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Cluster analysis of 55 Rice (*Oryza sativa* L.) germplasm.

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Abstract

Cluster analysis were carried out in rice germplasm for eight characters. The experiment was conducted at instructional cum Research Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) during *kharif* 2017 to access association analysis of the 55 germplasm accessions of rice along with popular standard checks Chattisgarh Zinc rice 1, Samleshwari Danteshwari, Indira Barani dhan and Indira Aerobic1. After evaluation of 55 accessions for eight quantitative characters, total 55 rice genotypes under this study were grouped into 5 clusters. Cluster I comprise 8 genotypes (14.54%), Cluster II, Cluster III, Cluster IV and Cluster V consisted 15 genotypes (27.27%), 7 genotypes (12.72%), 12 genotypes (21.81%) and 13 genotypes (23.63%) respectively. Cluster II has highest number of genotypes (15). The intra cluster distance ranged from 10.87 to 21.40. The maximum intra-cluster distance was observed for cluster III (21.40) followed by cluster IV (12.43) and cluster II (11.49). Cluster I (10.86) had minimum intra-cluster distance with more than one genotype. The inter-cluster distance varied from 78.547 to 24.495. The inter-cluster distance was maximum between clusters 3 and 4 (78.547) followed by clusters 1 and 3 (71.143) and minimum inter-cluster distance was observed between clusters 1 and 4 (24.495). On the basis of cluster mean values, top three accessions were identified for the yield improvement programme.

Keywords: Rice (*Oryza sativa* L.), agriculture, *kharif*

Introduction

Rice (*Oryza sativa* L.) ($2n=24$) is the most important cereal crop that has been referred as “Global Grain” because of its use as prime staple food in about 100 countries of the world. In world, rice has occupied an area of 160.6 million hectares, with a total production of 738.20 million tonnes and productivity 3424.41 kg/ha. In India rice is cultivated round the year in one or the other part of the country in diverse ecologies spread over 43.38 million hectares with a production of 104.32 million tonnes during 2015-16. Chhattisgarh popularly known as “Rice Bowl of India” occupies an area around 37.73 lakh hectares with the production of 60.28 lakh tonnes and productivity 1597 kg/ha. In any crop, germplasm plays as an important role as a source and provides scope for wide variability. The knowledge about genetic variability of yield contributing characters, inter relationship among them and their relation with yield are necessary for a effective breeding programme (Nayak *et al.*, 2016) [4].

Materials and Methods

The 55 accessions of rice were evaluated in the field during *kharif* 2017 at Research Cum Instructional Farm, Deptt. of Genetics & Plant Breeding, College of Agriculture, IGKV, Raipur. The field trials were conducted under irrigated transplanted condition. The plant materials were sown in raised bed nursery on 2nd July 2017. Twenty five days old seedlings were subsequently transplanted into the field in augmented design (only checks are replicated) in *kharif* -2017. Each entry was transplanted in two rows with 20 cm of spacing between row to row and 15 cm between plant to plant. The check varieties were randomized within blocks. Fertilizer dose @ of 80 N: 50 P: 30 K kg/ha was applied. The entire dose of phosphorus and potassium along with half the dose of nitrogen was applied as basal dose before transplanting. The remaining dose of nitrogen was applied in two splits, first at the time of beginning of tillering and second one week after it. The standard agronomic practices were adopted for normal crop growth.

Results and Discussion

Cluster Analysis based on yield and its attributing traits

Cluster analysis among 55 rice genotypes was studied. The clustering pattern of all genotypes has been presented in Table 1. The selection of parents with different genetic backgrounds is made easier by analyzing the general pattern of genetic variation and interactions among rice genotypes (Murphy *et al.*, 1986 and Souza and Sorrels, 1991) [3, 7]. Total 55 rice

genotypes under this study were grouped into 5 clusters based on K mean cluster analysis.

In Cluster analysis rice genotypes were grouped on basis of yield attributing traits, Cluster I comprise 8 genotypes (14.54%) out of 55 rice genotypes. Cluster II, Cluster III, Cluster IV and Cluster V consisted 15 genotypes (27.27%), 7 genotypes (12.72%), 12 genotypes (21.81%) and 13 genotypes (23.63%) respectively. Cluster II has highest number of genotypes (15).

Table 1: Distribution of 55 germplasm accessions of rice among five clusters

Cluster Number	Number of accession	Accession serial number	Name of accession
1.	8	1, 4, 10, 11, 12, 18, 23, 27	Hatiya, Jejne, Jugsay, Kachana, Kakai, Katuli, Kota Deshi, Lallo.
2.	15	2, 3, 5, 6, 7, 8, 14, 16, 17, 19, 21, 26, 28, 29, 30	Himga, Jatashankar, Bhatha Jhilli, Tikra Jhilli, Jodari Nadgi, Jodhari, Kanji, Karanga, Karmi, Khirasar, Koliha, Desi Lal Dhan, Lallu-14, Lalmijo,
3.	7	32, 34, 36, 47, 48, 49, 50	Bakai, Bakiya, Balchinga, Banaskupi, Banda, Kamka Banda, Bandi.
4.	12	9, 13, 15, 20, 22, 24, 25, 51, 52, 53, 54, 55	Jora Mallo, Kali Dhan, Kanjo, Kohikari, Kolya, Koto, Lal deshi, Indira Barani Dhan1, Indira Aerobic 1, Danteshwari, Chhatisgarh Zinc Rice 1, Samleshwari.
5.	13	31, 33, 35, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46	Bakadi, Bakal, Balaund, Baldular, Balesar, Balgi, Bal keshar, Baloda, Balra, Balsua, Balu, Bami sundari.

Inter Cluster Distances

The greater the distance among clusters, the greater the genetic variability between the genotypes. Highly variable genotypes would result in a wide range of variability in subsequent generations, allowing for further selection and improvement. The pattern of group constellation demonstrated that there is a substantial level of variation. The inter and intra cluster distances among 5 clusters were computed and are given in Table 2. Minimum distance was observed between cluster 1 and cluster 4 (24.495) followed by cluster 2 and cluster 4 (26.177). This shows that the genotypes

in these groups are connected through descent to the attributes being studied. Maximum distance was observed between Cluster 3 and cluster 4 (78.547) followed by cluster 1 and cluster 3 (71.143). It indicates that genotypes within the same group are more similar, while genotypes among clusters are more distinct. This suggests that these rice genotypes have considerable genetic diversity for the variables tested, with smaller within-class and larger between-class. This will assist breeders in implementing a focused breeding programme by selecting the most attractive and varied parents in order to improve selection and breeding efficiency

Table 2: Estimates of intra (Diagonal and bold) and inter cluster distances among five clusters

Cluster Number	I	II	III	IV	V
I	10.86				
II	26.461	11.49			
III	71.143	53.094	21.40		
IV	24.495	26.177	78.547	12.43	
V	53.748	28.341	33.950	51.635	11.26

Intra cluster distance

The distance among clusters ranged from 10.87 to 21.40. Cluster III has the greatest intra-cluster distance (21.40), followed by Cluster IV (12.43) and Cluster II (11.49). It was discovered that genotypes with a large level of heterogeneity within a cluster would generate more suitable breeding materials for obtaining optimum genetic advancement. On the other hand Cluster 1 (10.86) had the smallest intra-cluster distance with more than one genotype, showing that continuous selection was used in the past, which might have resulted in uniformity with less variation across genotypes (Rajesh *et al.*, 2010) [6].

The inter-cluster distance is greater than the intra-cluster

distance, showing that the genotypes have a lot of genetic variation. The distance across clusters ranged from 24.495 to 78.547. Clusters 3 and 4 had the greatest inter-cluster distance (78.547), followed by clusters 1 and 3 (71.143). Clusters 3 and 4; 1 and 3 had a large inter-cluster distance, indicating that they were highly divergent groupings. On the other hand, smallest inter-cluster distance was showing among clusters 1 and 4 (24.495), indicating close relationship among these clusters and hybridization among the genotypes of these clusters would not provide the encouraging results. Similar type of finding was reported by Pachauri *et al.* (2017) [5], Khare *et al.* (2014) [1], Tirkey *et al.* (2013) [8] and Maji *et al.* (2012) [2].

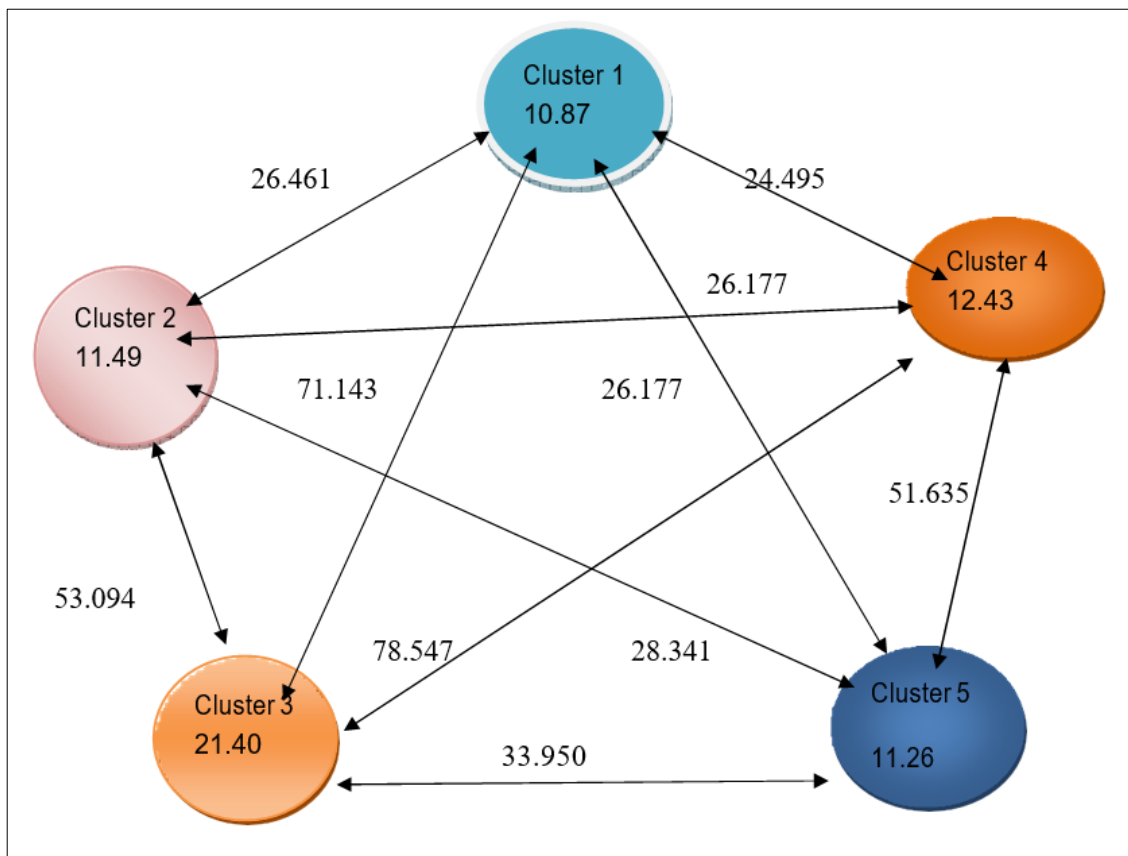


Fig 1: Cluster diagram of 55 rice genotypes

Cluster Mean

In order to visualize the pattern of clustering among rice genotypes, the mean performance of the clusters was calculated as shown in Table 3.

Days to 50% flowering and Days to maturity

Cluster 1 had lower mean values for days to 50% flowering (67.543) and days to maturity (97.83). This suggests that early duration trait breeding should consider germplasm from these clusters. As a result, we can select rice germplasm from these clusters with a low value for 50% blooming and days to maturity like Katuli, Kachana and Jugsay.

Number of effective tillers, panicle length and grain length width ratio

The number of effective tillers (6.67), panicle length (26.369) and grain length-width ratio (3.132) were all greatest in Cluster III. Cluster III has the most suited germplasm among the genotypes evaluated, which may be used in a breeding programme to enhance features like the number of effective tillers, panicle length and grain length to breadth ratio. As a result, we may choose rice germplasm from these clusters that has a high value for effective tillers, panicle length and grain length breadth ratio like Bakiya, Banda and Bal Chinga.

Plant height

Cluster IV showed a lower mean value for plant height (94.741) followed by cluster 1(112.5). As a consequence, dwarf genotypes can be created using genotypes from this cluster like Koto, Lal Deshi and Kolya.

100 grain weight and gain yield per plant

Cluster IV had higher mean value for 100 grain weight (2.864) and grain yield per plant (15.194). As a result, this is

the ideal cluster from which to choose a genotype for a breeding programme aimed at increasing grain output like Chattisgarh Zinc Rice 1, Samleshwari.

Table 3: Cluster mean (Figures in bold represents the highest or lowest mean value of a particular character) of five cluster for different characters in varying genotype of rice

Character	Cluster				
	I	II	III	IV	V
Days to 50% flowering	67.543	85.904	99.331	79.472	102.467
Number of effective tillers	6.129	5.952	6.670	6.423	5.943
Plant height	112.5	118.2	167.6	94.741	133.96
Panicle length	21.154	22.539	26.369	20.259	24.737
Days to maturity	97.833	115.8	129.377	108.98	132.38
Grain length width ratio	2.908	2.954	3.132	3.105	2.937
100 grain weight	2.303	1.901	2.240	2.864	2.284
Grain yield per plant	11.252	8.868	10.859	15.194	9.671

Conclusion

After evaluation of 55 accessions for eight quantitative characters, on the basis of cluster mean values, top three accessions were identified for the yield improvement programme, accessions like Katuli, Kachana and Jugsay of cluster I for days to 50% flowering; Bakiya, Banaskupi and Balchinga of cluster III for number of effective tillers; Koto, Lal deshi and Kolya of cluster IV for plant height; Banda, Balchinga and Bakai of cluster III for panicle length; Kachana, Katuli and Jugsay of cluster I for days to maturity; Balchinga, Bakiya and Banaskupi of cluster III for grain length width ratio; Chattisgarh Zinc Rice 1, Samleshwari and Danteshwari of cluster IV for 100 grain weight; Indira Barani dhan, Indira Aerobic1 and Samleshwari of cluster IV for grain yield per plant to be selected.

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