

# Variability and frequency distribution studies in $F_2$ population of two crosses of rice (*Oryza sativa* L.)

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An investigation was carried out at ZARS, VC Farm, Mandya during 2011-2012 to study the frequency distribution and variability produced in two  $F_2$  populations of rice viz., 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' for grain yield and its seven component characters. The  $F_2$  populations of both the crosses showed high PCV and GCV values coupled with high heritability and high genetic advance as per cent of mean for total tillers per plant, productive tillers per plant, grains per panicle and grain yield per plant. Skewness and kurtosis indicated dominance based complementary gene interaction involving large number of genes having decreasing effect in the inheritance of total tillers per plant, days to panicle emergence, productive tillers per plant, grains per panicle and grain yield in both the crosses and for 1000-grain weight in 'Jaya × BPHR-1'. However, duplicate interaction was noticed for panicle length in both the crosses; while, 1000-grain weight showed complete ambi-directional epistasis in the cross 'IR 64 × BPHR-1'. Contrary to this, plant height exhibited dominance based complete interaction for few segregating genes with majority of them having decreasing effect.

**Key words :** Frequency distribution, Gene interaction,  $F_2$  population, PCV, GCV

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## INTRODUCTION

Rice (*Oryza sativa* L.), the staple food of more than half the world's population, grows in a wide range of environments. To boost the production of rice in India, it is essential to increase through suitable breeding programmes, the yielding ability of currently available varieties and hybrids without altering grain quality. To achieve this objective, knowledge on inheritance pattern of yield and its components is very much essential. In addition, knowledge of genetic variability, heritability and genetic gain as per cent of mean of yield and yield component characters are of immense value in the selection of superior segregants.

The present investigations was, therefore, undertaken in  $F_2$  population of two crosses of rice with a view to assess the variability produced in respect of grain yield and its seven attributing traits and frequency distribution pattern based on skewness and kurtosis.

## RESEARCH METHODOLOGY

The material for the present experiment comprised of

$F_2$  population of two crosses of rice viz., 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' along with their two  $F_1$ 's and three parents. Twenty plants of each of the three parents, 10 plants of each of two  $F_1$ 's were planted in single rows of 4m, while 400  $F_2$  plants each of 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' were planted in plots of 4m length in ten rows each maintaining a row to row distance of 20 cm and plant to plant distance of 10 cm in wet lands at 'C' block of ZARS, VC Farm, Mandya during summer 2012. Data was recorded on 10 randomly chosen plants of non-segregating populations viz., parents (IR 64, Jaya and BPHR-1) and two  $F_1$  hybrids (IR 64 × BPHR-1 and Jaya × BPHR-1) and on 389 and 344 competitive plants in the  $F_2$  population of 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' crosses, respectively. The GCV and PCV values were computed by the formula suggested by Burton and De Vane (1953). Heritability and genetic advance as per cent of mean were estimated following the method of Johnson *et al.* (1955). Skewness, the third degree statistics and Kurtosis, the fourth degree statistics were estimated as per Snedecor and Cochran (1974) to understand the nature of distribution of 8 quantitative traits in  $F_2$  population of each

of the crosses.

## RESEARCH FINDINGS AND ANALYSIS

The variability parameters *viz.*, co-efficient of variability, heritability and genetic advance as per cent of mean are furnished in Table 1. The range of variability was high for all the characters studied except days to panicle emergence, plant height, panicle length and 1000-grain weight, which exhibited low to moderate variability in both the crosses.

The platykurtic (0.270 and 0.175) and positively skewed (0.525 and 0.350) distribution in 'IR 64 × BPHR-1' and 'Jaya

× BPHR-1', respectively indicated dominance based complementary gene interaction involving large number of genes having decreasing effect in the inheritance of total tillers per plant in both the populations (Fig. 1). Platykurtic (2.64 and 2.103 in 'IR 64 × BPHR-1' and 'Jaya × BPHR-1') and positively skewed (1.135 and 0.693 in 'IR 64 × BPHR-1' and 'Jaya × BPHR-1') distribution indicated dominance based complementary gene interaction involving presence of large number of genes having decreasing effect on the trait days to panicle emergence in both the populations (Fig. 2).

Productive tillers per plant appeared to be controlled by dominance based complementary gene interaction

Table 1: Variability parameters for eight quantitative characters in F <sub>2</sub> populations of two crosses of rice					
Characters	F <sub>2</sub> population	PCV (%)	GCV (%)	h <sup>2</sup> <sub>bs</sub> (%)	GAM (%)
Total tillers plant <sup>-1</sup>	IR 64 × BPHR-1	28.08	24.12	73.76	42.67
	Jaya × BPHR-1	31.99	18.87	34.81	22.93
Days to panicle emergence	IR 64 × BPHR-1	2.83	2.68	89.56	5.22
	Jaya × BPHR-1	5.35	5.25	96.60	10.64
Productive tillers plant <sup>-1</sup>	IR 64 × BPHR-1	41.42	34.23	68.28	58.26
	Jaya × BPHR-1	40.78	20.55	25.39	21.33
Plant height (cm)	IR 64 × BPHR-1	7.00	6.58	88.37	12.75
	Jaya × BPHR-1	10.69	10.38	94.36	20.78
Panicle length (cm)	IR 64 × BPHR-1	7.69	5.63	53.70	8.50
	Jaya × BPHR-1	7.38	6.47	76.78	11.67
Grains panicle <sup>-1</sup>	IR 64 × BPHR-1	27.53	26.96	95.92	54.40
	Jaya × BPHR-1	28.59	27.33	91.42	53.84
1000 grain weight (g)	IR 64 × BPHR-1	15.02	14.10	88.19	27.28
	Jaya × BPHR-1	18.76	16.71	79.29	30.65
Grain yield (g plant <sup>-1</sup> )	IR 64 × BPHR-1	47.46	44.41	87.56	85.60
	Jaya × BPHR-1	51.83	48.27	86.73	92.59

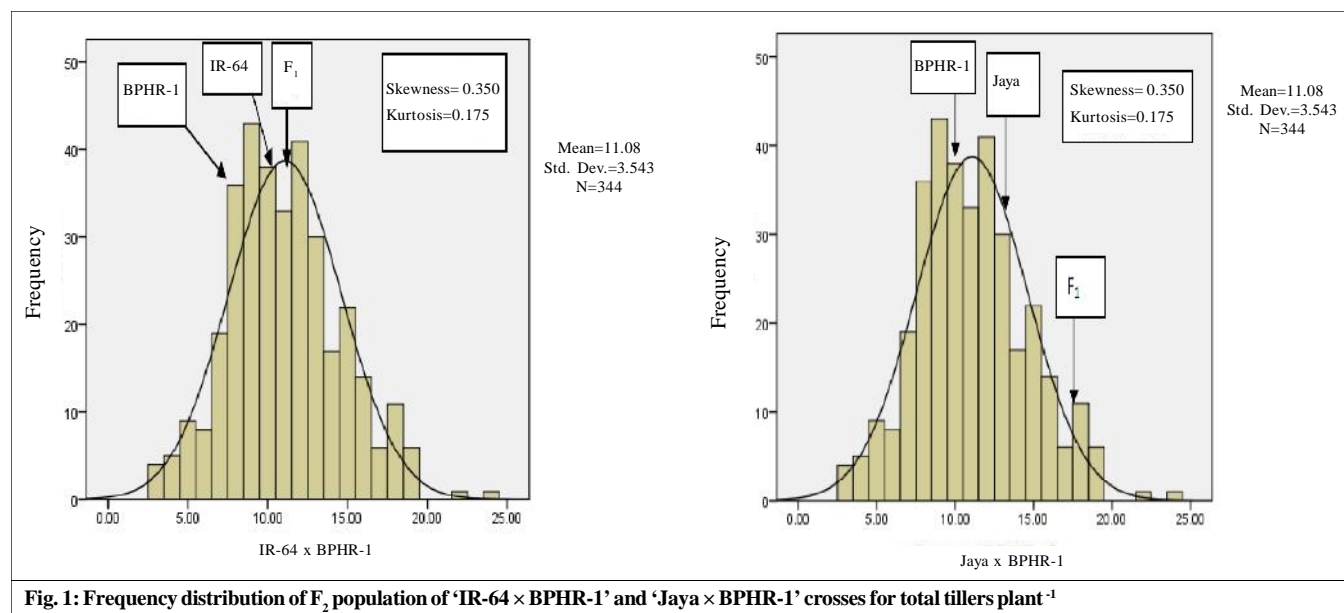


Fig. 1: Frequency distribution of F<sub>2</sub> population of 'IR-64 × BPHR-1' and 'Jaya × BPHR-1' crosses for total tillers plant<sup>-1</sup>

involving presence of large number of genes having decreasing effect on the character as evidenced by positively skewed (1.031 and 0.878) and platykurtic (1.292 and 1.214) distribution in both 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' populations, respectively (Fig. 3). The trait plant height appeared to controlled by few segregating genes with majority of them exhibiting decreasing effect and dominance based complementary gene interaction as indicated by the leptokurtic (12.68 and 7.074) and negatively skewed (-1.963 and -1.186) distribution in 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' population respectively (Fig. 4).

Panicle length appeared to be controlled by large

number of dominant genes with increasing effect and duplicate interaction in the inheritance as indicated by platykurtic (1.224 and 2.070) and negatively skewed (-0.553 and -0.597) distribution in 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' population, respectively (Fig. 5). The platykurtic (1.065 and 0.346) and positively skewed (0.669 and 0.205) distribution in both 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' populations, respectively indicated dominance based complementary gene interaction involving presence of large number of genes having decreasing effect in the inheritance of grains per panicle (Fig. 6).

Platykurtic (0.10) and symmetrical (0.00) distribution

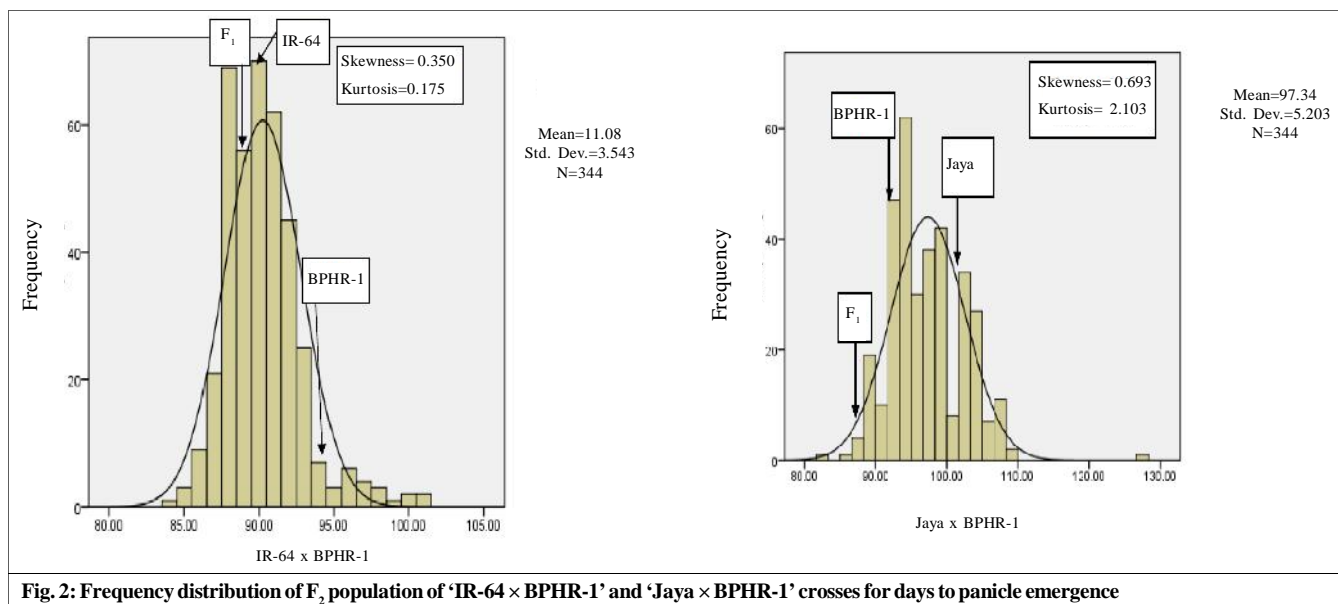


Fig. 2: Frequency distribution of F<sub>2</sub> population of 'IR-64 × BPHR-1' and 'Jaya × BPHR-1' crosses for days to panicle emergence

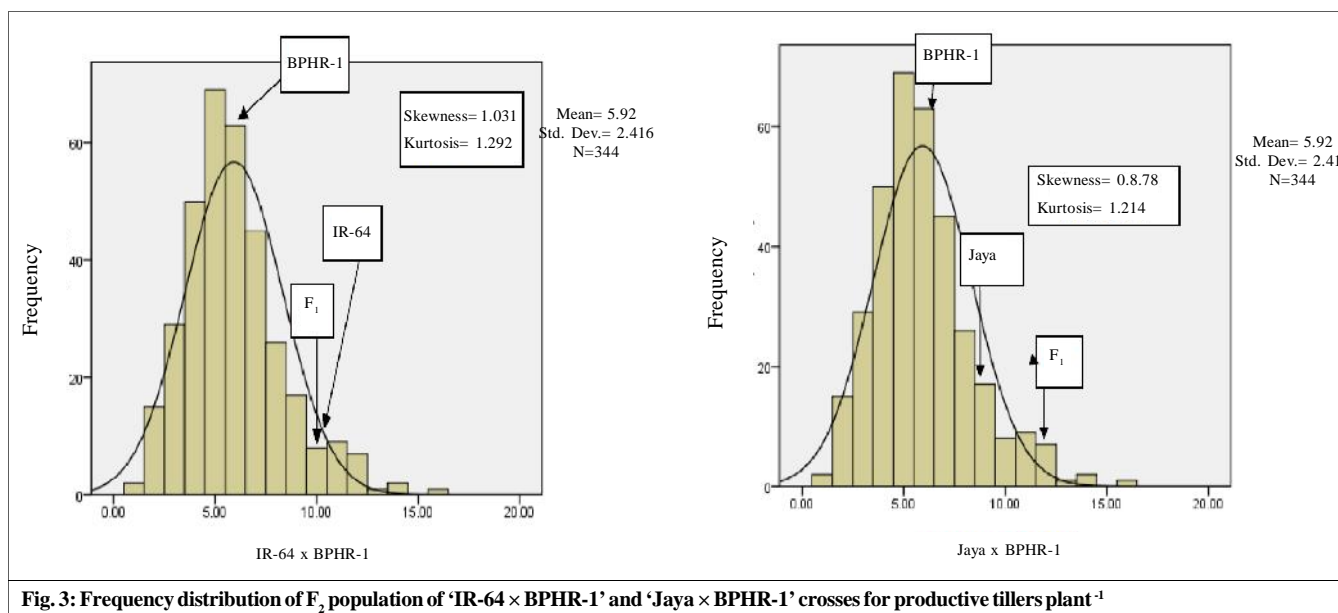


Fig. 3: Frequency distribution of F<sub>2</sub> population of 'IR-64 × BPHR-1' and 'Jaya × BPHR-1' crosses for productive tillers plant<sup>-1</sup>

in 'IR 64 × BPHR-1' indicated large number of dominant genes having complete ambi-directional epistasis in the expression of 1000-grain weight, while the same trait appeared to be controlled by larger number of genes having decreasing effect and involvement of dominance based complementary interaction as evidenced by platykurtic (1.67) and positively skewed (0.077) distribution in 'Jaya × BPHR-1' population (Fig. 7). Platykurtic (2.152 and 1.680) and positively skewed (1.113 and 1.017) distribution in 'Jaya × BPHR-1' and 'IR 64 × BPHR-1' populations, respectively suggested the dominance based complementary gene interaction involving presence of large number of genes

having decreasing effect in the inheritance of grain yield in both the populations (Fig. 8).

As expected, estimates of PCV values were relatively higher than GCV values in F<sub>2</sub> generation of both the crosses coupled with narrow differences which indicate less environmental influence on the expression of all the traits except total tillers per plant, productive tillers per plant and grain yield in both the F<sub>2</sub> populations.

Total tillers per plant exhibited higher values of GCV and PCV (28.08%, 31.99% and 24.12%, 18.87%, respectively) as well as high heritability (73.76% and 34.81%) coupled with high genetic advance as per cent of

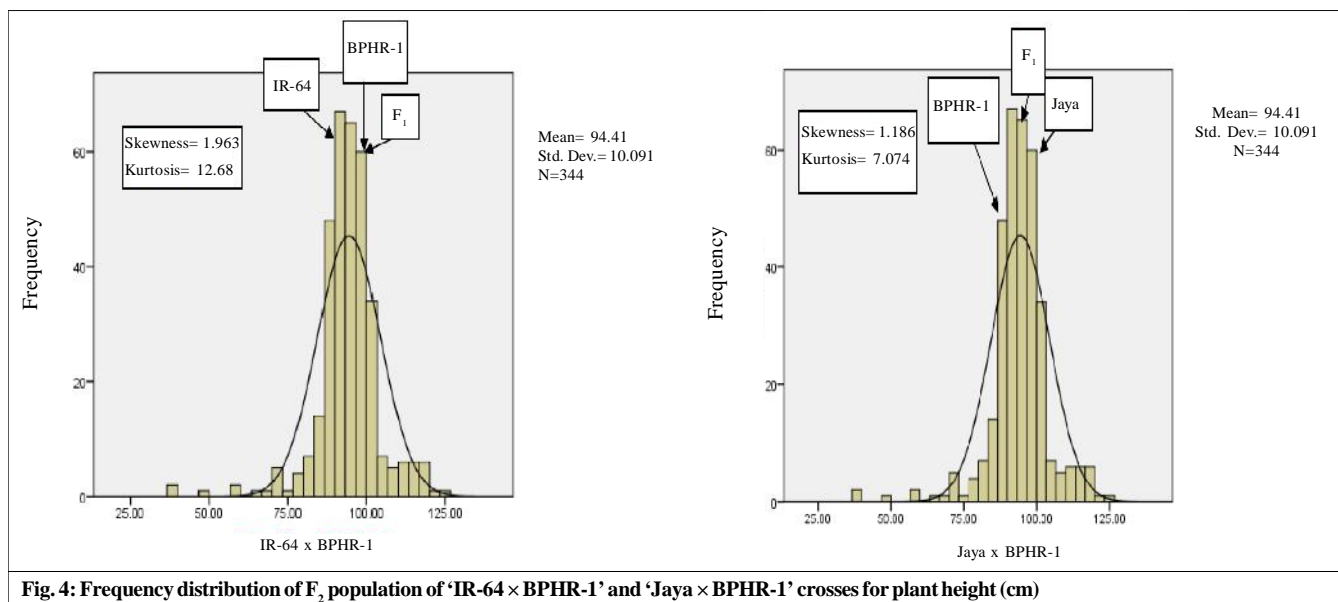


Fig. 4: Frequency distribution of F<sub>2</sub> population of 'IR-64 × BPHR-1' and 'Jaya × BPHR-1' crosses for plant height (cm)

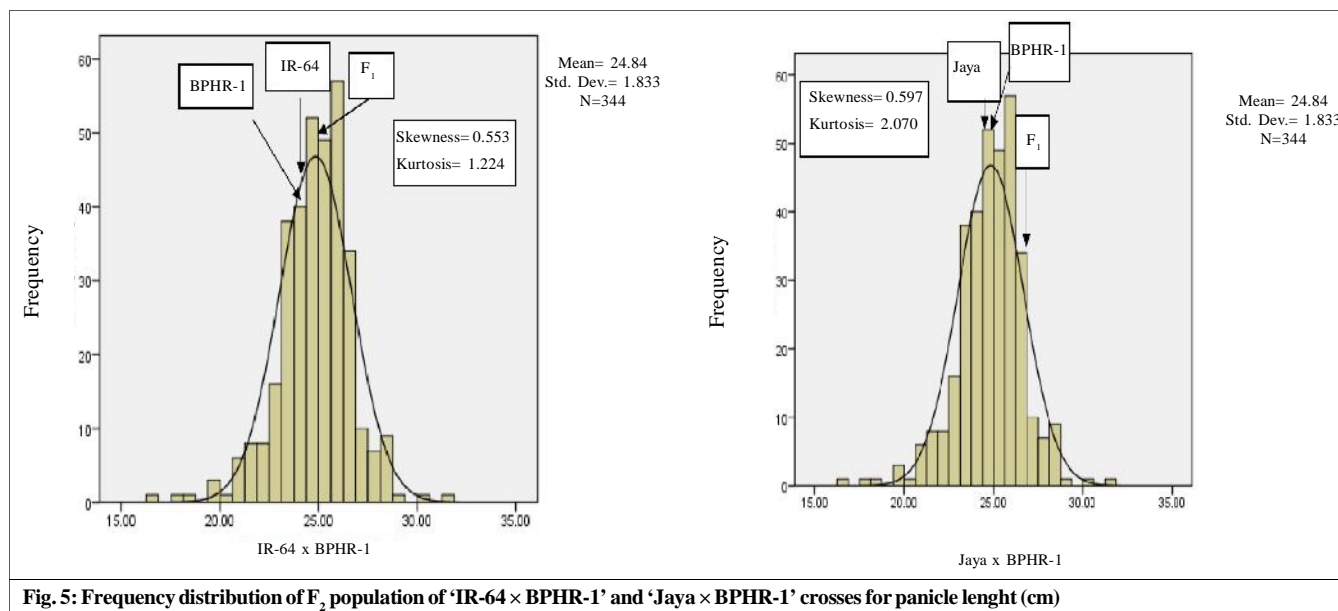


Fig. 5: Frequency distribution of F<sub>2</sub> population of 'IR-64 × BPHR-1' and 'Jaya × BPHR-1' crosses for panicle length (cm)

mean (42.67% and 22.93 %, respectively) in ‘IR 64 × BPHR-1’ and ‘Jaya × BPHR-1’ populations, which indicated major role of additive gene action in the genetic control of this trait in both the populations and this result was in accordance with the report of Chauhan *et al.* (1990).

Very low variability was noticed for days to panicle emergence as evidenced by lower values of PCV (2.83% and 5.35 %) and GCV (2.68% and 5.25%) in ‘IR 64 × BPHR-1’ and ‘Jaya × BPHR-1’ populations, respectively. Contrary to this, high heritability (89.56%) with low genetic advance as per cent of mean (5.22 %) in ‘IR 64 × BPHR-1’ population indicated major role of non-additive gene action while, high

heritability (96.60 %) and moderate genetic advance as per cent of mean (10.64 %) in ‘Jaya × BPHR-1’ population indicated role of additive gene action in respect of this trait. Kannan Bapu and Soundarapandian (1993) also reported similar result in respect of this trait.

Productive tillers exhibited wide variability and high influence of environment as evidenced by wide difference between GCV and PCV as well as higher values of PCV (41.46% and 40.78 %) and GCV (34.23% and 20.55 %) in ‘IR 64 × BPHR-1’ and ‘Jaya × BPHR-1’ population, respectively. High broad sense heritability (68.28% and 25.39 %) coupled with high genetic advance (53.70% and 21.33 %) as per cent of

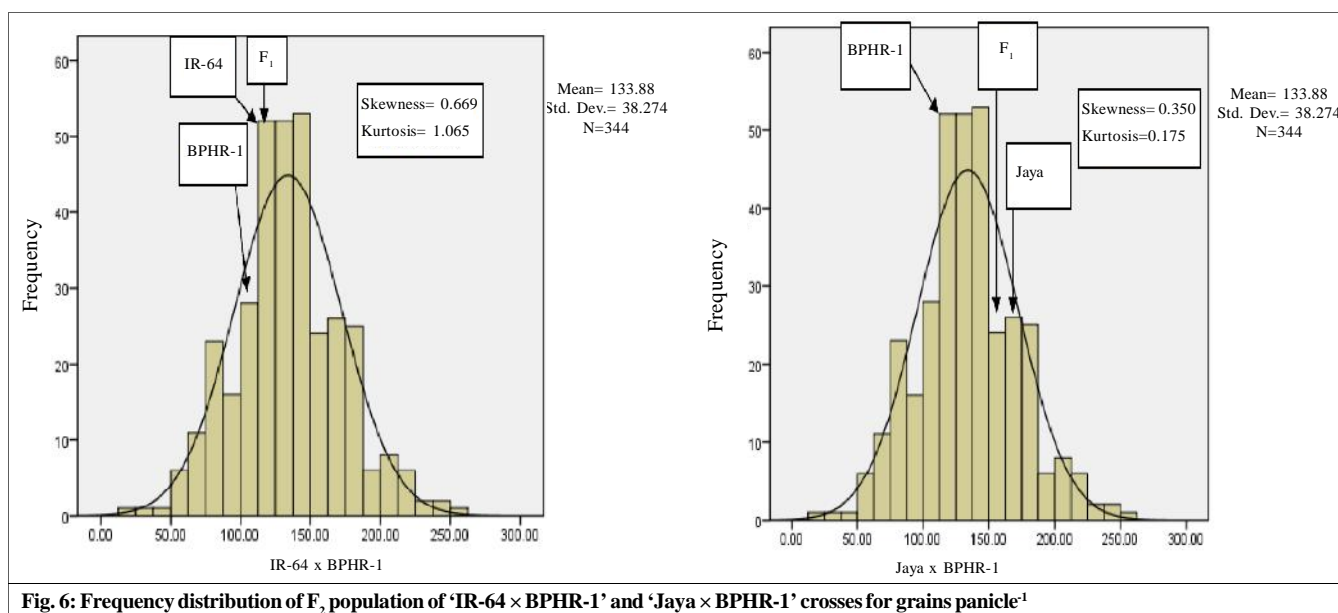


Fig. 6: Frequency distribution of  $F_2$  population of ‘IR-64 × BPHR-1’ and ‘Jaya × BPHR-1’ crosses for grains panicle<sup>-1</sup>

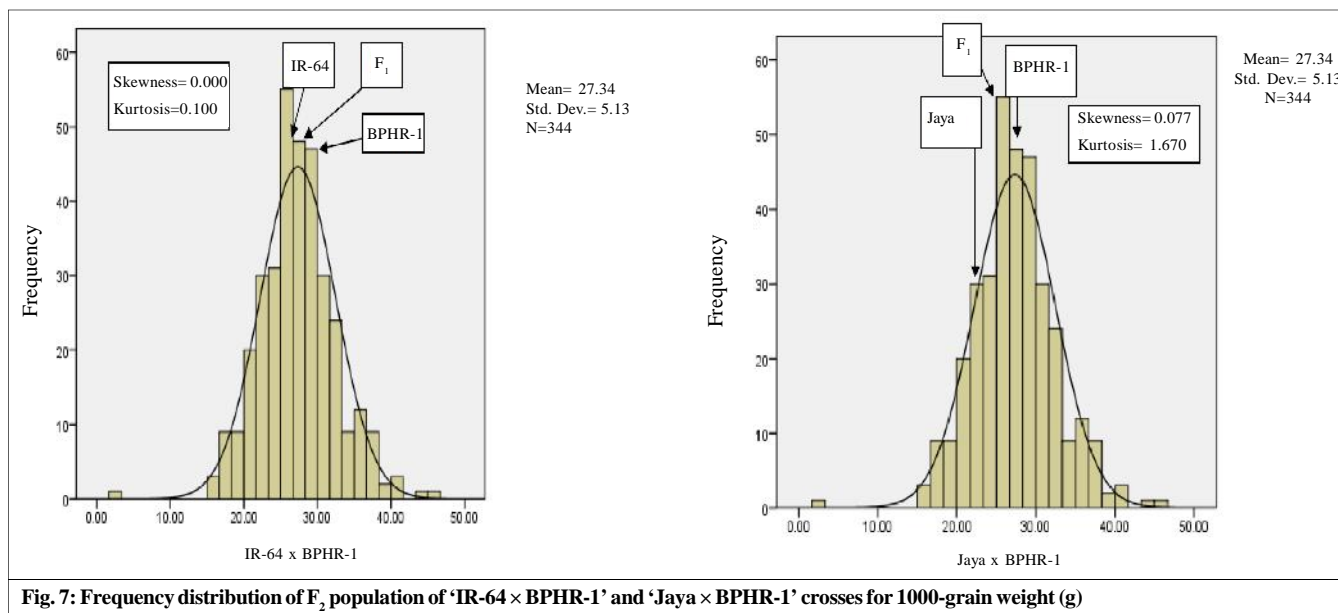


Fig. 7: Frequency distribution of  $F_2$  population of ‘IR-64 × BPHR-1’ and ‘Jaya × BPHR-1’ crosses for 1000-grain weight (g)

mean in 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' population, respectively revealed major role of additive gene action in the genetic control of this trait. Similar results were reported by Chauhan *et al.* (1990), Raju *et al.* (2004), Nayak (2008) and Nandeshwar *et al.* (2010).

PCV and GCV values (10.69 % and 10.38 %, respectively) in 'Jaya × BPHR-1' population indicated moderate variability for plant height. Results of present study are at par with the earlier reports of Kannan Bapu and Soundarapandian (1993) and Singh and Choudhary (1996). Contrary to this, low variability was noticed for this trait as evidenced by lower values of PCV and GCV (7.00 % and 6.58 %, respectively) in 'IR 64 × BPHR-1' population. These results are in agreement with earlier reports of Mohanthy and Singh (1969) and Chauhan *et al.* (1990). This trait exhibited high heritability coupled with low to moderate genetic advance expressed as per cent of mean in both the crosses indicating role of non-additive gene action in its genetic control. Results of present study are at par with the earlier reports of Suresh and Reddy (2002) and Kumar *et al.* (2005).

Panicle length in both the crosses registered lower values of PCV (7.69% and 7.38 %) and GCV (5.63% and 6.47 %), respectively. This is in accordance with the earlier observations made by Mohanthy and Singh (1969) and Paramasivan (1986). However, high broad sense heritability (53.70% and 76.78 %) but low genetic advance expressed as per cent of mean (8.50% and 11.67 %) in 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' population, respectively indicated predominant role of non-additive gene action in respect of this trait in both crosses. Agrawal (2003) reported similar results with

respect to heritability and genetic advance for this trait.

The PCV (27.53 % and 28.59 %) and GCV (26.96% and 27.33 %) values were high in 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' population, respectively for grains per panicle indicating wide variability for this trait. Estimates of broad sense heritability (95.92 % and 91.42 %) and genetic advance as per cent of mean (54.40 % and 53.84 %) were also high in 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' population, respectively revealing additive gene action in the control of this trait in both the populations. This is in accordance with the earlier observations made by Nayak (2008).

The PCV (15.02 % and 18.76 %) and GCV (14.10 % and 16.71 %) values were moderate coupled with high (88.19 % and 79.29 %) broad sense heritability and high genetic advance expressed as per cent of mean (27.28 % and 30.65 %) in 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' populations, respectively indicated moderate variability and major role of additive gene action in the control of 1000-grain weight in both the populations. Similar results were reported by Kannan Bapu and Soundarapandian (1993) and Chauhan and Chauhan (1994).

Wide variability was noticed for grain yield per plant as evidenced by relatively higher values of PCV (47.46 % and 51.83 %) and GCV (44.41 % and 48.27 %) in 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' populations, respectively. Estimates of broad sense heritability (87.58% and 86.73 %) and genetic advance expressed as per cent of mean (85.60 % and 92.59 %) were relatively high in 'IR 64 × BPHR-1' and 'Jaya × BPHR-1' populations, respectively indicating major role of additive gene action in the genetic control this trait in both the populations. Results of the present study are in

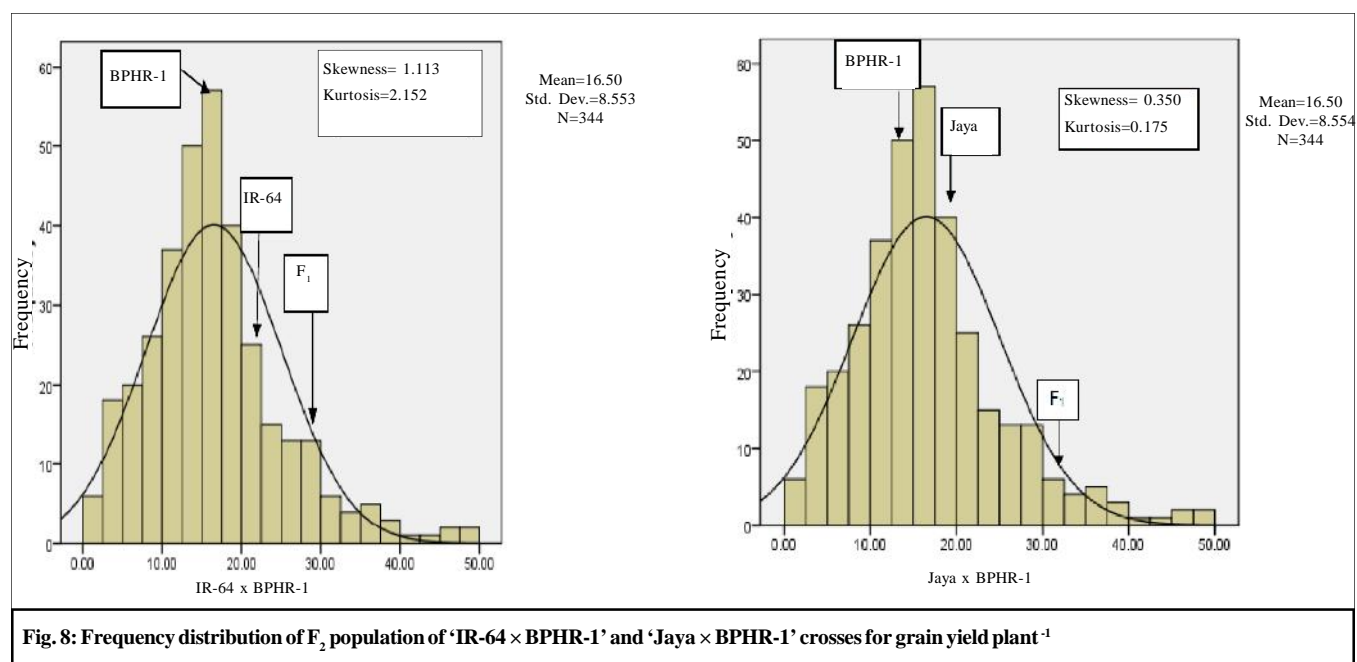


Fig. 8: Frequency distribution of  $F_2$  population of 'IR-64 × BPHR-1' and 'Jaya × BPHR-1' crosses for grain yield plant<sup>-1</sup>

conformity with the reports of Kumar *et al.* (2005) and Nayak (2008).

The results of the present study clearly indicate that, grain yield cannot be improved by direct selection as the trait is subjected to greater environmental effect. However, yield can be improved indirectly by selecting F<sub>2</sub> plants with high total tillers per plant, productive tillers per plant, grains per panicle and 1000-grain weight as these traits showed high heritability

coupled with high genetic advance as per cent of mean.

#### Conclusion :

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