

Original Research Article

<https://doi.org/10.20546/ijcmas.2018.703.289>

## Genetic Variability and Inter Relationship among the Gene Pyramided BC<sub>4</sub>F<sub>4</sub> Generation Lines for Yield and Yield Attributing Characters in Rice (*Oryza sativa* L.)

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### ABSTRACT

#### Keywords

Variability,  
Heritability, Genetic  
advance, Correlation,  
Path analysis

#### Article Info

Accepted:  
20 February 2018  
Available Online:  
10 March 2018

An investigation was carried out in the BC<sub>4</sub>F<sub>4</sub> generation with 95 plants for studying variability, correlation and path analysis. Low PCV and GCV values were recorded for the characters namely, days to fifty percent flowering, plant height, panicle length, number of productive tillers, grain length, grain width and hundred seed weight. High heritability coupled with high genetic advance as percentage of mean was observed for plant height, panicle length, number of productive tillers, grain width, seeds per panicle. The correlation studies revealed that the number of productive tillers and plant height recorded significant positive correlation with yield. The path coefficient analysis shows that the number of productive tillers recorded positive direct effect on the plant yield.

### Introduction

Rice (*Oryza sativa* L.) is the staple food for more than half of the world's population (Akhtar *et al.*, 2010). China and India account for more than half of the world's rice areas and consume more than three – quarters of the global rice production (Hossain, 1997; Maclean *et al.*, 2002). It is probably the most diverse crop as it is produced in a wide range of locations and under a wide variety of climatic conditions from the submerged areas in the world to the dried deserts. In the rice, major economic losses in the field are due to

various biotic stress including insect pests like stem borer, brown plant hopper (BPH), green leafhopper (GLH), leaf folder and gall midge and diseases like blast, bacterial blight (BB), sheath blight, leaf spot, sheath rot.

Among the biotic stresses, incidence of gall midge and diseases like blast, bacterial leaf blight are economically important as they cause significant yield reduction. Knowledge on genetic variability forms the basic prerequisite for any crop improvement programme. The present study was undertaken with the aim of phenotyping of BC<sub>4</sub>F<sub>4</sub>

generation for yield and yield component traits for studying variability, correlation and path analysis.

## Materials and Methods

The seed material from the selected gene pyramided plants of BC<sub>4</sub>F<sub>3</sub> population involving CO43 as the recurrent parent was used to take up sowing to generate BC<sub>4</sub>F<sub>4</sub> generation. F<sub>4</sub> generation of the cross involves viz., {[CO43\*4 //// (B<sub>95-1</sub> X Abhaya)]} / [CO43\*4 //// (B<sub>95-1</sub> X Tetep)] / [CO43\*4 //// (B<sub>95-1</sub> X Kavya)] involving CO43 as the recurrent parent were genotyped for Gall midge (*Gm1* and *Gm4*) and bacterial blight(*Xa21* and *xa13*) resistance genes using molecular markers. B<sub>95-1</sub> X Kavya was used as donor for *Gm1*, B<sub>95-1</sub> X Abhaya was used as donor for *Gm4* and *xa13*, B<sub>95-1</sub> X Tetep was used as donor for *Xa21*. The seeds of donor and recurrent parents were also sown along with the gene pyramided lines for evaluating the agronomic performance. The seeds were sown in separate rows in nursery beds. The seedlings were transplanted at 25DAS at a spacing of 20x10cm and recommended agronomic practices were followed. Randomised block design was followed for the field experiment with three replications. For measuring the biometric parameters of the gene pyramided BC<sub>4</sub>F<sub>4</sub> lines and their parents, five plants were selected for each replication and the mean values were calculated for all the replications. The mean value of all the three replications was considered as the final mean value for that character. The selected lines were evaluated for yield and yield attributing parameters like days to fifty percent flowering, plant height, number of productive tillers, panicle length, number of filled grains per panicle and single plant yield. Statistics analysis such as mean and phenotypic and genotypic co-efficient of variation (PCV and GCV) were computed based on the method given by Johnson *et al.*, (1955), heritability in

the broad sense by Lush (1940) and genetic advance by Johnson *et al.*, (1955). The correlation by Johnson *et al.*, (1955) and path analysis by Dewey and Lu (1959) were calculated.

## Results and Discussion

### Variability analysis for agronomic traits in BC<sub>4</sub>F<sub>4</sub> generation

The phenotypic and genotypic coefficient of variation (PCV and GCV) provides a measure to compare the variability present in the traits. High values of these parameters indicate the presence of the wider variability and *vice versa*. The existence of narrow differences between PCV and GCV implies lesser influence of environment on these traits. They were calculated for the selected gene pyramided lines of BC<sub>4</sub>F<sub>4</sub> generation. The PCV values were greater than the GCV values for all the traits studied, indicating the environmental influence on the phenotypic expression of the characters.

Low PCV and GCV values were observed for days to 50 percent flowering. Moderate PCV and GCV values were observed for panicle length and grain width. High PCV and GCV values were observed for seeds per panicle, hundred seed weight and single plant yield (Table 1). Similar results were obtained for grain length by Vanaja and Babu (2006), days to 50 percent flowering and panicle length by Bisne *et al.*, (2009), days to 50 percent flowering, plant height, number of productive tillers, hundred grain weight and panicle length by Seyoum *et al.*, (2012). Ogunbayo *et al.*, (2014) reported similar results for the traits plant height, panicle length, grain length, and grain width. The lower values of PCV and GCV for the traits mentioned above are due to the repeated backcrossing. The results were in agreement with the findings of Pandey *et al.*, (2012).

**Table.1** Genetic analysis in gene pyramided lines of BC<sub>4</sub>F<sub>4</sub> generation

Characters	PV	GV	PCV (%)		GCV (%)		h <sup>2</sup>		GA	GA as percentage of mean	
DFE	26.80	23.67	5.36	Low	5.04	Low	88.34	High	9.42	9.76	Low
PH	98.04	94.39	10.18	Moderate	9.99	Low	96.28	High	19.64	20.19	High
NPT	37.78	35.51	43.34	High	42.01	High	93.99	High	11.90	83.90	High
PL	8.73	5.59	17.80	Moderate	14.25	Moderate	64.05	High	3.90	23.50	High
SPP	594.38	579.56	20.78	High	20.52	High	97.51	High	48.97	41.75	High
GL	0.008	0.002	11.92	Moderate	6.21	Low	27.14	Low	0.05	6.67	Low
GW	0.002	0.001	16.86	Moderate	13.52	Moderate	64.30	High	0.06	22.34	High
HSW	857.77	3.62	46.22	High	30.52	High	0.42	Low	0.25	4.09	Low
SPY	58.55	55.89	34.95	High	34.15	High	95.46	High	15.05	68.74	High

**Table.2** Genotypic correlation between different traits in gene pyramided lines of BC<sub>4</sub>F<sub>4</sub> generation

Characters	DFE	PHT	NPT	PL	SPP	GL	GW	HSW	SPY
DFE	1.00	-0.40	-0.28	0.17	-0.15	-0.57	-0.67	-0.75	-0.26
PHT		1.00	0.37	0.00	0.07	-0.16	0.17	0.22	0.40*
NPT			1.00	0.24	0.47	0.27	0.04	0.57	0.74**
PL				1.00	0.59**	-0.01	0.31	0.95**	0.35
SPP					1.00	0.19	0.36	-0.06	0.48*
GL						1.00	0.45*	-0.50	0.14
GW							1.00	0.72**	0.23
HSW								1.00	0.02
SPY									1.00

\* Significant at 5% level; \*\* Significant at 1% level

**Table.3** Path analysis showing direct and indirect effects of different traits on single plant yield in gene pyramided lines of BC<sub>4</sub>F<sub>4</sub> generation

Characters	DFE	PHT	NPT	PL	SPP	GL	GW	HSW	Correlation
DFE	<b>0.1704</b>	-0.1019	-0.1604	0.0114	-0.0219	-0.0498	-0.029	-0.0833	-0.2645
PHT	-0.0687	<b>0.2528</b>	0.2079	0	0.0105	-0.0142	0.0075	0.005	0.4009
NPT	-0.048	0.0923	<b>0.5697</b>	0.016	0.0698	0.0238	0.0017	0.0127	0.738
PL	0.0287	-0.0001	0.1346	<b>0.0678</b>	0.0868	-0.0006	0.0135	0.0233	0.3541
SPP	-0.0252	0.018	0.2682	0.0397	<b>0.1483</b>	0.0165	0.0157	-0.0012	0.48
GL	-0.0964	-0.0408	0.1538	-0.0005	0.0277	<b>0.0881</b>	0.0195	-0.0111	0.1403
GW	-0.1145	0.0441	0.0221	0.0212	0.0541	0.0398	<b>0.0431</b>	0.1183	0.2282
HSW	-0.6382	0.0568	0.3263	0.0712	-0.0082	-0.0441	0.2295	<b>0.0222</b>	0.0154

Residual effect - 0.357, Diagonal values indicate the direct effect

### **Heritability and genetic advance as percent of mean for agronomic traits in BC<sub>4</sub>F<sub>4</sub> generation**

The fundamental principle involved in plant breeding is the application of selection on the genetic variability present in the breeding materials for various traits in order to develop improved genotypes possessing higher economic yield than the existing ones. Obviously genetic variability is the basis on which selections acts to bring improvement in architecture of plants (Pandey *et al.*, 2012).

The coefficient of variation doesn't offer full scope of heritable variation. Heritability and genetic advance as percent of mean were determined to study the scope of improvement through selection for many traits. The proportion of genetic variability which is transmitted from parents to progenies is reflected by heritability (Lush, 1949). Heritability in broad sense and genetic advance as percent of mean as direct selection parameters provide index of transmissibility of traits which gives indication about the effectiveness of selection of improving the characters (Johnson *et al.*, 1955).

High heritability combined with high genetic advance as percent of mean was observed in plant height, number of productive tillers, panicle length, seeds per panicle and single plant yield (Table 1).

The findings were supported by Prasad *et al.*, (2001), Bisne *et al.*, (2009) and Kole *et al.*, (2008). High heritability and genetic advance estimates indicated predominantly the presence of additive gene action in the expression of these traits and consequently greater chance of improving these traits through simple selection. Low heritability and genetic advance as percent of mean was observed in grain length and hundred seed weight.

### **Association analysis for various traits under study in BC<sub>4</sub>F<sub>4</sub> generation**

The degree of correlation among the characters is an important factor. Character association derived by correlation coefficient, forms the basis for selecting the desirable plants. Steel and Torrie (1984) stated that correlations are measures of the intensity of association between traits. The selection for one trait results in improvement of all the characters that are positively correlated and retrogress for characters that are negatively correlated.

From the present study, the genotypic correlation coefficients were studied for various characters. Plant yield showed positive and highly significant correlation with number of productive tillers (0.74). It showed positive and significant correlation with plant height (0.40) and seeds per panicle (0.48). It showed positive and non-significant correlation with panicle length (0.35), grain length (0.14), grain width (0.23) and hundred seed weight (0.02) (Table 2). This was supported by Ekka *et al.*, (2011) and Akhter *et al.*, (2014). It is also observed that, panicle length was having a positive and highly significant correlation with seeds per panicle and hundred seed weight.

The Path coefficient analysis is a tool which helps to separate the observed correlation coefficient into direct and indirect effects of yield components on single plant yield which provides a clear picture on character associations for formulating effective selection strategy. It differs from the simple correlations and it additionally reveals the causes and their relative importance (Pandey *et al.*, 2012).

From the present study, number of productive tillers recorded high and positive direct effect on the plant yield. The characters like seeds

per panicle, panicle length and plant height recorded moderate and positive direct effect on the plant yield (Table 3). This was supported by Prathap *et al.*, (2014). The days to 50 percent flowering recorded negative direct effect on the plant yield. The other characters namely grain length, grain width, hundred seed weight were showing moderate direct effect on the plant yield.

The estimates of variability, heritability, genotypic correlation coefficient and path analysis, indicated that the traits namely number of productive tillers, panicle length and seeds per panicle directly influence the single plant yield. More importance to be given to those characters while selecting for higher yielding genotypes.

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**How to cite this article:**

Krishnakumar, R. and Kumaravadeivel, N. 2018. Genetic Variability and Inter Relationship among the Gene Pyramided BC<sub>4</sub>F<sub>4</sub> Generation Lines for Yield and Yield Attributing Characters in Rice (*Oryza sativa* L.). *Int.J.Curr.Microbiol.App.Sci*. 7(03): 2502-2507. doi: <https://doi.org/10.20546/ijcmas.2018.703.289>