



# GENETIC DIVERGENCE AMONG RICE GENOTYPES STUDIED THROUGH NON-HIERARCHICAL EUCLIDEAN CLUSTER ANALYSIS

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## Abstract

The study of genetic divergence among 56 rice genotypes and three checks was performed by employing non-hierarchical Euclidean cluster analysis for twelve characters. The 59 genotypes were grouped into eight different non-overlapping clusters. Cluster II, having 16 genotypes, emerged with highest number of entries followed by cluster I with 15 genotypes. Cluster VIII had 10 genotypes and cluster VII possessed five genotypes. Cluster IV and cluster V contained 4 genotypes each. The highest intra-cluster distance was found for cluster I followed by cluster VI, IV and VIII. The maximum inter-cluster distance recorded between cluster VI and III followed by cluster V and III; cluster VII and III and cluster VII and IV. The minimum estimate for the inter-cluster distance recorded between cluster II and I followed by cluster VII and II; cluster VIII and II, cluster IV and II and cluster VII and I. The cluster VI and cluster VIII comprised of genotypes having tall stature; cluster III for PL followed by cluster IV; cluster V for EBT/P; cluster III with a cluster mean of 177.00 for S/P; Cluster I for FLA 28.65 cm<sup>2</sup>; cluster VI for SF; cluster VII for TW; cluster VII for BY/P. The highest cluster mean for grain yield per plant was observed in cluster VII while, high cluster mean for HI in cluster IV.

**Key words :** Rice, genetic diversity, cluster, germplasm and augmented design.

## Introduction

The information about the nature and magnitude of genetic diversity existing in the available germplasm of a particular crop is essential for selection of diverse parents, which upon hybridization may provide a wide spectrum of gene recombination for quantitatively inherited traits. Genetically, diverse parents are preferred for use in hybridization programme because crosses involving divergent parents have been found to provide greater possibility for obtaining desirable segregants in segregating generations. The importance of genetic diversity for selecting parents for recombination breeding in an autogamous crop such as aerobic rice to recover transgressive segregants has also been repeatedly emphasized (Griffing and Lindstorm, 1954; Moll *et al.*, 1962; Arunachalam, 1981). Earlier workers considered distances in place of origin as index of genetic diversity and used it for selection of parents for hybridization programme. However, the genetic diversity of the selected

parents has not found to be based on factors such as geographic diversity/place of release or ploidy level (Chandra *et al.*, 2007; Kumar *et al.*, 2008; Bose *et al.*, 2011; Ovung *et al.*, 2012). Hence, characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedures, such as non-hierarchical Euclidean cluster analysis. These procedures characterize genetic divergence using the criterion of similarity or dissimilarity based on the aggregate effects of a number of agronomically important characters.

## Materials and Methods

The present investigation was carried out at Crop Research Centre, Masodha, N.D. University of Agriculture & Technology, Faizabad (U.P.), India. The crosses were made during *Kharif*, 2012 and the germplasm lines, hybrids along with parental lines and check varieties were evaluated during *Kharif*, 2013. Geographically, this place is located in between 26.47°N latitude, 82.12°E longitude and at an altitude of 113 meters

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above from mean sea level.

### Germplasm evaluation

The 56-germplasm lines along with three checks *viz.*, Shusksamrat, NDR 2064 and NDR 359 were evaluated in augmented design during *Kharif*, 2013. The experimental field was sub-divided in to 4 blocks of 17 plots each. The checks were allocated randomly in each block, while remaining 14 plots in a block were used for accommodating the un-replicated test genotypes. Rice varieties under aerobic condition were directly sown on 23<sup>th</sup> June 2013 at 2-3 cm soil depth in dry and pulverized soil by hand plough with the seed rate of 60 Kg ha<sup>-1</sup> to maintain 3-4 seeds per hill. This method gave uniform seedling emergence for all the plots in 6-8 days. The experimental field under aerobic condition was irrigated for 15 days till plants reached 2-3 leaves. At this stage seedlings were thinned to keep 2 seedlings per hill so as maintain uniform plant number. Experimental plots were maintained at near saturation and re-watered only when soil moisture reached below 15 cm. Standard cultural procedures were adopted. Phosphorus (40 kg ha<sup>-1</sup> P<sub>2</sub>O<sub>5</sub>) and potassium (40 kg ha<sup>-1</sup> K<sub>2</sub>O) were applied as recommended before sowing/planting in aerobic and transplanted conditions. Urea was used as source of N in three splitdoses. The first application was made at 21 days after sowing, the second at active tiller initiation and the third at panicle initiation stages. The total nitrogen amount applied was 80 kg ha<sup>-1</sup>. All plant protection measures were taken. Weeds were controlled by treating plot by pre-emergence herbicide (Petrilachlore) after three days of sowing followed by one hand weeding. Non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973) was used to examine genetic divergence existing in germplasm collections.

## Results and Discussion

### Genetic divergence analysis

The Non-hierarchical Euclidean cluster analysis grouped 56 rice germplasm lines and three checks of the present investigation into eight distinct non-overlapping clusters (table 1). The discrimination of germplasm lines in to so many discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Earlier workers have also reported substantial genetic divergence in the rice materials (Bose *et al.*, 2011; Sharma *et al.*, 2011; Mahalingam *et al.*, 2013). Presence of substantial genetic diversity among the germplasm lines screened in the present study indicated that this material may serve as good source for selecting the diverse parents for hybridization programme aimed at isolating desirable

sergeant's for grain yield and other important characters. An examination of the clustering pattern of the 59 rice genotypes in to eight clusters revealed that the genotypes of heterogeneous origin were frequently present in same cluster. Although, the genotypes originated in same place or geographic region was found grouped together in same cluster, the instances of grouping of genotypes of different origin or geographical regions in same cluster were observed in case of most of the clusters. This indicated lack of any definite relationship or correlation between genetic diversity and geographic origin of the aerobic rice genotypes evaluated in the present study. Therefore, the selection of parental material for hybridization programme simply based on geographic diversity may not be rewarding exercise (Kumar *et al.*, 2008; Bose *et al.*, 2011; Mahalingam *et al.*, 2013). Among the eight clusters, Cluster II, having sixteen genotypes emerged with highest number of entries followed by cluster 1<sup>st</sup> (15), 8<sup>th</sup> (10) and 7<sup>th</sup> (5). Cluster 4<sup>th</sup> and 5<sup>th</sup> contained four genotypes each. Clusters 3<sup>rd</sup> and 6<sup>th</sup> were constituted by 2 and 3 entries, respectively. The estimates of average intra and inter-cluster distances for eight clusters, presented in table 2, revealed that the genotypes present in a cluster have little genetic divergence from each other with respect to aggregate effect of 12 characters under study, while much more genetic diversity was observed between the genotypes belonging to different clusters. Since, high or optimum genetic divergence is desired between the parents of hybridization plan for obtaining higher frequency of desirable recombinants, the chances of obtaining good segregants by crossing the little diverse genotypes belonging same cluster are very low. In order to increase the possibility of isolating good sergeants in the segregating generations it would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances. In the context, the maximum inter-cluster distance was recorded between cluster VI and III followed by cluster V and III, cluster VII and III and cluster VII and IV. In present investigation, the highest intra-cluster distance was found for cluster I followed by cluster VI, IV, VII, III, II, IV and cluster VII. The lowest inter cluster distance was required between cluster I and II, followed by cluster II and VIII; II and IV; I and VII. Thus, crossing between the genotypes of the above that cluster pairs having very low inter-cluster distances may not be rewarding owing to little genetic diversity among their genotypes. The intra-cluster group means for twelve characters (table 3) revealed marked differences between the clusters in respects of cluster means for different characters. The genotypes having DFF were grouped in cluster VIII with a cluster mean of 79.59 days. The

**Table 1 :** Clustering pattern of aerobic rice genotypes on the basis of Non-hierarchical Euclidean Cluster analysis for 12 characters.

Cluster number	Number of genotypes	Genotypes
I	15	IR 83614-673-B, IR 83614-354-B, IR 800B-B-141-4-1, IR 79913-B-99-B-2, IR 64, IR 55419-04, IR 79913-B-221-B-2, R-R-F-66, IR 79906-B-5-3-3, IR 84887-B-153-CRA-2-5-1, IR 84899-B-182-CRA-12-1, IR 81044-B-112-U-4-2, IR 77298-14-1-2, IR 84856-159-CRA-12-1, IR 80416-B-15-2-4
II	16	IR 79975-B-83-4-3, R-RF-60, IR 83614-564-B, IR 84894-B-139-CRA-8-1, IR 78878-53-2-2-2, I-7850-105-B-2-B, IR 83614-438-B, IR 79899-B-179-2-3, MTU 1010, IR 84614-203-B, NDR 2064, NDR 359, IR 8041-B-7-1, IR 79971-B-148-3-1, R-RF-45, LALIT
III	2	NDR 1045-2, IR 84894-B-143-CRA-17-1
IV	4	IR 78508-R-6-B-2-B, IR 82870-58, IR 78875-207-B-1-B, IR 77970-B-47-1
V	4	NDR 1119, IR 80416-B-152-4, IR 8364-281-B, IR 84500-B-149-CRA-2-1
VI	3	R-RF-65, IR 81063-B-94-U-3-2, BAU 358-02
VII	5	IR 84899-B-185-CRA-1-1, IR 79956-B-60-2-3, IR 81057-B-132-U-4-4, IR 78508-142-B-3-B, IR 83614-46-B
VIII	10	IR 83614-61-B, IR 81039-B-137-U-3-3, IR 83614-349-B, Shusksamrat, IR 72667-16-1-B-B-3, IR 78508-80-B-3-B, IR 74371-70-1-1, IR 78537-B-4-B-B-B, IR 844899-B-183-CRA-19-1, IR 83614-315-B-AROBIC-E-7

**Table 2 :** Estimates of average intra and inter-cluster distances for 8 clusters in aerobic rice.

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	<b>16.61</b>	18.12	38.46	27.29	27.51	29.60	24.88	26.52
Cluster II		<b>12.58</b>	27.47	24.04	27.47	29.79	19.26	20.48
Cluster III			<b>13.21</b>	38.65	61.29	73.29	47.79	35.85
Cluster IV				<b>11.69</b>	35.92	35.62	42.10	33.62
Cluster V					<b>15.18</b>	30.68	27.83	25.15
Cluster VI						<b>15.59</b>	29.58	35.02
Cluster VII							<b>11.17</b>	27.76
Cluster VIII								<b>14.52</b>

Bold figures represent intra-cluster distances.

**Table 3 :** Clusters means for 12 characters in aerobic rice.

Clusters	DFP	DM	PH (cm)	PL	EBT/P	S/P	FLA (cm <sup>2</sup> )	SF	TW (cm)	BY/P	GY/P (g)	HI (%)
Cluster I	91.08	119.93	98.11	22.57	8.16	100.63	28.65	30.47	23.66	19.47	8.18	42.13
Cluster II	85.64	123.89	89.87	23.11	7.48	102.02	24.67	24.99	24.17	20.42	8.68	42.85
Cluster III	82.75	129.00	84.79	26.00	4.59	177.00	25.81	14.83	21.89	14.94	6.99	46.26
Cluster IV	85.25	129.75	78.45	23.34	6.34	67.00	27.34	40.97	24.64	11.52	5.47	46.66
Cluster V	87.25	123.50	79.04	20.07	10.41	84.25	27.23	32.99	24.12	26.80	6.75	25.08
Cluster VI	85.08	127.00	113.00	19.25	8.58	53.28	24.93	46.42	25.19	23.62	9.48	40.42
Cluster VII	84.22	120.47	89.97	23.31	8.11	91.57	26.02	28.79	25.93	32.50	11.64	36.52
Cluster VIII	79.59	125.34	98.35	23.22	8.59	100.11	24.65	25.04	20.41	23.90	6.61	29.87

cluster I and V were constituted by the genotypes having DFP with cluster mean of 91.08 and 87.25 days, respectively. The early maturity days were grouped in cluster I with a cluster mean. For the trait PH, the desirable short stature genotypes were grouped in cluster IV and cluster V having clustered mean, respectively.

The cluster III exhibited highest cluster mean for PL followed by cluster IV. The genotypes having high number of EBT/P were grouped in cluster V. The maximum number of S/P was found in cluster III followed by cluster II. Cluster I possessed high cluster mean for FLA. The cluster VI, having only one genotype, showed highest

cluster mean for SF. The cluster VII had highest mean for TW. The cluster VII, having single genotype, showed highest cluster mean for BY/P. The highest cluster mean for GY/P was observed in cluster VII. The high cluster mean for HI was found in cluster IV. The above discussion clearly shows wide variation from one cluster to another in respect of cluster means for twelve characters, which indicated that genotypes having distinctly different mean performance for various characters were separated into different clusters.

### Conclusion

The crossing between the entries belonging to cluster pairs having large inter-cluster distance and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generations in rice. However, caution should be exercised in selecting very diverse genotypes, because the frequency of heterotic crosses and magnitude of heterosis for yield and its components were found to be higher in crosses between parents with intermediate divergence than the extreme ones.

### References

Beale, E. M. L. (1969). *Euclidean cluster analysis*. A paper contributed to 37<sup>th</sup> session of the International statistical Institute.

- Bose, L. K., O. N. Singh, H. N. Subudhi and G. J. N. Rao (2011). Genetic diversity in direct seeded aerobic rice. *International Journal of Agricultural Sciences*, **7** (2) : 321-324.
- Chandra, B. S., T. D. Reddy and N. A. Ansari (2007). Genetic divergence in rice (*Oryza sativa* L.). *Research on Crops*, **8**(3): 600-603.
- Kumar, S., D. Singh, A. Sirohi and Satyendra (2008). Genetic diversity in rice (*Oryza sativa* L.) under aerobic conditions. *Environment and Ecology*, **26** (2) : 606-608.
- Mahalingam, A., R. Saraswathi, J. Ramalingam and T. Jayaraj (2012). Genetic studies on divergence and phenotypic characterization of indigenous and exotic indica germplasm lines in rice (*Oryza sativa* L.). *African Journal of Agricultural Research*, **7**(20) : 3120-3128.
- Ovung, C. Y., G. M. Lal and P. K. Raj (2012). Studies on genetic diversity in rice (*Oryza sativa* L.). *International Journal of Agricultural Technology*, **7**(20) : 3120-3128.
- Sharma, S. K., R. Nandan, S. K. Singh, A. K. Sharma, S. Kumar, P. K. Sharma, M. K. Singh and V. Kumar (2011). Genetic divergence in rice (*Oryza sativa* L.) genotypes under irrigated condition. *Progressive Agriculture*, **11** (2) : 321-325.
- Spark, D. N. (1973). Euclidean cluster analysis. Algorithm. As. *Applied Statistics*, **22** : 126-130.