Research Article
Genetic diversity for agro-morphological traits in rice germplasm

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Abstract
Nature and magnitude of agro-morphological variation in 25 rice germplasm lines was studied with the help of Mahalanobis D^2 statistics. Notable genetic variability in all the traits studied indicated existence of sufficient variation among the germplasm lines. Variance estimates revealed that genotypic variance contributed maximum to phenotypic variance suggesting that such variation can be exploited through selection and hybridization. Based on D^2 values, 25 lines were grouped into six clusters. Among the six clusters, cluster IV consists of 9 lines, forming the largest cluster followed by cluster V (7 lines), cluster VI (5 lines), II (2 lines) while I & 3 had 1 line each. Inter cluster distances were found to be higher than intra cluster distances depicting wide diversity among the lines under study. The contribution of various characters towards the expression of total genetic divergence indicated that number of effective tillers/plant contributed a maximum level (21.86%) followed by days to 50 percent flowering (12.19%) and grain yield (11.40%). The variation present in the germplasm lines can be exploited through selection and hybridization.
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Key words
Rice germplasm, variability, dendrogram, genetic divergence

Introduction
Rice is one of the most important cereals, providing the caloric needs of millions of people daily. It contributes significantly in Indian Economy and also serves as staple food for more than 70 per cent of the people dwelling in Asia. In J & K rice is grown over an area of 271.49 thousand hectare with production and productivity of 5567 thousand quintals and 21.51 quintals hectare^{-1}, respectively (Anonymous, 2014) thereby, playing a important role in livelihood security of people of the state.

Crop improvement program solely depends on conservation and utilization of germplasm resources. However, the major thrust area for genetic improvement lies in identifying desirable parents for hybridization for which knowledge about germplasm diversity and genetic relationships among breeding materials serves as valuable aid. Selection of genetically divergent parents for hybridization depends upon categorization of germplasm on some basis, therefore in order to understand the usable variability, classification of germplasm is quite imperative.

Cross combinations involving divergent parents provide an opportunity for bringing together gene constellations of diverse nature and also promising segregant derivatives which result due to complementary interaction of divergent genes in parents are expected. Various workers in past had emphasized the importance of diversity for selecting desirable parents (Murthy and Arunachalam, 1996 and Rahman, *et al,* 1997).

Mahalanobis D^2 statistics for estimating genetic divergence had been emphasized by many workers (Roy and Panwar, 1993; Ramya and Senthilkumar, 2008). Therefore, an attempt was made through the present study to assess agro-morphological variation in few locally cultivated and advance breeding lines for their future exploitation.

Materials and methods
25 germplasm lines viz., GP1(SJR 76), GP2 (SJR80), GP3 (SJR 81), GP4 (SJR 92), GP5 (SJR 98), GP6 (SJR 105), GP7 (SJR 108), GP8 (SJR 115), GP9 (SJR 120), GP10 (SJR 121), GP11 (SJR 122), GP12 (SJR 123), GP13 (SJR 125), GP14 (SJR 129), GP15 (Basmati 370), GP16 (Ranbir Basmati), GP17 (Saanwal Basmati), GP18 (Basmati 564), GP19 (RR 600), GP20 (Basmati 1509), GP21 (SJR 70), GP22 (Local Basmati), GP23 (Local Basmati), GP24 (Local Basmati) and GP25 (Local Basmati)   constitute the material for the present study. All these lines were evaluated in a Randomized Block Design with three replications at the experimental area of Division of Plant Breeding & Genetics, Sher-e-Kashmir University of Agricultural Sciences & Technology Main Campus, Chatha Jammu during kharif 2015. Each germplasm line was sown in 4 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 per replication for days to 50 per cent flowering, plant height (cm), number of effective tillers, panicle length, days to maturity, grain yield (kg/plot), grain length (cm), grain breadth (cm) and grain length-breadth ratio. Observations on days to 50%

flowering and days to maturity were recorded on plot basis. Analysis of variance was calculated following the procedure of Panse and Sukhatme (1978). Genotypic and phenotypic coefficient of variation, heritability (broad sense), genetic advance was calculated following the procedure of Burton and Devane (1953) while Mahalanobis D^2 statistics (Rao, 1952) was employed to quantify the genetic variation.

Results and discussion

Analysis of variance for all the characters indicated reasonable variation among germplasm lines while estimates of components of variance and genetic parameters revealed that the genotypic variations contributed maximum to phenotypic variation for most of the characters thereby indicating that such variation can be successfully exploited through selection and hybridization among the component lines (table 1 & fig. 1)

Phenotypic coefficient of variation (PCV) was found to be higher than the genotypic coefficient of variation (GCV), depicting the influence of environmental agencies. Heritability estimates serve as predictive instrument in expressing the reliability of phenotypic value and high heritability helps in effective selection for a particular trait. In this study, high estimates of heritability in broad sense were recorded for almost all characters ranging from 62.12% (plant height) to 87.35% (grain yield) while number of effective tillers (52.70%) and panicle length (21.90%) exhibited moderate and low estimates respectively. Genetic advance is a useful indicator of the expected progress that results after attempting selection in a population. The genetic advance expressed as a percentage of mean ranged from 4.69 to 47.58 and the important characters like grain yield (47.58) recorded highest estimates. Characters that exhibits high heritability coupled with high genetic advance are controlled by additive gene action (Panse and Sukatme, 1957) and these characters can be improved through simple or progeny selection methods. Selection for such traits is likely to accumulate more additive genes. The characters showing high heritability along with moderate or low genetic advance can be improved by intermating superior genotypes of segregating population developed from recombination breeding (Samadia, 2005). On the basis of D^2 values the 25 germplasm lines were grouped by Tocher's method into six clusters (table 2 & fig. 2). Number of genotypes included in each cluster revealed that cluster IV had 9 and cluster V had 7 genotypes, thereby forming the largest clusters followed by cluster VI (5 genotypes), cluster II (2 genotypes) and cluster I & III (1 genotype each).

A perusal of the table 3 on cluster means revealed that cluster II could be characterized by genotypes having minimum days taken to 50% flowering (84.73), medium plant height (123.02) early maturity (125.35) and maximum grain length (9.15). Cluster III recorded maximum plant height (136.05) and minimum grain length (7.13 mm). Cluster I exhibited maximum number of effective tillers (15.73) while cluster VI exhibited maximum days taken to maturity (137.60). 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 contribution of characters towards total divergence revealed that grain length (16.85) exhibited maximum contribution followed by panicle length (14.52), grain yield (11.52), effective tillers (11.10), days to 50% flowering (10.19), plant height (8.44), grain breadth (8.23), days to maturity (4.47) while L/B ratio exhibited least contribution (0.02).

The inter and intra average distances among six clusters were computed and are presented in table 4. Inter cluster distances were higher than intra cluster distances indicating wider genetic diversity among the rice genotypes. 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 were 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. 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 II could be selected for early maturity, medium plant height and maximum grain length while genotypes in cluster I can be selected for maximum number of effective tillers cluster VI for late maturity could be used in crossing programmes to   identify

desirable segregants for isolating improved rice cultures with enhanced productivity.

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Table 1. Component of variance and estimates of genetic parameters

Character	Mean	σ^2 g	σ^2 p	GCV	PCV	h²(b.s)%	GA	GA as % of mean
Days to 50% flowering	109.76	26.79	34.50	5.71	7.88	77.65	9.40	8.56
Plant height	116.27	142.61	229.54	8.50	12.00	62.12	19.39	16.67
Number of effective tillers	7.93	0.39	0.74	13.60	18.80	52.70	0.93	11.72
Panicle length	27.89	1.84	8.40	7.60	9.04	21.90	1.31	4.69
Days to maturity	137.93	42.62	59.40	4.63	5.94	71.75	11.40	8.26
Grain yield	12.21	9.12	10.44	16.85	22.52	87.35	5.81	47.58
Grain length	6.71	0.43	0.54	8.42	10.20	79.62	1.21	18.03
Grain breadth	1.69	0.009	0.014	5.54	13.30	64.28	0.19	11.24
Grain L/B ratio	3.92	0.219	0.262	13.55	18.71	83.58	0.88	22.44

Table2. Clustering pattern germplasm lines (I-VI)

Cluster no.	No. of germplasm lines	Germplasm Entries
I	1	GP 1
II	2	GP 4
		GP 5
III	1	GP 14
IV	9	GP 6
		GP 7
		GP 10
		GP 8
		GP 9
		GP 13
		GP 12
		GP 2
		GP 11
V	7	GP 21
		GP 3
		GP 25
		GP 22
		GP 15
		GP 18
		GP 17
VI	5	GP 20
		GP 16
		GP 24
		GP 23
		GP 19

Table 3. Cluster means for eleven characters under study and their contribution to total divergence.

Character/Cluster	1	2	3	4	5	6	Contribution%
Days to 50% flowering	103.00	84.73	98.00	94.17	96.37	97.56	10.19
Plant height	120.92	123.02	136.05	125.52	107.90	122.90	8.44
Number of effective tillers	15.73	14.17	12.42	10.84	12.45	12.25	11.10
Panicle length	27.03	22.86	30.61	25.16	24.32	28.08	14.92
Days to maturity	135.40	125.35	129.80	136.28	113.46	137.60	4.47
Grain yield	22.23	26.63	27.44	23.70	25.37	23.40	11.52
Grain length	8.11	9.15	7.13	8.14	9.01	7.30	16.85
Grain breadth	1.67	1.63	1.82	1.52	1.76	1.66	8.23
Grain L/B ratio	5.01	5.11	4.63	4.43	5.08	4.15	0.02

Table 4. Intra and inter cluster D² values of six clusters.

Cluster	1	2	3	4	5	6
1	8.30	14.08	12.82	17.41	20.55	24.41
2		0.00	21.70	20.65	30.62	15.21
3			0.00	19.09	25.93	30.76
4				0.00	33.48	17.82
5					0.00	55.70
6						0.00

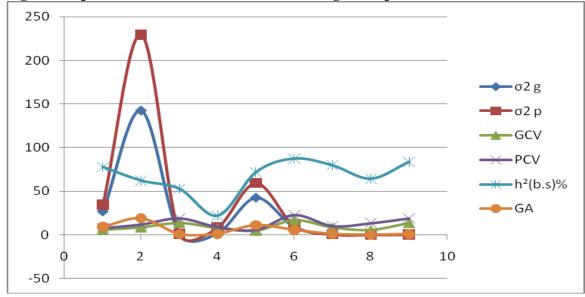**Fig 1. Components of variance and estimates of genetic parameters**

Fig 2. Dandogram depicting various clusters among 25 rice germplasm lines