Short Communication

Multivariate analysis of phenotypic diversity of rice (*Oryza sativa*) germplasm in North-West India

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Rice (*Oryza sativa* L.) is one of the most important cereal crop and a primary energy source for more than one half of world's population. In view of importance of rice as a major food crop, the origin and diversity of *Oryza sativa* has attracted great interest. The success of breeding programme largely depends on the selection of parents for hybridization from diverse base materials with built in genetic variability. Such materials serve as sources of desirable genes needed for relevant breeding programmes to improve yield and productivity and breeders across countries have recycled many traditional varieties as sources of genes of interest.

For breaking the yield plateau which generally is indicative of a narrow genetic, the widely followed approach involves diversification of parents for harnessing of the genetic diversity present in the germplasm. Genetic diversity analysis using genetic distance measures, derived from quantitative and agronomic characters, is an efficient tool to select best parents for hybridization programme and obtain desirable combinations in the segregating generations (Whitehouse 1969). Considering the above points, the present study was initiated to assess the extent of genetic diversity in rice germplasm using genetic distances calculated on the basis of morphological and agronomic traits as the measures.

The germplasm used in this study comprised 2142 rice accessions and six checks (Swarna, Pusa Basmati 1, NDR 97, Annada, IR 64 and Jaya) was obtained from the National Bureau of Plant Genetic Resources (NBPGR), New Delhi under the Establishment of national rice resource data base project. All the accessions along with checks were planted at CSSRI, Karnal experimental fields in *kharif* 2010-11 using augmented randomised complete block design (Federer 1961) in three rows plot having 20 plants spaced at 15 × 30 cm.

Recommended cultural practices were followed to grow a healthy crop and for proper expression of genotypes.

Five random but robust plants from inner rows were tagged from each plot for data collection. A total of ten quantitative traits namely; days to flowering, days to maturity, grain length (mm), grain width (mm), 100 seed weight (g), seedling height (cm), plant height (cm), panicle length (cm), number of effective tillers and grain yield/plant (g), were measured at particular stages of rice plant following the minimal descriptor of agri-hort crops and standard evaluation system of rice provided by NBPGR, New Delhi.

Analysis of variance was performed for quantitative characters using SAS software (Version 9.2) to estimate genetic variation for the traits. The Pearson's correlation coefficient (*r*) was analyzed to evaluate the relationships among different variables. Cluster analysis was carried out based on genetic distance matrix of the 2142 accessions along with six checks, applying the UPGMA (Unweighted Pair-Group Method using Arithmatic average) clustering method (Michener and Sokal 1957).

The analysis of variance showed significant block effects for all the traits except grain width where block effects were non-significant implying that blocking had no effect on the grain width. The accessions however showed significant differences for most of the traits, except number of effective tiller and grain yield/plant.

The genetic variability parameters including mean, standard error, coefficient of variation (CV) and minimum and maximum values of the various traits were also estimated. The checks had average days to maturity (129 days), 100-seed weight (2.3 g), grain yield/plant (18.5 g), effective tillers/plant (6.9) and panicle length (24.63 cm). The largest variation was observed in the yield/plant (CV = 64.66%) followed by the number of effective tillers, grain width and 100 seed weight having CV = 25.73, 19.26, and 15.78%, respectively. Seedling height followed by panicle length and days to maturity showed the lowest variation (CV = 0.87, 7.83 and 7.84%, respectively). Sanni *et al.* (2012) also

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reported variation for quantitative traits in rice germplasm. The accession IC 461817 recorded the longest flowering time (160 days after sowing), while IC 449551 recorded the earliest flowering time (72 days). Similarly, accession IC 330690 recorded the maximum number of effective tillers (17.2), whereas IC 394518 produced the minimum effective tillers (2.2). IC 392250 was the tallest accession with 221.4 cm plant height, whereas the shortest accession IC 385561 with 49.0 cm. The accession with least panicle length (12.6 cm) was IC 413457, while IC 459773 had the longest panicle of 41.8 cm. The accession that took the longest number of days to mature (178 days after sowing) was IC 450100, whereas IC 449656 was the earliest to mature, maturing in 106 days after sowing. The accession with the longest grain was IC 545222 with a grain length of 24.78 mm, whereas IC 459798 recorded the shortest grain of 4.2 mm. However, IC 114333 with the largest grain width of 11.42 mm had a broad grain shape, whereas IC 545299 had a width of 1.1 mm. Accession IC 382615 had the highest 100 - seed weight (3.5g) against the lowest (0.4g) width in IC 347612. Accession IC 333022 produced the maximum yield per plant (43.88g), while the lowest yield (1.2g) was recorded in IC 544956. Seedlings of IC 449774 were the tallest with 50.54 cm height, whereas IC 316314 had the shortest seedling height (4.38 cm). Thus, from the study of individual characters, it is clear that huge variations in all the characters is present in the present set of rice accessions in the germplasm set under evaluation and the same could be used for crop improvement programmes in rice (Chakravorty *et al.* 2013, Medhabati *et al.* 2013 and Wu *et al.* 2013).

Association between traits

Among the variables studied, the highest correlation coefficient recorded was between days to flowering and days to maturity with $r = 0.92**$ (Table 1). The trait presenting

highly significant but negative correlations with these two characteristics is the number of effective tillers ($r = -0.45**$ and $-0.46**$, respectively) showing the number of effective tillers tends to decrease as the duration of days to flowering and maturity increases. The positive and significant correlations among grain weight and grain width ($r = 0.44**$) and grain length ($r = 0.47**$) indicated that higher the grain weight, wider and longer the grain becomes. Estimated higher value of significant and positive correlation between number of effective tillers and yield/plant ($r = 0.59**$) revealed that grain yield is under direct influence as it tend to increase along with the increasing number of effective tillers. These findings are in conformity with Medhabati *et al.* (2013), Wu *et al.* (2013), Chakravorty *et al.* (2013), Soharabi *et al.* (2012), Sanni *et al.* (2012) and Lasalita-Zapico *et al.* (2010).

Cluster analysis

Analyses performed by the UPGMA grouped 2142 accessions into total eight clusters (Fig 1) with 1569 accessions in cluster I, 159 in cluster II, 155 accessions in cluster III, 370 accessions in the cluster IV, 69 accessions in cluster V, 8 accessions in cluster VI whereas cluster VII and VIII had only two accessions each (Table 2). The accessions in cluster VIII were primarily early flowering types with a mean of 77 days flowering duration. Number of effective tillers per plant was higher in clusters II, IV, V and VIII (7 to 8). Accessions in clusters VIII were taller (plant height 205.80 cm), whereas shorter accession were grouped in clusters II, V and VII having plant height between 87.33 to 91.0 cm. Cluster III had accession with the longest panicle (24.55 cm), the highest 100-seed weight (2.11 g), higher grain yield per plant (18.09 g) and the shortest seedling (17.88 cm). Early maturing accessions were grouped in cluster V and VI having mean maturity duration from 110 to 113 days. Cluster I, III, IV and VIII had the accession with the longest grain

Table 1   Correlation coefficient among ten quantitative traits in rice germplasm accessions

Traits	Correlation coefficients									
	Days to flowering	No. of effective tillers	Plant height (cm)	Panicle length (cm)	Days to maturity	Grain length (mm)	Grain width (mm)	100 seed weight (g)	Yield/ plant (g)	Seedling height (cm)
Days to flowering	1.00	-0.45**	0.27**	-0.16**	0.92**	-0.09*	-0.06	-0.19**	-0.10**	0.10**
No. of effective tillers		1.00	-0.23**	-0.02	-0.46**	-0.01	-0.05	-0.04	0.59**	-0.05
Plant height (cm)			1.00	0.18**	0.27**	0.08	0.07	0.10**	0.13**	0.01
Panicle length (cm)				1.00	-0.16**	0.12**	0.07	0.11**	0.31**	-0.01
Days to maturity					1.00	-0.09*	-0.06	-0.18**	-0.10**	0.11**
Grain length (mm)						1.00	-0.08	0.47*	0.12**	-0.02
Grain width (mm)							1.00	0.44*	0.09*	-0.02
100 seed weight (g)								1.00	0.14**	-0.01
Yield/plant (g)									1.00	-0.12**
Seedling height (cm)										1.00

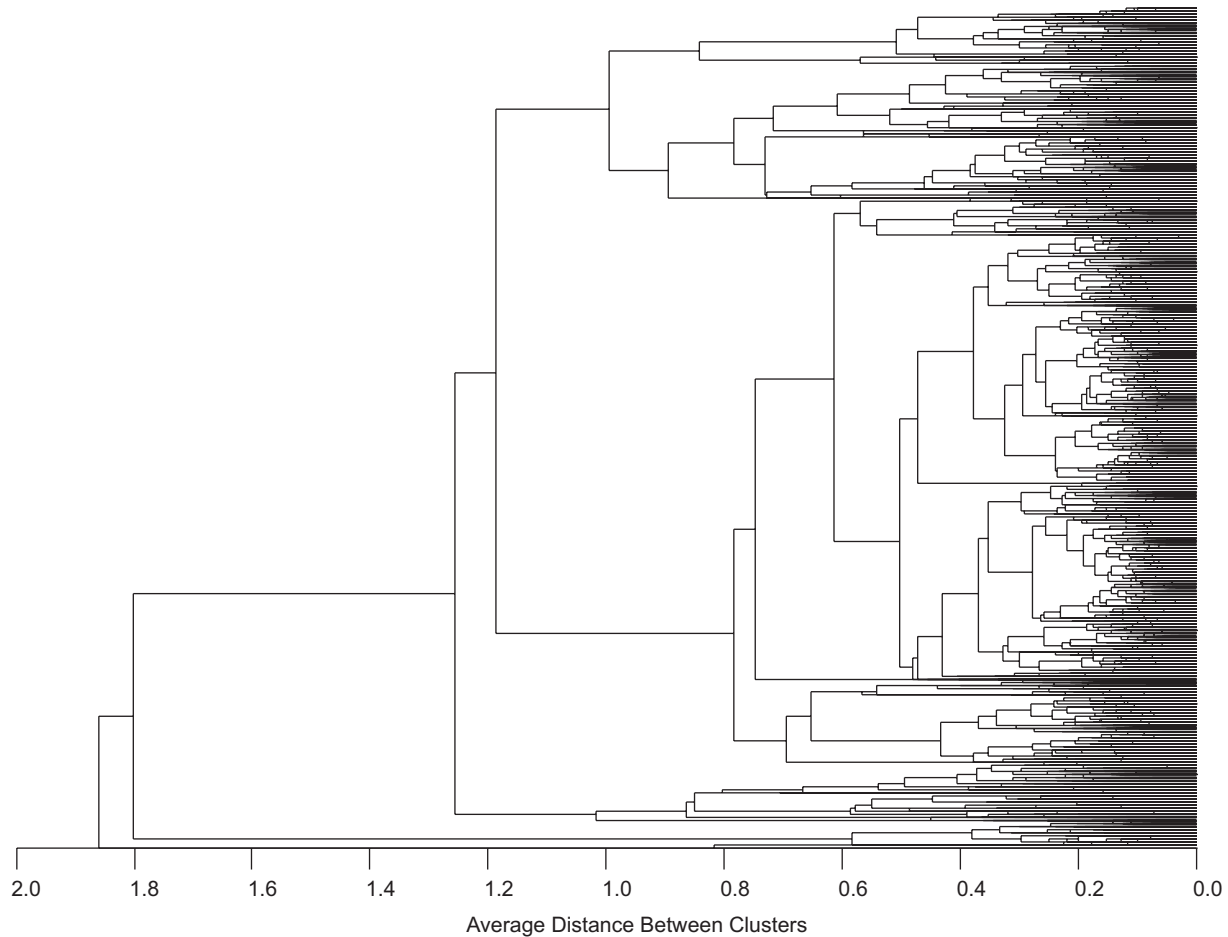*, **Significant at 5% and 1% level of significance, respectively

Fig. 1 Dendrogram of similarity patterns by the UPGMA method based on the average Euclidean Distance estimated from 10 agro-morphological traits analysed in 2142 accessions of Indian rice accessions used in the experiment.

(8.00 - 8.38 mm). Longer seedling accessions were grouped in cluster VI and VII with 22.15 to 23.59 cm height, respectively. Similarly, fine grain accessions were largely grouped in cluster VI with average grain size of 2.33 mm, whereas cluster VIII had accession with bolder grain having mean grain width of 2.73 mm (Table 2). Accessions falling under distant clusters could be hybridized to get the higher heterotic responses. Medhabati *et al.* (2013), Wu *et al.* (2013), Chakravorty *et al.* (2013), Sanni *et al.* (2012), Soharabi *et al.* (2012) and Latif *et al.* (2011) also reported similar findings from cluster analysis of the rice germplasm for agro-morphological traits diversity.

Table 2   Rice accessions grouped into eight different clusters using unweighted pair group method of the average linkage (UPGMA) based morphological dendrogram

No. of cluster	Correlation mean values of character										
	No. of member accessions	Days to flowering	No. of effective tillers	Plant height (cm)	Panicle length (cm)	Days to maturity	Grain length (mm)	Grain width (mm)	100 seed weight (g)	Yield/ plant (g)	Seedling height (cm)
CL I	1569	133.00	6.22	140.68	23.09	164.00	8.00	2.36	1.94	11.14	20.02
CL II	159	132.00	6.68	87.37	19.88	164.00	7.77	2.34	1.80	8.01	19.61
CL III	155	97.00	7.35	144.34	24.55	126.00	8.24	2.48	2.11	18.01	17.88
CL IV	370	110.00	7.04	105.64	22.62	139.00	8.12	2.34	2.00	12.39	19.29
CL V	69	77.00	8.26	88.11	22.46	110.00	7.97	2.35	2.03	14.59	19.17
CL VI	8	134.00	6.23	130.33	23.38	113.00	7.75	2.33	2.04	10.12	22.15
CL VII	2	90.00	5.2	91	20.9	164.00	7.85	2.44	1.55	10.1	23.59
CL VIII	2	99.00	7.4	205.8	22.5	140.00	8.38	2.73	1.9	9.4	20.52

Principal Component Analysis (PCA)

The first three principal components are often the most important in reflecting the variation patterns among accessions and the traits associated with these are more useful in differentiating accessions. In the present study, first three components account for about 44.12% of total variation (Table 3), giving a clear idea of the structure underlying the variables analyzed..However, the criterion of cut-off limit for the coefficients of the proper vectors greater than 0.3 having a large enough effect to be considered important while the traits having coefficient value lower than 0.3 were not considered to have important effects on the overall variation observed in the present study.

The first principal component accounted for 20.32% of total variance indicating that number of days to flowering, plant height, days to maturity and seedling height were the variables that contributed most negatively and also registered those with high yield component values (Table 3). The second component accounted for 10.0 percent of total variance which identified yield component variables (number of effective tillers, panicle length, weight of 100 grains and grain yield/plant) presenting positive contributions and the main characters responsible for classification. The third principal component accounted for 13.80% and was positively associated with grain length and grain width. This component was negatively associated with yield per plant, plant height and panicle length, thereby differentiating those accessions with their grain characteristics (Table 3). These results are corroborated by Medhabati *et al.* (2013), Wu *et al.* (2013), Chakravorty *et al.* (2013), Sanni *et al.* (2012), Soharabi *et al.* (2012), Lasalita-Zapico *et al.* (2010) and Rajiv *et al.* (2010).

The genotypes superior in some clusters might be usefully involved in multiple crossing programmes to recover

Table 3   Coefficients and vectors associated with the first three
         principal components

Particulars	First component	Second component	Third component
Eigen value	2.03	1.00	1.38
Variance (%)	20.32	10.00	13.80
Cumulative variance (%)	20.32	30.32	44.13
Coefficient Vector			
Days to flowering	–0.61	–0.13	0.24
No. of effective tillers	–0.14	0.55	0.23
Plant height (cm)	–0.35	0.24	–0.37
Panicle length (cm)	0.23	0.41	–0.49
Days to maturity	–0.69	0.08	–0.12
Grain length (mm)	–0.11	0.17	0.35
Grain width (mm)	–0.21	0.16	0.33
100 seed weight (g)	–0.23	0.37	0. 09
Yield/plant (g)	0.15	0.43	–0.55
Seedling height (cm)	–0.62	–0.27	0.25

transgressive segregants with high genetic yield potential and early maturity. The generated information can be helpful in reducing the overall time required to screen large populations for potential breeding stock. Accessions showing tall plant types for plant height may be useful as potential donors for increasing total plant biomass. The genotypes with early maturity, higher 100-seed weight, grain yield per plant, effective tillers per plant and panicle length might serve as potential donors for increasing grain yield of predominant rice varieties.

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SUMMARY

Genetic diversity of 2142 accessions of rice (*Oryza sativa* L.) from India based on the multivariate analysis for 10 agro-morphological traits was evaluated using augmented experimental design at CSSRI, Karnal, Haryana, in *kharif* 2010-11. In all, a total of 8 clusters were obtained based on the estimates of genetic diversity using the UPGMA. On the basis of their greater intercluster distance, high value of cluster mean according to the character to be improved and performance of the individual germplasms for the character, the germplasms could be used in hybridization programme for improvement of different plant characters in the rice germplasms. The results of PCA revealed that the first three principal components explained 40.12% of the total variation thus suggesting that traits such as plant height, days to flowering and maturity, number of effective tillers and grain size (weight, length and width) were the principal discriminatory characteristics. It is suggested that the genetic variation existing in the evaluated germplasm set can be usefully utilized in efforts towards genetic improvement of rice.

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