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Genetic Variability Studies in Advanced Backcross Derived Lines for Brown Plant Hopper and Blast Resistance in Rice (*Oryza sativa* L.)

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ABSTRACT: Among the biotic stresses in rice crop, the brown plant hopper (BPH) (*Nilaparvata lugens* Stal.) is one of the most destructive monophagous insect pests, causing substantial yield loss every year in rice grown throughout tropical, subtropical, and temperate areas in Asia. Rice blast (*Magnaporthe oryzae*) alone can cause yield loss ranging from 30 to 61 percent depending upon the stage of infection. The research articles was aimed to know the nature and magnitude of genotypic and phenotypic variability for yield and yield contributing characters present in elite advanced back cross derived rice genotypes for bph and blast resistance. The magnitude of difference between PCV and GCV was less for the traits indicating little influence of environment. Present study revealed that there was less amount of genetic variability in the traits except number of grains/panicle as the reason could be that they are back cross derived lines. For the development of high yielding varieties with good quality the information on variability and genetic parameter of grain quality attributes and their association with each other including grain yield is necessary to formulate suitable breeding strategies for grain quality improvement.

Keywords: Rice, GCV, PCV, Heritability, Genetic advance as percent of mean.

INTRODUCTION

In India, Rice crop plays a livelihood for millions of rural households. India has the largest area under rice. Among the biotic stresses, the brown planthopper (BPH) (*Nilaparvata lugens* Stal.) is one of the most destructive monophagous insect pests, causing substantial yield loss every year in rice grown throughout tropical, subtropical, and temperate areas in Asia (Park *et al.*, 2008). Rice blast (*Magnaporthe oryzae*) alone can cause yield loss ranging from 30 to 61 percent depending upon the stage of infection. In favourable conditions, this disease can devastate entire rice plants within 15 to 20 days and cause yield losses of up to 100 percent (Pradhan *et al*., 2018). Up to 25 to 55 percent of crops damaged is done by BPH (Madhuri *et al*., 2017).

Research work on development on BPH and Blast resistance was initiated to introgress Pi54 and Pi2 genes for blast resistance and Bph3 and bph4 genes for BPH resistance into popular rice variety Siddhi (WGL-44) at Regional Agricultural Research Station, Warangal with a view to develop most adaptable BPH and Blast resistance rice variety.

Advanced backcross derived lines with introgression of two significant, blast resistance genes (Pi2 and Pi54 from MIL-12) and BPH resistance genes (Bph3, bph4 from BM-71) in the genetic background of popular rice variety in Telangana State "Siddhi (WGL-44)" with the help of molecular markers were developed. Keeping in view the above perspectives to know the nature and magnitude of genotypic and phenotypic variability present in elite advanced back cross derived rice genotypes, the present investigation was carried out to estimate the variability.

MAREIALS AND METHOD

The experimental material comprised of 31 advanced backcross derived lines (BC_2F_5) developed by crossing between WGL-44 with inter cross F_1s (F_1 of first cross: WGL-44 × MIL 12 as donor parent for blast resistance genes *i.e.*, Pi2 and Pi54 and with F_1 of second cross: WGL 44 × BM-71 as donor parent for BPH resistance genes bph3 and bph4) possessing pi 54, pi2, bph3, bph4 genes for development of BC_1F_1s. In 2nd generation backcross was made with WGL-44 to get BC_2F_1 and advance to BC_2F_5. The present investigation was carried out at the Regional Agricultural Research Station, Warangal, which is located at an altitude of 304 M above MSL, 17.97° N latitude and 79.60° E longitude during *kharif*, 20121. The experiments were laid in randomized complete block design with three replications. Standard package of practices were followed to maintain a good crop in the field. Five randomly competitive plants were selected from each replication and used to record observations on yield traits. Estimates of phenotypic and genotypic coefficients of variation (Burton & De Vane 1952), heritability estimates in broad sense (Lush, 1940) and genetic advance (Johanson *et al.,* 1955) were calculated following standard statistical procedures.

RESULTS AND DISCUUSION

The analysis of variance exhibited the significant differences due to genotype for all the characters. (Table 1). The range, mean, variability estimates such as genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean are presented in Table 2. The genotypic and phenotypic coefficients of variation are classified (low: less than 10%, moderate: 10-20% and high: more than 20%) as suggested by Sivasubramanian and Madhava Menon (1973). The values of genotypic and phenotypic coefficients of variation (GCV and PCV) were moderate for all the traits studied under except for the traits No. of productive tillers per plant, Panicle length (cm). All the characters except number of productive tillers per plant, Panicle length the difference between GCV and PCV was less, indicating little influence of environment on the expression of these characters as they are back cross derived lines.

Heritability estimates are categorized (low: less than 30%, moderate: 30-60% and high: more than 60%) as recommended by Johnson *et al.* (1955). The range of genetic advance as percent of mean is classified (low: less than 10%, moderate: 10-20% and high: more than 20%) as suggested by Johnson *et al.* (1955). High heritability was observed for all the characters. High heritability coupled with high genetic advance as percent of mean was found for number of grains per panicle (Lingaiah *et al.*, 2014; Islam *et al*., 2016; Lingaiah *et al.* 2018; Setu Rani Saha, 2019) indicating the preponderance of additive type of gene action for the expression of this character and selection may be effective for improving this character. High heritability accompanied with low genetic advance as percent of mean for all the characters except number of grains per panicle reflected preponderance of non-additive gene action and selection for this trait may not be rewarding. These results are in accordance with findings of Gampala *et al*. (2015); Rukmini Devi *et al* (2016); Edukondalu *et al.* (2017); Sahu *et al*. (2017); Singh and Verma (2018). Present study revealed that there was less amount of genetic variability in the traits except number of grains/panicle as the reason could be that they are back cross derived lines.

Table 1: Analysis of variance for yield and its components in rice.

Sr. No.	Character	Mean sum of squares		
		Replication	Treatment	Error
		(d.f = 2)	(d.f= 66)	(d.f = 131)
1.	Days to 50% flowering	15.59	21.10 **	5.32
2.	Plant height (cm)	18.33	25.06**	11.01
3.	Number of productive tillers per plant	4.97	11.38**	3.19
4.	Panicle length (cm)	3.98	24.82**	1.38
5.	No. of grains per Panicle	236.36	2030.74**	113.33
6.	Grain yield per plant (g)	13.65	20.37**	4.57
7.	1000 grain weight (g)	1.74	1.02*	0.59
8.	Hulling (%)	2.64	8.84*	5.28
9.	Milling (%)	19.7	16.28**	8.08
10.	Head rice recovery (%)	14.57	8.36*	4.91
11.	Kernel length (mm)	0.003	0.154**	0.008
12.	Kernel breadth (mm)	0.002	0.042**	0.002
13.	Kernel L/B ratio	0.039	0.048**	0.023

* Significant at 5 per cent level, ** Significant at 1 per cent level

Table 2: Estimates of Variability, Heritability and Genetic advance as percent of mean for yield and its components in rice.

Sr. No.	Characters	Mean	Range		PCV (%)	GCV (%)	H (bs) (%)	Genetic Advance as %mean
			Min.	Max.				
1.	Days to 50% flowering	104.45	90.66	107.00	3.11	2.19	72.21	4.20
2.	Plant height (cm)	115.46	109.53	121.5	3.43	1.87	69.23	3.12
3.	No of productive tillers per plant	13.23	121.00	267.33	18.3	12.4	72.68	2.96
4.	Panicle length (cm)	25.98	20.76	31.86	11.66	10.75	77.54	6.80
5.	Number of grains per panicle	206.78	8.33	17.33	13.2	12.2	77.00	61.4
6.	1000 grain weight (g)	14.8	13.56	16.32	5.78	2.52	68.89	4.31
7.	Grain yield per plant(g)	27.5	18.49	30.66	11.38	8.32	73.23	4.4
8.	Hulling (%)	75.24	69.96	77.16	3.38	1.44	68.96	1.23
9.	Milling (%)	66.31	57.27	69.66	4.9	2.4	69.00	2.19
10.	Head rice recovery (%)	57.98	23.63	61.41	4.24	1.45	68.50	1.23
11.	Kernel length (mm)	5.46	4.75	6.23	4.36	4.03	77.13	5.30
12.	Kernel breadth (mm	1.61	1.37	1.93	7.78	7.08	77.00	2.72
13.	Kernel length breadth ratio	2.72	2.53	3.22	6.51	3.35	69.00	1.28

Min.-Minimum, Max.-Maximum, PCV-Phenotypic Coefficient of Variation, GCV-Genotypic Coefficient of Variation

CONCLUSION

The characters test weight, yield and plant height are attributable to additive gene effects which indicating that improvement in these characters is possible through Back cross followed by selection. The characters productive tillers per plant with low heritability with low genetic advance indicating the character is influenced by environmental effects and selection may not be useful.

FUTURE SCOPE

Cereals particularly Rice is the most important staple food-grown in over 100 countries, consumed regularly by over two billion people and the primary source of protein for millions. It is an excellent option for sustainable agri food systems of rainfed farming. The current yield is very low and stagnant around 4-5tons/ha in this crop. To combat the protein energy mal nutrition there is a need to enhance the productivity of this cereal. In this context the present study will aid the crop improvement researchers across the globe in selection of parents and to develop a strong breeding pipeline of rice crop.

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Conflict of Interest. None.

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