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IDENTIFICATION OF F_2 AND F_3 SEGREGANTS OF FIFTEEN RICE CROSSES SUITABLE FOR CULTIVATION UNDER AEROBIC SITUATION

F. KAHANI and S. HITTALMANI[*]

Marker Assisted Selection Laboratory, Genetics and Plant Breeding, University of Agricultural Sciences, GKVK,
Bangalore-560 065, India
[*]Corresponding author's email: shailajah_maslab@rediffmail.com

SUMMARY

Genetic variability studies provide basic information on genetic parameters of the population based on which selection of genotypes and breeding strategy could be formulated for crop improvement. The estimates of heritability, coefficients of variability and genetic advance were computed in F_2 segregating populations of the 15 crosses for 14 characters. The selected F_2 plants were forwarded to generate F_3 families during dry season under aerobic conditions. The estimates of phenotypic coefficients of variation (PCV) were high and moderate for days between flowering and maturity (11.3%), number of tillers (20.0%), number of panicles (23.4%), 100 grain weight (18.7%), panicle exertion (13.5%), panicle length (20.1%), leaf width (12.2%), straw weight (23.5%) and grain yield (36.2%) in different crosses. High estimates of heritability coupled with high and moderate genetic advance was observed for all the plant traits. Correlation analysis indicated that flowering time, plant height, number of tillers, number of panicles, grain length, grain width, panicle length and straw weight had exhibited significant positive association with grain yield plant^{-1}. The correlation and regression coefficient between F_2 and F_3 generation for crosses MAS26 × IM88, OYC145 × MAS946-1 and IR64 × IM192 were significant for 50% flowering time, maturity time, plant height, productive tiller per plant, 100 grain weight, panicle length and grain yield. This indicated the effectiveness of selection for these characters.

Key words: Rice, aerobic, genetic variability, heritability, genetic advance, selection

Key findings: There was significant effect of environment on the selection of the genotypes under aerobic condition. High heritability for most traits was observed. The selection for yield in early generations may not be effective; hence, selection could be done in advance generations. There was high correlation between tiller number, panicle number and grain yield. These two traits had direct effect on grain yield.

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INTRODUCTION

Rice (*Oryza sativa* L.) is one of the world's most important food crops, feeding two thirds of the world's population (Sathya and Jebaraj, 2013; Kahani and Hittalmani, 2015). Asia is the biggest rice producer and consumer, accounting for 90 per cent of the world's production and consumption of rice (Sala *et al*., 2015). It plays a pivotal role in Indian economy being the staple food for two third of the population. India stands second with 108 million tons as China occupies the first place with 144 million tons in the world's production table of 479.3 million tons (Kumar *et al*., 2013). It frequently faces abiotic stresses in all these ecosystems except irrigated ecosystem (Manjappa *et al*., 2014).To keep up the rice production during irrigation water shortage, alternate methods of cultivation of rice is essential (Hittalmani and Shivashankar, 1987). One such strategy is cultivation of rice under aerobic situation (Venkataravana and Hittalmani, 1999). Aerobic rice has been considered a promising rice cultivation system as water scarcity is increasing in the world. Compared with lowland rice, water requirement in aerobic rice is reduced by more than 50 per cent, and water productivity increases by 60 per cent. Hittalmani and Shivashankar (1987) demonstrated that rice could be cultivated in dry sowing (aerobic) involving crosses using local rice of Karnataka.

In plant breeding programme, evaluation of genetic variability available in crop species is the first step to select better performing lines among the divergent group later quantifying the extent of variability created for traits of interest. The knowledge of heritability and genetic advance assist the breeders to decide and select superior plants with high heritability and genetic advance so that the plants can perform superior for the traits of interest in subsequent generations. Grain yield and other yield attributing traits are complex trait not only influenced by its associated characters but also by the environment. Further genotype and environment interaction reduces the effectiveness of early generation selection (Whan *et al*., 1981, Rahman *et al*., 1986). Large environmental differences may lead to failure of parental yield to be indicative of the yield of progeny (Barman and Borah, 2012). So, direct selection for improvement of grain yield in segregating populations may not be effective. The parent progeny correlation and regression between two generations shows lesser susceptible to environmental effect and is very useful for selection in segregating population for the production of new, improved genotypes (Suwarto *et al.,* 2015).

This necessitates the segregation of genetic variability from the total variability to make selection through correlation coefficient gives the extent of association present between any two traits, but fails to reveal the direct and indirect effects of each components of yield. Path coefficient analysis (Wright, 1921) facilitates to partition the correlation coefficient into direct and indirect effects, providing the relative contribution of each character. It also helps to elucidate the intrinsic nature of observed association and imparts confidence in the selection scheme.

Direct selection for yield often does not result in expected gains. Even when the related characters are individually operated, the result would be similar because of loose association of grain yield with its component characters. In such situations the success of selection could be enhanced with the use of selection index technique as it facilitates simultaneous improvement of a number of characters. Hence integration of information on genetic variability, correlation coefficient and path analysis helps in the selection programme to obtain better results.

It is essential to estimate the various types of gene action for the selection of appropriate breeding procedure to improve the quantitative and qualitative characters (Banumathy *et al.*, 2003; Sathya and Jebaraj, 2013). Keeping in view the genetic studies in aerobic rice were undertaken to compute the heritability, coefficients of variability and genetic advance in F_2 segregating populations of the 15 crosses for 14 characters, and also the response of selection for yield and its component characters through mean, percentage of population mean and through parent progeny correlation and regression method in between F_2 and F_3 generations.

MATERIALS AND METHODS

Fifteen F_2 populations were generated using diallel mating design (Griffing, 1956) by crossing six parental genotypes i.e.*,* MAS26, IM88, IM192, IR64, MAS946-1 and OYC145. The selection of parents for crosses was made based on genotypes that were tolerant and susceptible for moisture deficit conditions. IR64 dis drought susceptible and rest of the parents are moderately tolerant (MAS26 and OYC145) and tolerant (MAS946-1, IM88 and IM192). Staggered sowing of the selected parental genotypes was done to achieve synchronization in the flowering for effective crossing programme to generate F_1. The seedlings were raised during dry season following all the recommended agronomic practices. At panicle emergence and flowering stage, the florets of female parents were hand emasculated early in the morning, before 7 a.m. and later the pollen was collected from male parent and dusted on to the stigma within 11 am. The seeds set on female plants were harvested, around 25-27 days after crossing event. Fifteen crosses were made by pair wise combination during dry season, at K block, UAS, Bangalore. The diallel design estimates combining ability of the parents/traits and helps to identify combination of traits desired by the breeder in the next generation.

Trait evaluation of F_2 generation population

The F_2 seeds of all the 15 crosses of rice were directly sown in the field under moisture scarce aerobic situation during dry season-2013. The crop was grown under aerobic condition non-transplanted and directly sown. The field was kept at field capacity. Irrigation was given at 2 cm depth twice a week at 4 days interval. A total of 480-500 mm of irrigation was provided (Gandhi *et al.*, 2012). Single seeds per hill were planted at spacing of 25 × 25 cm. An average of 300 population size for each cross was maintained along with two rows parental lines. Mean values were utilized for statistical analysis and the characters observed for eliciting the information are: flowering time, days between flowering and maturity, maturity time, plant height (cm), number of tillers plant^{-1}, number of panicles plant^{-1}, productive tillers plant^{-1}, mother panicle weight (g), 100 grain weight (g), panicle length (cm), panicle exertion (±cm), leaf length (cm), leaf width (cm), grain length (mm), grain breadth (mm), straw weight (g) and grain yield plant^{-1} (g).

Evaluation of F_3 families

F_3 families were raised during the dry season-2014. Among the 15 crosses that were evaluated in F_2, three best performing crosses were selected and 250 plants were forwarded to generate F_3 families. The crosses selected were MAS26 × IM88, OYC145 × MAS946-1 and IR64 × IM192. Two hundred fifty plants in each F_3 family were evaluated for traits 50% flowering time, maturity time, Plant height, Productive tiller per plant, 100 Grain weight, Panicle length and Grain yield. Progeny mean, range and percentage of population mean for selected individual for each population were estimated. Mean values were used to estimate the parent offspring correlation and regression between F_2 and F_3 generation.

Statistical analysis

The quantitative traits observed in the 15 crosses in F_2 and F_3 were subjected to for statistical analysis. The average of the traits were estimated for descriptive statistics Sunderaraj *et al.*, (1972) for mean, range, standard variation, skewness and curtosis were estimated as per Snedecor and Cochran (1974). SPSS (Version 11.0.1, SPSS Inc.) program was used to analyze the coefficient of the above statistical parameters Burton and De Vane (1953). Other parameters, genetic variability, PCV, heritability (h^2) and genetic advance were estimated as given by Johnson *et al*. (1955).

RESULTS AND DISCUSSION

The analysis of variance for parents and F_2 progenies revealed highly significant differences among the genotypes for all the characters studied, indicating the existence of enormous variability in the experimental material. Data on variability, heritability, genetic advance and genetic advance percent mean are presented for F_2 population is shown in Table 1. The estimates of GCV were lower than that of PCV for almost all the characters, indicating some influence of environment on the traits. However, relatively small differences between GCV and PCV for these characters indicated that these were predominantly governed by the genetic factors.

In F_2 population, maximum GCV was observed for grain yield plant^{-1} (35.9%) followed by number of panicles (22.8%), panicle exertion (22.7%). The phenotypic coefficients of variation (PCV) was maximum for characters grain yield plant^{-1} (36.2%) followed by straw weight (23.5%), number of panicle (23.4%) and number of tillers (20.0%). Similar findings were also reported by Panwar and Mathur (2007), Venkanna *et al.*, (2014) and Warkand *et al.*, (2014).

Heritability is a fraction of variance in phenotypic expression that arises from genetic effect. The nature of selection units and sampling errors also influences greatly the magnitude of heritability estimates. The heritability estimates in segregating generation helps to know genetic variance of genotype-environment interaction and genetic component to be expected from selection in the next generation.

Table 1. Genetic variability, heritability, genetic advance and genetic advance percent mean for F_2 population.

Characters	PCV	GCV	h^2	GA	GA % MEAN
FT	5.1	5.1	97.8	10.2	10.4
DFM	11.3	11.0	95.5	9.0	22.3
MT	6.8	6.7	99.0	19.1	13.8
PHT	11.1	10.7	92.2	12.6	21.2
NT	20.0	19.4	93.2	8.6	38.7
NP	23.4	22.8	94.9	8.7	45.8
100 GW	18.7	18.4	73.4	14.6	43.0
GL	11.9	10.6	62.1	0.2	13.5
GW	3.1	2.4	62.5	0.3	3.5
LW	12.2	11.6	86.7	8.0	34.3
PL	20.1	19.9	98.2	5.2	40.4
PE	13.5	22.7	68.3	0.4	4.3
SW	23.5	6.5	40.3	1.6	8.3
GYLD	36.2	35.9	98.2	6.0	40.2

Heritability was high for all the characters and ranged from 40.3% for straw weight to 99.0% for maturity, however the GA was low. According to Johnson *et al.* (1955), heritability estimates along with genetic gain would be more useful than the former alone in predicting the effectiveness of selection. Therefore, it is essential to consider the predicted genetic advance along with heritability estimate as a tool in selection programme for better efficiency. In this investigation, high heritability coupled with moderate genetic advance was observed for grain yield plant^{-1} (98.2%; 6.0), flowering time (97.8%; 10.2), maturity (99.0%; 19.1), plant height (92.2%; 12.6) and 100-grain weight (73.4%; 14.6). High heritability and moderate genetic advance suggested the predominant role of non-additive gene action in their inheritance and selection in later generation would be more effective. Suman *et al.,* (2005), Shukla *et al.*, (2005) indicated the same result.

Grain yield is the ultimate result of several complex characters, inheriting with one another and with the environment. Knowledge of association of different yield components with the yield and their interrelationships will help in improvement of yield through selection of component characters exhibiting strong favorable association. The relationship between yield and its main contributing traits, in segregating population of rice, has been studied by several researchers (Venkataramana and Shailaja, 1999b; Venkataramana and Shailaja, 2000). An overview of the correlation analysis (Table 2) indicated that flowering time, plant height, number of tillers, number of panicles, grain length, grain width, panicle length and straw weight had exhibited significant positive association with grain yield plant^{-1}. Thus, one can conclude from our findings that selection of traits with high positive significant association on grain yield can help in improving yield. Development of genotypes with higher number of panicles, panicle length might help in improving yield (Nandan *et al.*, 2010). Significant negative association was observed for traits days between flowering and maturity, 100-grain weight and panicle exertion with grain yield plant^{-1}. Negative correlation of 100-grain weight with yield suggest that enhancement of grain weight is not improving the grain yield (Nandan *et al.*, 2010).

Path coefficient analysis is used to partition the association among characters into direct and indirect effects and measures the relative importance of the causal factors involved. It allows separating the direct effect and their indirect effects through other attributes by apportioning the correlations (Wright, 1921) for better interpretation of cause and effect relationship. The results of the path analysis will help the breeder to decide the combination of the correlated traits for selection in an effective manner. The selection will be very effective by selecting more traits at a time to increase the yield directly by selecting the surrogate traits that enhance the grain yield in addition to the correlated traits and their magnitude (Figure 1). The estimates of path coefficient analysis are reported in Table 3.

Table 2. Phenotypic correlations among traits in F$_2$ generations.

Characters	FT	DFM	MT	PHT	NT	NP	100 GW	GL	GW	LW	PL	PE	SW	GYLD
FT	1													
DFM	0.13*	1												
MT	0.87**	0.6	1											
PHT	-0.42**	-0.15**	-0.39**	1										
NT	-0.21**	-0.29**	-0.29**	0.32**	1									
NP	-0.16	-0.3**	-0.26**	0.30**	0.99**	1								
100 GW	-0.29**	0.23**	-0.12	-0.11*	-0.51**	-0.55**	1							
GL	-0.40**	-0.11*	-0.43**	-0.08	0.21**	0.19**	0.04	1						
GW	0.27**	-0.13**	0.15	0.14**	0.09	0.15**	-0.57**	0.01	1					
LW	0.32**	-0.01	0.22**	-0.46**	0.01	0.06	0.06	0.25**	0.01	1				
PL	0.01	-0.27**	-0.15	0.07	0.32**	0.35**	-0.18**	0.57**	0.16**	0.32**	1			
PE	0.19**	0.11*	0.28**	0.01	-0.14**	-0.14**	0.06	-0.63**	0.11*	-0.38**	-0.27**	1		
SW	-0.03	-0.11*	-0.07	0.53**	0.63**	0.66**	-0.45**	0.09	0.47**	0.01	0.50**	-0.17**	1	
GYLD	0.17**	-0.26**	0.01	0.28**	0.65**	0.67**	-0.58**	0.17**	0.65**	0.06	0.53**	-0.13*	0.81**	1

*significant @ *P* = 0.01, **significant @ *P = 0.05*

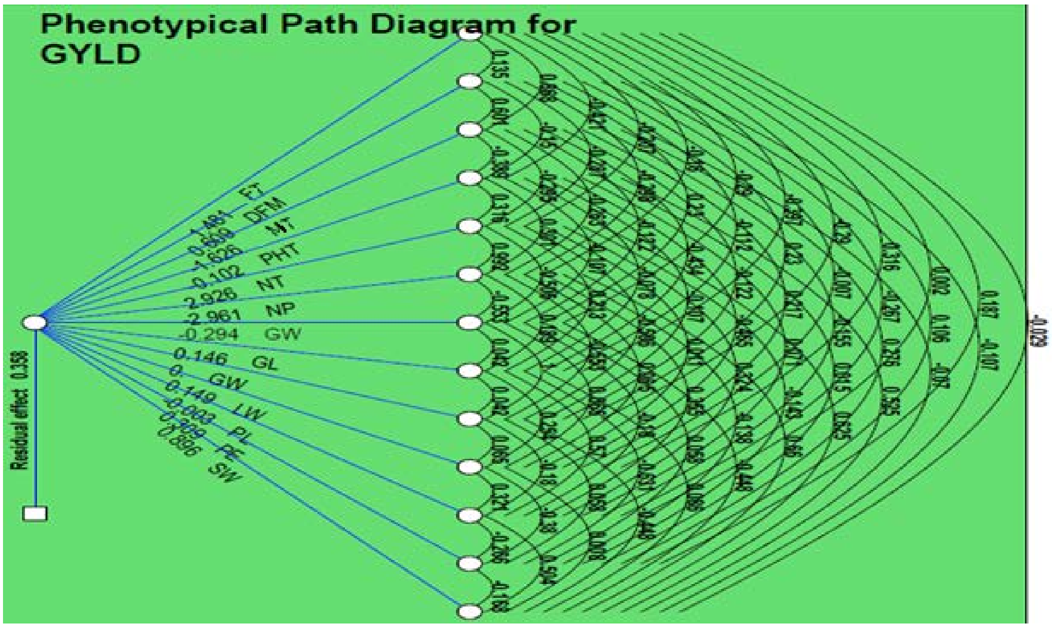
FT = flowering time, PHT = plant height, GW = grain width, LW = leaf width, SW = straw weight, DFM = days between flowering and maturity, NT = number of tillers plant^{-1}, GL = grain length, PL = panicle length, GYLD = grain yield plant^{-1}, MT = maturity time, NP = number of panicles, 100-GW = hundred grain weight, PE = panicle exertion

Table 3. Genotypic direct (diagonal) and indirect effects of different quantitative traits in F$_2$ generation.

Characters	FT	DFM	MT	PHT	NT	NP	100-GW	GL	GW	LW	PL	PE	SW	'r' values
FT	-1.36	-0.10	1.64	0.06	-0.43	0.19	-0.15	0.27	0.28	-0.10	0.01	-0.14	0.01	0.17**
DFM	-0.18	-0.80	1.13	0.02	-0.60	0.35	0.12	0.07	-0.14	0.01	-0.20	-0.08	0.04	-0.25**
MT	-1.18	-0.48	1.89	0.06	-0.60	0.30	-0.06	0.29	0.16	-0.07	-0.11	-0.21	0.02	0.01
PHT	0.57	0.12	-0.74	-0.14	0.66	-0.35	-0.06	0.05	0.15	0.15	0.05	-0.01	-0.18	0.27**
NT	0.29	0.23	-0.55	-0.05	2.06	-1.16	-0.26	-0.14	0.09	0.01	0.23	0.10	-0.21	0.65**
NP	0.22	0.24	-0.49	-0.04	2.04	-1.17	-0.28	-0.13	0.16	-0.02	0.26	0.10	-0.22	0.67**
100-GW	0.39	-0.18	-0.23	0.02	-1.05	0.64	0.50	-0.03	-0.60	-0.02	-0.13	-0.04	0.15	-0.58**
GL	0.54	0.09	-0.81	0.01	0.43	-0.22	0.02	-0.68	0.01	-0.08	0.42	0.46	-0.03	0.17**
GW	-0.37	0.10	0.28	-0.02	0.19	-0.18	-0.29	-0.01	1.05	0.01	0.12	-0.08	-0.16	-0.58**
LW	-0.43	0.01	0.41	0.07	0.02	-0.07	0.03	-0.17	0.01	-0.32	0.23	0.28	0.01	0.05
PL	0.01	0.22	-0.28	-0.01	0.66	-0.41	-0.09	-0.39	0.17	-0.10	0.73	0.20	-0.17	0.53**
PE	-0.26	-0.09	0.53	0.01	-0.29	0.16	0.03	0.43	0.12	0.12	-0.20	-0.74	0.06	-0.13*
SW	0.04	0.09	-0.13	-0.08	1.30	-0.77	-0.23	-0.06	0.50	0.01	0.37	0.13	-0.34	0.81**

* Residual effect = 0.358

FT = flowering time, PHT = plant height, GW = grain width, LW = leaf width, SW = straw weight, DFM = days between flowering and maturity, NT = number of tillers plant^{-1}, GL = grain length, PL = panicle length, GYLD = grain yield plant^{-1}, MT = maturity time, NP = number of panicles, 100-GW = hundred grain weight, PE = panicle exertion



FT = flowering time, PHT = plant height, GW = grain width, LW = leaf width, SW = straw weight, DFM = days between flowering and maturity, NT = number of tillers plant^{-1}, GL = grain length, PL = panicle length, GYLD = grain yield plant^{-1}, MT = maturity time, NP = number of panicles, 100-GW = hundred grain weight, PE = panicle exertion

Figure 1. Path diagram for F_2 population.

Among all the traits studied, number of tillers plant^{-1} (2.06) had highest positive direct effect on grain yield followed by maturity (1.89), grain width (1.05), panicle length (0.73) and 100-grain weight (0.50). The results are in conformity with the findings of Ekka *et al.*, (2011) for 100-grain weight and panicle length. The characters such as grain width and panicle length had positive correlation with grain yield plant^{-1} indicating the true relationship among these traits. This may indicate that the direct selection for panicle length would likely be effective in increasing grain yield in rice. However traits such as flowering time (-1.36), plant height (-0.14), number of panicles (-1.17), leaf width (-0.32), straw weight (-0.34), days between flowering and maturity (-0.80), grain length (-0.68), panicle exertion (-0.74) had negative direct effect on grain yield as suggested by Akthar *et al.*, (2011) and Ravindra Babu *et al.*, (2012).

The characters number of tillers had positive indirect effect on yield through flowering time (0.29) and days between flowering and maturity (0.23). 100-grain weight had positive indirect effect through flowering time (0.39) and number of panicles (0.64). Panicle length had a positive indirect effect through days between flowering and maturity (0.22), number of tillers (0.66) and panicle exertion (0.20). The lower residual effect indicated that different traits other than the characters considered in this study could influence grain yield considerably.

The yield performance and other attributing characters of F_3 families raised from the selected F_2 populations on the basis of phenotypic performance of the crosses did not show much encouraging results (Tables 4, 5 and 6). Out of 15 crosses only three families could be identified as promising families in F_3 generation. Thus, there was practically no relation between the yield of individual F_2 selection and the mean yield of corresponding F_3 families. Similar findings were also reported by Suwarto *et al.*, (2015), Barman and Borah (2012). Thus selection based on phenotypic performance for yield in early generation could be ineffective. Hence it is warranted that selection for grain yield be postponed until later generations.

In respect of plant height, number of productive panicles, 100 Grain weight, Panicle length and grain yield per plant in F_3 generation showed high mean performance and lower percentage of population mean than in F_2 generation in crosses MAS26 × IM88, OYC145 × MAS946-1 and IR64 × IM192.

Table 4. Mean performance of selected plants in F_2 and F_3 generation for different characters in cross MAS26 × IM88.

Characters	F_2 Population				F_3 Population			
	Range	Mean	% of F_2 population mean		Range	Mean	% of F_3 population mean	
			Min.	Max.			Min.	Max.
Flowering time	84 - 102	91	94	111	87 - 95	90	97	104
Maturity	119 - 143	131	93	108	123 - 137	130	95	105
Plant height	49 - 94	68	69	126	51 - 75	66	80	113
No. of productive panicles	8 - 33	25	126		10 - 30	26	115	
100 Grain weight	2.2 – 2.6	2.5	102		2.4 – 2.5	2.5	100.6	
Panicle length	12 - 27	20.2	118.9		13 – 26	21.1	117.8	
Grain Yield per plant	13- 58	39.2	134.9		14 - 50	40.4	120.9	

Table 5. Mean performance of selected plants in F_2 and F_3 generation for different characters in cross OYC145 × MAS946-1.

Characters	F_2 Population				F_3 Population			
	Range	Mean	% of F_2 population mean		Range	Mean	% of F_3 population mean	
			Min.	Max.			Min.	Max.
Flowering time	80 - 99	90	95	99	86 - 93	89	95	103
Maturity	113 - 145	126	89	114	116 - 134	125	91	106
Plant height	55 - 124	90	60	136	60 - 96	85	68	111
No. of productive panicles	12 - 39	27	139		13 - 40	28	138	
100 Grain weight	3.1 – 3.9	3.5	113.7		3.2 – 4	3.6	109.6	
Panicle length	17 - 26	22	112.7		17 - 25	23.2	102.8	
Grain Yield per plant	17 - 66	45	143.9		19 - 60	46.2	122.9	

Table 6. Mean performance of selected plants in F_2 and F_3 generation for different characters in cross IR64 × IM192.

Characters	F_2 Population				F_3 Population			
	Range	Mean	% of F_2 population mean		Range	Mean	% of F_3 population mean	
			Min.	Max.			Min.	Max.
Flowering time	87 - 104	96	88	106	89 - 98	95	92	102
Maturity	121 - 147	133	89	109	124 - 139	132	91	103
Plant height	42- 101	69	56	143	50 - 89	66	73	132
No. of productive panicles	10 - 35	22	148		14- 33	23	141	
100 Grain weight	2.5 –2.7	2.6	100.2		2.6 –2.7	2.64	100.3	
Panicle length	12 - 23	19	112.6		16 - 23	20.1	104.4	
Grain Yield per plant	20 - 50	40.3	121.2		22 - 49	40.6	117.1	

Moreover all the characters showed strong correlation and regression between F_2 and F_3 generation

The intergeneration correlation and regression for yield component characters are presented in Tables 7, 8 and 9. The F_2 generation showed significant positive correlation and regression with F_3 generation for 50% flowering time, maturity time, plant height, productive tillers per plant, 100 grain weight, panicle length and grain yield. The highest correlation in the cross MAS26 × IM88 was observed in plant height (0.94) and lowest is 100 grain weight (0.30). The highest correlation in the cross OYC145 × MAS946-1 was observed in maturity time (0.96) and lowest is panicle length (0.43). The highest correlation in the cross IR64 × IM192 was observed in maturity time (0.94) followed by 50% flowering time (0.93), grain yield (0.92) and lowest is panicle length (0.63). The findings were consistent with the findings Suwarto *et al.,* (2015), Barman and Borah (2012). This indicated the effectiveness of selection for these characters. These results were also consistent with the mean performance of the F_2 selection and F_3 progeny mean performance. (Tables 7, 8 and 9; Figures 2-4).

Table 7. Parent offspring correlation in F_2 and F_3 and regression of the crosses over segregating generation for different characters in cross MAS26 × IM 88.

Characters	Correlation coefficient F_2	Correlation coefficient of F_3	Correlation coefficient between F_2 and F_3	Regression coefficient between F_2 and F_3
Flowering time	-0.08	-0.01	0.62**	0.40**
Maturity	0.12*	0.04	0.87**	0.54**
Plant height	0.16**	0.04	0.94**	0.68**
Productive tiller per Plant	0.60**	0.44**	0.81**	0.63**
100 Grain Weight	-0.001	-0.08	0.30**	0.12**
Panicle Length	0.001	0.03	0.70**	0.78**
Grain Yield	-	-	0.80**	0.73**

* significant @ *P* = 0.05, ** significant @ *P* = 0.01

Table 8. Parent offspring correlation in F_2 and F_3 and regression of the crosses over segregating generation for different characters in cross OYC145 × MAS946-1.

Characters	Correlation coefficient F_2	Correlation coefficient of F_3	Correlation coefficient between F_2 and F_3	Regression coefficient between F_2 and F_3
Flowering time	-0.01	0.06	0.49**	0.30**
Maturity	-0.06	0.06	0.96**	0.81**
Plant height	0.02	0.03	0.77**	0.55**
Productive tiller per Plant	-0.05	0.06	0.85**	0.86**
100 Grain Weight	-0.11**	-0.06	0.53**	0.51**
Panicle Length	0.04	-0.05	0.43**	0.42**
Grain Yield	-	-	0.65**	0.53**

* significant @ *P* = 0.05, ** significant @ *P* = 0.01

Table 9. Parent offspring correlation in F_2 and F_3 and regression of the crosses over segregating generation for different characters in cross IR64 × IM 192.

Characters	Correlation coefficient F_2	Correlation coefficient of F_3	Correlation coefficient between F_2 and F_3	Regression coefficient between F_2 and F_3
Flowering time	0.05	0.002	0.93**	0.66**
Maturity	0.12*	0.09	0.94**	0.74**
Plant height	-0.04	-0.04	0.82**	0.69**
Productive tiller per Plant	0.07	0.04	0.81**	0.80**
100 Grain Weight	-0.05	0.15**	0.77**	0.70**
Panicle Length	0.012	0.12*	0.63**	0.41**
Grain Yield	-	-	0.92**	0.88**

* significant @ *P* = 0.05, ** significant @ *P* = 0.01

This study will help the breeders to select for between to flowering and maturity in early generation with grain yield. The results indicated that there is a substantial effect of environment on the traits observed under dry cultivation of rice under aerobic conditions. There was also influence of genotypes in some crosses. The selection of grain yield under aerobic condition is possible but it needs to be postponed to later generations and role of number of panicles had maximum positive effect on grain yield and could be used for selection. This investigation assists breeders to select desirable genotypes suitable for moisture deficit in aerobic conditions.

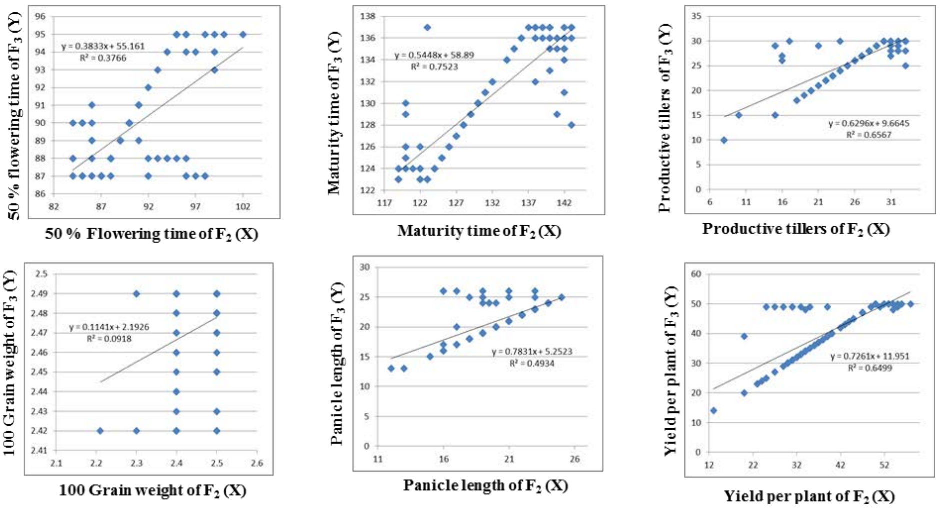


Figure 2. Parent progeny relationship in different traits (based on F_2, F_3) in cross MAS-26 × IM-88.

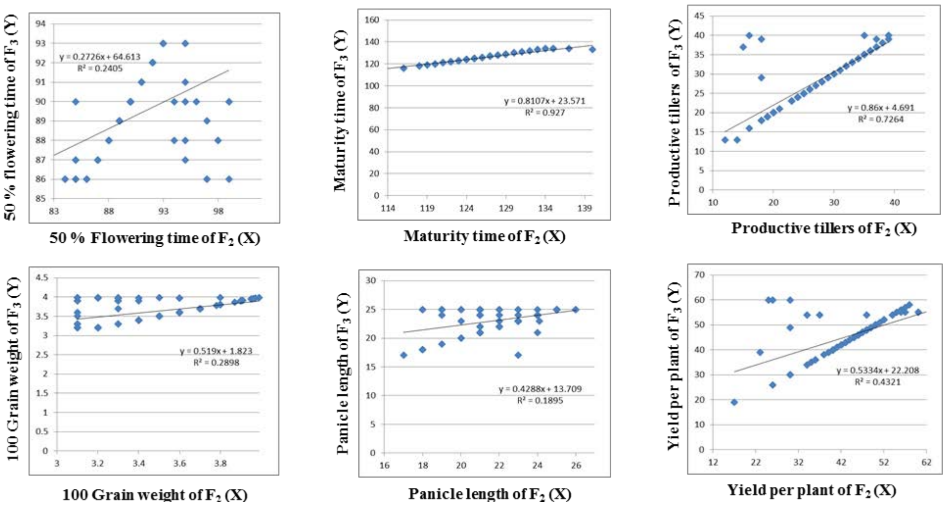


Figure 3. Parent progeny relation in different traits (based on F_2, F_3) in cross OYC-145 × MAS946-1.

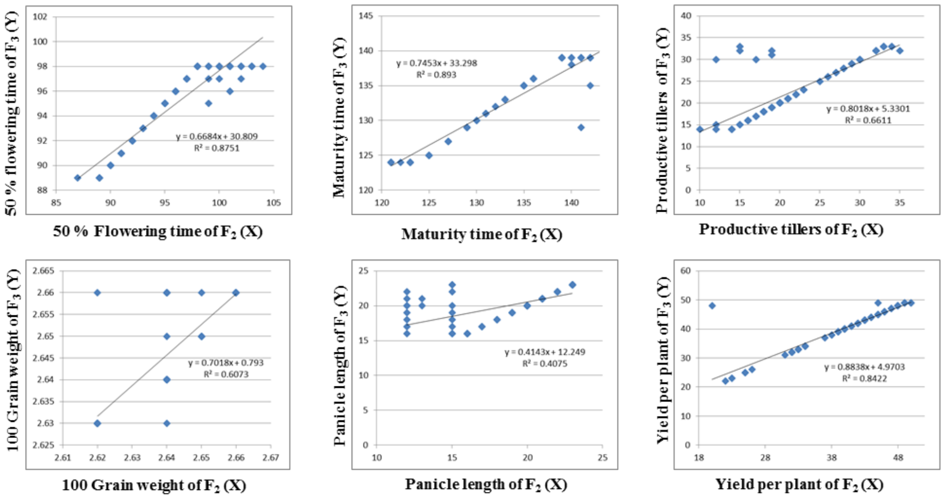


Figure 4. Parent progeny relationship in different traits (based on F_2, F_3) in cross MAS-26 × IM-192.

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