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Study of genetic divergence analysis for the selection of germpalsm in aerobic rice (*Oryza sativa* L.)

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Abstract
Aerobic rice intake low water use, so it can be produced in areas where lowland rice cannot be grown. Since aerobic rice is targeted at water-short areas, socio-economic comparisons must include water-short lowland rice and other upland crops. The development of high-yielding aerobic rice is still in its infancy and germplasm still needs to be improved and appropriate management technologies developed.

Keywords: germplasm, aerobic rice, cluster mean

Introduction
Aerobic rice is the new concept to further decrease water requirements in rice production in water short areas. Asia is considered as 'Rice bowl' of the world, occupying 90% world's rice area. More than 90 per cent of the world's rice is grown and consumed in Asia, where 60 per cent of Earth's people live. Rice accounts for 35 per cent to 75 per cent of the calories consumed by more than 3 billion Asians. In India rice is cultivated in an area of about 43.50 million hectares with an annual production of about 159.20 million tonnes with average productivity of 3659.8 kg per hectare (Anonymous, 2013) [1]. In Uttar Pradesh, the area of rice is about 13.84 million hectares and production is 14.00 million tones with productivity of 2358 kg per hectare (Anonymous, 2012) [2]. Aerobic rice is defined as high yielding rice grown in non-puddled and non-flooded aerobic soil. It is usually grown under supplementary irrigation and with fertilizer inputs. Aerobic rice cultivation has been a successful market integrated system in Brazil and it is also being grown in northern China with yield levels reported to be close to irrigated levels. To strategically address the projected water scarcity, IRRI has also developed an "aerobic rice" technology that aims to significantly reduce the crop's water requirement below current levels. Compared with lowland rice, water inputs in aerobic rice were more than 50% lower (only 470-650 mm), water productivities 64-88% higher, gross returns 28-44% lower (345-633 $ ha^{-1}) and labour use 55% lower. Because of its low water use, aerobic rice can be produced in areas where lowland rice cannot be grown. Since aerobic rice is targeted at water-short areas, socio-economic comparisons must include water-short lowland rice and other upland crops. The development of high-yielding aerobic rice is still in its infancy and germplasm still needs to be improved and appropriate management technologies developed. Ways must be found to decrease water use in rice production.

Materials and Methods
The investigation was carried out at the Crop Research Farm, Masodha, N.D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad. The germplasm along with check varieties were evaluated during *Kharif*, 2013. Geographically this place is located in between 26.47^{0}N latitude, 82.12^{0}E longitude and at an altitude of 113 meters above from mean sea level. This area falls in sub-tropical climatic zone. The climate of district Faizabad is semi-arid with hot summer and cold winter. The germplasm evaluation experiment involved evaluation of 56 germplasm lines along with three checks *viz.*, Shusksamrat, NDR 2064 and NDR 359. The 56 germplasm lines along with three checks were evaluated in augmented design during *Kharif*, 2013. The experimental field was sub-divided in to 4 blocks of 17 plots each. The three checks were allocated randomly to three plots in each block, while remaining 14 plots in a block were used for accommodating the unreplicated test genotypes.

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Result and Discussion

The study of genetic divergence among 56 rice genotypes and 3 checks was performed by employing Non-hierarchical Euclidean cluster analysis for twelve characters. The 59 genotypes were grouped into eight different non-overlapping clusters as presented in Table 1. 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 5 genotypes. Cluster IV and cluster V contained 4 genotypes each. Cluster VI and cluster III were constituted by 3 and 2 entries, respectively. The estimates of intra- and inter-cluster distances for eleven clusters are presented in Table 2. The highest intra-cluster distance was found for cluster I (16.61) followed by cluster VI (15.59), cluster IV (15.18), cluster VIII (14.52), cluster III (13.21), cluster II (12.58), cluster IV (11.69) and cluster VII (11.17).

The maximum inter-cluster distance was recorded between cluster VI and III (73.29) followed by cluster V and III (61.29), cluster VII and III (47.79) and cluster VII and IV (42.10). The inter-cluster distances between cluster pairs cluster IV and III (38.65), cluster III and I (38.46), cluster V and IV (35.92), cluster VIII and III (35.85) were also high. The minimum estimate for the inter-cluster distance was recorded between cluster II and I (18.12) followed by cluster VII and II (19.26), cluster VIII and II (20.48), cluster IV and II (24.04) and cluster VII and I (24.88).

The intra-cluster group means for twelve characters (Table 1) revealed marked differences between the clusters in respects of cluster means for different characters. The genotypes having lesser days to 50% flowering were grouped in cluster VIII with a cluster mean of 79.59 days, along with lowest cluster means for flag leaf area and 1000-grain weight. The cluster I and cluster V were constituted by the genotypes having days to 50% flowering with cluster mean of 91.08 and 87.25 days, respectively. The early maturity days were grouped in cluster I with a cluster mean of 119.93 days. The cluster IV and cluster III were constituted by the genotypes having late maturity with cluster mean of 129.75 and 129.00 days, respectively. For the trait plant height, the desirable short stature genotypes were grouped in cluster IV and cluster V having cluster mean of 78.45 and 79.04 cm, respectively. The cluster VI and cluster VIII were comprised of genotypes having tall stature with cluster mean *i.e.* 113.00 and 98.35 cm, respectively. The cluster III exhibited highest cluster mean

(26.00 cm) for panicle length followed by cluster IV (23.34 cm). The genotypes having high number of panicle bearing tillers per plant were grouped in cluster V (10.41). The maximum number of spikelets per panicle was found in cluster III with a cluster mean of 177.00, followed by cluster II (102.02). Cluster I possessed high cluster mean for flag leaf area 28.65 cm². The cluster VI, having only one genotype, showed highest cluster mean for spikelet fertility (46.42%) followed by cluster IV (40.97%). The cluster VII had highest mean for 1000-grain weight (25.93 g) followed by cluster VI with cluster mean of 25.19g. The cluster VII, having single genotype, showed highest cluster mean for biological yield per plant (32.50g) followed by cluster V (26.80 g). The highest cluster mean for grain yield per plant was observed in cluster VII (11.64 g) followed by cluster VI (9.48 g). The high cluster mean for harvest-index (46.66%) was found in cluster IV followed by cluster III with cluster mean of 46.26%. 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 recombinations for quantitatively inherited traits. Darwin (1859) [6] used the expression of divergence in characters to denote variation in genera, species and varieties. 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. 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 been always found to be based on factors such as geographic diversity/place of release or ploidy level (Murty, Bose *et al.,* 2011)[4]; Ovung *et al.* (2012)[8]. 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.

Table 1: Clusters means for 12 characters in aerobic rice

Clusters	Days to 50% flowering	Days to maturity	Plant height	Panicle length	Panicle bearing tillers per plant	Spikelets per panicle	Flag leaf area (cm²)	Spikelet fertility	1000-grain weight	Biological yield per plant	Grain yield per plant (g.)	Harvest index (%)
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

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

Table 3: Clustering pattern of aerobic rice genotypes on the basis of Non-hierarchical Euclidean Cluster analysis for 12 characters

Cluster number	No. 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

The Non-hierarchical Euclidean cluster analysis grouped 56 rice germplasm lines and three checks of the present investigation into eight distinct non-overlapping clusters. 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 (Sharma *et al.*, 2011) [7]. 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 segregants 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 were also found to be 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 all the clusters except the single entry cluster III. 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. The choice of suitable diverse parents based on genetic divergence analysis would be more fruitful than the choice made on the basis of geographical distances. This finding is in conformity with the previous reports advocating lack of parallelism between genetic and geographic diversity in rice (Bose *et al.*, 2011; Cheema *et al.* (2004) [5] advocated that the number of clusters formed, number of genotypes in the clusters and superposition of the genotypes within the clusters indicated the possibility of genetic improvement for yield and yield components. Among the eight clusters, Cluster II, having emerged with highest number of entries followed by cluster I, cluster VIII and cluster VII. Cluster IV and cluster V contained equal

genotypes each. Cluster VI and cluster III were constituted by 3 and 2 entries, respectively.

The estimates of average intra- and inter-cluster distances for eight clusters 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 present investigation, the highest intra-cluster distance was found for cluster I followed by cluster VI, cluster IV, cluster VII, cluster III, cluster II, cluster IV and cluster VII. 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. Thus, crossing between the genotypes of the above which 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 revealed marked differences between the clusters in respects of cluster means for different characters. The genotypes having days to 50% flowering were grouped in cluster VIII with a cluster mean of 79.59 days. The cluster I and cluster V were constituted by the genotypes having days to 50% flowering 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 plant height, the desirable short stature genotypes were grouped in cluster IV and cluster V having cluster mean, respectively. The cluster III exhibited highest cluster mean for panicle length followed by cluster IV. The genotypes having high number of panicle bearing tillers per

plant were grouped in cluster V. The maximum number of spikelets per panicle was found in cluster III followed by cluster II. Cluster I possessed high cluster mean for flag leaf area. The cluster VI, having only one genotype, showed highest cluster mean for spikelet fertility. The cluster VII had highest mean for 1000-grain weight. The cluster VII, having single genotype, showed highest cluster mean for biological yield per plant. The highest cluster mean for grain yield per plant was observed in cluster VII. The high cluster mean for harvest-index 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. 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.

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