

Genetic Divergence Studies in Rice (*Oryza Sativa*) Genotypes Suitable for Early Kharif Season

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ABSTRACT

Genetic divergence was assessed among 60 rice genotypes collected from different eco geographical areas using Mahalanobis D^2 analysis. The experimental materials were evaluated during 2016 at Agricultural Research Station, Nellore. The 60 rice genotypes were grouped into eight clusters. Cluster I was found to be the largest comprising of 27 genotypes followed by cluster II which had 25 genotypes and cluster VI had 3 genotypes. The clusters III, IV, V, VII and VIII were solitary in nature. The pattern of distribution of genotypes from different eco geographical regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters, 1000 grain weight, flag leaf width and days to maturity, contributed maximum towards genetic divergence among the genotypes. The highest inter-cluster distance ($D^2 = 839.69$) was recorded between clusters III and VIII followed by cluster V and cluster VIII (838.74). Selection of genotypes from these clusters may serve as potential donors for future hybridization programmes to develop recombinants with high yield coupled with desirable traits suitable for early *kharif* season.

Key words: *Early kharif, Genetic divergence, Geographical areas, Inter-cluster distance, Intra-cluster distance.*

Rice (*Oryza sativa* L.) is the most important crop providing food to over 75 % of Asian population and more than three billion of world population which represents 50 to 80 % of their daily calorie intake (Khush, 2005) and 55% of the protein intake in their average daily diet and aptly describes the slogan "Rice is life". Rice is majorly grown in *kharif* and *rabi* seasons and in some areas it is also being grown in *early kharif* season. In India, rice grown area during *early kharif* season is 1.82 M ha with a production of 3.00 Mt and productivity of 1645 kg ha⁻¹. The productivity of *early kharif* was very low when compared to *kharif* and *rabi* productivity of 2295 and 3291 kg ha⁻¹, respectively. In Nellore district of Andhra Pradesh, the rice is cultivated in an area of about 60,000 ha during *early kharif*. *Early kharif* season (March-May to June-October) was characterized by low (or) no rainfall, and high temperatures ranging from 35 to 45°C coupled with high velocity winds and these climatic factors had enormous effect on grain yield production in rice.

The success of any plant breeding programmes 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 yields and its components among genotypes is important for planning the future crossing programme to identify the genotypes suitable for *early kharif*. The use of Mahalanobis D^2 statistic for estimating genetic divergence has been emphasized by Shukla *et al.* (2006)

and Sarawgi and Rita Bisne (2007). The present investigation was carried to ascertain the value and magnitude of genetic diversity among 60 rice genotypes and to select suitable genotypes in breeding programme for the development of *early kharif* genotypes.

MATERIALS AND METHODS

The experimental material consisted of 60 diverse rice genotypes and was grown in a randomized block design with two replications at Agricultural Research Station, Nellore during 2016 *early kharif* season. The 28 days old seedlings were transplanted with a spacing of 15 x 10 cm to the main field and each genotype was grown in five rows of 5m length. Appropriate management and cultural practices were followed to raise a good crop. Observations on 17 yield and physiological characters namely *viz.*, days to 50 % flowering, days to maturity, plant height, number of ear bearing tillers per plant, panicle length, number of filled grains per panicle, number of ill-filled grains per panicle, 1000 grain weight, flag leaf length, flag leaf width, flag leaf area, SPAD chlorophyll meter reading, harvest index, grain length, grain width, grain L/B ratio and grain yield per plant were recorded based on ten randomly selected plants in each genotype in each replication. The genetic diversity between the genotypes was worked out using Mahalanobis D^2 (1928) statistic and grouping of genotypes into clusters was done using Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the genotypes for all the characters studied. The 60 genotypes were grouped into eight clusters (Table 1) based on Mahalanobis D^2 statistic. Cluster I was found to be the largest comprising of 27 genotypes followed by cluster II with 25 genotypes and cluster VI with 3 genotypes. The clusters III, IV, V, VII and VIII were solitary in nature indicating genotypes in those clusters with single and intra-cluster distance was present. The pattern of distribution of genotypes into various clusters was at random indicating that geographical and genetic diversity were not related, as genotypes from diverse sources were grouped into the same clusters *viz.*, I, II and VI and genotypes from similar origin were grouped into different clusters evidenced by the distribution of genotypes developed at Agriculture Research Station, Nellore into different clusters *viz.*, cluster I, II and VI. Grouping of materials of similar origin into different clusters was an indication of broad genetic base of the genotypes belonging to that origin. Bhatt (1970) and Raut *et al.* (1985) suggested that genetic drift and artificial selection could cause greater diversity than geographic distances.

Employing Mahalanobis generalized distance, the divergence in 60 genotypes of rice were estimated for yield and physiological characters during early *kharif* under natural situation. The clustering pattern based on D^2 values in rice genotypes are furnished in Fig.1. The intra-cluster average D^2 values ranged from 0.00-205.19 (Table 2). The highest intra cluster distance was observed in the cluster VI (205.19) indicating wide genetic variation among the genotypes included in this cluster.

It is reported that genotypes would produce more desirable breeding material for achieving maximum genetic advance with regard to yield *per se*, provided that there is adequate complementation of gene effects of parental lines (Rahman *et al.*, 1997). Therefore, genotypes from cluster VI should be given emphasis while selection of parents for hybridization programme. Since most of the elite breeding cultivars were included in this cluster.

The highest inter-cluster distance was observed between clusters III and VIII (839.69) followed by clusters V and VIII (838.74) indicating that the genotypes in cluster III were far diverse from those of cluster VIII. The lowest divergence was noticed between clusters IV and VII (146.02) followed by cluster I and II (168.17) indicating that genotypes included in them were closely related (Table 2). Choosing of genotypes belonging to distant clusters was expected to produce maximum heterosis in crossing and to be used in hybridization program for obtaining a wide spectrum of variation among the segregants.

It is observed that cluster III consists of only one genotype namely IR109A235 and recorded the highest means values for most of the characters like days to 50% flowering, days to maturity, number of ear bearing tillers per plant, ill filled grains per panicle, grain yield per plant, 1000 grain weight, grain length and grain L/B ratio. Cluster II had the highest mean values for flag leaf width, filled grains per panicle, while, cluster IV had the maximum values for grain width. Cluster V for plant height, panicle length, cluster VII for SCMR, harvest index and cluster VIII for flag leaf length and flag leaf area showed the desirable higher values. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits (Table.3).

Out of 17 characters studied the maximum contribution *i.e.*, (74.47%) towards total divergence was seen by four characters only *viz.*, 1000 grain weight (22.14%), flag leaf width (22.43), days to maturity (11.41) and flag leaf length (9.55). These characters should be taken into consideration while selecting parents for hybridization. On the other hand low contributing characters towards total genetic diversity were SCMR, flag leaf area and grain L/B ratio. Several workers reported contribution of grain yield attributes; Senapathi and Sarkar (2005) reported that the trait 1000 grain weight was the highest contributor to total genetic divergence. Devi *et al.* (2006) reported flag leaf length and flag leaf width were the highest contributors to total genetic divergence. While, Garg *et al.* (2010) reported days to maturity was the highest contributor to total genetic divergence. Ubarhande *et al.* (2009) reported that grain characters like grain length and grain width were the highest contributors to total genetic divergence and Sankar *et al.* (2005) reported grain yield per plant and grains per panicle were the major characters contributing towards divergence.

From the cluster analysis, high variability was observed between the genotypes in different clusters for different traits. The main aim of this study was to develop varieties suitable for early *kharif* season, so the selected genotypes should contain characters like early maturity, more number of ear bearing tillers per plant, high panicle length, more number of filled grains per panicle, high 1000 grain weight, and more grain yield per plant and physiological characters like high SCMR, high harvest index, high flag leaf area, low flag leaf length would be desirable for this season.

Clusters III (IR 109A235) and VIII (JGL 11118) had majority of the above mentioned desirable characters. Apart from this, these clusters also had highest inter cluster distance between them followed by clusters V (IR 11C 208) and VIII (JGL 11118). Thus, crosses involving the genotypes from these clusters would give wider and desirable recombinations, which will fit well in early *kharif* season.

Table 1: Clustering pattern of 60 genotypes of rice (*Oryza sativa* L.) by Tocher’s method.

Cluster No.	No. of genotypes	Name of the genotypes
I	27	IR 64, MTU 1010, NLR 33359, IR11C202, IR11C214, IR10C172, IR11C221, IR11C219, NLR 3414, NLR 3413, NLR 4002, IR11C228, NLR 3242, IR11C186, HHZ5-DT20-DT2-DT1, IR 62, NLR 3411, NLR 22671, NLR 3407, NLR 34303, NLR 40058, NLR 3366, NLR 3412, NLR 3217, NLR 3302, NLR 3415, MDT6.
II	25	NLR 3251, NLR 3369, NLR 3346, NLR 3354, NLR 3353, NLR34449, NLR3410, NLR 3417, NLR 3296, NLR 40024, NLR 40065, NLR 34242, NLR 3042, NLR 3408, NLR 30491, JGL 1798, NLR 3350, TN1, NLR 3367, White ponni, IR10F221, ADT 43, NLR 33358, MDT 10, NLR 3241.
III	1	IR 109A235
IV	1	ADT 45
V	1	IR 11C208
VI	3	NLR 33057, BG6367-2, IR64197
VII	1	ADT 37
VIII	1	JGL 11118

Table 2: Average intra-and inter –cluster D² values among nine clusters in 60 rice (*Oryza sativa* L.) genotypes.

Cluste NO	Cluster	Cluster	Cluster	Cluster	Cluster	Cluster	Cluster	Cluster
	I	II	III	IV	V	VI	VII	VIII
Cluster I	102.06	168.17	194.51	347.59	254.38	269	316.59	475.91
Cluster II		150.51	381.61	288.97	484.96	422.90	345.92	406.36
Cluster III			0.00	697.48	199.40	217.20	591.00	839.69
Cluster IV				0.00	718.24	636.84	146.02	202.75
Cluster V					0.00	245.08	539.41	838.74
Cluster VI						205.19	614.75	624.24
Cluster VII							0.00	362.08
Cluster VIII								0.00

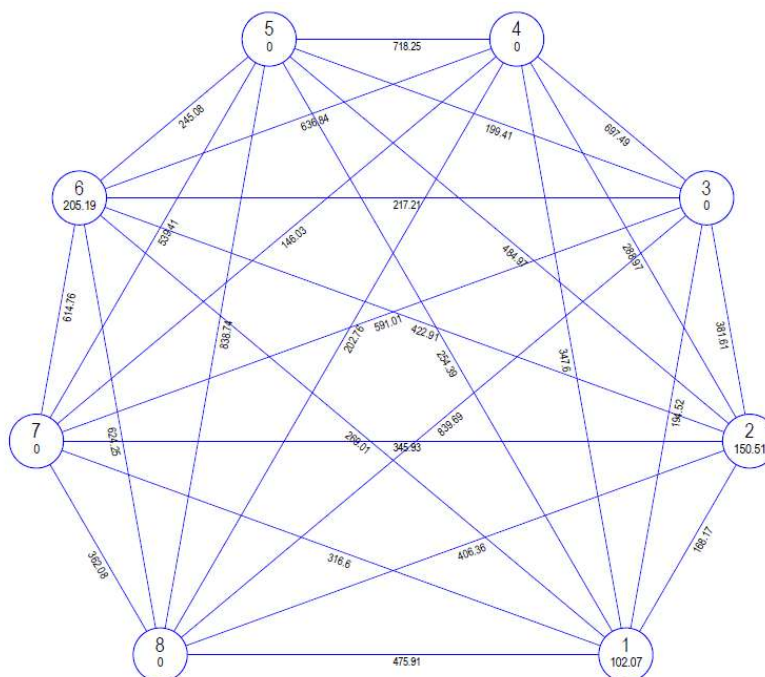


Fig 1. Intra and Inter cluster distances of rice based on euclidean D² distance

Table 3: Relative contribution of characters and Cluster Means of 60 genotypes in rice (*Oryza sativa* L.) : Tocher Method

	DFF	DM	PH (cm)	NEBT	PL(cm)	NFGP	NIFGP	1000 GW (g)	FLL (cm)	FLW (cm)	FLA (cm) ²	SCMR	HI (%)	GL (mm)	GW (mm)	GL/B Ratio	GYP
Cluster I	95.20	123.52	103.33	6.44	23.13	98.33	21.86	19.97	27.13	1.44	29.46	36.02	49.58	8.60	2.31	3.74	12.41
Cluster II	94.84	123.56	97.85	6.37	22.67	122.28	23.99	17.37	28.46	1.55	33.20	36.36	49.36	7.89	2.31	3.42	13.33
Cluster III	100.50	128.50	100.30	6.64	22.60	98.25	34.08	25.62	24.25	1.35	24.45	35.41	53.13	9.84	2.25	4.38	16.39
Cluster IV	80.50	109.50	84.20	4.79	21.00	113.38	17.74	17.39	28.64	1.34	29.81	32.78	48.06	7.62	2.76	2.77	9.64
Cluster V	94.50	121.50	133.25	5.50	24.25	92.56	32.80	21.75	29.69	1.28	28.51	35.18	39.98	8.79	2.53	3.47	11.22
Cluster VI	99.50	128.17	102.23	6.07	23.17	95.67	20.89	23.33	34.63	1.39	36.07	35.12	46.64	9.18	2.42	3.80	13.21
Cluster VII	80.50	108.00	97.90	6.36	22.60	93.64	11.42	22.60	25.82	1.42	27.58	45.28	62.45	7.32	2.52	2.91	13.92
Cluster VIII	79.50	107.50	87.35	6.07	21.85	116.85	19.18	16.55	39.42	1.45	42.73	40.76	45.15	8.40	2.02	4.17	11.75
Character contribution	1.24	11.41	2.77	1.36	1.92	1.36	2.49	23.45	9.55	22.43	0.28	0.73	3.16	3.22	7.63	0.17	6.84

DFF-days to 50 per cent flowering, DM-days to maturity, PH-plant height, NEBT-number of ear bearing tillers per plant, PL-panicle length, NFGP-number of filled grains per panicle, NIFGP-number of ill-filled grains per panicle, 1000 GW-1000 grain weight, FLL-flag leaf length, FLW-flag leaf length, FLA-flag leaf area, SCMR-spad chlorophyll meter reading, HI-harvest index, GL-grain length, GW-grain width, GL/B-grain L/B ratio, GYP-grain yield per plant.

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