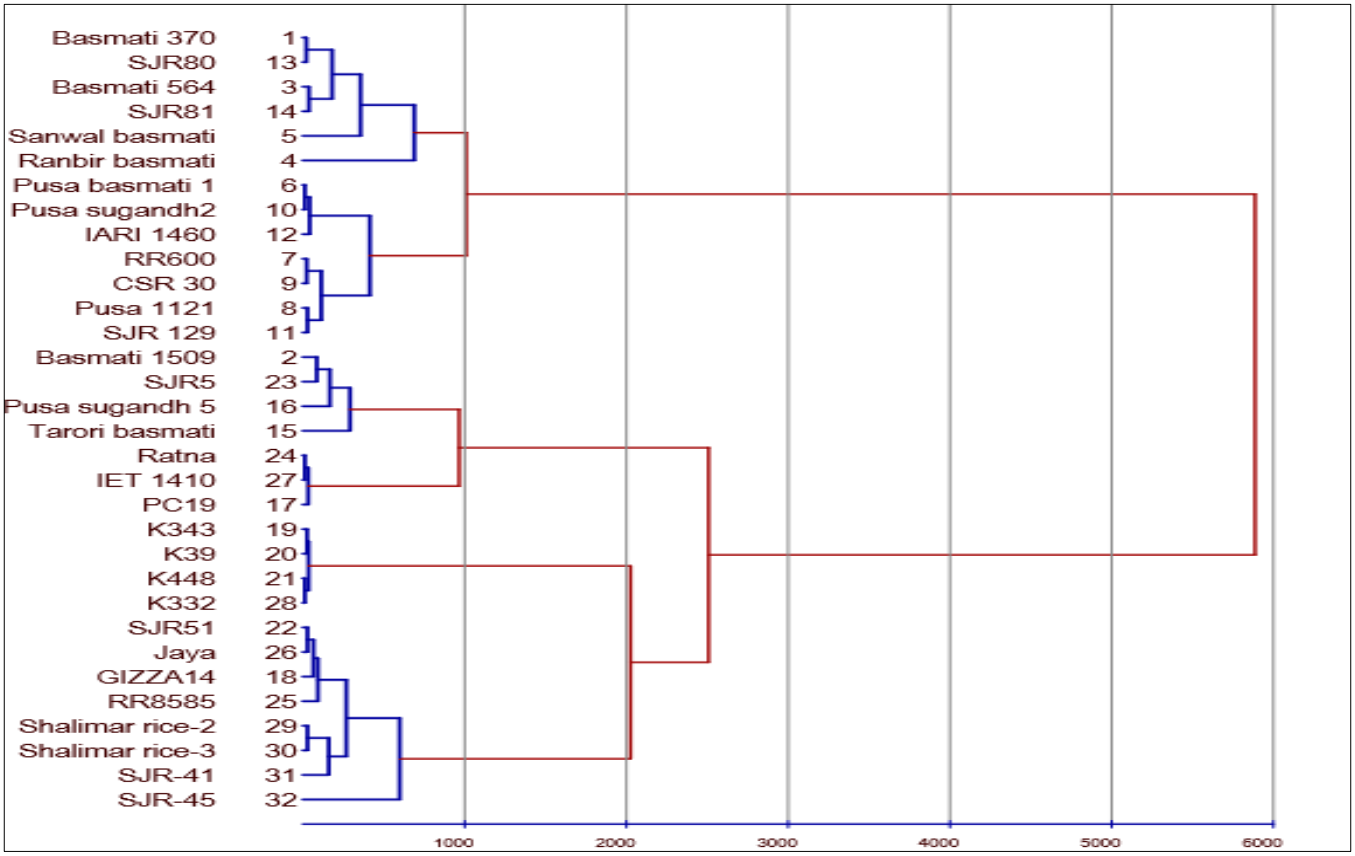

Fig 2: Distribution of genotypes in various clusters (I-VI)

genetic divergence still exists among the genotypes which could be utilized in yield improvement through recombination breeding. Inter cluster D^2 values (Table 3 and Fig 3) of six clusters, indicated that the highest divergence occurred between cluster I and cluster IV (2390.64) followed by cluster II and cluster IV (1748.39), cluster I and cluster VI (1705.93), cluster I and cluster V (1676.34), cluster III and cluster V (1605.53), cluster I and cluster III (1368.30), cluster II and cluster V (1145.65), cluster II and cluster III (1091.04), cluster III and cluster VI, cluster V and cluster VI (934.45), cluster IV and cluster VI (912.41), cluster IV and cluster V (869.27), cluster II and cluster VI (770.31), cluster III and cluster IV (714.49), cluster I and cluster II (617.76), cluster I and cluster I (514.44), cluster III and cluster III (363.51), cluster II and cluster II (211.97), cluster V and cluster V (49.74) and cluster IV and cluster IV (44.44) suggesting occurrence of broad spectrum

Table 3: Intra (diagonal) and Inter cluster average D^2 values

Cluster	I	II	III	IV	V	VI
I	514.44	617.678	1368.308	2390.645	1676.34	1705.936
II		211.97	1091.047	1748.396	1145.66	770.314
III			363.51	714.49	1605.53	992.758
IV				44.44	869.27	912.411
V					49.74	934.437
VI						356.99

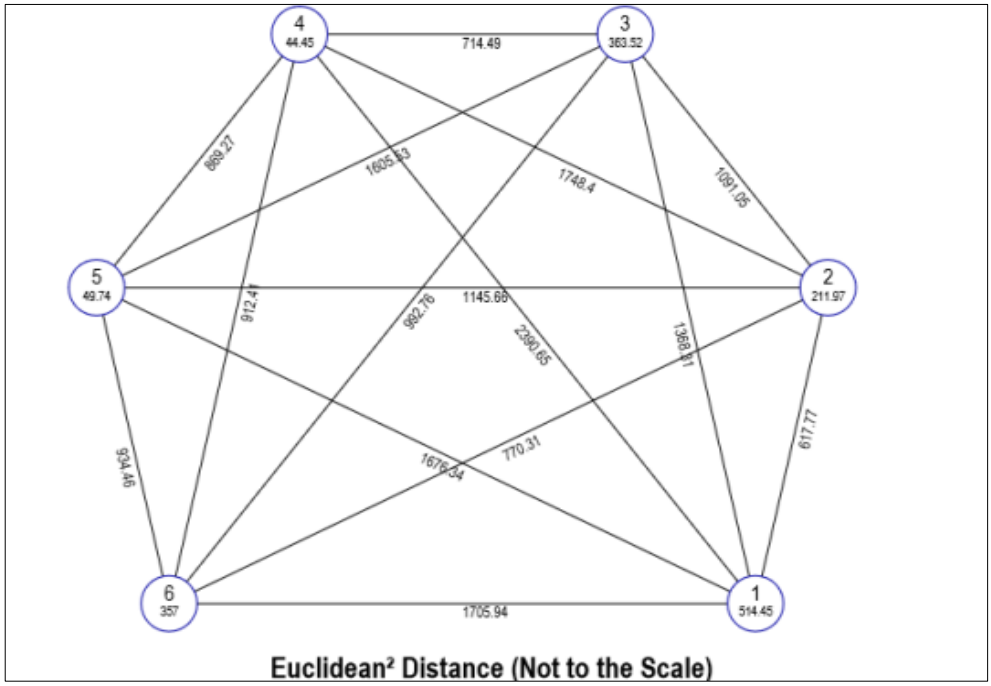

Fig 3: Intra (diagonal) and Inter cluster average D^2 values

of variation in segregating generations. Results of Bose and Pradhan (2005) [4] are also in confirmation with the results of present study thereby, suggesting that clustering of genotypes is probably due to free exchange of germplasm among breeders of different regions and or unidirectional selection practiced by breeders while tailoring promising cultivars for different regions (Chaturvedi and Maurya [6], 2005; Sabesan and Saravanam, 2008) [13]. Relative contribution of different characters (Table 4) towards divergence indicated that 1000 grain weight contributed

Table 4: Clusters means for yield, its components and quality traits in rice genotypes

Cluster / Character	I	II	III	IV	V	VI	Contribution (%)
Days to 50% flowering	108.37	104.74	113.96	95.56	89.33	97.14	5.13
Plant height	142.42	116.28	117.36	91.33	94.95	89.83	20.16
No. of effective tillers per plant	8.62	9.084	7.877	7.61	7.683	9.19	1.34
Peduncle length	40.87	41.52	41.62	39.13	35.03	38.27	0.81
Panicle length	31.36	30.43	28.09	22.37	22.24	21.56	1.41
Days to maturity	135.82	137.76	138.51	127.32	122.18	127.95	1.21
Grain yield per plot	1.82	2.03	2.06	2.22	2.19	2.00	14.92
1000 grain weight	20.01	22.35	23.71	23.32	25.81	22.93	38.25
Grain length	7.46	7.37	7.23	6.42	5.39	6.40	3.07
Grain breadth	2.68	2.84	1.57	1.43	2.30	2.07	0.40
Grain length/breadth ratio	2.85	2.58	4.59	4.47	2.33	3.11	0.40
Dry matter content	19.90	21.82	22.50	18.50	14.54	22.82	5.32
Total dry matter content	29.18	32.03	32.93	28.53	24.51	31.32	7.58

maximum to diversity (38.25%), followed by plant height (20.16%), grain yield per plot (14.92%), total dry matter content (7.58%), dry matter content (5.32%), days to 50% flowering (5.13%), grain length (3.07%), panicle length (1.41%), plant height (1.34%), days to maturity (1.21%), peduncle length (0.81%), grain breadth (0.40%), grain length /breadth ratio (0.40%). Selection of parents from different clusters having wide inter cluster distance coupled with good intra cluster diversity for a set of economic traits have been useful in creating broad spectrum segregants (Singh *et al.*,1996) [14]. Among the clusters cluster VI consists of 8 genotypes (SJR 51, Jaya, Giza 14, RR 8585, Shalimar rice 2, Shalimar rice 3, SJR 41 and SJR 45) forming the largest cluster followed by cluster II with seven genotypes (Pusa Basmati 1, Pusa sugandh 2, IARI 1460, RR 600, CSR 30, Pusa Basmati 1121 and Jammu Basmati 129), cluster I with six genotypes (Basmati 370, SJR 80, Basmati 564, SJR 81, Saanwal Basmati and Ranbir Basmati) cluster IIIrd and Vth with four genotypes each (Basmati 1509, SJR 5, Pusa Sugandh 5, Taroari Basmati and K-332, K-39, K-343, K-448) and cluster IV with three genotypes (Ratna, IET 1410 and PC 19). The pattern of distribution of genotypes into various clusters was at random indicating that geographical and genetic diversity were not related or may be due to the substantial variation in geographic and climatic conditions that houses different agro-ecosystems.

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