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## Genetic variability, heritability and genetic advance studies of segregating backcrossed generation (BC<sub>1</sub>F<sub>3</sub>) in rice (*Oryza sativa* L.)

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### Abstract

The study aimed to evaluate genetic variability, heritability and genetic advance in the BC<sub>1</sub>F<sub>3</sub> plant for yield and its attributes in non-replicated trial in Summer, 2023. Observations were taken on each individual plant of segregating population for ten different characters. Results showed wide range of variation within population and also confirmed that the mean values of all observed characters in the segregating population ranged between the mean values of parents. Moreover, the values of Phenotypic Coefficient of Variation (PCV) were observed slightly higher than the value of Genotypic Coefficient of Variation (GCV) for all ten observed characters under study indicating minor influence of environmental factors. High heritability was observed for all the ten traits under study revealed the least environmental influence. Higher heritability coupled with high genetic advance as per cent mean is observed for plant height, productive tillers per plant, panicle length, 100 grain weight, grains per panicle, straw yield per plant, harvest index and grain yield per plant indicated the role of higher additive gene action in these traits. The findings from this study provide valuable insights into the genetic architecture of the BC<sub>1</sub>F<sub>3</sub> generation, aiding breeders in selecting individuals with desirable traits for further advancement.

**Keywords:** Rice BC<sub>1</sub>F<sub>3</sub> population, variability, heritability and genetic advance

### Introduction

Rice (*Oryza sativa* L.) is a major cereal and staple crop, belongs to genus *Oryza* of family Poaceae. It is grown in 114 countries throughout the world. Furthermore, it is a major source of income and employment for more than half of the population worldwide. The *Oryza* genus includes a total of 24 species, among them 22 species are wild and other two species viz., *Oryza sativa* L. (Asian rice) and *Oryza glaberrima* Steud (African rice) are cultivated (Khush, 1997) [12] in Asia and Africa, respectively and diploid (2n = 2x = 24) in chromosome number.

Higher rate of segregation and recombination are most common in case of segregating populations, which can be a basic material for selection of superior progenies from a cross (Priyanka *et al.*, 2019) [16]. Improved lines generated from the backcrossing program can be evaluated for the yield and its attributes, which will further provide a better scope for a selection. Moreover, any crop improvement program is based on genetic variability for grain yield and its related traits along with the strategies of selection [Rani *et al.*, 2016] [17]. Wide variability, high heritability along with the high genetic advance will lead to the successful selection of genotypes. Understanding the direct and indirect association between yield and its related components provides the way for the selection of suitable breeding programs. So, it would be simple to generate or identify high yielding, stable and well adapted lines from the segregating population by utilising the better adaptation and stability of yield and its related qualities in breeding material.

Hence, looking view to those points, the experiment was conducted to evaluate the variability, heritability and association between yield and yield contributing various character to identify a better segregants in BC<sub>1</sub>F<sub>3</sub> generation of Gurjari × Tetep.

### Material and Methods

#### Experimental location and generation of material

The experimental study was conducted in Main Rice Research Station located at Navsari Agricultural University, Navsari. Gurjari, very popular and high yielding variety of Gujarat,

further susceptible to blast disease was used as a recurrent parent. Tetep harboring blast resistance genes was used as a donor for the introgression of the targeted genes. BC<sub>1</sub>F<sub>3</sub> progenies of plants harboring resistant genes and maximum recurrent parent genome recovery were selected through foreground and background selection, respectively. These selected BC<sub>1</sub>F<sub>3</sub> progenies were served as a material for the genetic variability, heritability and genetic advance studies. A non-replicated experiment block of 221 BC<sub>1</sub>F<sub>3</sub>s were raised along with parents and check variety GR-17 (Sardar). Observations were taken from the parents, check and an individual plant of segregating BC<sub>1</sub>F<sub>3</sub>s population for the ten quantitative parameters *viz.*, days to flowering, days to maturity, plant height (cm), productive tillers per plant, panicle length (cm), 100 grain weight (g), grains per panicle, straw yield per plant (g), harvest index (%) and grain yield per plant (g).

### Statistical analysis

The mean and variances in this study were analyzed with a formula given by Singh and Chaudhary (1977) [20]. The phenotypic variance is calculated using the individual observations collected for each trait on the F<sub>2</sub> population. Because all individuals in non-segregating generations (P<sub>1</sub>, P<sub>2</sub> and Sardar) have identical genotype, environmental variance can be estimated from the mean phenotypic variance of the P<sub>1</sub> (Gurjari) and P<sub>2</sub> (Tetep) and check (Sardar) population. Furthermore, the genotypic and phenotypic coefficient of variation, heritability and genetic advance expressed as per cent of mean was computed according to Burton and Devane (1953) [5], Allard (1960) [1] and Johnson *et al.* (1955) [22], respectively.

## Results and Discussion

### Analysis of Mean, Range and Variance

In present study, large phenotypic differences were observed

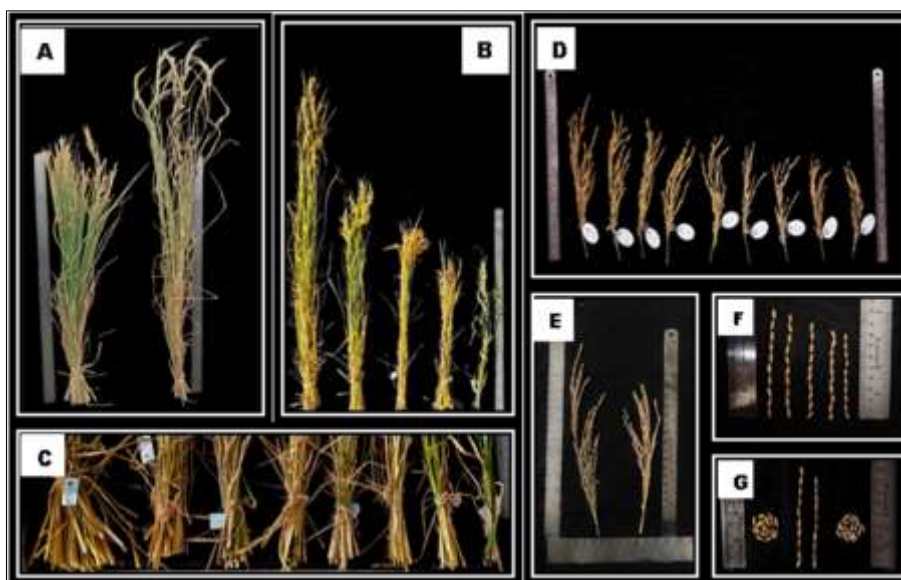
between the minimum and maximum values within a BC<sub>1</sub>F<sub>3</sub> population on overall basis. (Photo 1). The wide range of variation obtained in experimental population may be due to segregation and recombination.

The mean values of both parents, individual 221 BC<sub>1</sub>F<sub>3</sub> plants and check for different attributes are presented in Table 1. The comparison of mean performance between the segregating backcrossed populations and parents indicated that mean values for all mentioned characters in the population ranged between the mean values of parents, which depicted graphically in Fig 1. Additionally, the segregating populations manifested decreased mean values over the recurrent parent (Gurjari) for grains per panicle, harvest index and grain yield per plant. Furthermore, the BC<sub>1</sub>F<sub>3</sub> population recorded a nearly similar mean value with Gurjari for panicle length and 100 grain weight. However, days to flowering, days to maturity, productive tillers per plant and straw yield per plant exhibited increased mean value over recurrent parent (Gurjari). Vaibhav *et al.* (2019) [21] also reported a similar kind of result.

Among all characters studied, straw yield per plant exhibited the highest variance followed by harvest index, plant height and grain yield per plant, while 100 grain yield was recorded with the lowest magnitude of variance followed by panicle length and productive tillers per plant. These results pointed towards the presence of a sufficient amount of variability in segregating population. Large differences were observed in the variances for most of the characters in BC<sub>1</sub>F<sub>3</sub> population. Basavaraj *et al.* (2020) [3] and Chukwu *et al.* (2020) [6] also reported the large phenotypic variation among segregating population. Hence, it may be concluded that in rice, an increase in mean value as a result of hybridization indicates scope for further improvement in traits in subsequent generations.

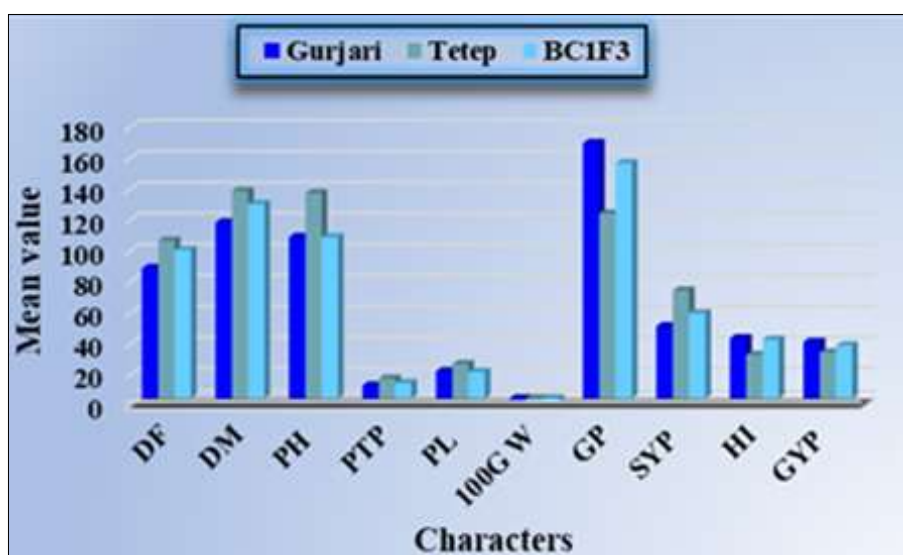
**Table 1:** Mean, range and variance values in parents (Gurjari, Tetep), check variety (Sardar) and BC<sub>1</sub>F<sub>3</sub> population for ten traits in rice

Characters	Mean ± Standard Error				Range	Variance			
	Gurjari	Tetep	Sardar (Check)	BC <sub>1</sub> F <sub>3</sub>	BC <sub>1</sub> F <sub>3</sub>	Gurjari	Tetep	Sardar	BC <sub>1</sub> F <sub>3</sub>
Days to flowering	89.20±0.28	106.90±0.33	101.90±0.30	100.90±0.51	65-118	0.76	1.09	0.89	58.11
Days to maturity	115.90±0.45	138.80±0.56	129.90±0.10	130.47±0.55	95-147	2.04	3.16	0.09	65.91
Plant height (cm)	109.20±4.89	137.50±2.71	106.00±2.36	109.04±1.49	64-190	239.36	73.85	56.00	487.56
Productive tillers per plant	13.50±1.31	17.80±1.09	17.30±1.30	15.09±0.45	1-35	17.05	11.96	16.84	44.46
Panicle length (cm)	22.70±0.74	27.20±0.61	21.20±0.70	22.16±0.23	14-31	5.41	3.76	4.96	11.52
100 grain weight (g)	2.16±0.06	1.72±0.06	2.54±0.07	2.17±0.01	1.3-3.1	0.04	0.04	0.04	0.11
Grains per panicle	169.90±16.60	124.40±6.63	128.00±7.87	156.90±3.49	49-340	2756.49	440.84	619.20	2691.94
Straw yield per plant (g)	51.70±3.75	74.70±8.26	55.50±3.69	60.08±3.57	4-451	140.41	683.41	136.45	2821.82
Harvest index (%)	43.89±2.21	33.23±2.32	50.38±1.43	42.99±0.85	3.90-79.19	48.88	53.98	20.48	159.57
Grain yield per plant (g)	41.58±4.52	34.72±1.48	55.68±2.33	39.25±1.44	3.5-112.3	204.12	22.04	54.54	457.88



**Fig 1:** Phenotypic variation BC<sub>1</sub>F<sub>3</sub> population and parents

**A:** Plant height of Gurjari and Tetep; **B:** Variation in plant height in BC<sub>1</sub>F<sub>3</sub> population; **C:** Variation in the total number of tillers in the BC<sub>1</sub>F<sub>3</sub> population; **D:** Variation in panicle length of BC<sub>1</sub>F<sub>3</sub> population; **E:** Variation in panicle length parents; **F:** Variation in seed size of BC<sub>1</sub>F<sub>3</sub> population; **G:** Variation in seed size of BC<sub>1</sub>F<sub>3</sub> parents



**Fig 2:** Mean values of parents and BC<sub>1</sub>F<sub>3</sub> population for different characters

### Variability parameters, Heritability and Genetic Advance Study of BC<sub>1</sub>F<sub>3</sub>

The results of variability parameters are shown in Table 2. The moderate to high, as well as closer values of genotypic and phenotypic variance, were observed for days to flowering, days to maturity, 100 grain weight and straw yield per plant. Additionally, slightly higher PCV value than GCV value depicted for majority of characters in BC<sub>1</sub>F<sub>3</sub> population revealed less environmental influence in character expression. Therefore, these traits could be easily exploited through selection. The same result was depicted by work of Immanuel *et al.* (2011)<sup>[8]</sup>, Kahani and hitalmani (2015)<sup>[10]</sup>, Mallimar *et al.* (2015)<sup>[14]</sup>.

Balakrishnan *et al.* (2016)<sup>[2]</sup>, Hemant *et al.* (2018)<sup>[7]</sup>, Bhargava *et al.* (2022)<sup>[23]</sup>, Prajapati *et al.* (2022)<sup>[15]</sup> and Renuprasath *et al.* (2023)<sup>[19]</sup> for different characters.

In the present investigation, plant height, productive tillers per plant, grains per panicle, straw yield per plant, harvest index and grain yield per plant exhibited higher values of GCV and

PCV indicating the greater scope of improving this character by applying the selection in an appropriate direction and also showed greater variation within BC<sub>1</sub>F<sub>3</sub> population for these traits. Similar results were reported by Immanuel *et al.* (2011)<sup>[8]</sup>, Kiran *et al.* (2012)<sup>[13]</sup>, Basavaraj *et al.* (2020)<sup>[3]</sup>, Bhargava *et al.* (2022)<sup>[23]</sup> and Prajapati *et al.* (2022)<sup>[15]</sup>.

Moderate GCV and PCV values were observed for the traits *viz.*, panicle length and 100 grain weight. This indicated that the extent of response of these traits for selection would be less. However, days to flowering and days to maturity were reported with low GCV and PCV values indicating a narrow range of variability for these traits and restricting the scope of selection for these traits. The result of low and moderate GCV and PCV was in accordance with findings of Mallimar *et al.* (2015)<sup>[14]</sup>, Balakrishnan *et al.* (2016)<sup>[2]</sup>, Kayande *et al.* (2017)<sup>[11]</sup>, Prajapati *et al.* (2022)<sup>[15]</sup> and Renuprasath *et al.* (2023)<sup>[19]</sup>. The magnitude of genotypic and phenotypic variance was recorded at 364.31 and 457.88, respectively for grain yield per plant. High estimates of GCV (48.62 %) and PCV (54.51 %)

were recorded. Furthermore, it exhibited high estimates of heritability (89.20 %) coupled with high genetic advance as per cent of mean (100.15 %).

High heritability was observed for all of the ten traits under study indicating that all were majorly governed by additive genes and thus had the least environmental influence. The same result was depicted by work of Kayande *et al.* (2017) [11], Hemant *et al.* (2018) [7], Vaibhav *et al.* (2019) [21], Bhargava *et al.* (2022) [23] and Renuprasath *et al.* (2023) [19] for most of the traits.

The genetic advance as per cent mean was recorded high for

all traits except days to flowering and days to maturity (Fig. 2). Higher heritability coupled with high genetic advance as per cent mean is observed for plant height, productive tillers per plant, panicle length, 100 grain weight, grains per panicle, straw yield per plant, harvest index and grain yield per plant. This confirmed higher additive gene action thus improvement could be brought by direct phenotypic selection over the genotypes. Higher heritability with medium genetic advance as per cent is observed in days to flowering and days to maturity indicating the effect of non-additive gene action.

**Table 2:** Estimate of genetic variability parameters for ten quantitative characters in BC<sub>1</sub>F<sub>3</sub> population

Characters	Mean	$\sigma^2 p$	$\sigma^2 e$	$\sigma^2 g$	GCV %	PCV %	ECV %	h <sup>2</sup> (b) %	GA	GAM %
Days to flowering	100.90	58.11	0.91	57.20	7.50	7.55	0.95	99.21	15.58	15.44
Days to maturity	130.47	65.91	1.76	64.15	6.14	6.22	1.02	98.65	16.50	12.65
Plant height (cm)	109.05	487.56	123.07	364.49	17.51	20.25	10.17	86.46	39.33	36.06
Productive tillers per plant	15.09	44.46	15.28	29.18	35.80	44.19	25.91	81.01	11.13	73.74
Panicle length (cm)	22.16	11.52	4.71	6.81	11.78	15.32	9.79	76.89	5.38	24.26
100 grain weight (g)	2.17	0.11	0.04	0.07	12.08	15.34	9.46	78.74	0.54	24.89
Grains per panicle	156.90	2691.94	1272.18	1419.76	24.01	33.07	22.73	72.62	77.62	49.47
Straw yield per plant (g)	60.09	2821.82	320.09	2501.73	83.24	88.41	29.78	94.16	103.04	171.48
Harvest index (%)	42.99	159.57	41.11	118.45	25.32	29.38	14.91	86.16	22.42	52.15
Grain yield per plant (g)	39.26	457.88	93.57	364.31	48.62	54.51	24.64	89.20	39.32	100.15

GCV = Genotypic coefficient of variation (%); PCV = Phenotypic coefficient of variation (%); GAM = Genetic advance as per cent of mean (%)  
 $\sigma^2_{GG}$  = Genotypic variance;  $\sigma^2_{PP}$  = phenotypic variance; GA = Genetic advance (%);  $h^2_{BS}$  = Heritability (Broad sense)

**Conclusion**

Study of variability in BC<sub>1</sub>F<sub>3</sub> revealed wide range of variation among segregating population, which falls between the mean values of parents. Values of GCV, PCV and heritability indicate the negligible influence of environmental factors for most of the characters under investigation. Moreover, inclusion of more characters in a variability study might increase accountable variation in future.

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