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Genetic Divergence for Yield and other Quantitative Traits in Rice (*Oryza sativa* L.)

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A B S T R A C T

Rice is an important versatile food crops which feeds over half of the world's population and provides essential food elements, employment opportunity as well as raw materials for different products used by human kind. An investigation was carried out with the twenty six genotypes of rice to study the nature and magnitude of genetic divergence using D^2 statistics in 2015. Eleven quantitative traits were recorded on the genotypes raised in the RBD Design with three replications. The twenty six genotypes were grouped into six clusters based on Euclidean cluster analysis with cluster I containing the maximum of 11 genotypes. Maximum intra-cluster distance was observed in cluster III indicating greater genetic divergence between the genotypes belonging to this cluster. The cluster IV having highest average compared to other five groups in terms of seven traits. Maximum inter-cluster distance was recorded between cluster III and IV followed by cluster I and VI indicating wide genetic diversity and it may be used in rice hybridization programme for improving grain yield. The maximum contribution of individual trait to the divergence among genotypes recorded in number of spikelet per panicle. Thus, these genotypes hold great promise as parents for obtaining promising elite lines through hybridization and to create further variability for these characters.

Introduction

Rice (*Oryza sativa* L.) is the most important food crop of world grown under 149 mha area (FAO, 2006). Being grown worldwide, it is the staple food for more than half of the world's population. It is a nutritious cereal crop, provides 20% calories and 15% protein requirements of world population. Besides being the cheapest source of carbohydrate and protein in Asia, it is also a source of minerals and fiber. About 92% of the world's rice is produced and consumed in Asia. A major part of Asian rice grown under flooded irrigation and water is the main limiting factor for increased production of rice (Akinbile *et al.,* 2011). The global need of rice has been forecasted to rise by 25% from 2001 to 2025 in order to cope with the increasing population (Maclean *et al.,* 2002). As a cereal grain, it is the most widely consumed staple food for a large part of the world's human population, especially in Asia. It is the agricultural commodity with the third-highest worldwide

production (rice, 741.5 million tonnes in 2014), after sugarcane (1.9 billion tonnes) and maize (1.0 billion tonnes). India is the world's second largest producer of rice, wheat and other cereals. The huge demand for cereals in the global market is creating an excellent environment for the export of Indian cereal products. According to the final estimate for the year 2014-15 by Ministry of Agriculture of India, the production of rice stood at 105.48 million tonnes (According to APDEA report, 2016). Genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization programme. The divergence can be studied by technique using D^2 statistics developed by Mahalanobis (1936). This is considered as the most effective method for qualifying the degree of genetic diversity among the genotypes included in the study. The present investigation aimed to estimate the magnitude of genetic divergence present in the 26 rice genotypes and to identify the diverse genotypes for future breeding programme.

Materials and Methods

The present investigation was conducted at the Student instructional Farm, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad, in normal irrigation condition during 2015. The experiment material comprised 26 genotypes of rice. The seeds of rice genotypes were sown in nursery bed. After 25 days single seedling per hill was laid out in a randomized block design with three replications of 3m length. Row to row and plant to plant spacing were maintained at 20×15 cm. The observations were recorded on five randomly taken plants from each plot for eleven quantitative traits *viz.*, Seedling vigor (cm), Days to 50% flowering (days), Plant height (cm), Panicle bearing tillers per plants, Number of spikelet per panicle, Number of grain per panicle, Spikelet fertility (%), Test

weight (g), Biological yield per plant (g), Grain yield per plant (g) and Harvest index (%). Planting Operation like preparing the main land, transplanting, irrigation, weeds and diseases and fertilizer were conducted in accordance with local custom. The analysis of genetic divergence was done using Mahalanobis (1936) D^2 statistics. Intra and inter-cluster distances and mean performance of the clusters for the characters were also computed.

Results and Discussion

Based on D^2 values, all the genotypes could be grouped into five clusters using non-hierarchical Euclidean cluster analysis (Table 1). The genotypes within each cluster were closer to each other than the genotypes in different clusters. Eleven morphological traits clustered 26 rice genotypes in to six major groups. From Figure 1 and Table 1 it is found that cluster I was the largest (containing 11 genotypes) namely, IR 91167-31-3-1-33, IR 68144-2B-2-2-3-1-120, Nedu, Shusk Samrat, IR 68144-2B-2-2-3-1-127, Taramon, Saponyo, Barani Deep, Ngobanyo Red Cover, Nagina-22 And IR 83668-35-2-2-2and cluster II having seven genotype namely *i.e.* R-RHZ-2, IR-64, Kuhusoi-Ri-Sareku, IR92960-75-1-3, Sarjoo-52, NDR-359 and Maigothi, Cluster III having five NDR-97, NDR-118, NDR-1, IR91167-133-1-1-2-3, Gopalbhok (Local). Cluster IV, V as well as cluster VI (containing one member namely Amker, Ayaar and Pusa Basmati-1, respectively) were the smallest group. Clusters II and III comprised of seven and five genotypes, respectively. Thus, these genotypes hold great promise as parents for obtaining promising elite lines through hybridization and to create further variability for these characters (Mishra and Pravin, 2004). The fourth group had the highest average compared to other five groups in terms of seven traits (Table 2) namely, Panicle Bearing Tillers/ Plant (11.50), Number of

spikelets per Panicle (185.33), Number of grains per Panicle (169.33), Spikelet Fertility (91.27%), Test Weight (24.20g), Harvest Index (42.96%) and grain Yield per Plant (22.59g). The third group included the highest average for four traits such as number of Seedling Vigor (71.70cm), Days to 50% Flowering (141.333 days), Plant Height (145.77 cm) (Table 2). The UPGMA dendrogram broadly clustered the rice genotypes in to six major groups, which implied a high level of morphological diversity in the rice genotypes. Result of this study unveiled the better resolution power of quantitative traits for grouping of *O. sativa* genotypes. On the basis of 18 morphological traits 58 rice varieties were clustered in to four groups in a study conducted by Ahmadikhah *et al.,* (2008) while Veasey *et al.,* (2008) observed that 23 rice populations were clustered in to 10 different groups based on 20 morphological traits.

Genotypes from same geographic location fell into different clusters indicating that clustering of populations did not follow their geographic or location distribution. Average intra and inter-cluster distances have been shown in Table 3. The maximum intra cluster distance was recorded in cluster III (889.03) followed by cluster IV (671.37%) and cluster V (539.17%). The maximum inter cluster distance was recorded between cluster III and IV (3081.32%) followed by cluster I and VI (2943.43%), cluster I and VI (2623.69%) and cluster III and VI (2148.36%) (Sandhyakishore *et al.,* 2007 and Patil *et al.,* 2005). Remaining traits had very little or no contribution towards genetic divergence and hence, they were of less importance.

Since varieties with narrow genetic base are increasingly vulnerable to diseases and adverse climatic changes, availability of the genetically diverse genotypes for hybridization programme become more important. Since days to maturity contributed maximum towards the genetic divergence, we may go for direct selection of this rate for diversity purpose.

Table.1 Clustering pattern of 26 rice genotype on the basis on D^2 analysis for yield and other 10 quantitative traits

Cluster No.	No. of genotypes	genotype
Cluster I	11	IR 91167-31-3-1-33, IR 68144-2B-2-2-3-1-120, Nedu, Shusk Samrat, IR 68144-2B-2-2-3-1-127, Taramon, Saponyo, Barani Deep, Ngobanyo Red Cover, Nagina-22, IR 83668-35-2-2-2
Cluster II	7	R-RHZ-2, IR-64, Kuhusoi-Ri-Sareku, IR92960-75-1-3, Sarjoo-52, NDR-359, Maigothi
Cluster III	5	NDR-97,NDR-118, NDR-1, IR 91167-133-1-1-2-3, Gopalbhok (Local)
Cluster IV	1	Amker
Cluster V	1	Ayaar
Cluster VI	1	Pusa Basmati-1

Table.2 Mean values of yield and other 10 quantitative traits for six groups revealed by cluster analysis among 26 genotypes of *Oryza sativa* L.

Characters	SV	DTF	PH	PBT	SP	GP	SF	TW	BY	HI	GY
Cluster I	36.78	89.400	84.265	9.26	61.66	51.40	83.66	18.61	31.56	32.74	10.43
Cluster II	39.74	94.848	105.48	10.84	102.87	88.51	86.36	23.24	44.30	27.61	12.34
Cluster III	71.70	141.333	145.77	7.66	64.33	57.66	89.63	23.16	53.76	26.23	14.10
Cluster IV	40.01	92.83	131.87	11.50	185.33	169.33	91.27	24.20	52.78	42.96	22.59
Cluster V	40.63	95.83	106.04	11.00	157.94	134.27	85.01	22.56	45.58	31.52	15.22
Cluster VI	34.40	106.33	103.74	9.667	163.00	125.00	76.68	23.06	16.00	39.24	6.27

SV- Seedling Vigor (cm), DTF-Days to 50% Flowering (days), PH-Plant Height (cm), PBT-Panicle Bearing Tillers per Plant, SP-Number of spikelet per Panicle, GP-Number of grains per Panicle, SF-Spikelet Fertility (%), TW-Test Weight (g), BY- Biological Yield per Plant (g), HI-Harvest Index (%), GY-Grain Yield per Plant (g)

Table.3 Estimation of average intra and inter cluster D^2 value under for yield and other 10 quantitative traits among 26 genotypes of *Oryza sativa* L.

| Cluster	I	II	III	IV	V	VI
Cluster I	830.35	1895.48	2989.00	11059.77	6250.28	6506.65
Cluster II		686.09	2145.44	5338.70	2413.44	3086.66
Cluster III			0.00	8870.69	5136.84	5429.44
Cluster IV				536.42	1564.12	3237.34
Cluster V					975.05	1650.12
Cluster VI						0.000

Table.4 Eigen vectors and Eigene values of the first five principal components

|	1 Vector	2 Vector	3 Vector	4 Vector	5 Vector
Eigene Value (Root)	**4.19**	**2.35**	**1.54**	**1.00**	**0.62**
% Var. Exp.	**38.11**	**21.37**	**14.00**	**9.09**	**5.63**
Cum. Var. Exp.	**38.11**	**59.48**	**73.49**	**82.58**	**88.22**
SV	0.12	0.53	0.13	0.25	0.23
DTF	0.08	0.38	0.41	0.34	0.19
PH	0.32	0.31	-0.09	0.09	-0.28
PBT	-0.04	-0.21	0.56	0.30	-0.67
SP	0.38	-0.21	0.33	-0.12	0.19
GP	0.39	-0.25	0.28	-0.05	0.19
SF	0.13	0.48	0.12	-0.49	-0.12
TW	0.37	0.04	-0.12	-0.32	-0.41
BY	0.33	0.07	-0.44	0.31	-0.24
HI	0.41	-0.18	0.05	-0.21	0.18
GY	0.35	-0.18	-0.24	0.44	0.13

Table.5 Contribution (%) for yield and other 10 quantitative traits among
26 genotypes of *Oryza sativa* L.

Character	Times ranked 1st	Contributon %
SV	1.23	1.23
DTF	10.46	10.46
PH	1.54	1.54
PBT	0.01	0.00
SP	60.00	60.00
GP	3.08	3.08
SF	0.31	0.31
TW	4.62	4.62
BY	3.69	3.69
HI	13.54	13.54
GY	1.54	1.54

Fig.1 The dendrogram showing relationship among 26 rice genotypes (*Oryza sativa* L.) using 11
quantitative traits
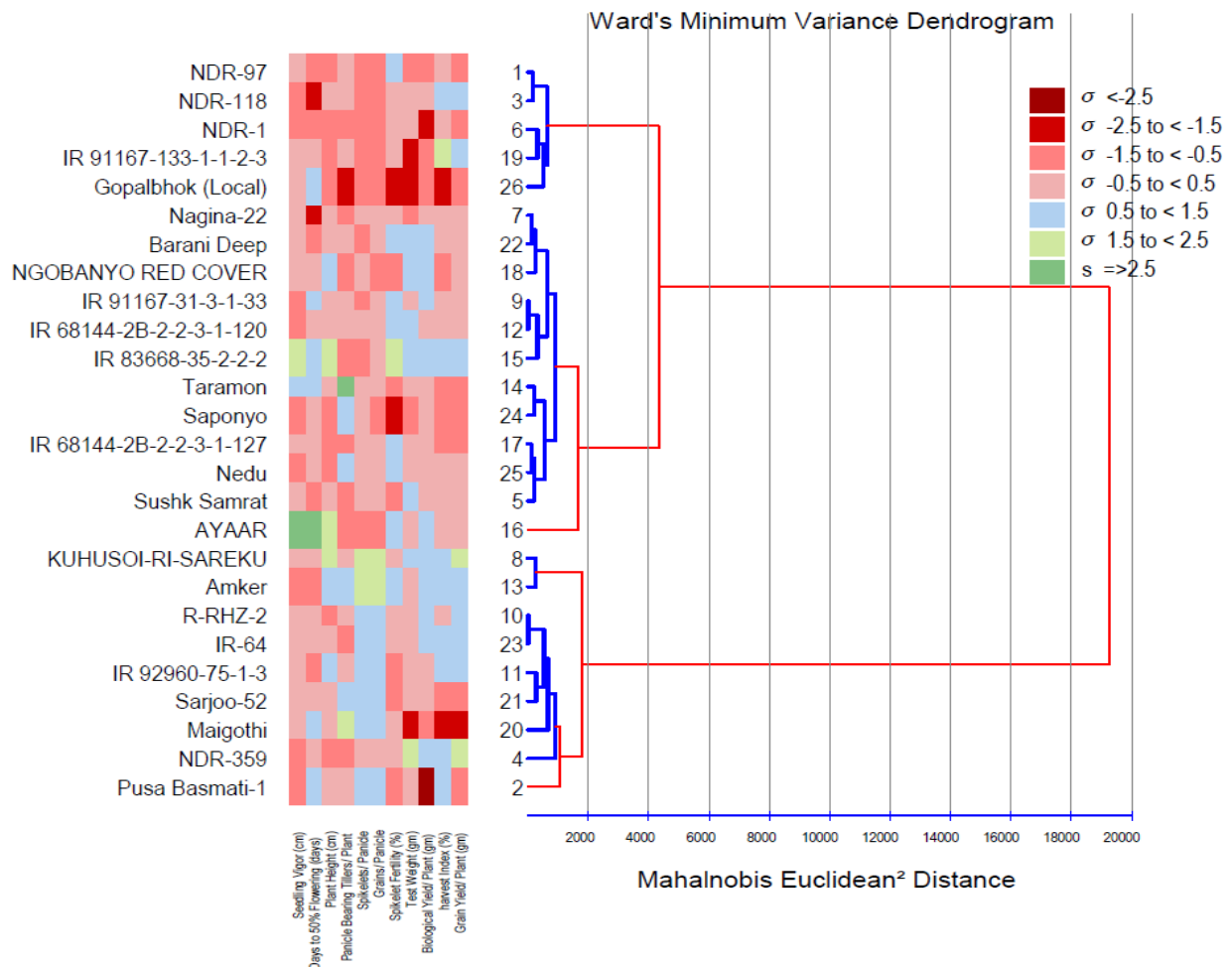
Fig.2 Two-dimensional plot of PCA showing relationships among 25 rice genotypes using 11 quantitative traits
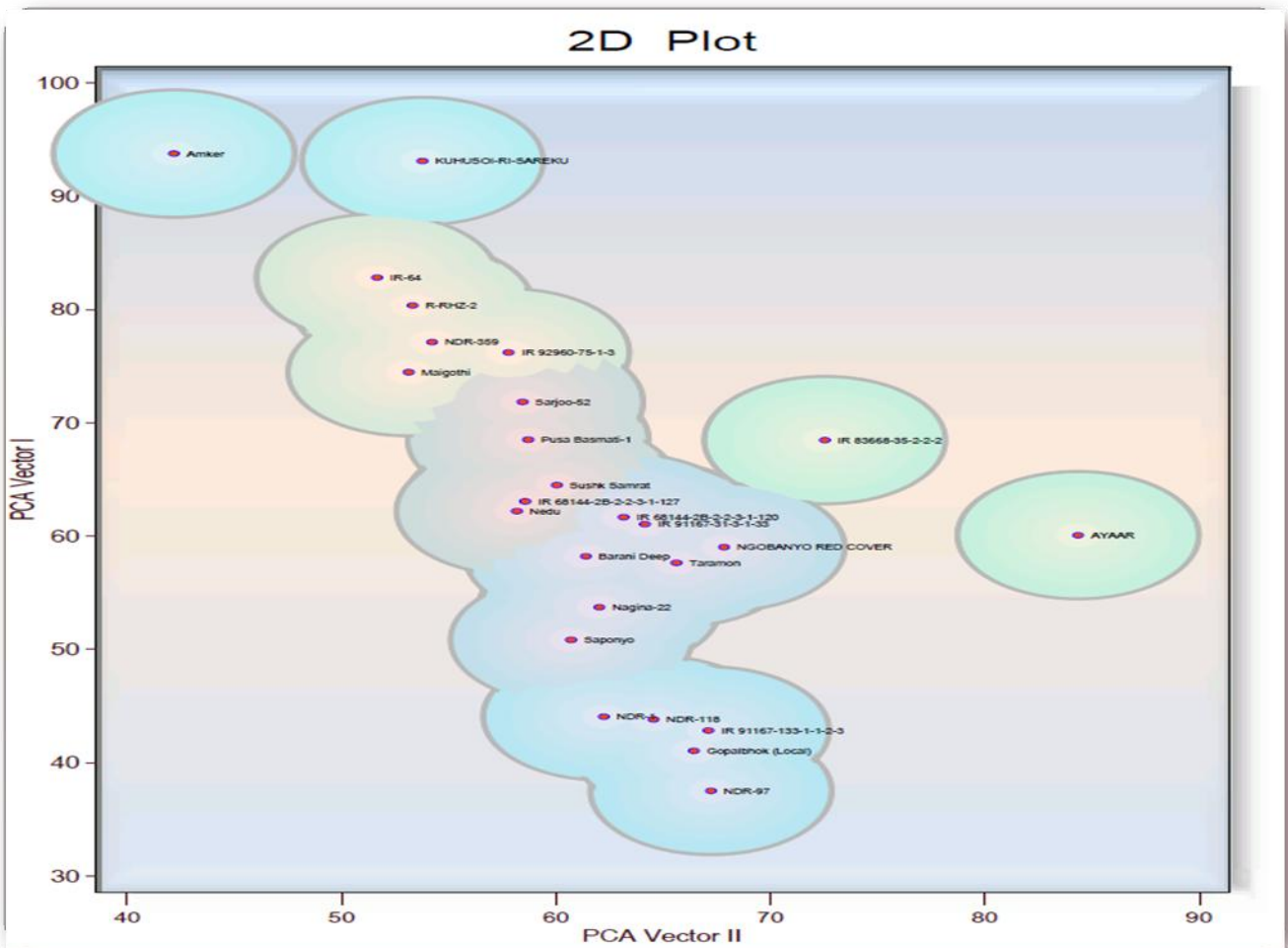
The PCA mostly confirmed the cluster analysis. In case of distant genotype Pusa Basmati-1 which formed its own group alone both in cluster analysis and PCA analysis (Fig. 1 and 2). However, genotype Ayaar which was clustered alone in group V of cluster analysis came closer to some other genotypes in PCA and formed group IV with other genotypes. According to PCA, the first four principal components accounted for about 88.22% of total variation for all morphological traits and exhibited high correlation among the characteristics analyzed. From the Eigen vectors analysis it was found that 38.11, 21.37, 14.00, 9.09 and 5.63 % variation of morphological traits could be explained in respect by the first five principal components (Table 4). The presence of broad morphological differences among genotypes was further confirmed by principal component analysis, which indicated that the overall diversity observed could be elucidated by a few Eigen vectors. Caldo *et al.,* (1996) reported, the first 10 principal components accounted for 67% of total variation, implied a strong correlation among traits which were studied. Lasalita-zapico *et al.,* (2010) also noticed 82.7% of total variation among 32 upland rice varieties, where almost 66.9% variation showed by PC1 and 15.87% by PC2.

The contribution of individual trait to the divergence among genotypes is presented in Table 5. Spikelets per panicle contributed maximum towards genetic divergence (60.00%) followed by index (13.54%) and days to 50% flowering (10.46%). Similar kinds of observations were made by earlier workers (Sandhyakishore *et al.,* 2007 and Patil *et al.,* 2005). Remaining traits had very little or no contribution towards genetic divergence and hence, they were of less importance. Since varieties with narrow genetic base are increasingly vulnerable to diseases and adverse climatic changes, availability of the genetically diverse genotypes for hybridization programme become more important. Since spikelet per panicle contributed maximum towards the genetic divergence, we may go for direct selection of this trait for diversity purpose.

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