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Genetic Divergence for Quantitative and Quality Traits in Rice (*Oryza sativa* L.)

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A B S T R A C T

An investigation was carried out with 42 genotypes of rice to study the nature and magnitude of genetic divergence using Mahalanobis D^2 statistics. Based on 12 morphological quantitative and quality characters namely, days to 50 per cent flowering, plant height, number of productive tillers per plant, panicle length, hundred grain weight, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant, these genotypes were grouped into six clusters. Cluster III with sixteen genotypes was the largest cluster followed by cluster VI with thirteen genotypes. Cluster I (7 genotypes), clusters II, IV and V comprised two genotypes each were also observed. Geographical origin was not found to be a good parameter of genetic divergence. The intra cluster distance was maximum (D=174.228) in cluster VI. The maximum inter cluster distance (D=230.709) was recorded between clusters II and VI. Cluster VI recorded highest mean value for hundred grain weight, kernel length, kernel L/B ratio and grain yield per plant. Grain yield per plant (46.69 per cent) followed by kernel length (18.28 per cent) and hundred grain weight (14.96 per cent) contributed maximum to total divergence. Hybridization among genotypes from II and VI which had maximum inter cluster distances and desirable values for quantitative and quality traits is likely to produce heterotic combinations and wide variability in segregating generations.

Introduction

Rice is a cereal crop belonging to genus *Oryza* of family *Poaceae*. About half of the world's population depends on rice for their survival. Rice is being cultivated in around 113 countries of the world. The present world rice area, production and productivity is 158.93 mha, 465.03 mt and 4.36 t/ha, respectively. In India, it is being grown in 45.10 mha area with production of 103.60 mt and productivity of 3.51 t/ha and contributes 25% to agricultural GDP (Foreign Agriculture Services/USDA, Office of Global analysis, April 2013).To feed the ever growing population, the targeted rice production of the world, China and India for the year 2030 is envisaged as 771.02, 168.90 and 130.02 million tonnes respectively.

The major objective in rice breeding programme is to maintain the desirable traits with an increase in the yield potential. Genetic improvement mainly depends on the amount of genetic variability present in the population.

The estimation of genetic diversity between different genotypes in the crop of interest is the first and foremost process in any plant breeding programme. However assessment of genetic diversity of rice has not given much thrust. We need to identify the genetically diverse accession with desired genes for better utilization in crop breeding programme. Hence the present study was undertaken to evaluate 42 rice genotypes for genetic divergence.

Materials and Methods

The experimental material comprised of 42 genotypes (Table 1) were evaluated during samba season (September-January) 2014 and 2015 at the Plant Breeding Farm (11°24′ N latitude and 79°44′ E longitude ± 5.79m MSL), Annamalai University, Annamalainagar, Tamilnadu, South India. Seeds of the 42 genotypes were sown in raised nursery bed. The seedlings were transplanted to the mainfield at the rate of one seedling per hill, after 25 days, with a spacing of 20 cm × 15 cm. The experiment was arranged in a randomized complete block design with three replications, in four – row plots of 3 m 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. Twelve traits *viz.,* days to 50 per cent flowering, plant height (cm), number of productive tillers per plant, panicle length (cm), hundred grain weight (g), grain length (mm), grain breadth (mm), grain L/B ratio, kernel length (mm), kernel breadth (mm), kernel L/B ratio and grain yield per plant (g) were recorded. Mahalanobis (1936) D^2 analysis Sarawagi and Rita Binse (2007) was used to estimate genetic divergence among the 42 genotypes. Grouping of genotypes into clusters was carried out following Tocher's Methods Rao (1952). Mean value of the variables, calculated based on measurements on plants from blocks and each genotype, were used in the cluster analysis.

Results and Discussion

The analysis of variance showed significant difference among the forty two genotypes for all the twelve characters indicating the existence of high genetic variability among the genotypes for all the traits (Table 2). The forty two genotypes were grouped in to six different clusters based on the relative magnitude of D^2 values.

Cluster III, the largest cluster, comprised sixteen genotypes, followed by cluster VI with thirteen genotypes (Table 4). The cluster I with seven genotypes, the clusters II, IV and V comprised two genotypes each. The clustering pattern revealed that the genotypes from different sources clustered together indication that there was no association between ecogeographical distribution of genotypes and genetic divergence. The possible reason for grouping of genotypes of different states in one cluster could be the free exchange of germplasm among the breeders of different regions, or unidirectional selection practiced by breeder in tailoring the promising cultivars for different regions Verma and Mehta (1976). Similar findings were reported by Chaturvedi and Maurya (2005), Sabesan and Saravanan (2008) and Bhati *et al.,* (2015). This indicated that, in general selection has been towards the same goal in the different centers of origin of these genotypes and yet, there is sufficient genetic variability, which distinctly differentiates them into six clusters. On the other hand, our study has also revealed that genotypes from the same centre of origin were distributed in different clusters, which may be due to differential adaptation to varied agro-ecosystems Kandamoorthy and Govindarasu (2005), Sabesan *et al.,* (2009) and Kumari Priyanka *et al.,* (2015).

Table.1 List of genotypes selected for D^2 analysis

Genotype code	Genotype names	Origin
G1	ADT-36	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G2	ADT-37	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G3	ADT-38	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G4	ADT-39	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G5	ADT-40	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G6	ADT-41	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G7	ADT-42	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G8	ADT-43	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G9	ADT-44	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G10	ADT-45	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G11	ADT-46	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G12	ADT-47	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G13	ADT-48	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G14	ADT-49	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G15	CR-1009	Central Rice Research Institute (CRRI), Cuttack, Orissa, India.
G16	BPT-5204	Agriculture college, Bapatla, Andhra Pradesh, India.
G17	IR-64	International Rice Research Institute (IRRI), Philippines.
G18	WHITE PONNI	Paddy breeding station, Coimbatore, Tamil Nadu, India.
G19	TRY-1	Agricultural College and Research Institute, Trichy, Tamil Nadu, India.
G20	TRY-2	Agricultural College and Research Institute, Trichy, Tamil Nadu, India.
G21	TRY-3	Agricultural College and Research Institute, Trichy, Tamil Nadu, India.

Contd…

Genotype code	Genotype names	Origin
G22	CSR-30	Central Saline Soil Research Institute (CSSRI), Karnal, Haryana, India.
G23	ANANDA	Gujarat, India.
G24	CO-49	Paddy Breeding Station, Coimbatore, Tamil Nadu, India.
G25	MTU-1001	Rice Research Station, Marteru, Andhra Pradesh, India.
G26	MARANTHONDI	Traditional Variety, Kerala, India.
G27	MDU-5	Agriculture College and Research Institute, Madurai, India.
G28	SWATHI	Directorate of Rice Research (DRR), Hyderabad, Andhra Pradesh, India.
G29	MTU-1010	Rice Research Station, Marteru, Andhra Pradesh, India.
G30	ASD-16	Rice Research Station, Ambasamuthiram, Tamil Nadu, India.
G31	ASD-17	Rice Research Station, Ambasamuthiram, Tamil Nadu, India.
G32	ASD-19	Rice Research Station, Ambasamuthiram, Tamil Nadu, India.
G33	MAHAMAYA	Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh), India.
G34	POORNIMA	Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh), India.
G35	KARMA MAHSURI	Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh), India.
G36	JALAKARA PONNI	Traditional variety, Tamil Nadu, India.
G37	SHYAMALA	Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh), India.
G38	ANNAPURNA	Regional Agricultural Research Station, Pattambi, Kerala, India.
G39	ASD-18	Rice Research Station, Ambasamuthiram, Tamil Nadu, India.
G40	BPT-5202	Agriculture college, Bapatla, Andhra Pradesh, India.
G41	GAYATHRI	Central Rice Research Institute (CRRI), Cuttack, Orissa, India.
G42	SWARNA	Rice Research Station, Marteru, Andhra Pradesh, India.

Table.2 Analysis of variance for 12 morphological characters in 42 rice genotypes

Source	df	MSS											
		DFF	PH	NPT	PL	HGW	GL	GB	GLBR	KL	KB	KLBR	GYD
Replication	2	3.094	0.765	2.869	1.801	0.024	0.009	0.033	0.007	0.004	0.006	0.027	1.083
Genotype	41	392.290**	897.104**	15.337**	55.264*	0.533**	0.036**	0.008**	2.319**	0.022**	0.216**	0.468**	7.941**
Error	82	1.067	10.923	1.793	36.020	0.008	0.004	0.012	0.004	0.002	0.003	0.009	2.005

*Significant at 5 per cent level
**Significant at 1 Per cent level

Table.3 Cluster means of 42 rice genotypes for various characters

Cluster	DFF (Days)	PH (cm)	NPT	PL (cm)	HGW (g)	GL (mm)	GB (mm)	GLBR	KL (mm)	KB (mm)	KLBR	GYD (g)
I	85.524	101.952	20.410	21.935	2.283	0.799	0.299	2.726	0.585	0.214	2.737	27.106
II	85.500	93.703	24.233	21.050	1.488	0.715	0.215	3.320	0.515	0.211	2.427	26.530
III	81.479	101.131	21.888	23.421	2.271	0.883	0.258	3.586	0.639	0.210	2.983	26.848
IV	84.167	112.683	22.633	20.703	2.370	0.814	0.314	2.601	0.615	0.219	2.869	28.111
V	91.167	103.217	24.000	23.550	2.027	0.814	0.214	3.808	0.614	0.209	2.860	27.277
VI	84.538	97.909	22.149	20.223	2.397	0.857	0.254	3.608	0.668	0.215	3.115	28.140
General mean	83.881	100.567	21.970	21.947	2.268	0.847	0.262	3.400	0.631	0.215	2.945	27.349

DFF – Days to 50 per cent flowering
pH – Plant height
NPT – Number of productive tillers per plant
PL – Panicle length
HGW – Hundred grain weight
GL – Grain length
GB – Grain breadth
GLBR – Grain L/B ratio
KL – Kernel length
KB – Kernel breadth
KLBR – Kernel L/B ratio
GYD – Grain yield per plant

Table.4 Composition of D^2 clusters for 42 rice genotypes

Cluster	Number of genotypes	Name of genotypes
I	7	ADT36, ADT37, ADT38, ADT39, ADT40, MTU1001, MDU5
II	2	ADT47, ADT49
III	16	ADT41, ADT42, ADT43, ADT44, ADT45, ADT46, ADT48, CR1009, BPT5204, IR64, WHITE PONNI, TRY1, TRY2, TRY3, ASD17, BPT5202
IV	2	POORNIMA, SWARNA
V	2	CO49, MAHAMAYA
VI	13	CSR30, ANANDA, MARANTHONDI, SWATHI, MTU1010, ASD16, ASD19, KARMA, MAHSURI, JALAKARA PONNI, SHYAMALA, ANNAPURNA, ASD 18, GAYATHRI

Table.5 Average inter (D^2) and intra (D) cluster values for 42 rice genotypes

Cluster	I	II	III	IV	V	VI
I	17614.209 (132.719)	25457.107 (159.553)	22801.158 (151.001)	8211.706 (90.618)	12961.501 (113.849)	30810.082 (175.528)
II		62.919 (7.932)	38001.336 (194.939)	24008.752 (154.948)	17083.168 (130.703)	53226.840 (230.709)
III			21626.939 (147.061)	13728.705 (117.170)	12038.848 (109.722)	25159.533 (158.618)
IV				129.204 (11.367)	5629.074 (75.027)	20246.965 (142.292)
V					311.559 (17.651)	19106.977 (138.228)
VI						30355.225 (174.228)

Table.6 Contribution of different characters to genetic divergence

S. No.	Characters	Contribution of each characters (%)
1	Days to 50 per cent flowering (days)	1.54
2	Plant height (cm)	0.17
3	Number of productive tillers per plant	1.20
4	Panicle length (cm)	2.35
5	Hundred grain weight (g)	14.96
6	Grain length (mm)	0.32
7	Grain breadth (mm)	0.41
8	Grain L/B ratio	8.81
9	Kernel length (mm)	18.28
10	Kernel breadth (mm)	4.37
11	Kernel L/B ratio	0.90
12	Grain yield per plant (g)	46.69

The relative divergence of each from other cluster *i.e.,* inter-cluster distance indicated greater divergence between cluster II and cluster VI (D^2=230.709). It was characterized by genotypes with heavier grain yield per plant and low hundred grain weight (Table 5). It was followed by cluster II and cluster III (D^2 = 194.939) with cluster II having highest number of productive tillers per plant and cluster III with earliness in days to 50 per cent flowering. Parental lines selected from these clusters may be used in hybridization programme, since hybridization between divergent parents is likely to produce wide variability and transgressive segregations with high heterotic effects (Rama, 1992). Such recommendations were also made by Sabesan *et al.,* (2009) and Satheeshkumar and Saravanan (2012). The smallest inter-cluster distance was observed between clusters IV and V (D^2 = 75.027) followed by cluster I and IV (D^2 = 90.618). The lines belonging to these clusters were relatively closer to each other, in comparison to lines grouped in other clusters. Such analysis was meant to avoid selection of parents from genetically homogenous clusters, and to maintain a relatively broad genetic base.

The largest intra-cluster distance was recorded for cluster VI (174.228) followed by clusters III (147.061) and I (132.719) the lines included in cluster I, III and VI were more diverse than those in the other clusters. Heterosis is generally attributed to genetic divergence among the parental lines in involved in the crosses. Nevertheless, the genetic divergence for the maximum expression of the heterotic effect has a limit (Arunachalam and Bandyopadhyay, 1984) and (Moll *et al.*, 1965).

The cluster mean values showed a wide range of variation for all the traits under study (Table 3). Cluster VI was characterized with high mean values for hundred grain weight, kernel length, kernel L/B ratio and grain yield per plant. Cluster II exhibited a low mean for plant height, hundred grain weight, grain length, kernel length, kernel L/B ratio and grain yield per plant. Cluster IV had high mean for plant height, grain breadth and kernel breadth. Cluster V had high mean for panicle length and grain L/B ratio. Cluster III had high mean for grain length and early for days to 50 per cent flowering.

In all the combinations of inter cluster distance each character is ranked on the basis of inter cluster distances. Rank I is given to the character having highest mean difference and rank P is given to the character having lowest mean difference, where P is the numbers of characters. Percentage contribution of each character is calculated on the basis of occurrence of these ranks. With 46.69 per cent contribution, the grain yield per plant, 18.28 per cent for kernel length and with 14.96 per cent contribution of hundred grain weight were the major force of discrimination among the genotypes tested (Table 6). Similar finding were made by Karthikeyan (2002), Sabesan and Saravanan (2008), Rajesh *et al.,* (2010) and Kumari Priyanka *et al.,* (2015) for filled grains per panicle, hundred grain weight and grain yield per plant, respectively. Plant height had the minimum (0.17 per cent) contribution to the total divergence. Similar results were reported by Senapati and Sarkar (2005).

Considering the importance of genetic distance, relative contribution of characters towards total divergence and yield potential of genotypes, the present investigation suggests that parental lines selected from cluster II (ADT 47 and ADT 49) for slender grains. Cluster VI (CSR 30, ANANDA, MARANTHONDI, SWATHI, MTU1010, ASD16, ASD19, KARMA, MAHSURI, JALAKARA PONNI, SHYAMALA, ANNAPURNA, ASD 18 and GAYATHRI) for high mean for hundred grain weight, kernel length, kernel L/B ratio and grain yield per plant. Cluster IV (POORNIMA and SWARNA) for high mean for plant height, grain breadth and kernel breadth could be used in a hybridization programme, since hybridization between divergent parents is likely to produce wide variability and transgressive segregations. Crosses between unrelated lines tend to exhibit heterosis. Thus,

diverse lines from different clusters should be chosen for crossing in a hybrid rice breeding programme.

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