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Studies of genetic diversity analysis in rice (*Oryza sativa* L.) genotypes for yield and yield contributing characters

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Abstract

Rice (*Oryza sativa* L.), an autogamous crop, is the staple food of most of the people of South-Eastern Asia. Around 90% of all rice grown in the world is produced and consumed in the Asian region specifically China followed by India. Hundred genotypes (indigenous collection) from NBPGR with four checks were evaluated at N. E. Borlaug Crop Research Centre of G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India, during kharif season, 2015-17. Analysis of variance indicated adequate genetic variability among the experimental materials. Based on Hierarchical cluster analysis, the 104 genotypes including check were grouped into 8 clusters. The maximum numbers of genotypes (44) were grouped in Cluster III and minimum (1) in Clusters I and VIII. The maximum divergence was observed between Clusters I and VII (415.80) and least divergence was observed between Clusters IV and V (90.23). Cluster I have most desirable genotypes as it exhibited highest cluster mean values for majority of the characters under study. Based on inter-cluster distance, cluster mean values and per se performance, the potential parental combinations that could be considered for enhancing the overall yield levels in rice were, IC75747, IC75738, IC75843, IC75968, IC75828, IC75811, IC75839, IC458780.

Keywords: Genetic diversity, rice, cluster analysis

Introduction

Rice (*Oryza sativa* L.) is a cleistogamous, C_3 and self-pollinated crop. It belongs to Oryza Genus (22 wild species and 2 cultivated species) and Poaceae family. Rice is the most essential food of more than 60% of the world's population. It is expected to world population reach eight billion by 2030 and rice production must increase by 50 per cent to meet the growing demand (Khush and Brar 2002) [9]. It is mainly used as a major source of human food besides animal feed, production of alcoholic beverages like wine, rice bran oil, fuel and manufacture of insulation materials (Chakravarthi and Naravaneni, 2006). Yield is the complex trait which is associated with different yield contributing traits. Genetic diversity is an important tool for a crop improvement programme, as it helps in the development of superior recombinants (Manonmani and Khan, 2003) [11]. Genetic divergence among the genotypes plays an important role in selection of parents having wider variability for different traits (Nayak *et al.*, 2004) [12]. Genetic diversity in crop plants is essential to withstand level of high productivity (Tripathi *et al.*, 2013) [13]. The availability of morphogenetic variation in agronomic characters of a crop would be of considerable importance in determining the best method to improve the yield of that crop.

Material and methods

A total of hundred rice germplasm line and four checks Jaya, Swarna, Pusa Basmati 1 and IR 64 consisted of experiment materials for the investigation (Table 1). The genotypes were evaluated in augmented design –II (Federer, 1956 & 1977). Hundred test entries were planted once without replication in five blocks, each block had twenty test entries and the five checks were randomized within the block and replicated across the five blocks. Each plot consists of 2 rows of 2 m length (plot size 0.8 m^2) with between rows and within rows spacing of 20 cm and 15 cm, respectively.

The observations were recorded on 15 morphological characters Days to 50% flowering, Plant height (cm), Tiller number per plant, Panicle length (cm), Number of grains per panicle, Filled grains per panicle, Unfilled grains per panicle, 1000 grain weight (g), Grain weight per panicle (g), Grain yield per plant (g), Grain yield per plot (g), Grain yield per ha (q), Kernel length (mm), Kernel breadth (mm), LB ratio on plot basis as well as based on five randomly chosen competitive plants from each plot.

Statistical analysis

The genetic divergence was estimated using the Hierarchical cluster analysis which was performed on the basis of Euclidean distance between the genotypes. The Euclidean distance between ith and kth accession was calculated by $D_{ik} = \left[E_{j=1}^{n}\left(A_{ij} - A_{kj}\right)^2\right]^{1/2}$ Where, D_{ik} is Euclidean distance between ith and kth accession, A_{ij} is performance of ith accession for jth character, A_{kj} is performance of kth accession for jthcharacter, m is number of accessions (I or k = 1, 2… m), n is number of characters (j =1, 2…n).

Table 1: List of the rice genotypes/codes

S. No.	Genotypes identity code No. (IC No.)	S. No	Genotypes identity code No. (IC No.)	S. No.	Genotypes identity Code No. (IC No.)	S. No	Genotypes identity code No. (IC No.)	S. No.	Genotypes identity Code No. (IC No.)	S. No	Genotypes identity code No. (IC No.)	S. No.	Genotypes identity Code No. (IC No.)
1	459770X	16	75741	31	75771	46	75829	61	75844	76	75861	92	75982
2	458768	17	75747	32	75773	47	75846	62	75864	77	75891	93	75957
3	454588	18	75737	33	75783	48	75819	63	75865	78	75894	94	75969
4	449549X	19	75756	34	755785	49	75830	64	75872	79	75896	95	75970
5	449560X	20	75782	35	75790	50	75843	65	7574	80	75889	96	75955
6	454612	21	75799	36	75793	51	75845	66	75879	81	75913	97	75958
7	458780	22	75789	37	75795	52	75847	67	75882	82	75919	98	75960
8	75735	23	75791	38	75797	53	75839	68	75877	83	75920	99	75965
9	75748	24	75800	39	75798	54	75822	69	75855	84	75927	100	75966
10	75754	25	75801	40	75803	55	7525	70	75856	85	75930		
11	75757	26	75802	41	75804	56	75832	71	75857	86	75956		
12	75761	27	75767	42	75786	57	75811	72	75859	87	75968		
13	75732	28	75768	43	75772	58	75821	73	75860	88	75972		
14	75731	29	75769	44	75775	59	75828	74	75849	89	75961		
15	75738	30	75770	45	75779	60	75834	75	75851	90	75963		

Results and Discussion

Estimation of Genetic Divergence through Hierarchical Cluster Analysis (HCA)

The adjusted mean of genotypes were subjected to Hierarchical Cluster Analysis (HCA) and the genotypes were grouped based on 40% dissimilarity level and same study by (Ward Jr, J. H. (1963) [14]. Hundred test genotypes and four checks were grouped in 8 clusters based on hierarchical cluster analysis. Cluster III had the highest number of genotypes (44) followed by Cluster V with 37 accessions, Cluster VII with 8 accessions, cluster II with 6 accessions, cluster VI with 2 accessions, cluster I and VIII with only1 accessions per genotype.

Inter and intra-cluster distance

Highest intra-cluster distance was recorded for cluster III (72.11) followed by cluster VII (58.32) and lowest for cluster I and cluster VIII (0.0). The inter-cluster distance was highest between cluster I and cluster VII (416.80) followed by cluster I and cluster VIII (395.78) on the other hand lowest inter-cluster distance was estimated between cluster IV and cluster V (90.23) (Table 2). Highest inter-cluster distance between cluster I and cluster VII revealed that these two clusters and genotypes of these clusters are distinctly related to each other. Diverse clusters would generate a high variability to scope for effective selection in the segregating generations for the development of high yielding rice cultivars. For grain yield per ha, the accessions IC75747, IC75738, IC75843, IC75968, IC75828, IC75811, and IC75839 have been identified as promising donors. One Accession IC75828 was identified to be promising donor for characters number of grains per panicle, grain yield per plant, grain yield per plot, grain yield per ha. These yield contributing characters possessing accessions can be used as donors in yield improvement. Donors for earliness in flowering were identified, IC454588, IC458768, IC75821 and IC459770X.Whereas accessions IC75839, IC75737, IC75843, IC75856 identified as donors for more tillers per plant (Table 3). Therefore these genotypes could be used to breed short duration and high yielding cultivars. Accessions IC458780, IC75828 had significantly higher grain yield per plant than best check (Jaya 51.76g). Accession IC458780 showed significant grain weight per panicle than best check [Jaya (2.34g)] accession IC449549X had significantly plant height, filled grains per panicle than best check Jaya. Accession IC449549X also had number of grains per panicle which is superior to Pusa Basmati 1. No accession showed more kernel length and LB ratio than check. There was more number of Accessions for more plant height and only one had dwarf plant height. The accession IC75799 had dwarf stature than superior check Swarna (Table 3).

Table 2: Intra (diagonal) and inter -cluster (Off-diagonal) distances based on Hierarchical Cluster Analysis of rice germplasm:

Cluster	I	II	III	IV	V	VI	VII	VIII
I	0.0	128.16	234.00	306.30	335.83	367.12	416.80	395.78
II		55.37	147.08	224.77	249.98	302.08	333.20	306.55
III			72.11	110.98	125.43	183.28	204.35	183.41
IV				30.75	90.23	137.37	145.87	101.53
V					54.80	103.36	101.42	109.29
VI						17.27	100.27	151.41
VII							58.32	107.22
VIII								0.0

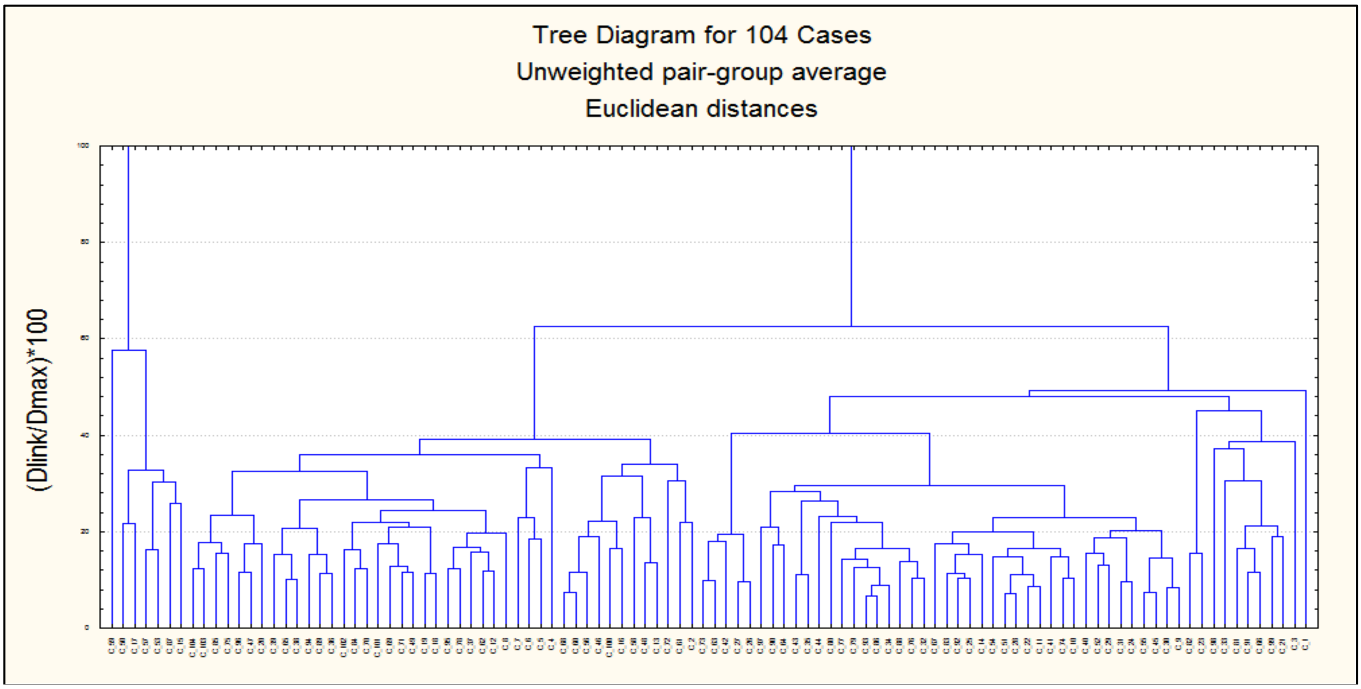

Fig 1: Clusters of 100 genotypes and 4 checks using Hierarchical cluster analysis method

Conclusion

In the context of all the above observations, it can be summarized that adequate amounts of genetic diversity for yield and its contributing characters existed among the experimental materials (100 genotypes + 4checks) taken up for the present study. High inter-cluster distance between certain clusters obtained through genetic diversity analysis indicated that hybridization between superior genotypes obtained from these clusters would be highly promising to bring about yield improvement in rice.

Table 3: Potential donor identified for different characters

S. No.	Characters		Donor
1.	Days to 50% flowering	Early	IC454588, IC458768, IC75821, IC459770X,
		Late	IC75965, IC75790, IC75793, IC75798, IC75963, IC75961.
2.	Plant height (cm)	Dwarf	IC75799.
		Tall	IC454612, IC459770X, IC458780, IC449549X, IC75732.
3.	Tillers/plant		IC75839, IC75737, IC75843, IC75856.
4.	Panicle length (cm)		IC75801, IC75800, IC75849, IC75894.
5.	Number of grains/ Panicle		IC449549X, IC75865, IC75828, IC 75860, IC75889
6.	Filled grains/panicle		IC449549X.
7.	Unfilled grains/panicle	Low	IC454588, IC459770X, IC458768, IC75802.
8.	1000 grain weight (g)		IC454612, IC75956.
9.	Kernel length (mm)		
10.	Kernel breadth (mm)	Low	IC75773, IC75829, IC75811.
		high	IC75958, IC75822, IC75978.
11.	L B ratio		IC75799, IC75847, IC75859, IC75851
12.	Grain weight/ panicle (g)		IC458780.
13.	Grain yield/plant (g)		IC458780, IC75828.
14.	Grain yield/plot (g)		IC75747, IC75738, IC75843, IC75968, IC75828, IC75839.
15.	Grain yield/ha (q)		IC75747, IC75738, IC75843, IC75968, IC75828, IC75811, IC75839.

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