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Genetic Diversity Analysis of Rice Germplasm Lines for Yield Attributing Traits

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Abstract: **Genetic divergence is an efficient tool for the selection of parents used in hybridization programme. In the present study, forty rice genotypes were raised at Experimental Field of Department of Genetics and Plant Breeding, SHIATS, during *Kharif* 2013 for identify diverse genotypes using D^2 analysis. The forty genotypes were grouped into seven clusters based on Torcher cluster analysis with cluster III containing the maximum of 10 genotypes followed by 9 genotypes in cluster II, 7 genotypes in cluster I, 6 genotypes in cluster IV, 4 genotypes in cluster VI and 2 genotypes each in cluster V & VII. The highest inter cluster distance was observed between cluster IV and VII followed by cluster III and VII, cluster III and VI these lines may be utilized in further breeding programme for the exploitation of hybrid vigour. The intra cluster distance was maximum in cluster III followed by II and I indicate hybridization involving genotypes within the same clusters may result in good cross combinations. Among the thirteen traits studied, maximum contribution was made by number of spikelets per panicles (38.08%) followed by grain yield (23.08%) plant height (13.59%) and flag leaf length (13.21%). Therefore, these characters may be given importance during hybridization programme.**

Keywords: **Rice, genetic diversity, cluster.**

1. INTRODUCTION

Rice (*Oryza sativa* L.) is the staple food for 2.5 billion people and growing rice is the largest single use of land for producing food, covering nine percent of the earth's arable land **Khan *et al.*, (2009).** Rice is the predominant staple food for 17 countries in Asia and the Pacific, nine countries in Africa. Rice provides 20 per cent of the world's dietary energy supply, while wheat supplies 19 per cent and maize 5 per cent. Among the rice growing countries, India has the largest area (43.97 m ha) followed by China and Indonesia. In India production is of 104.70 M tons and productivity of 2.17 t/ha. It is estimated that the demand for rice will be 121.2 million tons by the year 2030, 129.6 million tons by 2040 and 137.3 million tons by 2050 for internal consumption **Directorate of Rice Research Annual Report (2013-14**). In order to meet the food requirement of growing population, development of high yielding varieties is essential. The success of any breeding programme depends on the selection of parents for hybridization. The parents involved in the development of varieties should be divergent. The germplasm provides immense scope for wide variability.

Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for breeding programme **Vivekanandan and Subramanian, (1993).** The D^2 technique is based on multivariate analysis developed by **Mahalanobis (1936)** had been found to be a potent tool in quantifying the degree of divergence in germplasm. Success in recombination breeding depends on the suitable exploitation of genotypes as parents for obtaining high heterotic crosses and transgressive segregants. For this, the presence of genetic variability in a base population is essential so research should be done for creating of variation. The crosses between parents with maximum genetic divergence are generally the most responsive for genetic improvement **(Arunachalam, 1981).** Recognizing the importance of genetic variability in plant breeding experiments, the main objective of present research work was to assess the genetic diversity for yield and yield contributing character.

2. MATERIALS AND METHODS

The experiment consisted of 40 high yielding rice genotype collected from Department of Genetics & Plant breeding SHIATS, Allahabad represented at Field Experimental Centre of the Department of Genetic and Plant Breeding. The seedlings were transplanted into the main field at the rate of one seedling per plant, after 25 days, with a spacing of 20cm x15cm. The experiment was arranged in a randomized block design with three replications, in four row plots of 3m length. The recommended agronomical practices and plant protection measures were followed to ensure a normal crop. Observations were recorded on five randomly selected plants in each replication from the two centre rows. Thirteen traits observations were recorded and the data was subjected to statistical analysis. The genetic distance between the genotypes was worked out using **Mahalanobis D^2 analysis (1936)** and grouping of varieties into clusters was done following the Tochers method as detailed by **Rao, 1952**.

3. RESULTS & DISCUSSION

The use of Mahalanobis D^2 statistics for estimating genetic divergence has been emphasized by many workers **(Roy and Ponwar, 1993; Ramya and Senthil Kumar, 2008).** Hence, based on relative magnitude of D^2 statistics the 40 genotypes of rice were grouped into 7 clusters as shown in Table 1. Maximum number of genotypes (10) were included in cluster III followed by 9 genotypes in cluster II, 7 genotypes in cluster I, 6 genotypes in cluster IV, 4 genotypes in cluster VI and 2 genotypes each in cluster V & VII. Genotypes from the same centre of origin were distributed in different clusters which may be due to differential adaptation to varied agro-ecosystems as explained by **Sabesan *et al.* (2009) and Banumathy *et al.* (2010).** The intra and inter cluster average distances among 7 clusters were variable as indicated in table 2. The highest intra-cluster distance was recorded for cluster III (107.03) followed by cluster II (102.80) and cluster I (62.82) indicating genetic diversity among the genotypes belonging to these clusters. Highest inter-cluster distance was observed between clusters IV and VII (995.92) suggesting wide diversity between these clusters followed by cluster III and VII (834.19), cluster IV and VI (550.17), cluster III and VI (529.50). Therefore, genotype belonging to these clusters may be used in hybridization programme for the improvement of rice. Crosses involving parents belonging to the most divergent clusters would be expected to manifest maximum heterosis and wide variability of genetic architecture **(Souroush *et al.*, 2004).** The diversity was also supported by the appreciable amount of variation among the cluster means for different characters (Table 5). Cluster II and III showed maximum cluster mean for plant height and days to maturity respectively. Cluster IV showed the maximum cluster means for tillers/plant, panicles/ plant and flag leaf length. For cluster V recorded the maximum cluster mean values for biological yield, test weight and economical yield and cluster VI showed maximum values for days to 50% flowering and flag leaf width. Maximum values for number of spikelets/panicle and harvest index were recorded by cluster VII. Thus, these genotypes hold great promise as parents for obtaining promising elite lines through hybridization and to create further variability for these characters **(Mishra and Pravin, 2004).** The contribution of individual trait to the divergence among genotypes is presented in Table 3. Number of spikelets per panicle contributed maximum towards genetic divergence (38.08%) followed by plant height (13.59%) and flag leaf length (13.21%). Remaining traits had very little or no contribution towards genetic divergence and hence, they were of less importance. Since varieties with narrow genetic base are increasingly vulnerable to diseases and adverse climatic changes, availability of the genetically diverse genotypes for hybridization programme become more important. Since number of spikelets per panicle contributed maximum towards the genetic divergence, we may go for direct selection of this trait for diversity purpose.

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APPENDIX – A

List Of Tables:

Table 1: Distribution of 40 genotypes of rice into different clusters

S. No.	Cluster Numbers	Number of genotypes	Genotypes included
1	I	7	IR 09A104, PEPE, AAIR-203, IR-098228, IR-81852-15-2-2-3, IR-72860-74-1-2-1, IR-82355-5-2-6
2	II	9	IR-8070-7-69-1-3-3, IR-78091-6-3-1-1, IR-10A125, IR-10A142, IR-02A149, IR-05N412, KARJAT-7, NSIC RC-160, IR-06N211
3	III	10	AAIR 205, IR-79478-15-2-2-2, VK-18, IR -79228-9-2-3-1, CHATTE-4, IR-78119-24-1-2-2-2, IR- -82786-43-3-2-1, RP-4075-345-132-27, MITHILA, MR-258
4	IV	6	AAIR-102, IR 09A102, IR -77186-148-3-4-3, CT-15675-7-1-4-3-1-M, IR-70454-144-1-1-3-2, IR-73888-1-4-5
5	V	2	IR-82019-54-1-2, NDR-359 (Check-2)
6	VI	4	IR-09N127, IR-09N522, IR-06M134, IR-64 (Check-1)
7	VII	2	OM-6070, NSIC RC-154

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Table 2: Intra (diagonal) and inter cluster average distance (D^2) in rice genotypes

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster
1 Cluster	**62.802**	115.417	158.607	300.322	173.613	261.791	485.790
2 Cluster		**102.801**	232.994	386.403	219.424	275.910	364.813
3 Cluster			**107.030**	173.608	286.304	529.506	834.197
4 Cluster				**0.000**	245.919	550.171	995.923
5 Cluster					**0.000**	175.584	483.100
6 Cluster						**0.000**	242.520
7 Cluster							**0.000**

Table 3: Mean values of seven clusters for 13 morphological characters in 40 rice genotypes and contribution %

	Days to 50 % Flowering	Plant Height (cm)	Flag Leaf Length (cm)	Flag Leaf Width (cm)	Tillers / plant	Panicles/ plant	Panicle Length (cm)	Number of Spikelets/ Panicle	Days to Maturity	Biological Yields (g)	Harvest Index %	Test Weight	Economical Yields (g)
I Cluster	90.55	107.11	32.86	1.39	18.39	16.49	25.88	171.34	120.69	68.67	41.57	22.46	28.58
II Cluster	89.73	123.63	36.80	1.50	18.05	16.22	27.03	193.48	120.26	77.50	46.54	20.03	35.60
II Cluster	86.58	106.48	41.13	1.26	18.22	16.07	30.12	128.05	116.54	58.91	52.08	21.73	30.38
IV Cluster	90.66	88.25	59.71	1.38	20.26	18.13	30.10	131.73	119.3	44.40	54.34	22.86	24.13
V Cluster	88.00	94.02	47.88	1.38	16.93	15.66	27.62	206.86	118.66	90.76	49.12	28.23	44.56
VI Cluster	100.33	100.66	37.55	1.93	15.66	13.00	30.58	236.13	130.33	55.97	54.28	25.90	29.80
VII Cluster	91.33	118.32	28.10	1.72	15.26	12.86	21.93	272.13	130.33	58.06	78.13	17.63	44.33
Contribution%	0.77	13.59	13.21	2.05	0.13	0.00	2.44	38.08	2.18	2.44	0.90	1.15	23.08