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Research Article

Genetic divergence for yield contributing characters in F_5 families of rice (*Oryza sativa* L.)

Abinash Mishra, P. C Kole, Soumya Satpathy and Rosevellina Mohanta

Department of Genetics and Plant Breeding, Institute of Agriculture, Visva-Bharati, Sriniketan -731235, Birbhum, West Bengal
E-Mail: abinash.siram83@gmail.com

Abstract
Twenty-one different F_5 families derived from eight different crosses involving seven improved parental genotypes of West Bengal were studied for genetic diversity on the basis of yield and its attributing characters. Based on D^2 analysis, the 21 families were grouped into 8 clusters. Cluster I consisted maximum of 6 families followed by Cluster II with 4 families. Wilk's Lambda criterion = 0.7×10^{-7} and V=716.42 with 240 df revealed a highly significant difference among the genotypes for the pooled effects of all the characters. The clusters VII and VIII were mono-familial although there was a common parent. The maximum inter-cluster distance was found between cluster III and IV. Relative contribution of 100-grain weight to the total divergence was highest, followed by plant height, days to 50% flowering and straw yield.

Key words
Rice, genetic diversity and D^2 analysis.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important cereal crops belonging to the tribe oryzae of the family Gramineae (Poaceae). The cultivated rice is diploid having 24 chromosomes (2n = 2x = 24). It ranks first among the three major cereals, followed by wheat and maize. *O. sativa* and *O. glaberrima* are believed to have evolved independently from a common ancestor *O. perennis*. The genus Oryza contains 25 recognized species, of which 23 are wild species and two, *O. sativa* and *O. glaberrima* are cultivated (Morishima, 1984; Vaughan, 2008; Brar and Khush, 2003). Grain yield is a complex polygenic quantitative trait which is greatly affected by environment and determined by the magnitude and nature of their genetic variability (Singh *et al*., 2000). Study of genetic divergence would help to initiate hybridization programme between genotypes. The more is diversity among the parents, the chance of obtaining heterotic hybrids is greater. Estimation of the degree of the divergence between biological population and computation of relevant contributions of different components to the total divergence is done by Mahalanobis's (1936) generalized distance estimated by D^2 statistics.

MATERIALS AND METHODS

The field experiments were conducted at the Agricultural Farm, Institute of Agriculture, Visva-Bharati, Sriniketan, which is located at sub-humid lateritic belt. The present investigation was carried out with 21 different F_5 families derived from eight different cross combinations during warm wet (*kharif*) season (July-December) in 2018. The seven parents involved in the 21 different families were Dudheswar (DS), Shantibhog (SNT), Shitabhog (STB), Kerala Sundari (KS), IET14142 (IE2), IET14143 (IE3) and Subhasita (SS). Each parental genotype was having some peculiar characteristics (**Table 1)**. Thirty-day old single seedling per hill was transplanted in randomized complete block design (RCBD) with three replications. Each plot consists of 5 rows each with 20 plants with a spacing of 20 cm × 15 cm spacing. Observations were recorded on following twelve different quantitative characters *viz.* plant height, days to flowering, flag leaf area, panicle exertion, panicle length, panicle number,

Table 1. Characteristics of parental genotypes used in crosses

SL No.	Genotype	Source/origin/ geographical Distribution	Characters
1	**Subhasita**	Sub Research Rice Station, Chakada (B.C.K.V, West Bengal)	Medium long grain, awn absent, scented, susceptible to false smut, moderately resistance to lodging, acute leaf angle.
2	**Shitabhog**	Sub Research Rice Station, Chakada, (B.C.K.V, West Bengal)	Short grain with higher number of spikelets, awn absent, aromatic, tall stature
3	**Kerala Sundari**	Purulia, Burdwan, North 24 Pargonas, Sagar Island of South 24 Pargonas, Hoogly, Nadia (W.B)	Medium bold grain, awn absent, scented, High yield folk rice, gives grain yield- 4.2-5.4 t/ha: comparable with HYVs. Short duration varieties (seed to seed-130 days)
4	**Shantibhog**	Sub Research Rice Station, Chakada (B.C.K.V, West Bengal)	Long bold grain, awn present with low expressivity, scented rice, sturdy stem.
5	**Dudheswar**	North and South 24 Pargonas,	Medium grain fine rice, awn absent, non- aromatic. Boro paddy – partial photo insensitive, tasty fine rice
6	**IET 14142**	Dept. of Genetics and Plant Breeding (Visva-Bharati)	Mutant of "Tulaipanji", awn present with low expressivity, extra primary branch arises from the base of the panicle (neck), mild aromatic.
7	**IET 14143**	Dept. of Genetics and Plant Breeding (Visva-Bharati)	Small grain, reduced height true breeding mutant derived from scented traditional race i.e. Tulaipanji, awn present, unique trait such as semi dwarf with high tillering ability.

primary branches panicle^{-1}, secondary branches panicle^{-1}, grain number panicle^{-1}, 100-grain weight, straw yield and grain yield plant^{-1}.

RESULTS AND DISCUSSIONS

The present investigation on genetic divergence was carried out on 21 different F_5 families derived from 8 different crosses based on twelve quantitative characters viz. plant height, days to 50% flowering, flag leaf area, panicle exertion, panicle length, panicle number, primary branches panicle^{-1}, secondary branches panicle^{-1}, the number of filled grain, 100-grain weight, straw yield and grain yield. Analysis of variance revealed that mean square due to F_5 families was highly significant for all the characters under study, indicating considerable genetic variation among the F_5 families derived from the eight crosses. The significance of genotypes assuredly stipulated the significant pooled effect of all the traits between different genotypes. Hence, further analysis was made to estimate genetic divergence by employing Mahalanobis's D^2 statistic (Mahalanobis, 1936). Wilk's 'V' (statistic) criterion was estimated to reveal the significant differences between the groups based on the pooled effects of all the characters. Wilk's Lambda criterion = 0.7 × 10^{-7} and V=716.42 with 240 df revealed highly significant difference among the genotypes for the pooled effects of all the characters. D^2 value ranged from (13.31) [IE2 × SS (1) and IE2 × SS (2)] to (338.5) [SNT × SS (2) and IE2 × SS (3)]. The 21 different families were assorted into six clusters basing upon Tocher's method(Rao, 1952; Singh and Choudhary, 1977). Cluster-I comprised maximum number of 6 families: IE2 × SS (1), IE2 × SS (2), STB × IE3 (3), STB × IE3 (1), KS × IE3 (1) and KS × IE2. Cluster-II contained four families representing SNT × IE2 (1), SNT × IE2 (2), SNT × IE2 (3) and KS × IE3 (2). Cluster-III had three families viz. SNT × SS (1), SNT × SS (2) and IE2 × DS. Cluster-IV, V and VI were composed of two families each KS × IE2 (1) and IE2 × SS (1), SNT × KS (3) and STB × IE3 (2), and SNT × KS (5) and KS × IE2 (2), respectively. Cluster-VII and VIII had each a single family IE2 × SS (4) and KS × IE2 (3), respectively (**Table 2**).

Cluster -I comprised two families from same cross IE2 × SS and one family from cross KS × IE2 and hence these families were having IE2 as a common parent. This cluster was also comprised of two families from STB × IE3 and one family from KS × IE3 and hence, these families were having IE3 as a common parent. All the families were having either IE2 or IE3 as a parent which were the mutants produced from same parent Tulaipanji. Cluster -II contained three families from the same cross SNT × IE2 and one from KS × IE3. IE2 and IE3 were derived from the same Tulaipanji parent by mutagenesis. Cluster -III had two families from the same cross SNT × SS and one from IE2 × DS. Cluster-IV comprised one family from KS × IE2 and one from IE2 × SS and hence these families were having IE2 as the common parent and were included in the same cluster. Cluster -V was represented by one family from the cross SNT × KS and another family from the cross STB × IE3 with no common parentage. Cluster-VI with one family from the cross SNT × KS and one from the cross KS × IE2 had KS as the common parent which could be the cause of inclusion in the same cluster. The other two clusters were mono-familial although there was a common parent. Mono-familial types of clusters were also previously reported through various experiments (Ashok *et al*., 2017; Singh *et al*., 2019). The clustering pattern showed no clear-cut parentage relations, although relatedness of parents was somewhat responsible for cluster formation. However,

Table 2. Distribution of 21 families into different clusters

Cluster	Number of genotypes	Genotypes included in each cluster
I	6	IE2 × SS (1), IE2 × SS (2), STB × IE3 (3), STB × IE3 (1), KS × IE3 (1) and KS × IE2.
II	4	SNT × IE2 (1), SNT × IE2 (2), SNT × IE2 (3) and KS × IE3 (2)
III	3	SNT × SS (1), SNT × SS (2) and IE2 × DS
IV	2	KS × IE2 (1) and IE2 × SS (3)
V	2	SNT × KS (3) and STB × IE3 (2)
VI	2	SNT × KS (5) and KS × IE2 (2)
VII	1	IE2 × SS (4)
VIII	1	KS × IE2 (3)

segregation pattern of the crosses and subsequent selection history might have played important role in grouping the advanced generation families.

The statistical distance is used as the index of genetic diversity among clusters. The study revealed that the average intra-cluster distance ($\sqrt{D^2}$) varied from (5.44) in cluster-I to (6.48) in cluster-VI (**Table 3**). The maximum inter-cluster distance (15.16) was found between cluster III and IV, followed by cluster IV and VI (13.99), cluster III and VI (13.27), cluster VI and VIII (13.09) and so on. This indicated considerable amount of divergence within and between the clusters. Hence, recombinants possessing desirable agronomic features could be selected from different families, falling under different clusters of greater inter- cluster distance and employed in hybridization programme to generate superior heterotic F_1 individuals as well as potent transgressive segragants in advance generations of crosses (Rama,1992; Mishra *et al*., 2003; Chaturvedi and Maurya, 2005; Bhati *et al*.,2015). Selections and crossings of parental genotypes belonging to two different clusters of wide inter-cluster distance led to generation of a wide range of desirable recombinants in the F_2 and subsequent generations (Mishra *et al*., 2003; Bose and Pradhan, 2005; Chaturvedi and Maurya, 2005). The inter-cluster distance was minimum between cluster I and VII (6.83), followed by cluster III and VIII (8.34). The families belonging to these clusters were relatively closer to each other, in comparison to families grouped under other clusters. Hence, the families belonging to these genetically homogeneous clusters, should not be manoeuvred in the crossing programme, as there would be no significant exploitation of heterosis in the F_1 generation (Bhati *et al*., 2015). The minimum intra- cluster distance was found for cluster I (5.44), while it was zero for cluster VII and cluster VIII and the maximum intra- cluster distance was for cluster VI (6.48), followed by cluster V (6.14), cluster II and III (6.06) and so on. This revealed that the recombinants of the families belonging to the groups VI, V, II and III were more genetically diverse as compared to the genotypes of other families.

Table 3. Inter and Intra $\sqrt{D^2}$ values

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**5.44**	8.57	9.51	10.76	8.66	9.69	6.83	8.62
II		**6.06**	10.7	8.54	8.83	9.37	9.56	11.11
III			**6.06**	15.16	12.03	13.27	11.96	8.34
IV				**5.66**	10.99	13.99	8.41	13.03
V					**6.14**	9.42	9.68	11.66
VI						**6.48**	10.58	13.09
VII							**0**	9.25
VIII								**0**

Cluster-I was characterized by lowest mean for flag leaf area (20.13) and high mean values for plant height (141.56), days to 50% flowering (122.99), panicle length (24.39) and secondary branches panicle^{-1} (25.04) and moderate mean values for rest of the characters (**Table 4**). Cluster-II showed a high mean value for panicle number (10.43) and low mean values for plant height (113.69) and straw yield (34.35) and moderate for rest of the characters. Cluster-III recorded a highest mean value for panicle number (10.77) and the lowest mean values for plant height (104.66), panicle exertion (1.74), primary branches panicle^{-1} (10.18), secondary branches panicle^{-1} (17.87) and the number of filled grains (78.41). Cluster -IV had la owest mean value for days to 50% flowering

(111.5) and high mean value for secondary branches panicle^{-1} (26.36) and straw yield (36.53) and moderate mean values for rest of the character. Cluster-V was characterized by the lowest mean value for panicle length (20.94) and the highest mean value for panicle exertion (7.26) and high mean values for plant height (143.68), flag leaf area (32.28) and secondary branches panicle^{-1} (25.37) and rest of the characters showed moderate mean value. Cluster-VI was exerted the highest mean value for days to 50% flowering (125.67), flag leaf area (38.03), primary branches panicle^{-1} (12.49), secondary branches panicle^{-1} (32.87), the number of filled grains (152.13), 100- grain weight (2.29), straw yield (61.98) and grain yield (21.98). Cluster-VII showed the highest mean values plant height (150.58) and panicle length (26.39) and the moderate mean values for rest of the characters. Cluster-VIII had the lowest mean values for panicle number (5.53), the number of filled grains (98.5), 100-grain weight (1.44), straw yield (31.88) and grain yield (10.96) and high mean values for days to 50% flowering (123.33), panicle length (24.51) and secondary branches panicle^{-1} (27.67).

Table 4. Cluster means of twelve quantitative characters in F_5 segregating population of rice

Cluster	Plant height (cm)	Days to 50% flowering	Flag leaf area (cm^2)	Panicle exertion (cm)	Panicle length (cm)	Panicle number	Primary branches panicle^{-1}	Secondary branches panicle^{-1}	Number of filled grains	100-grain weight (g)	Straw yield (g)	Grain yield (g)
I	141.56	122.99	**20.13**	3.21	24.39	9.50	11.22	25.04	104.49	1.89	42.93	16.33
II	**113.69**	119.83	27.78	3.16	22.22	10.43	10.51	21.1	102.82	2.08	34.35	20.92
III	104.66	125.44	23.30	**1.74**	22.25	**10.77**	**10.18**	**17.87**	**78.41**	1.75	45.57	11.38
IV	130.66	**111.5**	25.48	2.57	23.13	8.02	11.23	26.36	109.39	1.76	36.53	15.49
V	143.68	122.33	32.28	**7.26**	**20.94**	7.52	10.66	25.37	138.75	2.08	42.95	17.33
VI	150.35	**125.67**	**38.03**	2.86	24.52	7.92	**12.49**	**32.87**	**152.13**	**2.29**	**61.98**	**21.98**
VII	**150.58**	120	33.21	2.27	**26.39**	10.26	11.19	21.33	111.85	1.71	47.54	17.35
VIII	126,42	123.33	31.31	2.31	24.51	**5.33**	11	27.67	98.5	**1.44**	**31.88**	**10.96**
Relative contribution %	**10.79**	**9.81**	**8.06**	**8.05**	**7.86**	**5.93**	**7.28**	**5.97**	**8.89**	**10.98**	**9.39**	**6.97**

Relative contribution of various characters towards the divergence would give an idea about the worth of various traits (Table 4). Relative contribution of 100-grain weight to the total divergence was highest (10.98), followed by plant height (10.79), days to 50% flowering (9.81) and straw yield (9.39). Similar results have been reported for 100- grain weight (Chandra *et al*., 2007; Panday and Anurag, 2010; Monohara and Singh, 2013 and Gangapur *et al*., 2014), plant height (Singh *et al*., 2006; Grag *et al*., 2011 and Monohara and Singh, 2013).

Considering the genetic divergence, relative importance of traits in determining yield in this particular population and the mean performance of 21 different families, crossing between inter-cluster families [(SNT ×KS-5) × (KS × IE2-1)], [(SNT ×KS-5) × (KS × IE2-1)], [(SNT ×KS-5) × (IE2 × SS-3)], [(KS × IE-2) × (IE2 × SS-3)] and [(STB × IE2-1) × (SNT ×KS-5)] and intra-cluster families [(IE2 × SS-2) × (STB × IE3-3)], [(STB × IE3-3) × (KS × IE-2)] and [(SNT × KS-5) × (KS × IE2-2)] would most likely to produce heterosis in the F_1 generation and a wide range of desirable recombinants in the F_2 and subsequent generations.

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