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Genetic divergence in rice varieties having iron and zinc

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Abstract
The objective of this study was to estimate the genetic diversity of fourteen iron and zinc genotypes of rice for yield and quality traits using Mahalanobis D^2. The clustering pattern of 11 genotypes was grouped into four non-overlapping clusters. Cluster III having highest number of genotypes, The maximum intra cluster distance was recorded in cluster II (3459.43) indicating greater genetic divergence between the genotypes belonging to this cluster. Spikelets per panicle, days to maturity, grains per panicle, plant height Grain yield per plant, days to 50% flowering, plant height, number of filled grains per panicle, contributed 88.45% towards total divergence. Cluster-II has highest mean value for Spikelets/panicle and Grains/panicle. The maximum inter cluster distance recorded between cluster II and IV (14289.25) followed by I and IV (9461.13), cluster III and IV (6053.272), cluster II and cluster III (4033.25) indicating wide genetic diversity and it may be used in rice hybridization programme for improving grain yield.

Keywords: Rice, iron, zinc, genetic divergence

Introduction
Rice is the staple food for billions of people throughout the developing world. But beyond easing hunger pains and providing carbohydrates for energy, it has little nutritional value. Over two billion people worldwide suffer from micronutrient deficiencies due to a lack of essential vitamins and minerals in their diet. Iron (Fe) and zinc (Zn) deficiencies are the most widespread human micronutrient deficiencies and are particularly prevalent in resource-poor countries where there is a heavy dietary reliance on staple crops (Sands *et al.*, 2009) [16]. Biofortification of rice (*Oryza sativa* L.) with micronutrients is widely recognized as a sustainable strategy to alleviate human iron (Fe) and zinc (Zn) deficiencies in developing countries where rice is the staple food. Genetic engineering is considered a valuable strategy to alleviate Fe deficiency in rice based societies, as increases of Fe concentrations in transgenic polished rice grain have exceeded levels achieved by conventional breeding (Johnson *et al.*, 2011; Lee *et al.*, 2012; Trijatmiko *et al.*, 2016) [8, 9, 18].

Materials and Methods
The experiment was carried out at the Experimental field and Green house, Department of Plant Molecular Biology and Genetic Engineering, N.D. University of Agriculture and Technology, Faizabad (U.P.) during Kharif season. The plant materials used in the research work included Shusk Samrat, Barani Deep, Narendra Usar Dhan 3, Narendra Usar Dhan 2, Swarna sub 1, Jalmagna, NDR 359, Sarjoo-52 and Kalanamak and two $F_{1(s)}$ namely NDR-359×Kalanamak, NDR-359×Barani Deep made in background of NDR 359. Taken Data on Days to 50% flowering, Days to Maturity, Plant height, Flag leaf Area, Panicle bearing tillers per plants, Number of spikelets per panicle, Grain per panicle Spikelet fertility (%), Test weight (g), Biological yield (g), Harvest index (%), Unpolished Zinc (ppm), Polished Zinc (ppm), Unpolished Iron (ppm), Polished Iron (ppm), Grain yield (g) were recorded. Based on genetic distances (D2 values), the genotypes were grouped into clusters of genetically closer related groups following the Tocher's method (Rao, 1952) [15].

Results and Discussion

The importance of genetic divergence in plant breeding has been emphasized by several scientists (Griffing and Lindstrom, 1954 [4]; Moll *et al.*, 1962 [13]; Arunachalam (1981) [1] and Hawkas (1981) [5]. Mahalanobis D^2 statistic has been utilized by several workers for the assessment of genetic divergence in different crops (Malhotra and Singh, 1971) [11].

In the present study, the 11 genotypes of rice were grouped into four different non-overlapping clusters (Table 1), suggesting considerable amount of genetic diversity in the material. Cluster III having highest number of genotypes (4) namely, NUD-3, NUD-2, NDR 359, Kalanamak×NDR 359. Cluster I having three rice genotypes namely, Sushk Samrat, Barani Deep×NDR 359, Barani Deep. Cluster II having Sarjoo-52 and Swarna sub 1. Cluster IV having Jalmagna and Kalanamak as supported by earlier finding of Cheema *et al.* (2004); Devi *et al.* (2006); Hosan *et al.* (2010); Ismail *et al.* (2010); Mall *et al.* (2011) and Ovung *et al.* (2012) [2, 3, 6, 7, 12].

The estimates of average intra and inter cluster distances presented in Table 2, revealed that the maximum intra cluster distance was exhibited by the genotype of cluster III (18.50) followed by cluster I (16.15) and cluster II (3459.43) while the maximum inter cluster distance was recorded between the genotypes of cluster II and IV (14289.25) followed by cluster I and IV (9461.13) and cluster III and IV (6053.272). Cluster-II has highest mean value for Spikelets/panicle and Grains/panicle followed by cluster-III. As heterosis can be best exploited and chances of getting transgressive segregants are maximum when generating diverse lines are crossed (Zaman *et al.,* 2005 and Saxesena *et al.,* 2013) [19, 17]

Table 1: Clustering patterns of 11 rice genotypes on the basis of D2 analysis for 16 characters

Cluster No.	No. of genotype	Genotype
I	3	Sushk Samrat, Barani Deep×NDR 359, Barani Deep
II	2	Sarjoo-52, Swarna sub 1
III	4	Narendra Usar Dhan-2, NDR-359, Narendra Usar Dhan-3, Kalanamak×NDR 359
IV	2	Jalmagna, Kalanamak

Table 2: Estimates of average intra and inter cluster D^2 value

Cluster No.	I	II	III	IV
I	549.891	2997.094	2449.201	9461.131
II		3459.426	4033.253	14289.250
III			1736.086	6053.272
IV				3187.877

Table 3: Cluster means for different characters for rice genotypes under normal condition.

S. No.	Days to 50% flowering	Days to maturity	Plant height (cm)	Panicle bearing tillers/plant	Flag leaf area (cm²)	Spikelets/panicle	Grains/panicle	Spikelet fertility (%)	Test weight (g)	Biological yield (g)	Harvest index	Unpolished seed (Zn)	Polished seed (Zn)	Unpolished seed (Fe)	Polished seed (Fe)	Grain yield /plant (g)
1 Cluster	75.711	100.433	77.381	12.696	24.153	147.466	137.978	93.600	23.376	27.987	41.349	7.371	7.544	37.577	35.956	11.573
2 Cluster	111.000	139.000	76.348	13.933	28.122	173.088	165.062	95.372	23.323	27.298	37.230	4.222	3.312	52.453	63.353	10.163
3 Cluster	105.117	134.283	91.063	11.965	27.900	154.984	145.186	93.627	22.763	31.350	41.410	6.507	7.497	31.539	27.844	12.956
4 Cluster	118.500	145.833	133.777	11.910	29.842	142.625	127.900	89.898	26.890	31.497	37.637	8.433	7.693	32.708	106.507	11.852

Conclusion

Analysis of Genetic divergence indicate that Cluster III having highest number of genotypes followed by cluster I and II. maximum intra cluster distance was exhibited by the genotype of cluster III followed by cluster I and cluster II while the maximum inter cluster distance was recorded between the genotypes of cluster II and IV followed by cluster I and IV and cluster III and IV. Cluster-II has highest mean value for Spikelets/panicle and Grains/panicle followed by cluster-III. Genetic variability between germplasm suggesting that these clusters could be used as parents in hybridization programme to develop desirable type because crosses between genetically divergent lines will generate heterotic segregants. As heterosis can be best exploited and chances of getting transgressive segregants are maximum when generating diverse lines are crossed.

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