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RESEARCH ARTICLE

GENETIC DIVERGENCE STUDIES FOR YIELD AND YIELD COMPONENTS IN RICE (*ORYZA SATIVA* L.)

Nutan A. Ramteke, J.P. Devmore*, P.B. Vanave, T.J. Bedse, M.P. Gawai and B.D. Waghmode

Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth
Regional Agricultural Research Station, Karjat – 410201, Dist. Raigad. M.S.
Email: jalinder443@gmail.com

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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 Regional Agricultural Research Station, Karjat during *Kharif*, 2020 to identify diverse genotypes. They were evaluated for fifteen yield and yield attributing characters using D^2 analysis, to study the diversity pattern among the genotypes. Based on the analysis, the genotypes were grouped into 6 clusters. Maximum number of genotypes i.e. 33 and 11 were grouped under cluster I and II, respectively and while clusters III, IV, V, VI were solitary. Maximum inter cluster D^2 value was observed between cluster IV and VI (D= 22.174) followed by cluster V and VI (D = 22.138), cluster II and V (D= 22.066), cluster II and III (D=21.455), cluster III and VI (D=19.528), cluster II and VI (D =17.256) and cluster I and VI (D = 17.217). The greater the distance between two clusters, the wider the genetic diversity among the genotypes of those clusters. The intra cluster distance was maximum in cluster II (D=9.890) followed by cluster I (D=8.839). The cluster III, IV, V and VI recorded no intra cluster distance being solitary.

Keywords: Cluster, Genetic divergence, Genotypes, Rice

INTRODUCTION

The slogan 'Rice is life' aptly describes the importance of rice in food and nutritional security. It is a primary food source for over one third of world's population. Due to population explosion, the demand for food production in the world especially rice is likely to increase in the coming decades. In order to meet the future food demand, the yield potential of the varieties has to be improved; this of course is difficult due to narrow genetic base of the popular varieties. To break the yield plateau, it is essential to broaden the genetic base of the varieties which can only be achieved and sustained by introgressions from newer gene pools.

The success of any plant breeding programme largely depends on the existence of diversity among the genotypes (Allard, 1960). This helps in the choice of parents for hybridization in yield improvement programmes. Hence, estimation of genetic diversity for yield and its components among genotypes is important for planning the future hybridization programme. The D^2 statistics is a tool to evaluate large number of germplasm lines for their genetic diversity and helps in the identification of genetically divergent parents for their exploitation in hybridization programmes, a hybrids between lines of diverse origin display a greater heterosis than those between closely related strains. Murthy and Arunachalam (1966) stated that multivariate analysis with Mahalanobis's D^2 statistics is a powerful tool to know the clustering pattern to establish the relationship between genetic and geographic divergence and to determine the role of different quantitative characters towards the maximum divergence. Hence, the present investigation was carried out to ascertain the value and magnitude of genetic diversity of 48 rice genotypes and to select suitable genotypes.

MATERIALS AND METHODS

The present investigation was carried out during *kharif*, 2020 at Agricultural Research Farm, Regional Agricultural Research Station, Karjat Dist. Ratnagiri (MS). The experimental material consisted of forty

*Corresponding Author

eight rice genotypes obtained from Rice Specialist, RARS Karjat, which were sown in nursery beds and transplanted into the main field in Randomized Block Design in three replications with spacing of 20 x 15 cm. Single plant observations were recorded on five plants selected at random per genotype per replication for recording observations on fifteen yield and yield attributing characters *viz;* days to 50 per cent flowering, plant height (cm), number of tillers per plant, panicle length (cm), number of filled spikelets per panicle, number of unfilled spikelets per panicle, total number of spikelets per panicle, spikelet fertility (%), test weight (g), straw yield per plant (g), harvest index (%), grain length (mm), grain breadth (mm), length/breadth ratio and grain yield per plant (g). All the agronomic practices were followed to maintain good crop stand. Genetic divergence analysis was done following the D^2 statistics proposed by Mahalanobis (1936). The genotypes were grouped into different clusters according to Tocher's method. (Rao, 1952).

RESULTS AND DISCUSSION

In the present study, analysis of variance showed significant differences for all the fifteen characters studied, indicating existence of a good amount of genetic variability. The forty eight rice genotypes were grouped into six clusters using Mahalanobis D^2 statistics (Table 1). Clustering pattern indicated that, cluster I was the largest cluster comprising of 33 out of 48 genotypes followed by cluster II comprising 11 genotypes whereas cluster III, IV, V and VI were solitary. The formation of distinct solitary clusters may be due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adoptable gene complexes must be responsible for this genetic diversity (Devi *et al*. 2019). The clustering pattern revealed that the genotypes from different origin clustered together indicating that there was no association between eco geographical distribution of genotypes and genetic divergence. Similar results of non association of geographical region with the genetic diversity were earlier reported by Banumathy *et al*. (2010), Ovung *et al*. (2012), Ahamed *et al*. (2014) Bhati *et al*. (2015), Chandramohan *et al*. (2016) and Kumari *et al*. (2016).

Inter and intra cluster distances are presented in Table 2 and depicted in fig 1. The intra and inter-cluster D^2 values among six clusters revealed that intra-cluster average D^2 values ranged from 0 to 9.890 and inter-cluster average D^2 values ranged from 8.839 to 22.174. Statistical distances represent the index of genetic diversity among clusters. Inter-cluster distance was higher than intra-cluster distance, indicating wider genetic diversity among the genotypes. The maximum inter cluster distance was observed between cluster IV and VI (D= 22.174) followed by cluster V and VI (D = 22.138), cluster II and V (D= 22.066), cluster II and III (D=21.455), cluster III and VI (D=19.528), cluster II and VI (D =17.256) and cluster I and VI (D = 17.217). The greater the distance between two clusters, the wider the genetic diversity among the genotypes of those clusters. Such highly divergent, high performing genotypes would be of great use in recombination breeding programme in order to get high desirable segregants (Soundharya *et al*. 2020). While cluster IV and V (D = 15.296), cluster III and IV (D= 15.904), cluster I and II (D= 14.873), cluster II and IV (D = 14.068), recorded moderate inter cluster distances.

The highest intra cluster distance was noticed for cluster II (D=9.890) followed by cluster I (D=8.839). The cluster III, IV, V and VI recorded no intra cluster distance being solitary. Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which would be made use of in improvement through inter-varietal hybridization Banumathy *et al*. (2010).

Cluster means of all the characters is presented in Table 3. Cluster II with eleven genotypes exhibited the highest mean values for spikelet fertility (87.95) and grain breadth (2.15). Cluster III containing only one genotype showed highest mean value for harvest index (44.46) while cluster IV with one genotype recorded highest mean value for test weight (19.89). Cluster V contained genotype with highest mean values for days to 50 per cent flowering (111.00), plant height (117.73), panicle length (27.27), grain yield per plant (12.67) and straw yield per plant (30.53). Cluster VI exhibited highest mean values for number of tillers per plant (7.67), number of filled spikelets per panicle (238.20), number of unfilled spikelets per panicle (41.80), total number of spikelets per panicle (280.0) and grain length (6.35).

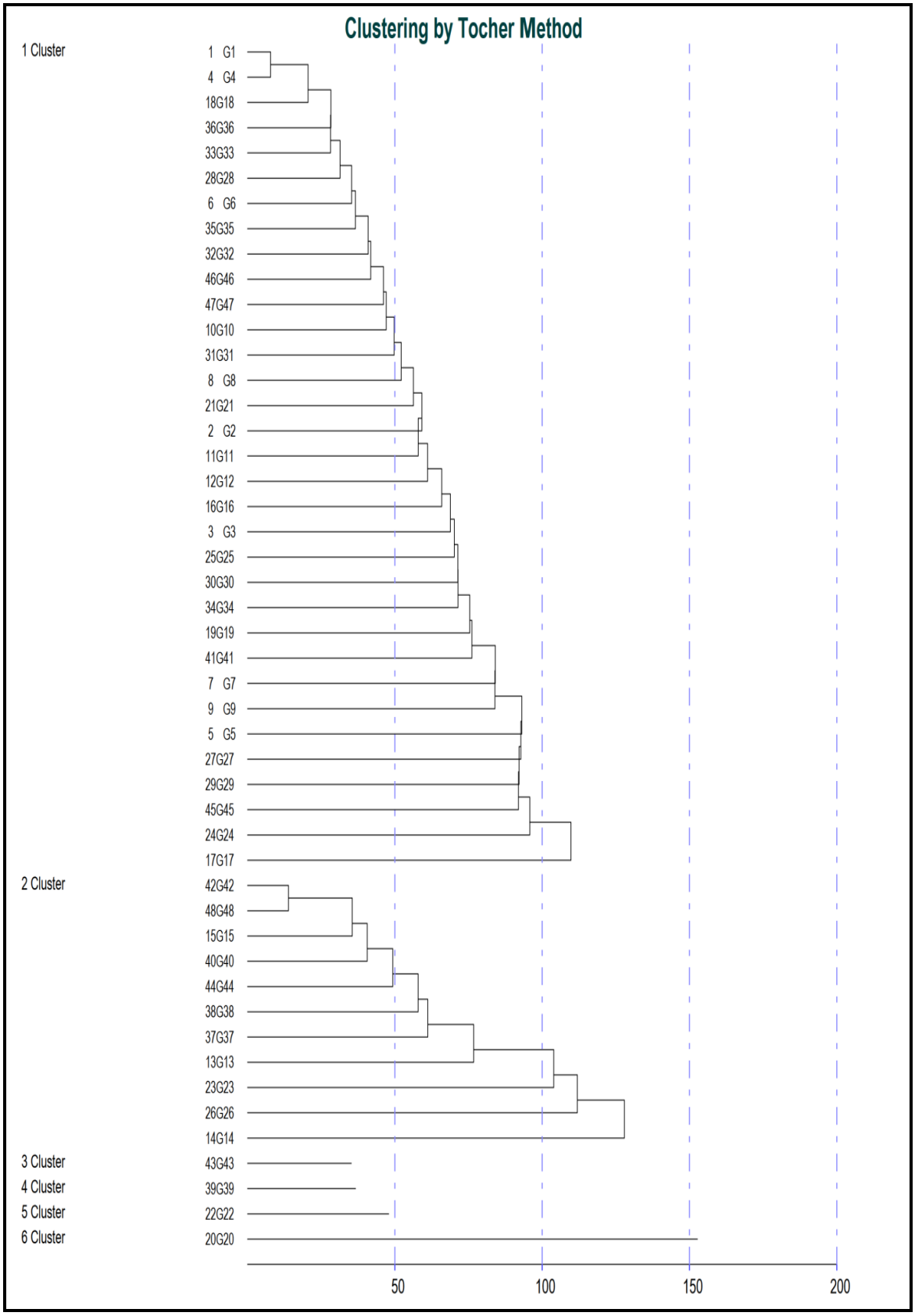

Fig. 1: Clustering by Tocher Method

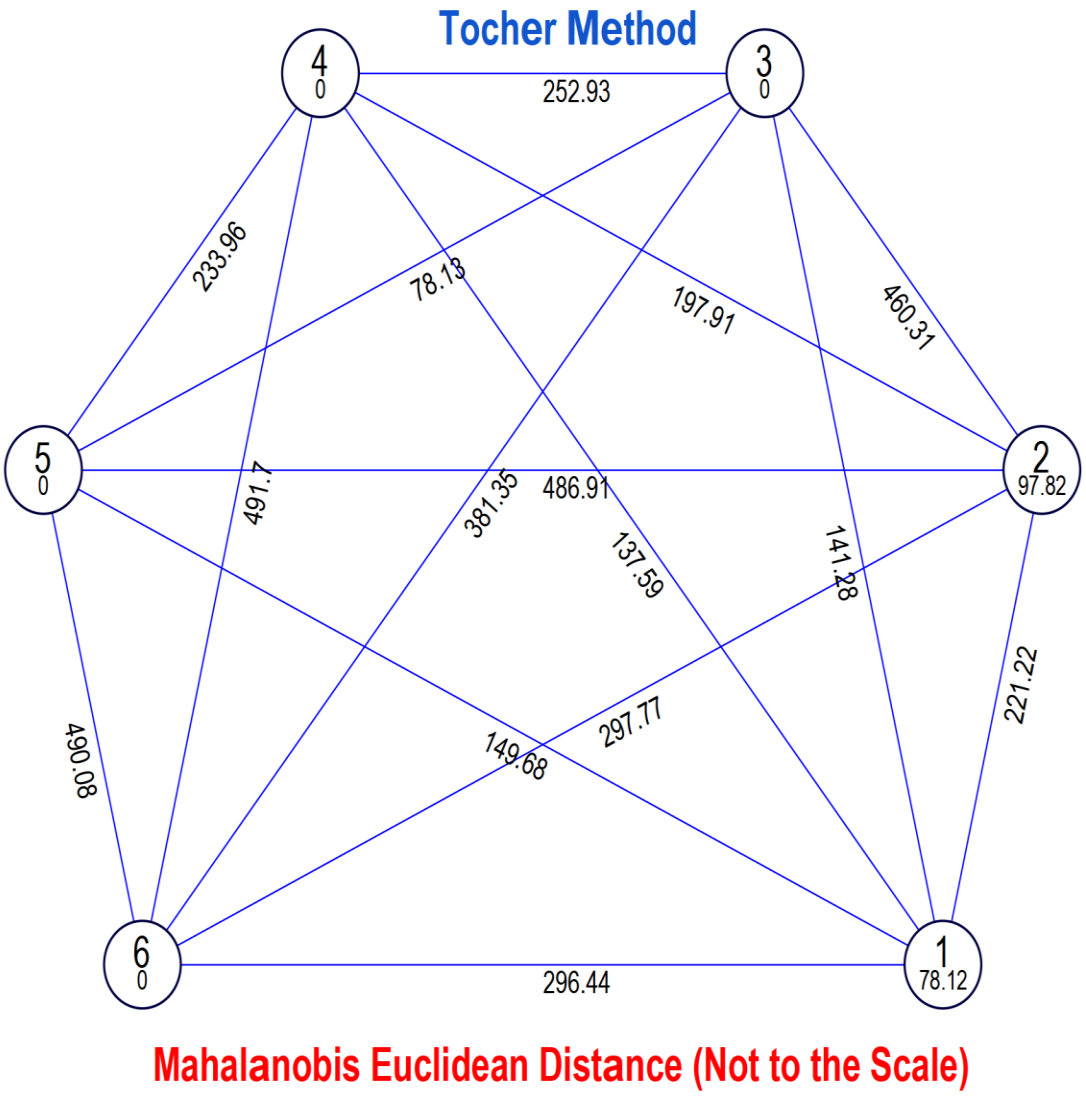

Fig. 2: Cluster diagram

Table 1. Clustering pattern of 48 rice genotypes.

Clusters	Number of Genotypes included	Name of Genotypes
I	33	GNV 1904, Pusa 1702-10-271, JGL 32485, KPS-6262, MTU 1320 (RM 135-33-1-2-1) (HR L 4), NWGR 15022, CR 4208-12-2-2-1, RP 6333-59-11-6-2, BARC KKV 25, PNP 8064, BPT 5204 (NC), WGL 14 (NC), Pusa 1702-10-289, MTU 1326 (MTU 2513-24-2-2), CR 3553-9-2-1-1-2-2, CR 3783-3-2-1-1-1-4-1, RP 6300-188-23-7, RP 6112-MS-M-6-55-2-3-4-3-2-5, NVSR 2565, RNR 28362, NWGR 13052, RTN 1313-6-3-1-1-2-4, P 3237, SKL 07-11-177-50-65-60-267, JGL 33124, RP 5977-MS-M-20-3-2-3-4-3-2, BPT 2846, SKL -07-11-177-50-40-12-40, GNV 1907, RP 6366-JBC 154-1-14, RP 6365- JBC 166-7-1, RP 6354-10-21-6-3, NVSR 2529.
II	11	CRAC 3998-41-2, RP 6329-100-8-2-1, Karjat 9 (Local Check), RP 6166-47, RP 6334-111-5-2-1, KNM 6871, CR 3511-1-1-1-4-1-1, CR 4069-1311-1-1-4-5-7, RP 5963-13, MTU 1321 (MTU 2284-103-1-7), NVSR 441.
III	1	RNR 26121
IV	1	KNM 6854
V	1	AD 16168
VI	1	Pusa 5268-40

Table 2. Estimates of average intra and inter cluster values in six clusters (D) = ($\sqrt{D^2}$) in rice.

Clusters	I	II	III	IV	V	VI
I	8.839	14.873	11.886	11.730	12.234	17.217
II		9.890	21.455	14.068	22.066	17.256
III			0	15.904	8.839	19.528
IV				0	15.296	22.174
V					0	22.138
VI						0

Table 3. Cluster mean performance for fifteen characters in forty eight rice genotypes.

Sr. No.	Characters	Clusters						Population mean
		I	II	III	IV	V	VI	
1	Days to 50 per cent flowering	102.29	101.39	102.67	97.67	**111.00**	105.67	103.45
2	Plant Height (cm)	104.14	98.43	103.93	108.67	**117.73**	94.47	104.56
3	Number of tillers per plant	6.52	6.71	6.73	7.27	6.40	**7.67**	6.88
4	Panicle Length (cm)	23.07	22.36	25.20	22.13	**27.27**	23.80	23.97
5	Number of filled spikelets/panicle	237.78	196.14	175.73	160.73	149.53	**238.20**	193.02
6	Number of unfilled spikelets/panicle	35.91	26.44	26.80	24.40	28.13	**41.80**	30.58
7	Total number of spikelets/panicle	273.69	222.58	202.53	185.13	177.67	**280.00**	223.60
8	Spikelet fertility (%)	86.64	**87.95**	86.58	86.84	84.22	85.10	86.22
9	Test Weight (g)	15.69	19.14	12.17	**19.89**	13.80	13.62	15.72
10	Grain yield per plant (g)	9.85	9.08	7.37	7.84	**12.67**	10.99	9.63
11	Straw yield per plant (g)	21.94	17.52	9.20	14.27	**30.53**	22.00	19.24
12	Harvest Index (%)	31.08	34.64	**44.46**	35.97	30.68	33.05	34.98
13	Grain Length (mm)	5.60	6.05	5.34	5.43	5.32	**6.35**	5.68
14	Grain breadth (mm)	1.97	**2.15**	1.82	1.95	1.83	1.80	1.92
15	Length/ Breadth Ratio	2.85	2.82	2.93	2.78	2.90	**3.52**	2.97

CONCLUSION

It is well known that crossess between divergent parents usually produce greater heterotic effect than between closely related ones. Considering the importance of genetic distance and relative contribution of characters towards total divergence, the present study indicated that the genotype selected from cluster V (AD 16168) for days to 50 per cent flowering, plant height, panicle length, grain yield per plant and straw yield per plant and cluster VI (Pusa 5268-40) for number of tillers per plant, number of filled spikelets per panicle, number of unfilled spikelets per panicle, total number of spikelets per panicle and grain length could be used in crossing programmes to achieve desired segregants.

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