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Estimates of Genetic Divergence in Advance Breeding Lines of Rice (*Oryza sativa* L.)

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Abstract The study was carried out with 42 genotypes of rice representing diversity for yield contributing and quality traits in advance breeding lines of rice including 3 check varieties. Nature and magnitude of genetic divergence was assessed using Mahalanobis D^2 statistics through which the 42 genotypes were grouped into seven clusters. Cluster IV having 17 genotypes was largest, whereas cluster I and VII were found monogenotypic clusters. The maximum inter-cluster distance was found between cluster II and VII (98.237) indicating suitability of genotypes from these clusters for hybridization. The parental lines selected from cluster VI (UPR 3837-2-2-1-3, UPRI 2013-10, UPR 3912-21-2-1, UPR 3926-12-1-1, UPR 3837-7-2-1-1, UPRI 2013-4, Pant Dhan-4) for panicle length, number of panicles per plant and grain yield per plot, from cluster VII (UPR 3929-8-1-1) for number of grains per panicle, filled grains per panicle, grain length, alkali spreading value and amylose content could be used in hybridization program to obtain desirable segregants for yield and quality traits.

Keywords Divergence, Tochers method, Cluster, Cluster distance, Hybridization.

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Introduction

Rice (*Oryza sativa* L.) (2n=24) belonging to family Poaceae deserves a special status among cereals as worlds most important wetland crop. There are two cultivated species namely, *Oryza sativa* and *O. glaberrima*, while other twenty-two species are wild.

About 20% of the total calorie supply worldwide comes from rice. More than 90% rice of world is produced and consumed in South and South East Asia, where approximately 60% of the population of the world is living. In India, it is staple food for more than 65% of the people. It provides about 29.4% of total calories/capita/day in Asian countries. In India it is grown on 43.4 million hectares of land and producing approximately 106.3 million tons rice grain with an average productivity of 2.42 tons per hectare [1]. The demand of rice is continuously increasing due to unabated growth of population. To cope up with the ever increasing population and self-sufficiency in rice production as well as for maintaining price stability there is need for new genes and improved genetic recombinants. Approximately 150 million tons of rice is needed by 2030 to feed 1.378 billion Indian people and ~850 million tons to feed 5 billion rice consumers in the world (at least 1.1% yield increase is required every year) [2]. Biological diversity and genetic resources have great role to play in achieving sustainable agricultural development and the ecological health of the earth. Plant breeding program with diverse genetic base could sustain a high level of crop yield. The narrow genetic base of semi-dwarf varieties is likely to make them vulnerable to different biotic

Table 1. Clustering patterns of 42 genotypes of rice on the basis of D^2 values. Through the cluster diagram D^2 values and D values are extracted as shown in Table 2.

Cluster number	Genotypes included	Number of genotypes
I	UPR 3907–2–2–1	1
II	UPR 3907–20–2–1, UPR 3943–8–1–1, UPR 3948–18–1–1	3
III	UPR 3919–6–2–1, UPR 3926–6–1–1, UPR 3930–18–1–1, UPR 3947–20–1–1, UPR 3806–3–1–1–1, UPR 3837–7–2–1–6, UPRI 2013–5	7
IV	UPR 3931–8–1–1, UPR 3947–23–2–2, UPR 3947–23–2–3, UPR 3837–2–2–1–2, UPR 3841–1–1–1–1, UPRI 2013–1, UPRI 2013–6, UPR 3906–18–2–1, UPR 3923–2–1–1–2, UPR 3926–3–1–1–1, UPR 3838–6–1–1–1, UPR 3860–6–1–1–1, UPR 3876–5–1–1–1, UPRI 2013–3, UPRI 2013–14, UPRI 2013–16, Pant Dhan–12	17
V	UPR 3819–9–1–1–1, UPR 3871–8–1–2–2, UPR 3911–4–1–2, UPR 3920–2–1–1–1, UPR 3879–4–2–1–1, Govind	6
VI	UPR 3836–2–2–1–3, UPRI 2013–10, UPR 3912–21–2–1, UPR 3926–12–1–1, UPR 3837–7–2–1–1, UPRI 2013–4, Pant Dhan–4	7
VII	UPR 3929–8–1–1	1

and abiotic stresses. Therefore, to meet the ever-increasing demand of food grains, for higher production emphasis should be given to the genetic improvement of the existing varieties of rice. Genetic diversity and the diverse gene pools are the basis of plant breeding. In addition to new gene pool providing building blocks for further improvement, genetic diversity is essential if higher level of productivity is to be achieved and sustained during the process of varietal development. Genetic divergence is an outcome of several factors such as exchange of breeding material, genetic drift, natural variation and artificial selection other than ecological and geographical diversification. Any crop improvement program should aim at broadening the genetic base of the breeding stock. Wide genetic resources may be required to either increase the gene pool for germplasm improvement or for the development of new cultivated varieties [3]. Genetic divergence among parents is of paramount importance in selecting parental genotypes for crossing programs. The more diverse the parents, greater the chances of achieving heterotic progeny

Table 2. Inter and intra-clusters (Diagonal) average D^2 values and genetic distances (D values). Bold values (diagonal value) are intra-cluster distance and data in parentheses are D–values.

Clusters	I	II	III	IV	V	VI	VII
I	**0.000**	23.043	34.132	44.369	32.403	62.304	85.878
	(0.000)	(4.800)	(5.842)	(6.661)	(5.692)	(7.893)	(9.267)
II	23.043	**14.842**	52.571	60.426	26.364	80.108	98.237
	(4.800)	**(3.853)**	(7.250)	(7.773)	(5.135)	(8.950)	(9.912)
III	34.132	52.571	**22.779**	15.057	46.111	30.382	60.85
	(5.842)	(7.250)	**(4.773)**	(3.880)	(6.791)	(5.512)	(7.800)
IV	44.369	60.426	15.057	**29.568**	50.589	20.828	53.377
	(6.661)	(7.773)	(3.880)	**(5.438)**	(7.113)	(4.564)	(7.306)
V	32.403	26.364	46.111	50.589	**39.241**	70.750	90.154
	(5.692)	(5.135)	(6.791)	(7.113)	**(6.264)**	(8.412)	(9.495)
VI	62.304	80.108	30.382	20.828	70.750	**51.185**	45.098
	(7.893)	(8.950)	(5.512)	(4.564)	(8.412)	**(7.154)**	(6.716)
VII	85.878	98.237	60.851	53.377	90.154	45.098	**0.000**
	(9.267)	(9.912)	(7.800)	(7.306)	(9.495)	(6.716)	**(0.000)**

Table 3. Cluster mean values for different characters in advance breeding lines of rice.

Characters Clusters	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle no per plant	Grains no per panicle	Filled grains per panicle	Grain length (mm)	Grain breadth (mm)
I	106.667	87.667	28.700	11.000	184.333	158.333	4.800	2.500
II	101.667	90.378	28.767	12.867	170.000	145.000	5.967	1.822
III	103.810	88.576	27.214	12.476	211.286	177.190	6.038	1.976
IV	101.980	89.439	29.873	11.761	212.275	187.196	6.069	1.896
V	90.944	80.933	24.439	13.167	179.611	153.556	6.000	1.872
VI	103.571	91.976	31.100	13.743	225.286	202.476	5.752	1.933
VII	89.667	132.000	30.833	13.600	227.333	210.000	6.233	2.267

Table 3. Continued.

Clusters	L/B ratio	1000 grain weight (gm)	Alkali spreading value	Content of amylose (%)	Gel-consistency	Days to maturity	Grain yield per plot (kg)
I	1.919	24.950	4.810	20.677	57.667	141.667	3.527
II	3.307	28.901	4.225	21.084	66.111	137.111	3.463
III	3.084	26.471	4.796	21.010	63.714	136.429	3.525
IV	3.234	26.264	5.554	20.592	74.216	134.745	3.345
V	3.239	25.755	5.537	20.351	76.333	123.343	3.393
VI	3.043	24.802	5.222	22.024	71.143	136.333	3.809
VII	2.763	26.077	6.555	22.150	73.333	123.333	3.687

and a broad spectrum variability in segregating generations. Thus assessment of genetic diversity for different traits in the germplasm is essential for the identification of suitable parents in the hybridization program [4].

Materials and Methods

The present investigation on estimates of genetic divergence in advance breeding lines of rice (*Oryza sativa* L.) was carried out during *kharif* season 2014 at the NE Borlaug, Crop Research Center (CRC) of GB Pant University of Agriculture and Technology, Pantnagar. Each genotype considered as one treatment, the experimental material was planted in randomized complete block design with three replications in main plots in the month of June, 2014. Each plot had 5 m × 1.6 m (8m^2) area and 45 cm apart. Twenty seven days old seedlings raised in nursery were transplanted at spacing of 20 cm× 15 cm. The recommended package of agronomic practice was followed to raise a healthy crop.

The observations were recorded on five randomly selected competitive plants from each plot in all replications for plant height, panicle length, number of panicles per plant, number of grains per panicle, filled grains per panicle, whereas, on the whole plot basis the observations were recorded for days to 50% flowering, days to maturity and yield per plot and on the composite sample basis 1,000 grain weight and their means were used for the statistical analysis. A series of quality test also conducted in Rice Breeding Laboratory of Department of Genetics and Plant Breeding, College of Agriculture.

Results and Discussion

The analysis of variance revealed highly significant differences among the 42 genotypes for fifteen characters studied. This indicated significant amount of variability among the genotype for the characters studied. The genetic divergence was estimated by Mahalanobiss D^2 statistics as described by Rao [5]. Based on the D^2 values, the constellation of genotypes into clusters was done following Tochers method. All the 42 genotypes were grouped into seven clusters. The clustering pattern of these genotypes is given in Table 1.

Inter and intra-cluster average D^2 values

The inter cluster average D^2 value (98.237) was maximum between cluster VII with one genotype and cluster II with three genotypes followed by D^2 value (90.154) between VII with one genotype and cluster V with six genotypes and D^2 value (85.878) between cluster VII and I both contain single genotype (Table 2), indicating that , these clusters contained genetically more diverse advance breeding lines. Therefore, hybridization between the genotypes should be done from those clusters having more inter cluster distance to achieve maximum variability and hybrid vigor effects. Hence, the highest divergence between above clusters may be used in heterosis as well as in recombination breeding to get more number of desired segregants and inter varietal hybridization [6]. The greater the distance between two clusters, wider the expected genetic distance between their genotypes. The genetic distance between the parents largely governs the variability spectrum generated in the segregating generation and also the F_1 heterosis. Similar suggestions were given by Chauhan and Singh [7]. Therefore, the crosses should be made between the genotypes of clusters separated by large inter-cluster distances [8, 9].

The minimum inter cluster average D^2 (15.057) value was observed between cluster IV with seventeen genotypes and cluster III with seven. It indicates that genotypes of these clusters are very close to each other and providing a relatively narrow range of diversity.

Intra cluster average D^2 values ranged from 0.0 to 51.185. It was maximum in cluster VI (51.185) with seven genotypes followed by cluster V (39.241) with six genotypes, cluster IV (29.568) with seventeen genotypes, cluster III (22.043) with seven genotypes and cluster II (14.842) with three genotypes. The lowest intra-cluster D^2 was observed (0.0) for two mono genotypic cluster I and VII, due to presence of only one genotype in each cluster.

Cluster mean values

Cluster mean values for fifteen characters are presented in Table 3. The cluster mean value analysis of different characters indicated considerable differences between the clusters mean for all the characters studied. Hence selection within these cluster may be carried out based on the highest mean for the desirable trait, which could be applied for significant improvement through inter varietal hybridization. Thus, these genotypes hold great promise as parents for obtaining promising elite lines through hybridization and to create further variability for these characters [10].

References

1. Anonymous (2013-2014) Economic survey. Min Finance, GOI, New Delhi.
2. Goyal SK, Singh JP (2002) Demand versus supply of food grains in India: Implications to food security. 13th Int Farm Mgmt Cong. 7—12 Jul 2002 Wageningen, The Netherlands, pp 20.
3. Subudhi HN, Meher J, Bose LK, Das Sanjukta (2006) Genetic diversity studies of promising rice varieties of eastern India based on quality characters. Oryza 46 : 224—227.
4. Sharma V, Panwar IS (2007) Genetic divergence for yield, its component and quality traits in bread wheat. Haryana Agric Univ J Res 37 : 27—31.
5. Rao CR (1952) Advance statistical methods in biometrical research. 2nd edn. John Willey & Sons, New York.
6. Joshi MA, Singh Pritpal, Sarao NK, Sharma RC, Bharaj TS (2008) Genetic diversity among the rice varieties cultivated in Punjab. Oryza 45 : 277—279.
7. Chauhan JS, Singh KH (2003) Genetic divergence analysis using quality traits in upland rice (*Oryza sativa* L.). Ann Agric Res 24 : 673—675.
8. Sandhyakishore N, Babu VR, Ansari NA, Chandran R (2007) Genetic divergence analysis using yield and quality traits in rice (*Oryza sativa* L.). Crop Improve 34 : 12—15.
9. Chandra BS, Reddy TD, Ansari NA (2007) Genetic divergence in rice (*Oryza sativa* L.). Res Crops 8 : 600—603.
10. Mishra LK, Pravin J (2004) Variability and genetic diversity in rice (*Oryza sativa* L.). Mysore J Agric Sci 38 : 367—375.