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GENETIC DIVERGENCE AND PRINCIPLE COMPONENT ANALYSIS IN UPLAND RAINFED RICE (*ORYZA SATIVA* L.)

RR DHUTMAL* AND HV KALPANDE[1]

Agriculture Research Station, Tuljapur, Dist. Osmanabad, (VNMKV, Parbhani) Maharashtra, India

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Abstract

Genetic divergence and principle component analysis were worked out in 73 upland rainfed rice genotypes consisting traditional varieties, local selections, advanced breeding lines and popular varieties for upland rainfed ecology from different regions of India. Based on ten agro-morphological characters, these genotypes were grouped into nine clusters. The composition of different clusters varied from 1 to 23 genotypes. The maximum number of genotypes (23) was grouped in cluster IV followed by cluster V, I, VIII, II, IX, III, VI and I. Local selection from Marathwada region of Maharashtra exhibited maximum diversity and were represented in all the clusters except cluster VII. However, no parallelism was observed between geographic diversity and genetic diversity. Days to 50% flowering contributed maximum towards genetic divergence (40.64%) followed by effective tillers per m^2 (12.21%), yield per hectare (11.72%), spikelet fertility (10.69%) and plant height (8.98%). These could form the basis for selection of parents from distantly paced cluster to obtain high heterotic combinations. Six principle components, accounting 92.78 of total variance were obtained from principle component analysis. First three PCs i.e. PC I, PC II and PC III, contributed 28.71, 20.57 and 14.81% of total variance with the discriminating power of 2.87, 2.57 and 1.48, respectively.

Introduction

Upland rice is grown under diverse agro-climatic conditions (Sinha *et al.* 1991). Traditional cultivars and local selection have wide range of adoptability to different agro-ecological conditions. Owing to their adaptation to a wide range of agro-ecological conditions, traditional land races show tremendous genetic variability which is not found in modern varieties. These cultivars can therefore be exploited to significantly enhance rice productivity in marginal upland areas. Genetic uniformity among new rice varieties increased the vulnerability of the rice crop to disease epidemics and insect infestation, is an alarming situation confronting the rice industry (Morishima and Oka 1995). Cluster analysis and principle component analysis allows preliminary groupings of cultivars based on cluster similarities and inter cluster morphological variations. The present investigation has been carried out to ascertain the nature and magnitude of genetic diversity present in traditional cultivars, local selections and some upland rainfed rice varieties based on morpho-agronomic variations. Thompson (1998) used PCA to determine the optimum number of clusters, Lombard *et al.* (2000) to complement cluster analysis and Mohammadi and Prasanna (2003) to investigate patterns of genetic diversity.

Materials and Methods

Seventy three geographically diverse upland genotypes consisting traditional varieties, local selections, advanced breeding lines and popular varieties for upland rainfed ecology from different regions of India were evaluated under upland rainfed ecology, during *kharif* 2010 at Experimental Farm of Agriculture Research Station, Tuljapur, Osmanabad (Maharashtra). The experiment was

*****Author for correspondence: <rr_dhutmal@rediffmail.com>. [1]Sorghum Research Station, VNMKV, Parbhani 431 402, Maharashtra, India. VNMKV, Parbhani 431 402, Maharashtra, India.

conducted in randomized block design with two replications at the spacing of 30 cm between rows, keeping row length 4 m in a single row plot. The recommended agronomical practices and plant protection measures were followed to raise a normal healthy crop. Observations were recorded on days to 50% flowering, plant height, panicles per plant, panicle length, effective tillers per square meter, effective tillers per plant, number of spikelets per panicle, number of grains per panicle, fertility %, 1000-grain weight and yield per plant. The data were subjected to analysis of variance and multivariate analysis using statistics (Mahalnobis 1928). Based on genetic distances (D^2 values), the genotypes were grouped into clusters of genetically closer related groups following the Ward's method. Cluster analysis was done to yield a Ward's minimum variance dendrogram showing the morphological relatedness. Principal component analysis was also done to detect underlying sources of morphological variability. All analysis were done using Windostat Version 9.2.

Results and Discussion

The analysis of variance revealed significant difference among genotypes for all the characters, indicating existence of a good amount of genetic variability. The genotypes differed from each other with respect to the characters.

On the basis of D^2 cluster analysis all the 73 genotypes (including checks) were grouped into 9 clusters (Table 1). The composition of different clusters varied from 1 to 23 genotypes. The maximum number of genotypes (23) was grouped into cluster IV followed by cluster V, I, VIII, II, IX, III, VI and I. The distribution of genotypes from different eco-geographical regions into these

Table 1. Distribution of 73 genotypes of rice among clusters on the basis of D^2 analysis.

Cluster No.	No. of genotypes	Genotypes
I	10	Vandana, CR 143-2-2, MAULS 7, Brown gora, Birsagora, IET 20312, Tuljapur-1, N-22, Anjali, Varalu
II	7	MAULS 32, MAULS 36, MAULS 12, MAULS 34, MAULS 37, MAULS24, Lalankanda
III	4	MAULS 10, MAULS 35, MAULS 8, MAULS 28
IV	23	Sathi-34-36, MAULS 11, MAULS 23, MAULS 6, IET 20316, Parag 5, MAULS 5, MAULS 27, MAULS 29, Ranjit, Prabhavati, MAULS 2, MAULS 18, MAULS 14, MAULS 16, IET 2602, MAULS 17, MAULS 1, Terna, Ambika, MAULS 19, MAULS 22, MAULS 20
V	11	IURON 46, IURON 47, Annada, Tulsi, Avishkar, CH 45, Kalakeri, IURON 55, MAULS 26, IURON 39, IURON 84
VI	2	Dehula, MAULS 38
VII	1	IURON 86
VIII	9	Tharra, IET 20313, IET 19258, MAULS 31, MAULS 9, MAULS 15, MAULS 30, MAULS 33, MAULS 21
IX	6	IET 20314, IET 20315, IET 19839, IET 19850, IET 20319, MAULS 4,

clusters was apparently random. Genotypes of similar origin *viz.*, MAULS genotypes were grouped into different clusters and *vice versa*, thereby indicating non-relationship between geographical and genetic diversity. Similar findings were also reported by Rajesh *et al.* (2010), Chandra *et al.* (2007) and Nayak *et al.* (2004). This tendency of genotypes to occur in clusters cutting across geographical boundaries demonstrates that geographical isolation is not the only

factor causing genetic diversity (Sihag *et al.* 2004). This also suggests that the genotypes within cluster may have some degree of ancestral relationship. Similar findings were also reported by Lang *et al.* (2008).

Selection of parents for hybridization should be based on genetic diversity rather than geographic diversity to get more heterotic recombinants and desired transgressive segregants. However, caution should be taken in selecting divergent genotypes because such crosses may not yield proportionate heterotic response. Arunachalum (1981) also observed that the more diverse the parents are within their overall limits of fitness, the greater are the chances of heterotic expression of F_1s and a broad spectrum of variability in segregating generations.

The statistical distances among the different clusters are presented in Table 2. The maximum intra-cluster distance was observed in cluster VII (100.171), followed by cluster III (58.386) indicating wide genetic variability within the genotypes of these two clusters. The maximum inter-cluster distance was observed between cluster VII and VIII (563.614) followed by cluster VII and IX (437.776), which indicated maximum diversity between the genotypes of these clusters. Therefore, it is suggested that if the diverse genotypes from these groups along with the other desirable attributes are used in breeding programmes, it is expected through better segregants for high grain yield and yield contributing traits due to non-allelic interaction.

The minimum inter-cluster distance between clusters II and IV (51.493) indicated that the genotypes of these clusters were genetically least diverse and almost of the same genetic architecture. Such genotypes can also be used in breeding programmes for developing biparental crosses between the most diverse and closest groups to break the undesirable linkages between yield andits associated traits.

Table 2. Average inter- and intra distances involving 73 genotypes of rice.

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX
I	32.10	54.33	110.66	60.03	80.87	177.77	274.29	88.88	78.99
II		22.14	122.04	51.49	80.26	151.56	240.17	132.27	102.47
III			58.38	101.66	134.11	304.42	428.78	124.64	136.13
IV				29.95	58.67	260.96	366.12	78.63	92.96
V					37.31	302.97	303.54	151.97	183.12
VI						100.17	172.06	335.09	207.25
VII							0.00	563.6	437.77
VIII								33.25	58.69
IX									32.91

The diversity was also supported by the significant amount of variation among the cluster means for different characters (Table 3). Cluster VIII exhibited the highest mean value for spikelet fertility, effective tillers per m^2, and effective tillers per plant and yield per hectare. Highest mean value for spikelets per panicle and grains per panicle was reported in cluster V, and for plant height was observed in cluster VI. For days to 50% flowering, lowest and highest mean value was observed in cluster IX and VII, respectively. Cluster III exhibited lowest and highest mean values for spikelet fertility and test weight, respectively. Cluster VII exhibited the least mean value for plant height, panicle length and spikelets per panicle, grains per panicle, effective tillers per m^2,

Table 3. Cluster mean values for 10 morphological traits.

Cluster number	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Spikelet/ panicle	Grains/ panicle	Spikelet fertility (%)	Effective tillers/ m²	Effective tillers/ Plant	Test weight	Yield/ ha
I	78.50	93.16	20.88	94.04	87.72	93.39	240.30	4.22	23.14	2666.60
II	83.57	113.96	21.41	86.29	79.86	92.68	239.86	4.21	22.63	1731.29
III	78.25	104.95	22.87	109.35	88.00	80.78*	274.25	5.00	23.40**	2700.00
IV	82.78	116.05**	21.89	102.86	95.40	92.90	275.43	4.73	22.78	2771.04
V	91.95	98.60	21.94	109.40**	101.00**	92.60	267.09	4.64	21.86	3019.09
VI	72.00	109.70	23.00**	92.50	86.00	93.32	154.50	2.20	22.35	1105.50*
VII	96.00**	92.40*	19.40*	77.20*	71.00*	91.93	100.00*	1.30*	21.50*	2356.00
VIII	68.78	107.11	21.49	100.30	94.28	93.83**	302.78**	5.20**	23.12	3071.67**
IX	65.50*	115.80	20.80	91.47	85.50	93.37	252.50	4.33	22.57	2759.33

*, ** significant at 5 and 1% levels of significance.

and effective tillers per plant and test weight. Cluster VI exhibited lowest and highest mean values for yield per hectare and panicle length, respectively. These results showed that different clusters were superior for different characters.

The contribution of individual trait to divergence among genotypes is presented in Table 4. Days to 50% flowering contributed maximum towards genetic divergence (40.64%) followed effective tillers per m^2 (12.21%), yield per hectare (11.72%), spikelet fertility (10.69%) and plant height (8.98%). Similar observation were also reported by Rajesh *et al*. (2010) for days to 50% flowering, grain yield and plant height, Sebesan *et al*. 2009 for days to 50% flowering, Bisht (2007) for effective tillers and plant height. Remaining traits had little or no contribution towards genetic divergence and hence, they were of less importance. Since days to 50% flowering contributed maximum towards the genetic divergence, we may go for direct selection of this trait for diversity purpose.

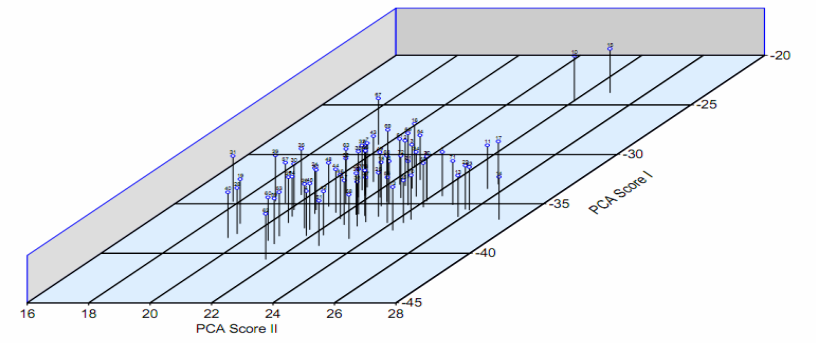

Fig. 1. PCA plot of 73 upland rainfed rice genotypes.

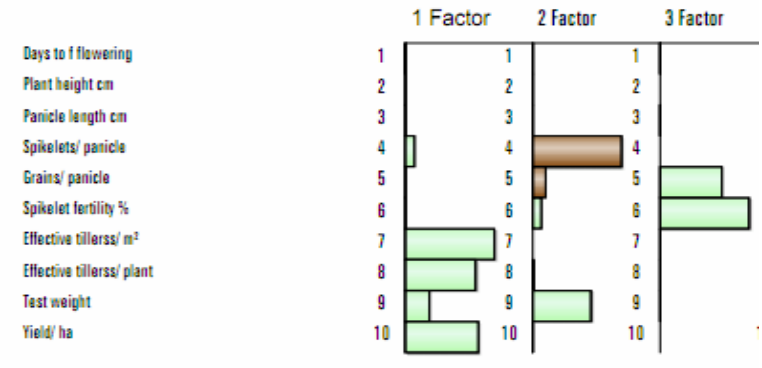

Fig. 2. Trait contribution towards principle components.

Total six principle components, accounting 92.78 of total variance, were obtained from principle component analysis (Fig. 1). First three PCs i.e. PC I, PC II and PC III, contributed 28.71, 20.57 and 14.81% of total variance with the discriminating power of 2.87, 2.57 and 1.48 respectively. First principle component was correlated with effective tillers per square meter, effective tillers per plant, and yield per hectare while, spikelets per panicle contributed to the second components and spikelet fertility percentage to third component (Fig. 2).

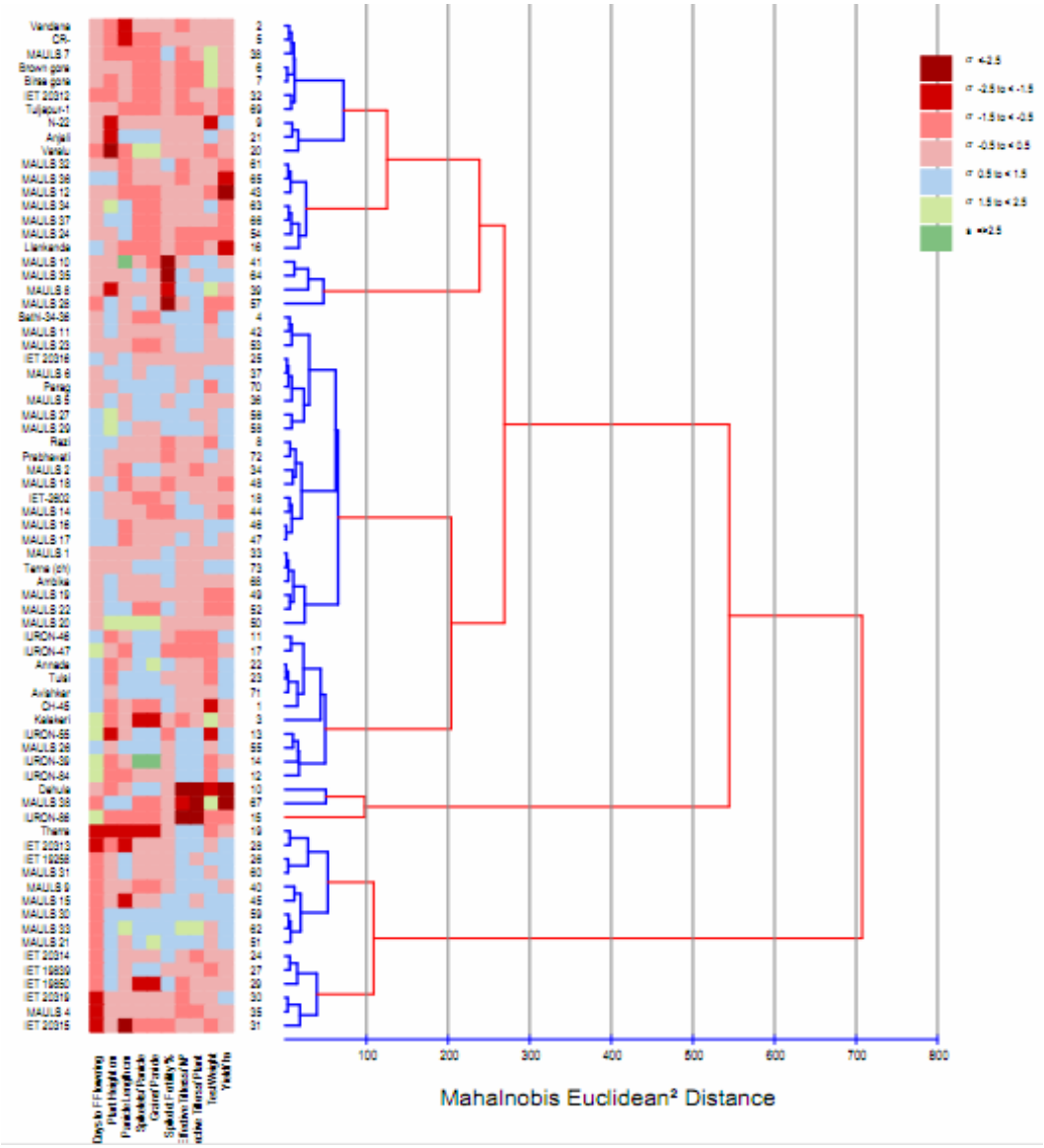

Fig. 3. Ward' minimum variance dendogram based on Mahalnobis Euclidean^2 distance.

The results obtained from PCA were further corroborated by cluster analysis using UPGMC (Unweighted Paired Group Method using Centroids). Seventy three upland rainfed cultivars were classified into nine morphologically distinct clusters (Fig. 3). UPGMC proved to be useful in showing high internal (within cluster) homogeneity and external (between clusters) heterogeneity within cultivars, as previously reported Florence (2010) and Mohammadi and Prasana (2003). The resulting clusters were well resolved in terms of morphological characteristics. Cluster IX comprised of very early and tall genotypes, genotypes grouped in cluster VIII consisted of early and genotypes with high number of effective tillers per square meter, high number of effective

tillers per plant, and high yielding genotypes. Cluster VII consisted of mainly late and short genotypes. Furthermore, late high yielding genotypes were mainly clustered in cluster V, tall genotypes with high number of grains were concentrated in cluster II and short and early genotypes consisted of cluster I.

Table 4. Relative contribution (%) of individual trait to the divergence among genotypes.

Characters	Contribution (%)
Days to 50% flowering	40.64
Plant height	8.98
Panicle length	4.34
Spikelets/panicle	2.89
Grains/panicle	0.08
Spikelet fertility %	10.69
Effective tillers/m²	12.21
Effective tillers/plant	5.14
Test weight	3.31
Yield/ha	11.72

According to Lie *et al.* 2002 diversity analysis based on phenotypic values may not be the perfect representation of natural grouping of cultivars. More reliable results can be obtained after employing suitable molecular markers such as SSR by reducing environmental effects or experimental errors. The discriminating power principle of component analysis is not conclusive due to the small number of traits evaluated and their susceptibility to environmental conditions.

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