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Genetic Diversity in Upland Rice Germplasm Accessions (*Oryza sativa* L.) of Chhattisgarh, India

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A B S T R A C T

The present study was undertaken to find out the clustering pattern of 100 rice genotypes for 12 metric traits including five checks. Clustering of genotypes was done by following the method of Non Hierarchical Euclidean cluster analysis. All the genotypes were grouped into eight clusters revealing the presence of considerable amount of genetic diversity in the material for different studied traits. According to the results, Cluster V is having the largest cluster with maximum of 23 genotypes, followed by Cluster I (21 genotypes) and Cluster III (20 genotypes). Cluster VIII is the smallest cluster comprising of only 2 genotypes. On the basis of inter-cluster distance, the most diverse clusters were cluster VIII and IV (7.29), followed by cluster VIII and VI (6.96) which indicated maximum diversity between the genotypes of these clusters. Cluster VIII was characterized by genotypes with early maturity, high tillering capacity, high panicle length, high grain yield, longest grain length and high L/B ratio. Cluster IV was characterized by genotypes having less height and long grains. Cluster VI is represented by genotypes with highest number of filled grains per panicle. The conclusion drawn by the cluster analysis is that high variability was observed in the studied population between the genotypes in different clusters for different characters. The genotypes Banspor and Chingi can be used as potential donors in future hybridization programmes to develop rice variety with good grain yield and quality traits.

Keywords

Cluster analysis, Genetic divergence, Rice germplasm, Non hierarchical euclidean cluster analysis, Rice (*Oryza sativa* L.)

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Introduction

Rice (*Oryza sativa* L.) is one of the most important crops that provide food for more than half of the world population. It is no longer a luxury food but has become the cereal that constitutes a major source of calories for the urban and the rural (Sasaki and Burr, 2000). With an increasing global population, the demand for rice will continue to rise, which raises challenges for the breeding of high-yielding rice cultivars. The continued development and utilization of the genetically diverse rice germplasm resources to constantly expand and enrich the genetic basis of the breeding parents is, therefore, extremely important for the promotion and development of rice breeding and production (Lu, 1998). In crop improvement programme, to increase the productivity breeder needs to maintain a pool of diverse desirable donor parents (Joshi *et al.,* 2013). Genetic diversity plays a key role in selecting the suitable parents for hybridization programme resulting in superior hybrids and desirable transgressive segregants (Rathi *et al.,* 2011). Genetic diversity is pre-requisite for any crop improvement programme as it helps in the development of superior recombinants (Manonmani and Fazlullah Khan, 2003) Genetic divergence among the genotypes plays an important role in selection of parents having wider variability for different characters (Nayak *et al*, 2004). Genetic divergence analysis quantifies the genetical distance among the selected genotypes and reflects the relative contribution of specific traits towards the total divergence (Iftekharuddaula *et al*, 2002). The crosses between parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam, 1981). This study will help in selection of more distantly related parents for crossing programme to develop high yielding rice varieties.

Materials and Methods

The present research work was conducted at Instructional and Research Farm, Department of Genetics and Plant Breeding, Indira Gandhi Agricultural University, Raipur (Chhattisgarh) during *kharif* 2014. The experimental material consisted of 100 upland genotypes collected from different districts of Chhattisgarh including 5 check varieties of rice. Each genotype was grown in single row. Normal agronomic practices were followed throughout the crop period. Five plants from each row were randomly selected and were tagged for recording characters *viz*., Days to 50 per cent flowering, Effective tillers per plant, Plant height (cm), Panicle Length (cm), Filled Grains per panicle, Chaffy Grains per panicle, Total Number of Grains per panicle, 1000 grain weight, Grain yield per plant, Grain Length (mm), Grain Breadht (mm) and Grain Length Breadth Ratio (LB ratio). Panicle and grain characters were recorded on five panicles of selected plants. Cluster analyses for the above characters were done by following Non Hierarchical Euclidean cluster analysis in order to classify the genotypes into different groups based on their similar and dissimilar performance for the traits. Genetic divergence among genotypes was studied through Non Hierarchical Euclidean cluster analysis. (Beale, 1969 and Spark, 1973) and genotypes were grouped into different clusters by Tocher's method (Rao, 1952). Intra and inter cluster distances and mean performance of the clusters for the characters were also computed.

Results and Discussion

Analysis by non-hierarchical Euclidean cluster method grouped 100 rice genotypes into eight distinct clusters (Table 1) revealing the presence of substantial genetic diversity among the genotypes screened. This indicated that materials under study may serve as good source for selecting the diverse parents for hybridization programme for isolating transgressive segregants for grain yield and its attributes. The existence of high degree of genetic divergence in rice has also been reported by Nayak *et al.,* (2004), Suman *et al.,* (2005), Gahalain (2006), Chandra *et al.,* (2007), Shahidullah *et al.,* (2009) and Pratap *et al.,* (2011). Among the eight clusters formed, Cluster V is having the largest cluster with maximum of 23 genotypes, followed by Cluster I (21 genotypes) and Cluster III (20 genotypes). Cluster VIII is the smallest cluster comprising of only 2 genotypes. Average intra and inter cluster distance in studied rice genotypes are presented in Table 2. The highest intra- cluster distance value was found for cluster VIII (3.468), followed by cluster VI (2.730) and II (2.484) and lowest intracluster distance was found in Cluster I. The maximum inter- cluster distance was recorded between Cluster VI and Cluster VIII (6.966), followed by Cluster III and Cluster VIII (6.422) and minimum inter- cluster distance was observed between Cluster I and Cluster III (2.332) as depicted in Table 2. Cluster VIII was characterized by genotypes with early maturity, high tillering capacity, high panicle length, high grain yield, longest grain length and high L/B ratio. Cluster IV was characterized by genotypes with lowest mean plant height having long slender grains. Cluster VI is represented by genotypes with highest number of filled grains per panicle. The conclusion drawn by the cluster analysis is that high variability was observed in the studied population between the genotypes in different clusters for different characters. The Genotypes Banspor and Chingi can be used as potential donors in future hybridization programmes to develop rice variety with good grain yield and quality traits. Based on results, genotypes grouped into different clusters showed more valuable heterotic pool that could be utilized in crossing the genotypes selected from those clusters which have maximum inter- cluster and intra- cluster distance in developing the desirable segregants. Cluster mean for twelve traits is given in Table 3, the perusal of traits showed Cluster I genotypes exhibiting maximum mean for 1000 grain weight, Cluster IV genotypes exhibited maximum mean for grain breadth. Cluster VI genotypes exhibited maximum mean for days to 50% flowering, filled grains per panicle, chaffy grains per panicle and total number of grains per panicle. Cluster VII genotypes exhibited maximum mean for plant height whereas Cluster VIII genotypes exhibited maximum mean for effective tillers per plant, panicle length, grain yield per plant, grain length and grain length breadth ratio. Crossing between genotypes from the cluster III and VIII may produce maximum diversity in the segregating population for panicle length. Similarly crossing between genotypes from the Cluster I and VIII may be useful in developing high yielding cultivars.

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Table.1 Clustering pattern of rice genotypes

Clusters	Name of Genotypes
I	BAKAL, DHABALI BANKO, BARHI, CHANDA, DESHI SAFED, DAGAD DESHI, DOKRA MENCHHA, DUBRAJ, GADUR SELA, GANDHAK, GANDHI, GANDHO, GODA DHAN, POORNIMA, DESHI GURMATIYA, JENJANE, BHATHA JHULI, KANJI, KANJI (KALI), KANTA BUTA, KOLIHA.
II	BAKHALA SAL, BHAYA GODA, DUDH BURSI, DUDHIA DANWAR, GODA DANI, GUJIYA, JAL SAR, KOLIYA, KOLIYARI, KHERA BASANT, LAICHI.
III	BUNDIA BANKO, BUTANI, CHAR KHOTALI, DHAN SAFED, DUDH KARAN, GARANJI, GUDMA (SUKMA), JHILLI, JHINNI, JONDHARI NADGI, KACHANA, KAJAROO, KAKAI, KEKAI, KALASU, KANJI, KANJI (KALI), KARANGA, KARDHANA, KOHI KARI.
IV	BATROO, DESHI NO: 17, JENJANE, JHILLI, KAKERI, KANTA DHAN.
V	BANKO II, BADAL PHOOL, BADAL PHOOL, BARHI, BADI BARIK, BASA BHOG, BENISAR (HALKA), BEWARA, BUDALI, BUTABARI, CHHOTA KABRI, CHIGGI, DESI, DAGAD DESHI, DUDHYA POTIYA, BAKAI GODA, DANI GODA, NAGPURI GURMATIYA, HARDI GUDI, KAKERI, KARDHANA, KARAHANI, LAJI.
VI	CHHOTA KABRI, DESHI LAL, DAGAD DESHI , GURMATIYA, JOGI BHOG, KARI KHUJI, KOLIYARI, KUWLARI, KUDESAR.
VII	BANSPOR (LOCAL), BHAYA, BOHITA, DESHI LAL DHAN, KARI, KOSAWARI, KOTO, LAL BHADAINU.
VIII	BANSPOR, CHINGI.

Table.2 Average intra and inter cluster distance in rice genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**1.922**	3.776	2.332	4.998	2.974	5.095	3.753	6.028
II		**2.484**	5.019	5.541	3.451	3.278	4.082	5.923
III			**2.294**	3.896	3.18	6.292	4.663	6.422
IV				**2.400**	2.898	5.459	4.775	7.29
V					**1.980**	3.688	2.915	5.923
VI						**2.730**	4.283	6.966
VII							**2.420**	4.726
VIII								**3.468**

*****Diagonal values in bold are intracluster

Table.3 Cluster means for twelve characters in rice genotypes.

Clusters	Days to 50% flowering	Effective Tillers per plant	Plant height (cm)	Panicle Length (cm)	Filled Grains Per panicle	Chaffy Grains Per panicle	Total Number of Grain Per panicle	Grain Yield /Plant (gms)	1000 Grain Weight (gms)	Grain Length (GrL) mm	Grain Breadht (GrW) mm	Grain Length Breadth Ratio (L/B ratio)
I	85.48	8.69	132.74	23.17	80.80*	14.96	95.74	14.18*	2.74**	8.70	2.70	3.23
II	86.64	9.06	141.39	24.91	119.55	20.06	139.61	14.34	1.93*	8.31	2.24*	3.72
III	82.55	9.63	120.25	21.16*	81.56	12.33*	93.87*	15.18	2.66	8.07	2.89	2.80
IV	84.50	9.77	118.72*	22.72	142.59	22.16	164.75	20.8	2.27	7.11*	3.03**	2.34*
V	84.65	8.58	142.84	24.02	129.68	18.26	145.64	18.72	2.44	7.86	2.74	2.87
VI	87.89**	7.00*	150.66	25.74	161.95**	36.70**	198.65**	17.00	2.16	8.51	2.48	3.44
VII	86.88	11.17	155.12**	25.58	119.97	20.04	140.01	25.8	2.58	8.68	2.73	3.19
VIII	76.5*	12.99**	134.16	27.00**	116.97	15.49	132.47	30.44**	2.47	9.36**	2.41	3.87**

Note: * indicate lowest and ** indicate highest value.

The conclusion drawn by the cluster analysis is that high variability was observed in the studied population between the genotypes in different clusters for different characters. The genotypes Banspor and Chingi can be used as potential donors in future hybridization programmes to develop rice variety with good grain yield and quality traits.

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