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Genetic variation, heritability and diversity analysis of exotic upland rice (*Oryza sativa* L.) germplasms based on quantitative traits

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Abstract

Upland rice is important for sustainable crop production to meet future food demands. The expansion in area of irrigated rice faces limitations due to water scarcity resulting from climate change. Therefore, this research aimed to identify potential genotypes and suitable traits of upland rice germplasm for breeding programmes. Twenty two genotypes were evaluated in a randomized complete block design with three replications during *Kharif* 2013, *Kharif* 2014 and *Rabi* 2015. All genotypes exhibited a wide and significant variation for 16 traits. The highest phenotypic and genotypic coefficient of variation was recorded for the filled grains/panicle, spikelet per panicle and plant height. The highest heritability was found for filled grains/panicle, spikelet per panicle, plant height, test weight, flag leaf length and yields/plant (g). Cluster analysis based on 16 traits grouped the 22 rice genotypes into five clusters. Cluster I was the largest and consisted of 13 genotypes. The first five principle components of 16 traits accounted for about 83.71% of the total variation and indicated a wide variation among the genotypes. The selected best trait of the number of filled grains/panicle and spikelet/panicle which showed high heritability and high genetic advance, could be used as a selection criterion for hybridization programmes in the future.

Keywords: upland rice, genetic diversity, principle component analysis and cluster analysis

1. Introduction

Upland rice has been gaining popularity, because current high-yielding varieties have led to an increase in genetic vulnerability, a scarcity of water for irrigation, and a breakdown of resistance genes against emerging races of pathogen due to intensive cultivation. In recent decades, the increases in world rice production that have resulted from successes in research and the transfer of modern technology have mainly concerned irrigated high-yielding varieties. Research into upland rice has been very limited and most of the research findings have not been published; therefore, these successes have had virtually no effect on upland rice production. It is a nutritious cereal crop, provides 20 per cent of the calories and 15 per cent of protein consumed by world's population. In India, rice is grown in an area of 44.6 million ha (23% of gross cropped area) with an annual production of 90 million tons. It is also important in cropping systems, because of the lack of irrigation facilities and lower cost of production (Fageria *et al.* 2014) [16]. To boost the yield potential of upland rice, it is necessary to identify cultivars with improved yield and other desirable agronomic characters, to overcome the global problem of hunger and starvation, especially in eastern India (Mustafa *et al.* 2012) [11]. Genetic variation is the basis of plant breeding and provides a great array of genotypes that can be selected to develop new varieties or breeding materials (Pandey *et al.* 2009) [18]. Variability in terms of genetic divergence for agronomic traits is the key component of breeding programmes for broadening the gene pool of rice and requires reliable estimates of heritability to plan an efficient breeding programme (Akhinwale *et al.* 2011). Knowledge concerning heritability helps plant breeders to predict the nature of the succeeding generation, to make an appropriate selection and to assess the magnitude of genetic improvement through selection (Khutan *et al.* 2007). This study was therefore conducted to select potential genotypes and to identify the most important characters for breeding programmes by exploiting the genetic variation, heritability, and diversity analysis of yield and related attributes of 22 upland rice genotypes.

Material and Methods

The experimental for the present study was conducting during *kharif 2013 and kharif 2014* at the field experimentation centre of Department of Genetics and Plant Breeding, SHUATS, Allahabad the experimental material comprised of 22 rice genotypes and it was laid out in randomised block design with three replications. Observations were recorded for sixteen quantitative traits viz., days to 50% flowering, Days to Maturity, flag leaf length, flag leaf width, Panicle length, tillers/Plant, Plant height, Test Weight, Spikelets per Panicle, Filled spikelet/panicle, spikelet fertility, root length (20DAS) and shoot length (20DAS), Biological Yield per Plant, Harvest Index and Grain Yield per Plant. Standard Statistical procedure were used for the analysis of variance, genotypic and phenotypic coefficient of variance (Burton (1952) [3], heritability (Iush 1940) [12], genetic advance and diversity analysis was conducted by NTSYS-PC software (version 2.1) and Minitab software (version 15).

Results and Discussion

In the present investigation the magnitude of PCV was higher than the GCV for all the quantitative characters, indicated that these characters were less influenced by environment. High GCV and PCV was observed for spikelet filled grain while shoot length, grain yield per plant, test weight, tiller/plant and flag leaf length show moderate GCV and PCV. Higher GCV and PCV were earlier reported by Zahid *et al.*, 2006 [26] and Pandey *et al.*, 2010 [19]. Higher GCV and PCV show high variance and low effect of environment which suggest that the selection of this trait may efficient for improvement. Moderate GCV and PCV for grain yield per plant had earlier been reported by Rahman *et al.* (2012) [22]. The trait number of tillers per plant showed moderate PCV value but extent of GCV is low for this trait, indicated the higher effect of

environment on this trait. Rest yield component traits viz., days to 50 per cent flowering, harvest index, biological yield, panicle length and root length exhibited low GCV and PCV estimates indicated that it may be governed by non additive genes and recombination breeding may helpful for improvement of grain yield through selection of these traits. The low GCV and PCV values for days to 50 per cent flowering was also observed by several workers viz., Anandrao *et al.* (2011) [2], Paul *et al.* (2011) [20], Singh *et al.* (2011) [23] and Quatadah *et al.* (2012) [21]. Heritability measures the possibility of joint transmission of two correlated characters through selection of one character. (Dabholkar 1992; Falconer and Mackay 1996) [5, 6]. In the present study traits like number of spikelet/panicle, spikelet filled grain, plant height, test weight, flag leaf length and grain yield/plant Chaubey and Singh (1994) [4] and Atlin (2003) [1] showed high heritability estimate while biological yield, spikelet fertility, root length, flag leaf width, panicle length, shoot length and harvest index show moderate heritability. Therefore selection from these traits will be valuable for further rice improvement. Days to 50% flowering and tiller/ plant showed low heritability. Estimates of heritability are more advantageous when expressed in terms of genetic advance Johnson *et al.*, (1955) [10] predicting the resultant effect of selecting the best trait. In the present study high estimates of heritability coupled with high value of genetic advance as a percentage of means was observed for plant height, flag leaf length, number of spikelet per panicle, spikelet filled grain, test weight and grain yield per plant, while root length, tiller/plant, flag leaf length. Similar finding has earlier been reported by Verma (2010) [24]. Thus the heritability estimates will be reliable, if accompanied by high genetic advance.

Table 1: Genetic parameter for sixteen yield and its component traits in exotic rice genotypes.

S. No	Characters	Mean	VG	VP	GCV	PCV	h ² bs	GA	GAM
1	50% flowering	82.15	6.19	15.51	3.03	4.79	40	3.24	3.94
2	Flag leaf length	26.33	11.20	13.50	12.71	13.95	83	6.28	23.86
3	Flag leaf width	1.10	0.02	0.03	11.77	14.80	63	0.21	19.30
4	Tiller/plant	6.03	0.53	1.15	12.11	17.78	46	1.02	17
5	Maturity	112.16	6.19	15.39	2.22	3.50	40	3.25	2.90
6	Panicle length	22.46	2.59	4.29	7.17	9.22	60	2.58	11.48
7	Plant height	96.24	84.89	92.22	9.57	9.98	92	18.21	18.92
8	Spikelet/panicle	124.38	266.22	274.39	13.02	13.32	96	32.61	26.22
9	Test wt	17.67	5.77	6.68	13.59	14.63	86	4.60	26.03
10	Spikelet filled grain	100.49	322.65	346.33	17.87	18.52	93	35.71	35.54
11	Spikelet fertility %	80.50	34.79	53.13	7.33	9.05	65	9.83	12.22
12	Root length	5.63	0.37	0.56	10.74	13.28	65	1.01	17.89
13	Shoot length	4.64	0.45	0.75	14.43	18.50	59	1.06	22.92
14	Biological yield	22.87	2.86	4.27	7.39	9.03	67	2.85	12.46
15	Harvest index	50.14	11.04	19.53	6.63	8.81	57	5.15	10.27
16	Grain yield/plant	11.49	2.32	2.93	13.24	14.83	79	2.79	24.27

VG= Genotypic variance, VP=Phenotypic variance, GCV= Genotypic Coefficient of Variation, PCV= Phenotypic Coefficient of Variation, h²bs= Heritability in broad sense, GA=Genetic advance, GAM= Genetic Advance as per cent of Mean

The Euclidean distance was calculated using standardised morphological data and a UPGMA dendrogram was constructed using these values for 22 upland rice genotypes. Cluster I contained the maximum number of genotypes (13), which consisted of 59.09% of all genotypes, mostly originating from the Philippines. The second highest was

cluster II, which consisted of 5 members. Clusters III, IV, and V consisted of one, two and one genotypes, respectively. The results of PCA partly confirmed the findings of cluster analysis in PCA, the genotypes also clustered into five groups (Figure 1), with only few differences between groups III and V compared to cluster analysis. This demonstrates that the data obtained from this experiment were accurate, precise, and reliable. The PCA analysis showed that the first five principal components accounted for about 83.71% of the total variation and exhibited a very high correlation among them. The first, second, third, fourth and fifth principle components

explained about 42.61%, 61.28%, 70.54%, 78.21 and 83.71% of the variation observed in the eigenvector analysis (Table

2). In the first PC: Days to 50% flowering (0.17) and days to maturity (0.06) were the most.

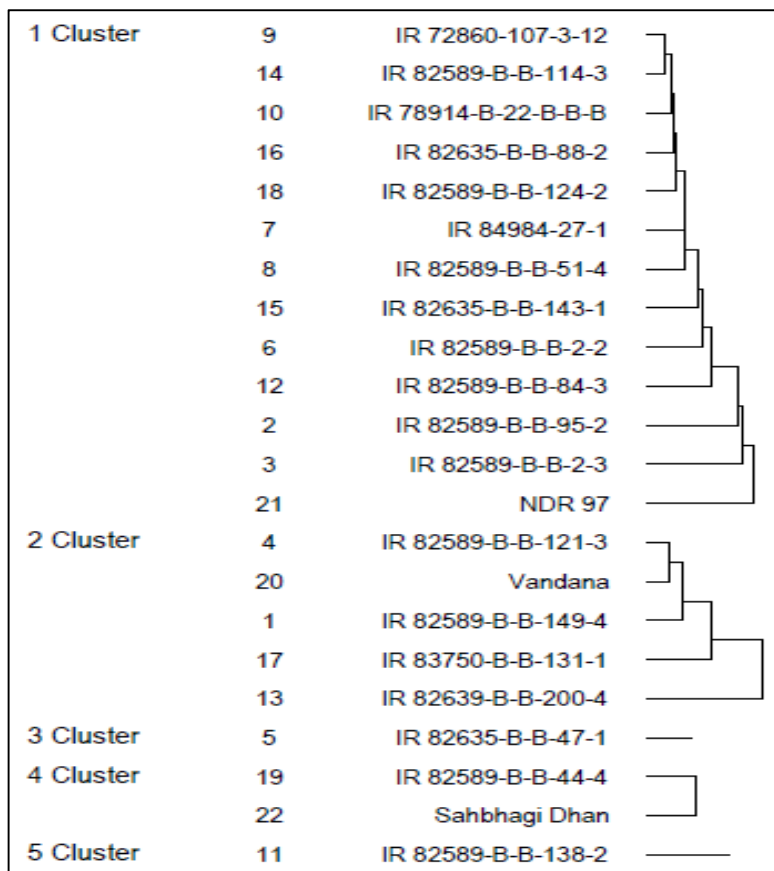


Fig 1: Cluster analysis of 22 upland rice genotypes based on yield and yield associated characters.

Important contributing traits; similarly Days to 50% flowering (0.40), flag leaf length (0.37), flag leaf width (0.28) and days to maturity (0.21) were the important parameters of the second PC. The 22 upland rice genotypes clustered into five groups based on the dendrograms of cluster analysis and PCA. The groupings of hierarchical cluster analysis exhibited a similar dendrogram topology and cluster membership to that produced using PCA analysis, thereby confirming the accuracy of the constructed dendrogram. Principal component analysis helps to understand how the genotypes of similar categories group together compared to dissimilar ones. The results of PCA can clarify or verify the cluster analysis; if the results of one analysis support those of another, this confirms that the data are more precise and accurate. The presence of strong differences among 22 upland rice genotypes in the present study was also further confirmed by PCA. The first five principal components accounted for 83% of the total variation, which indicated a very strong correlation among the characters being studied. The first PC, which solely contributed to 42.61% of the variation, was the most significant. Accordingly, in the first PC, the traits DFF, DM were important in separating the genotypes due to their high loadings. For the selection of parents, genetic diversity is one of the important decisive factors (Mazid *et al* 2013) [15]. Similarly, Worede *et al* (2014) [17] explained 61.2% of the total variability using the first and second PCs. Approximately, 82.7% of the total variation among 32 upland rice varieties was also noted by Lasalita-Zapico *et al.* (2013) [8].

Table 2: Eigenvectors and eigenvalues of the first five principle components of 16 traits.

	PC 1	PC 2	PC 3	PC 4	PC 5
Eigene Value	6.819	2.987	1.481	1.228	0.880
% Var. Exp.	42.616	18.668	9.258	7.675	5.499
Cum. Var. Exp.	42.616	61.284	70.542	78.217	83.717
Day to 50% flow.	0.175	0.408	0.222	0.029	0.098
Days to Maturity	0.062	0.218	0.443	0.261	0.637
Flag Leaf Length	-0.181	0.372	0.322	-0.104	0.021
Flag Leaf Width	-0.200	0.285	-0.459	0.078	0.172
Panicle Length	-0.283	0.061	-0.356	0.202	0.224
Tillers/ Plant	-0.342	-0.080	-0.075	-0.124	0.109
Plant Height	-0.272	0.283	0.028	0.157	-0.144
Test Weight	-0.290	-0.135	0.074	0.410	-0.139
Spikelets/ Panicle	-0.225	-0.237	0.185	-0.019	0.015
Spikelet Filled Grain	-0.358	0.009	0.107	0.026	0.084
Spikelet Fertility (%)	-0.187	-0.292	0.462	0.194	-0.196
Root Length	-0.363	0.053	0.024	-0.143	0.053
Seed Yield/ Plant	-0.225	-0.329	0.049	0.009	0.050
Biological Yield	-0.006	-0.377	-0.058	-0.287	0.621
harvest Index	-0.338	0.214	-0.055	-0.064	-0.042
Shoot Length	-0.166	0.133	0.182	-0.720	-0.119

Note: PC1, first principle component; PC2, second principle component; PC3, third principle component; PC4, four principle component and PC5 fifth principle component.

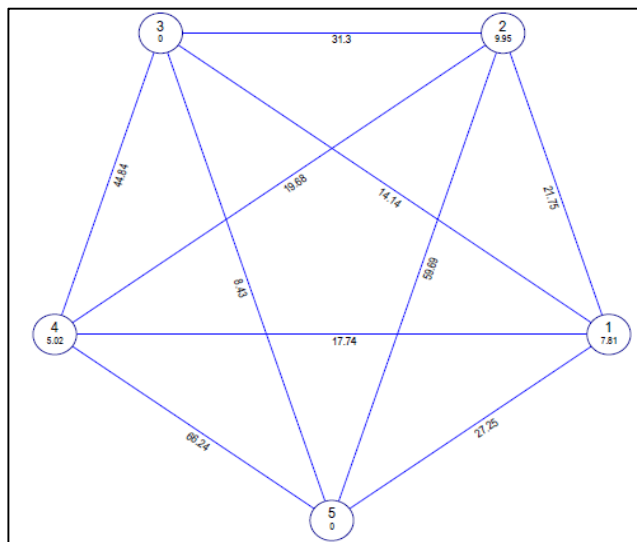


Fig 1: Cluster analysis of 22 upland rice genotypes based on yield and yield associated characters.

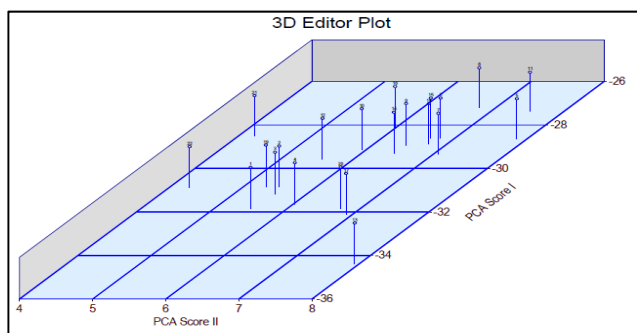


Fig 2: Three-dimensional graph of 22 upland rice genotypes based on yield and yield associated characters (principal component analysis).

5. Conclusions

The present study showed the existence of a considerable level of diversity among the 22 upland rice genotypes. The highest heritability recorded for the parameters spikelet/panicle, spikelet filled grain, plant height, test weight, flag leaf length and grain yield/plant demonstrates that these traits could be successfully transferred to offspring, if selection for these characters is performed in the hybridisation programme. The aforementioned traits of number of filled grains/panicle and number of spikelet per panicles showed a very high genetic advance, which implies that these characters could be used to select upland accession genotypes for a notable improvement in cultivation in changing environments, particularly under conditions of water scarcity in the tropics. Principal component analysis has identified few characters that plays prominent role in classifying the variation existing in the germplasm set. The analysis identified days to 50% flowering, days to maturity, spikelet fertility, test weight, biological yield and flag leaf length in different principal components are the most important for classifying the variation. Thus the results of principal component analysis used in the study have revealed the high level of genetic variation existing in the population panel and explains the traits contributing for this diversity. Hence the results will be of greater benefit to identify parents for improving various morphological traits analyzed in this study.

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