

Selection in advanced generation (F₄) based on agro-morphological traits in fine rice

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Abstract

Advanced generation (F₄) derived from inter-varietal crosses were evaluated with a view to evolve superior fine rice varieties. The experiment was conducted at Plant Breeding Research Field during transplant Aman season (1st July-December) of 2016. The experimental materials comprised with 32 advanced generation (F₄) derived from eight crosses involving six fine rice parental lines. A total of thirteen characteristics viz plant height (cm), productive tillers/hill (maximum vegetative stage), panicle length (cm), fertile grains/panicle, sterile grains/panicle, panicle weight (g), sterility (%), lodging (%), 1000-grain weight (g), grain yield/hill (g), days to 50% flowering, days to maturity and harvest index were studied to assess genotypic and phenotypic correlations and genetic diversity pertained among the advanced lines. The means of different traits were separated by DMRT test, the advanced line, PL6 derived from Kataribhog × Chinigura produced the highest grain yield/hill (41.51g) but ranking of the advanced lines based on yield enhancing traits, PL5 derived from the same cross showed the best performance for yield potential. Among the 13 characters, fertile grains per panicle, panicle weight and 1000-grain weight exhibited positive and significant correlation with grain yield both at genotypic and phenotypic levels, suggested inherent association of these traits to increment gain yield in the advanced lines. All the 32 advanced lines were incorporated in the genetic diversity analysis based on 13 traits. The lines were distributed into six clusters; cluster II comprised with eight lines and the cluster V only with two lines. The intra-cluster distance was maximum (1.14) in the cluster IV, indicated six advanced lines included in the cluster were relatively more diversified from each other. The inter-cluster distance (16.59) was between the cluster I and V. Therefore, further genetic diversity might be extended through crossing or direct selection of promising parental lines. Since the main objective of breeding is to increase yield potential in advanced lines, cluster mean of the traits must be taken into deliberation. Accordingly, the cluster I might be deliberately selected to improve yield potential in the advanced lines. The simultaneous consideration character association both at genotypic and phenotypic levels and genetic and genetic diversity fertile grains per panicle, panicle weight and 1000-grain weight along with the advanced line, PL6 may be included in further breeding to evolve better quality fine rice varieties suitable for our country.

Keywords: Rank, correlation coefficient, genetic divergence and fine rice

Introduction

Rice is the staple food of about 135 million people of Bangladesh. It provides nearly 48% of rural employment, about two-third of total calorie supply and about one-half of the total protein intake of an average person in the country. Rice sector contributes one-half of the agricultural GDP and one-sixth of the national income in Bangladesh. Almost all of the 13 million farm families of the country grow rice. Rice is grown

on about 10.5 million hectares which has remained almost stable over the past three decades. About 75% of the total cropped area and over 80% of the total irrigated area is planted to rice (Shelley *et. al.*, 2016)

Aromatic rice is rich with natural chemical compounds which gives it a distinctive scent. Numerous varieties of rice are aromatic, ranging from the famous Basmati to much lesser known Radhunipagal. It can be used just like

conventional rice for cooking, but adds a new dimension of flavor and aroma to meals. In the 1990s, aromatic rice began to explode on the popular market, leading to increased consumer demand and the development of numerous specific cultivars with unique flavors and aroma all their own. It is a delicious exportable excellent product of Bangladesh with attractive flavor which creates hunger. In any festival for making rich food like Polaow, Biriyani, Khichury, Firni, Kheer, and special dishes.rice etc. In addition, aromatic rice is very suitable for better health and digestion. In Bangladesh there are two varieties of Aromatic rice is found. Name of one is Chinigura and another is Kalijira. Both are small rice with attractive scent. Before export these rice are properly cleaned and make free from impurity. These two popular aromatic rice can be supplied from Bangladesh round the year with fluctuating price.

Measurement of correlation coefficient helps to identify the relative contribution of component characters towards yield (Panse, 1957). Moreover, the correlation between grain yield and a component character may sometimes be misleading due to an over estimation or under estimation for its association with other characters. Thus, yield components have influence on ultimate yield both directly and indirectly (Turkey, 1954). Splitting of total correlation into direct and indirect effects, therefore, would provide a more meaningful interpretation of such association. Path coefficient, which is a standard partial regression coefficient, specifies the cause and effect relationship and measures the relative importance of each variable (Wright, 1921). Therefore, correlation in combination with path coefficient analysis will be an important tool to find out the association and quantify the direct and indirect influence of one character upon another (Dewey and Lu, 1959). Considering the above facts the present study has been undertaken to assess the character association and contribution of characters towards grain yield of selected genotypes, and to find out the direct and indirect effect of component characters on grain yield with the help of correlation coefficient analysis.

The genetic diversity of various traits in local cultivars of rice is greatest in the area extending from Assam in India and Bangladesh to

Myanmar and northern Thailand, and to Yunnan Province in China (Oka, 1988). This area is characterized by topographical and hydrological heterogeneity, and is considered the center of diversity. Today genetic diversity in this area is being lost, since many rice growers are now growing modern cultivars.

The present investigation will be undertaken with the following objectives-

- To understand the association among grain yield and its component characters which ultimately would help for ranking of the characters enhancing yield.
- To study the diversity of 32 F₄ lines using cluster analysis and principle component analysis..
- To select the outstanding advanced lines with high grain yield and aroma content for further breeding.

Materials and Methods

The experiments were conducted in the Plant Breeding Research Field, Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur during T Aman season (1st July-December) of 2016. A total of thirty two F₄ lines were collected from the Department of Genetics and Plant Breeding The name of the parental lines with their F₄ generations is listed in Table 1 and Table 2. Data on different yield and yield contributing characters were recorded on plot and hill basis at different dates as per experimental requirement. Data recorded on the plant characters are shown in Table 3.

The genotypic and phenotypic correlation coefficients of yield and its different contributing characters were estimated by the formulae given by Johnson *et al.* (1955) and Singh and Chaudhary (2010). The data were subjected to principal component analysis (Rao, 1964) to group the lines into different clusters using non-hierarchical classification based on maximum variance and succeeded components with latent roots greater than unity (Jeger *et al.*, 1983). Genetic divergence based on thirteen characters was computed using GENSTAT 5.5 software program and the lines were clustered by using on hierarchical classification through covariance matrix. The intra and inter-cluster distances were measured following the D² statistics proposed by Mahalanobis (1936).

Table 1. Outline for the development of 32 F₄ lines through half diallel model

	FR1	FR2	FR3	FR4	FR5	FR6
FR1	xx	FR1×FR2 (Success)	FR1×FR3 (Success)	FR1×FR4 (Success)	FR1×FR5 (Failed)	FR1×FR6 (Failed)
FR2		xx	FR2×FR3 (Success)	FR2×FR4 (Success)	FR2×FR5 (Success)	FR2×FR6 (Failed)
FR3			xx	FR3×FR4 (Success)	FR3×FR5 (Failed)	FR3×FR6 (Failed)
FR4				xx	FR4×FR5 (Success)	FR4×FR6 (Failed)
FR5					xx	FR5×FR6 (Failed)

Note: FR1= Kataribhog, FR2= Kalozira, FR3= Chinigura, FR4= Badshabhog, FR5= Begunbichi and FR6= BRR1 dhan34

Table 2. List of the 32 advanced lines (F₄) of fine rice

Experimental cross	Selected F ₄ (PL) Lines
FR1×FR2	PL1, PL2, PL3 and PL4
FR1×FR3	PL5, PL6, PL7 and PL8
FR1×FR4	PL9, PL10, PL11 and PL12
FR2×FR3	PL13, PL14, PL15 and PL16
FR2×FR4	PL17, PL18, PL19 and PL20
FR2×FR5	PL21, PL22, PL23 and PL24
FR3×FR4	PL25, PL26, PL27 and PL28
FR4×FR5	PL29, PL30, PL31 and PL32

The F₄ generation of 32 advanced lines will be received from the department of Genetics and Plant Breeding

Table 3. Data on different yield and yield contributing characters of fine rice

Sl. No.	Name of the characters	Contribution on yield	Abbreviation	Sl. No.	Name of the characters	Contribution on yield	Abbreviation
1	Plant height (cm)	Negative	PH	7	Sterility percentage	Negative	SP
2	Productive tillers/hill (max. vegetative stage)	Positive	PTPH	8	Lodging percentage	Negative	LP
3	Panicle length (cm)		PL	9	1000-grain wt. (g)	Positive	TGW
4	Fertile grains/panicle	Positive	FGPP	10	Grain yield/hill (g)	Positive	GYPH
5	Sterile grains/panicle	Negative	SGPP	11	Days to 50% flowering		DTF
6	Panicle weight (g)	Positive	PW	12	Days to maturity		DTM
				13	Harvest index		HI

Results and Discussion

Analysis of variance

Highly significant mean squares due to genotypes were observed for all traits, indicated the existence of sufficient variation among the genotypes for yield and yield component characters and therefore, there is a scope for effective selection.

The panicle length varied due to variety shown in Table 4. Advanced lines are generally characterized by having longer panicles indicating their efficiency in partitioning of

assimilates to reproductive parts. This is one of the attributes of higher yields in advanced lines. According to Zhende (1988) hybrid rice have bigger panicles and more spikelets per panicle and thus in the study, PL 23 (29.57 cm) and PL 26 (28.97 cm) had produced the longest panicle among the advanced lines as seen in Table 4. The shortest panicle was registered by PL 25 (21.90 cm) The grand mean value for this trait was 25.66 cm. The significant differences in panicle length among the advanced lines of rice could be attributed to their genetic make-up. The number of fertile grains/panicle is another important as well as major yield contributing character in rice.

It directly contributes to the grain yield and maximum mean value was highly desirable for this trait. Genotypes evaluated here significantly differed in terms of the number of fertile grains per panicle. PL 6 (201.80) and PL 31 (190.00) produced maximum fertile grains/panicle, PL 27 produced the lowest number that is 130.10. The grand mean value for this trait was 160.81. Fernandez (2002) supported that hybrid rice produces long roots and broad leaves that enable them to take up more nutrients and produce more grains. Among all the genotypes PL13 and PL27 showed highest lodging percentage (29.33%) and PL 6 showed lowest percentage (6.00%), with a grand mean of 17.18%. The highly performing group was constituted by the genotypes PL6 (6.00%), PL7, PL8, PL16, PL22 and PL31 (10.33%) respectively. The lines which showed lowest performance of this trait were PL 13 (29.33%), PL 27 (29.33%), PL 3, PL4, PL12, PL14, PL18 and PL 25 (25.33%), respectively.

Among all the genotypes PL6 showed highest 1000-grain weight (19.83 g) and PL 30 showed lowest weight (8.78 g), with a grand mean of 15.118g. The highly performing group was constituted by the genotypes PL6 (19.83 g), PL 22 (19.58 g) and PL 23 (18.78 g), respectively. The group which showed lowest 1000-grain weight was PL 30 (8.78 g), PL 32 (10.78 g) and PL 14 (11.58 g), respectively. Grain yield is a function of interplay of various yield components such as number of productive tillers, grains/panicle. The highest grain yield/hill (41.51g/hill) was found in PL 6 and the lowest yield (8.77 gm/hill) was recorded in PL 13 with a grand mean of 20.66. Sinha and Bhattacharya (1980) observed that the genetic advance expressed as a percentage of the mean was highest for yield per plant. A comparative view of results of mean values for grain yield per hill (g) parameter of 32 advanced lines (F₄) of fine rice has been mentioned. Early maturing advanced lines are desirable as they produce more yields per day and fit well in multiple cropping systems. Highly significant difference was noted among the cultivars on the number of days from sowing to maturity. The range for days to maturity among all the genotypes varied from 94.00 days (PL 5) to 125.00 days (PL 29). The grand mean for days to maturity of all the genotypes was 105.02 days. The group of genotypes that showed maximum

days to maturity was constituted by PL 29 (125.00 days) and PL 24 (124.00 days), respectively. The group of genotypes which showed least number of days to maturity was constituted by PL 5 (94.00 days) and PL 27 (96.00 days), respectively. The earlier ripening of tested varieties was attributed to their varietal differences; others have shorter life span and attained physiological maturity stage faster than the other varieties. Hence this result shows the similarity of the findings that different varieties differ in their performance and adaptability to a certain environment (Ahmed *et al.*, 2010 and Bhuiyan *et al.*, 2014). The mean harvest index of the hybrids was recorded 32.41 percent and range varied from 27.50 percent (PL 1) to 35.67 percent (PL 5). Among all the genotypes, PL 5 showed maximum harvest index (35.67%) and PL 1 showed least harvest index (27.50%). The highly performing group included PL 5 (35.67%), PL 9 (35.48%) and PL 15 (34.64%), respectively. Moreover, the group with least performance for this character was constituted by the genotypes PL 1 (27.50%), PL 25 (28.66%) and PL 2 (29.48%), respectively. In the present study, the advanced line PL 5 (35.67%) is superior to all compared varieties for yield components. The yield increase of dwarf over tall varieties mainly resulted from higher harvest index; while the yield increase of hybrid rice over the dwarf varieties was mainly from higher biomass production (Jiang *et al.*, 1995). Yield differences among cultivars were due to HI. The superiority of hybrids for biomass over conventional varieties is reported widely (Kiniry *et al.*, 2001). 10-20% superiority of hybrids for total biological yield and grain yield (Blanco *et al.*, 1990). But the harvest indices were in general low in all the advanced lines.

Correlation coefficients estimation of yield and yield attributing characters

The genotypic and phenotypic correlations for yield and yield components are presented in Table 5. The genetic and phenotypic correlation coefficients among F₄ generation of rice yield and yield contributing traits showed that most of the traits have higher genetic correlation coefficients than corresponding phenotypic correlation coefficients. A perusal of these results revealed phenotypic and genotypic correlations to be of similar direction and significance. However, genotypic correlations had recorded a higher

Table 4. Mean values of different characters in F₄ generation of fine rice

Genotypes	PH	PTPH	PL	FGPP	SGPP	PW	SP	LP	TGW	GYPH	DTF	DTM	HI
1PLF ₄	139.0 k	8.33 d-g	27.38 de	180.600 f	28.400 a	2.877 ij	13.380 a	14.000 i	14.730 i	25.450 h	91.670 b	108.0 cd	27.500 n
2PLF ₄	136.8 lm	9.600 ab	25.62 g-i	143.900 r	17.17 hi	1.923 n	10.790 g	18.330 e	11.79mn	19.77 o	81.0 gh	109.0 bc	29.480 l
3PLF ₄	141.9 gh	9.267 bc	25.37 h-j	131.8 v	16.57 i-k	2.309 l	11.030 f	25.330 b	15.820 g	17.600 q	81.0 gh	106.7 de	31.570 i
4PLF ₄	136.8 lm	8.20 d-h	25.950 g	180.500 f	25.100 c	2.796 ij	11.980 c	24.330 b	14.000 j	18.510 p	80.0 g-i	96.670	32.63 fg
5PLF ₄	137.700 l	7.867 f-i	26.380 f	189.30 bc	25.230 c	3.445 cd	11.350 e	14.330 i	15.270 h	26.050 f	78.330 ij	94.000 k	35.670 a
6PLF ₄	124.8 r	8.867 cd	26.420 f	201.800 a	27.230 b	4.574 a	11.44 de	6.000 m	19.830 a	41.510 a	79.000 hi	96.000 J	34.3 cd
7PLF ₄	135.5 n	8.33 d-g	27.200 e	168.600 h	24.070 d	3.469 c	12.300 b	10.330 l	18.450 c	29.560 b	91.0 bc	104.000 f	34.60 bc
8PLF ₄	143.100 f	9.600 ab	25.120 j	161.900 k	16.6 i-k	2.799 ij	9.206 p	10.330 l	15.690 g	28.870 d	86.000 f	101.00 g	32.930 f
9PLF ₄	136.7 lm	9.267 bc	25.900 g	157.100 l	14.43 m	2.801 ij	8.449 u	14.33 i	16.490 f	25.820 g	86.670 ef	107.0 de	35.480 a
10PLF ₄	145.6 c	8.47 d-f	24.530 k	174.700 g	17.23 hi	3.320 c-f	8.781 rs	16.67 fg	16.890 ef	22.470 k	90.0 b-d	106.0 de	34.210 d
11PLF ₄	141.0 hi	8.50 d-f	23.53 lm	183.600 e	17.53 gh	2.973 hi	8.268 v	16.330 g	13.810 j	24.080 j	89.0 cd	108.0 cd	34.5 b-d
12PLF ₄	140.1 i-k	6.93 k-n	25.77 gh	187.80 cd	17.60 gh	2.741 j	8.791 r	25.330 b	13.040 k	15.810 s	81.330 g	107.0 de	32.63 fg
13PLF ₄	161.00 a	6.000 o	23.50 lm	135.100 u	16.30 jk	1.883 n	10.550 h	29.330 a	12.750 k	8.766z	86.000 f	105.00 ef	30.51 j-k
14PLF ₄	136.7 lm	7.53 h-k	23.13 m	162.60 jk	11.53 op	2.158 lm	6.670 z	24.670 b	11.580 n	16.020 s	88.00 de	104.000 f	32.890 f
15PLF ₄	144.4 de	8.0 e-h	27.72 cd	187.000 d	20.070 e	3.288 d-f	9.478 n	13.670 ij	14.850 i	24.360 i	90.0 b-d	104.000 f	34.640 b
16PLF ₄	136.4mn	8.33 d-g	24.370 k	163.800 j	20.570 e	3.376 c-e	10.950 f	10.330 l	18.950 b	29.290 c	91.0 bc	107.0 de	32.540 g
17PLF ₄	151.20 b	7.967 E-i	25.43 h-j	150.90 op	19.270 f	2.552 k	11.490 d	18.330 e	15.720 g	19.750 o	91.670 b	109.0 bc	30.730 j
18PLF ₄	142.6 fg	8.000 E-i	25.220 ij	156.000 l	14.70 m	1.855 n	8.637 t	25.330 b	11.99 l-n	12.270 x	95.00 a	110.00 b	30.300 k
19PLF ₄	145.3 cd	6.033 o	23.52 lm	152.1 no	13.070 n	2.971 hi	8.104 w	21.670 d	18.63 bc	14.540 v	92.000 b	107.0 de	32.060 h
20PLF ₄	130.3 p	6.367n-o	26.530 f	166.800 i	16.8 h-j	3.244 ef	9.116 pq	17.33 ef	17.640 d	18.510 p	92.000 b	107.0 de	30.710 j
21PLF ₄	144.2 e	6.7 l-o	23.630 l	141.400 s	11.370 p	3.072gh	7.563 y	18.33 e	18.72 bc	20.08 n	89.0 c-d	104.000 f	32.490 g
22PLF ₄	135.7mn	8.000 e-i	25.950 g	151.2 n-p	15.470 l	3.251 ef	9.370 o	10.330 l	19.580 a	28.490 e	86.000 f	99.000 h	34.4 b-d
23PLF ₄	130.70 p	7.13 j-m	29.570 a	152.8 mn	17.17 hi	3.178 fg	9.970 k	12.330 k	18.78 bc	21.750 l	92.000 b	108.0 cd	33.270 e
24PLF ₄	127.20 q	7.300 i-l	24.620 k	164.200 j	17.07 h-j	2.289 l	9.097 q	22.33 cd	12.02 lm	16.790 r	81.0 gh	124.00 a	33.480 e
25PLF ₄	129.90 p	6.100 o	21.900 n	139.200 t	13.070 n	1.789 n	8.682 st	25.330 b	11.71mn	10.260 y	81.0 gh	97.000 ij	28.66 m
26PLF ₄	133.30 o	7.933 e-i	28.970 b	150.3 o-q	16.83 h-j	2.697 jk	9.803 l	13.330 ij	17.010 e	20.76 m	86.00 f	102.00 g	32.78 fg
27PLF ₄	140.20 ij	6.5 m-o	24.400 k	130.100 v	9.600 q	1.624 o	6.955 z	29.330 a	12.260 l	9.762 z	76.670 j	96.000 j	31.760 hi
28PLF ₄	143.5 ef	8.567d-f	27.63c-e	138.00 t	15.90 kl	1.827 n	10.230 j	15.330 h	11.72mn	15.55 t	82.00 g	102.00 g	32.450 g
29PLF ₄	135.7mn	7.300 i-l	25.050 j	150.000pq	18.170 g	2.772 j	10.36 i	13.670 ij	16.570 f	20.75 m	78.000 ij	125.0 a	32.06 h
30PLF ₄	139.50 jk	7.833 f-j	27.970 c	154.100 m	13.230 n	2.098 m	7.670 x	22.670 c	8.780 p	12.76 w	81.00 gh	98.330 hi	32.460 g
31PLF ₄	126.8 q	7.70 g-j	27.63c-e	190.00 b	12.130 o	3.858 b	5.863 z	10.330 l	17.940 d	29.750 b	86.000 f	102.0 g	32.76 fg
32PLF ₄	136.3mn	8.43 d-g	25.35 h-j	148.800 q	16.43 i-k	1.860 n	9.615 m	12.67 jk	10.78 o	15.290 u	90.0 b-d	107.0 de	30.72 j
Total	4293.100	250.966	821.210	5146.000	555.940	87.669	305.938	549.610	483.790	660.998	2749.340	3360.700	1037.140
Mean	134.159	7.843	25.664	160.813	17.373	2.740	9.561	17.175	15.118	20.656	85.906	105.022	32.411

The mean values having same the letter (s) didn't differ significantly at 5% level of probability.

magnitude compared to phenotypic correlations indicating the masking effect of environment. Besides, Ganapati *et al.* (2014) reported that character association analysis among grain yield and yield contributing characters revealed that in most of the cases the genotypic correlation coefficient were higher than the respective phenotypic correlation coefficients. This indicated that the suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. Similar results were reported by Madhavalatha *et al.*, (2005). Since the phenotypic relationship was affected by environment at phenotypic level, it is resulted the low phenotypic correlation coefficients (Chaubey and Singh, 1994 and Ojo *et al.*, 2006). Grain yield revealed significant positive genetic association with productive tillers per hill, fertile grain per plant, panicle weight, 1000-grain weight and harvest

index both at genotypic and phenotypic levels. The findings suggest that grain yield can be improved in these rice genotypes by using these traits as selection criteria in succeeding generations. The results got conformity with the findings of Prasad *et al.* (2001) and Zahid *et al.* (2006) who showed positive correlations with these traits. Sterile grains per plant and lodging percentage were found negatively and significantly correlated with grain yield. Negative correlation coefficient of these two characteristics with grain yield indicated that low translocation of photosynthates from vegetative parts to spikelets at the time of fertilization and tallness in rice reduced the grain yield due to less grain filling and seed formation which is resulted lodging susceptibility (Tahir *et al.*, 1988 and Zahid *et al.*, 2006). Moreover, plant height and sterility percentage showed negative and non-significant association. Therefore, priority should be given to

these traits, while making selection for yield improvement. The findings are in agreement with the reports of Manikaminnie *et al.* (2013) for productive tillers per hill and Sudharani *et al.* (2013) for number of fertile grains per panicle. On the contrary, non-significant association was noticed for grain yield with panicle length only. The findings are in consonance with the reports of Yadav *et al.* (2010).

In the present study, days to 50% flowering exhibited a positive but non-significant association with panicle length (Yolanda and Das, 1995) and days to maturity (Debchoudhary and Das, 1998), and negative non-significant association was estimated for productive tillers per hill, which was opposite interpretation shown by Sawant *et al.* (1995). The results indicated a scope for simultaneous improvement of the traits. Similar results were reported by Sankar *et al.* (2006) and Singh *et al.* (2006).

The degree of correlation among the characters is an important factor especially in economic and complex character as yield. Steel and Torrie, (1984) stated that correlations are measures of the intensity of association between traits. The selection for one trait results in progress for all characters that are positively correlated and retrogress for traits that are negatively correlated. Plant breeders usually select for yield component traits which indirectly increase yield. The relationship between rice yield and its contributing characters has been studied widely at phenotypic level (Akinwale *et al.*, 2011; Hairmansis *et al.*, 2010; Sadeghi, 2010 and Ullah *et al.*, 2011). The grain yield is a complex trait, quantitative in nature and a combined function of a number of constituent traits. So the selection for yield may not be much satisfying unless other yield component traits are taken into consideration (Kumar and Saravanan, 2012). Understanding of correlation between yield and yield components are basic and foremost effort to find out strategies for plant selection. Correlation between yield and its component traits has effectively been used in identifying useful traits as selection criteria to improve grain yield in rice (Hasan *et al.*, 2013; Akinwale *et al.*, 2011; Sadeghi, 2010; Kole *et al.*, 2008; Mustafa and Elsheikh, 2007).

Genetic divergence analysis based on yield and yield contributing characters

The analysis of variance revealed significant differences among the genotypes for all the characters (Table 6). Based on D² values, all the genotypes could be grouped into six clusters using non-hierarchical Euclidean cluster analysis. The use of Mahalanobis D² statistics for estimating genetic divergence has been emphasized by many workers (Roy and Ponwar, 1993; Ramya and Kumar, 2008). Hence, based on relative magnitude of D² statistics the 32 F₄ genotypes of rice were grouped into six clusters. Maximum number of genotypes (eight) were included in cluster II followed by cluster VI with seven genotypes, cluster III and IV each comprised with six genotypes, cluster I included three genotypes and cluster V with 2 genotypes. The advanced lines (F₄) from the same cross combination were distributed in different clusters which may be due to differential adaptation of parental lines in different agro-ecosystems (Sabesan *et al.*, 2009 and Banumathy *et al.*, 2010). The intra and inter cluster average distances among six clusters were variable as indicated in Table 7. The highest intra-cluster distance was recorded for cluster IV (1.13) followed by cluster V (1.23) and cluster I (1.03) indicated genetic diversity among the genotypes belonging to these clusters. The genotypes belonging to the highest intra-cluster distance in the parenthesis (cluster IV) might develop good segregants by crossing the genotypes of the cluster. The clusters having low intra-cluster distances may not evolve good segregants upon hybridization (Kishore *et al.*, 2007 and Chandra *et al.*, 2007). The highest inter-cluster distance was observed between clusters I and V (16.53) suggested wide diversity between these clusters followed by cluster III and V (15.07), cluster IV and V (14.04) and cluster II and V (13.85). Therefore, advanced lines belonging to these clusters may be further used in hybridization program 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 least inter-cluster distance was observed between clusters II and IV (2.52) followed by clusters I and III (3.20) indicated close relationship between the genotypes of these clusters and hence, may not be

emphasized upon to be used in hybridization programs. The intra and inter- cluster distances among 32 F₄ are also presented by in the Fig. 1. The overall composition of the clustering pattern showed that parental lines collected from the same geographic origin were distributed in different clusters. Similar findings of non-correspondence of geographic origin with genetic diversity were also reported by Shanmugasundaram *et al.*, (2000) and Nayak *et al.*, (2004). Based on the values of principal component score 1 and 2 obtained from the PCA, a two-dimensional scatter diagram (Z1-Z2) using component score 1 as X-axis and component score 2 as Y-axis was constructed (Fig.2). The position of the genotypes in the scatter diagram was apparently distributed into six groups indicated the existence of considerable diversity among the genotypes. The clustering pattern confirmed the results obtained by divergence analysis (Ahmed *et al.*, 2010). The diversity was also supported by the appreciable amount of variation among the cluster means for different characters (Table 8).

Cluster VI and cluster I showed maximum cluster means for plant height (142.50cm) and productive tillers per hill (8.14), respectively. Cluster I showed the maximum cluster means for panicle length, fertile grains per panicle, grain yield and harvest index. For cluster IV recorded the maximum cluster mean value for days to 50% flowering and cluster II produced maximum cluster mean for 1000-grain weight. Thus, these genotypes hold great promise as lines for obtaining 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 9. Plant height contributed maximum towards genetic divergence (38.83 %) followed by productive tillers per hill (14.02 %) and panicle length (11.16 %). Remaining traits had little contribution towards genetic divergence and hence, they were of less importance. Since plant height and productive tillers contributed maximum towards the genetic divergence, Initiate direct selection based on correlation with grain yield of these two characteristics for diversity purpose.

Table 5. Genotypic and phenotypic correlation of yield and yield attributing characters in fine rice

		PTPH	PL	FGPP	SGPP	PW	SP	LP	TGW	GYPH	DTF	DTM	HI
PH	r _g	-0.103	-0.289	-0.339	-0.130	-0.359	0.076	1.175**	-0.206	-0.405	0.233	0.001	-0.147
	r _p	-0.087	-0.286	-0.337	-0.129	-0.358	0.075	1.165**	-0.205	-0.403	0.228	0.002	-0.146
PTPH	r _g		0.308	0.227	0.394	0.144	0.373	-0.502*	0.006	0.552*	-0.028	-0.031	0.195
	r _p		0.284	0.211	0.370	0.134	0.343	-0.469	0.001	0.515*	-0.026	-0.012	0.180
PL	r _g			0.265	0.342	0.318	0.276	-0.487*	0.195	0.345	0.060	-0.116	0.208
	r _p			0.261	0.338	0.315	0.273	-0.480*	0.191	0.341	0.055	-0.117	0.205
FGPP	r _g				0.589*	0.726**	0.243	-0.430	0.251	0.635**	0.064	-0.125	0.420
	r _p				0.585*	0.725**	0.242	-0.427	0.250	0.634**	0.063	-0.121	0.418
SGPP	r _g					0.494*	0.866**	-0.431	0.253	-0.562*	-0.017	-0.048	0.091
	r _p					0.492*	0.861**	-0.428	0.250	-0.559*	-0.015	-0.045	0.091
PW	r _g						0.171	-0.708**	0.818**	0.864**	0.172	-0.143	0.543*
	r _p						0.171	-0.705**	0.815**	0.863**	0.168	-0.142	0.541
SP	r _g							-0.273	0.177	-0.307	-0.013	0.058	-0.159
	r _p							-0.272	0.177	-0.306	-0.013	0.056	-0.159
LP	r _g								-0.615*	-0.864**	-0.228	0.023	-0.396
	r _p								-0.611*	-0.861**	-0.219	0.023	-0.393
TGW	r _g									0.690**	0.304	-0.021	0.376
	r _p									0.688**	0.294	-0.022	0.371
GYPH	r _g										0.083	-0.134	0.503*
	r _p										0.192	-0.133	0.500*
DTF	r _g											0.202	-0.108
	r _p											0.201	-0.107
DTM	r _g												-0.156
	r _p												-0.154

**and* indicates significant at 1% (0.01) and 5% (0.05) level of probability, rg= Genotypic correlation coefficient and rp=Phenotypic correlation coefficient

Table 6. Number and distribution of genotypes under different clusters in fine rice

Clusters	No. of Genotypes	Genotypes included
I	3	5PLF ₄ , 6PLF ₄ , 31PLF ₄
II	8	7PLF ₄ , 8PLF ₄ , 9PLF ₄ , 16PLF ₄ , 20PLF ₄ , 22PLF ₄ , 23PLF ₄ , 26PLF ₄
III	6	1PLF ₄ , 4PLF ₄ , 10PLF ₄ , 11PLF ₄ , 12PLF ₄ , 15PLF ₄
IV	6	14PLF ₄ , 17 PL F ₄ , 18PLF ₄ , 19PLF ₄ , 30PLF ₄ , 32PLF ₄
V	2	24PLF ₄ , 29PLF ₄
VI	7	2PLF ₄ , 3PLF ₄ , 13PLF ₄ , 21PLF ₄ , 25PLF ₄ , 27PLF ₄ , 28PLF ₄

Table 7. Inter and intra cluster distances (D² values) in F₄ generation of fine rice

	I	II	III	IV	V	VI
I	1.036					
II	7.885	0.798				
III	3.207	4.680	0.687			
IV	10.408	2.528	7.201	1.139		
V	16.534	13.853	15.071	14.045	1.232	
VI	13.686	5.871	10.504	3.509	13.397	0.949

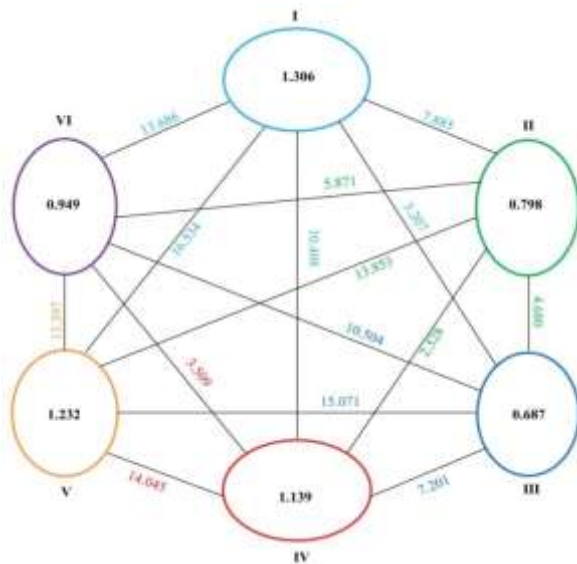


Fig.1. Graphical representation of Intra and Inter cluster distances in fine rice

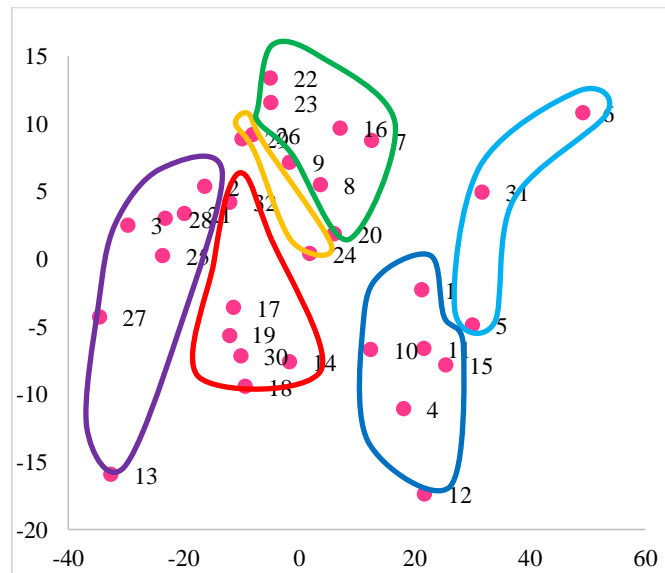


Fig. 2. Cluster diagram of 32 genotypes of fine rice developed from D² statistics and PCA I and PCA II values

Table 8. Cluster means of yield and yield attributing characters in fine rice

	I	II	III	IV	V	VI
PH	129.500	135.213	141.150	141.933	131.450	142.500
PTPH	8.145	8.121	6.683	7.633	7.300	7.547
PL	26.810	26.701	25.813	25.103	24.835	24.579
FGPP	193.700	159.063	182.367	154.083	157.100	137.071
SGPP	21.530	17.743	20.993	14.705	17.620	14.283
PW	3.959	3.1018	2.999	2.249	2.531	2.061
SP	9.551	9.896	10.106	8.698	9.864	9.411
LP	10.220	11.039	18.388	20.890	18.000	23.044
TGW	17.680	17.824	14.553	12.913	14.295	13.539
GYPH	32.437	25.381	21.780	27.645	18.770	14.541
DF	81.110	88.834	87.000	89.612	79.500	82.381
DM	97.333	104.375	104.945	105.888	124.500	102.814
HI	34.243	33.335	32.685	31.527	32.770	30.989

Table 9. Estimation of contribution towards genetic diversity in fine rice

Parameters	PH	PTPH	PL	FGPP	SGPP	PW	SP	LP	TGW	GYPH	DTM	DTF	HI	TOTAL
Contribution to genetic diversity (%)	38.83	14.02	11.16	8.12	7.36	6.50	5.71	4.83	1.80	1.30	0.20	0.13	0.04	100

Since the advanced lines with narrow genetic base are increasingly vulnerable to diseases and adverse climatic changes, availability of the genetically diverse genotypes for hybridization programs become more important.

Thirty-two advanced lines of rice were evaluated for yield and other twelve yield attributing characters. The present study brings out the retention of significant association among certain characters where selection may be practiced in the following generation. In this particular cross, the association among the characters and also with yield was high. Results of the present investigation on character association revealed the importance of productive tillers per hill and fertile grains per panicle, panicle weight and 1000-grain weight appeared as selection criteria for effective yield improvement of fine rice. The study also indicated the need for balanced selection in light of negative association of sterile grains per panicle and lodging percentage with yield per plant in crop yield improvement programs. Therefore, selection in any of these characteristics might result in the simultaneous improvement of other traits and finally resulting in increased grain yield. Further based on the aforementioned results it can be concluded that selection for the characters which were widely varied among genotypes would be more effective to bring simultaneous improvement for yield and yield components of rice.

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