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GENETIC VARIABILITY AND ASSOCIATION STUDIES FOR BLAST DISEASE AND YIELD TRAITS IN F_2 POPULATION OF CROSS HUR 3022 × TETEP IN RICE (*ORYZA SATIVA* L.)

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Abstract

Analysis of variance revealed significant differences for the traits studied except, weight of panicle and length breadth ratio of grain, indicating the existence of high genetic variability among individuals of F_2 population. Less difference was observed between phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) for all the characters studied, indicating absence of considerable effect of the environment. Higher value for both GCV and PCV were observed for number of effective tillers per plant, weight of panicle, number of filled grains per panicle, grain yield per plant, disease severity per cent and area under disease progress curve. High heritability with high genetic advance observed for number of filled grains per panicle, number of unfilled grains per panicle, spikelet fertility percent and area under disease progress curve hence selection will be highly effective for these traits. Number of effective tillers per plant, number of filled grains per panicle, plant height and spikelet fertility % showed significant positive correlation with grain yield per plant, thus performing selection for these traits will be resulted into improvement of grain yield per plant. Leaf blast infection cause significant decrease in grain yield per plant because both blast disease related traits (disease severity % and area under disease progress curve) in this study showed significant negative correlation with the grain yield per plant.

Key words: Phenotypic Coefficients of Variation, Genotypic Coefficients of Variation, Disease Severity per cent, Area Under Disease Progress Curve.

Introduction

Rice is a primary food crop that provides > 20% of calories per day to nearly half of the world's population. Highest production areas as well as largest number of consumers of rice in the world belongs to Asian countries (Khush, 2005; Khush, 2013). To feed increasing world population with the existing land an increase of 26% in the rice production within next 20 years will be required (Khush, 2013). But rice is reported to be attacked by more than 70 diseases caused by different fungi, bacteria, viruses and nematods (Song and Goodman, 2001). Among these diseases, rice blast caused by fungus *Magnaporthe oryzae* belonging to the class Ascomyceta and the genus *Magnaporthe,* is one of the most significant, potentially damaging and a costly constraint for rice production at global level (Latif *et al.,* 2011). A global loss of 35–50% in rice yield is caused by rice blast (Padmavathi *et al.,* 2005). Before starting a program to breed for resistant cultivars with improved yield, a knowledge of magnitude of genetic variability present in the population, extent to which the desirable genes are heritable and association between blast resistance traits and grain yield is prerequisite (Savitha and Ushakumari, 2014).

Hence, this study was undertaken mainly to know the genetic variability and character association in F_2 population of a cross between blast susceptible and blast resistant cultivar of rice for the traits contributing to the yield as well as blast disease related traits under artificial inoculation for blast pathogen in the field condition.

Materials and Methods

Experimental Site

The present research was carried out at Agricultural

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Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (25°18′ North latitude and 83°03′ East longitude and at altitude of 123.23 m from sea level) during *kharif* 2018. The disease reaction was evaluated in field condition after artificial inoculation with *Magnaporthe oryzae* isolate *LB-TN-2.*

Experimental Material

The seed from F_2 population of a cross between HUR 3022 (Blast susceptible variety) and Tetep (Blast resistant variety) was used as study material for present experiment. 21 days old seedlings were transplanted in the field along with parents and a check (C0 39), in a complete family randomized block design with three replications maintaining a spacing of 15 × 20 cm plant to plant and row to row, respectively.

Traits Observed

Observations were recorded for total fourteen disease related and yield traits. Days to 50 percent flowering and days to maturity were recorded on plot basis. For remaining traits, data were recorded on five plants from each replication respectively, for plant height (cm), number of effective tillers per plant, panicle length (cm), weight of panicle, number of filled grains per panicle, number of unfilled grains per panicle, test weight (g), grain yield per plant (g) and length breadth ratio. Spikelet fertility per cent, disease severity % and Area Under Disease Progress Curve were calculated using standard formulae.

Statistical Analysis

Analysis of variance (ANOVA) were performed using replicated data of all the traits in online freely available software OPSTAT. Estimation of various genetic parameters like genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were carried out as per formula suggested by Burton and De-Vane (1953). While, broad sense heritability (h^2) and genetic advance (GA) were calculated as per the formula given by Allard (1960). Classification of genetic parameters values into three categories- low, medium and high were performed as per scale suggested by Sivasubramanian and Menon (1973) for GCV and PCV, as per scale suggested by Johnson *et al.,* (1955) for heritability and genetic advance, as per scale suggested by Searle (1965) for correlation coefficient, respectively.

Results and Discussion

Analysis of variation and genetic parameters

Analysis of variance indicated the presence of highly significant differences among the F_2 genotypes for all the characters except two characters- weight of panicle and length breadth ratio of grain (Table 1). These results revealed the presence of high magnitude of variation among the experimental material which is necessary for any successful crop improvement programme. These results were in conformity with the earlier reports of Salgotra *et al.,* (2009); Dhanwani *et al.,* (2013); Pallavi *et al.,* (2017); Sandhya *et al.,* (2017); Goswami (2018).

In present experiment phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all characters, clearly indicating that the phenotype was resulted not only due to genotype but environmental is also involved in the final expression of the character (Table 2). However, in present study little difference observed between GCV and PCV for all the characters revealing that role of environmental factors were very less and these characters are predominantly influenced by genetic factors. Higher value for both GCV and PCV were observed for number of effective tillers per plant, weight of panicle, number of filled grains per panicle, grain yield per plant, disease severity per cent and area under disease progress curve. Similar results were earlier reported for number of effective tillers (Badri *et al.,* 2016; Bharath *et al.,* 2018), for weight of panicle (Singh *et al.,* 2018), for number of filled grains per panicle and grain yield per plant (Behera *et al.,* 2018; Singh *et al.,* 2018). Hence, simple selection could be practiced for further improvement in above characters. Moderate value of

Table 1: Analysis of Variance (ANOVA) for fourteen blast disease related and yield traits of F_2 population under blast disease condition.

Source of variation	d.f.	DOF	DOM	PH	NET	PL	WP	NFG	NUG	SFP	TW	GY	L/B ratio	DSP	AUDPC
Genotypes	69	80.95**	82.06**	194.72**	39.41**	13.12**	1.16	3275.15**	1922.13**	464.96**	10.25**	23.57**	0.43	238.56**	50168.85**

** Significant at 1% level of significance. d.f. = degree of freedom

(DOF) Days to 50 per cent flowering, (DOM) days to maturity, (PH) plant height, (NET) number of effective tillers per plant, (PL) panicle length,(WP) weight of panicle, (NFG) number of filled grains per panicle, (NUG) number of unfilled grains per panicle, (SFP) spikelet fertility per cent, (TW) test weight, (GY) grain yield per plant, (L/B ratio) length breadth ratio of grain, (DSP) disease severity per cent and (AUDPC)area under disease progress curve both GCV and PCV were observed only for two characters which includes spikelet fertility per cent and test weight. Similar observation was earlier reported for test weight (Singh *et al.,* 2018) and for both the characters (Behera *et al.,* 2018). These results revealed that vigorous selection required for the improvement in these two traits. Lower value for both GCV and PCV were observed for days to 50% flowering, days to maturity, plant height, panicle length and length/breadth ratio of grain. Similar findings were reported for days to flowering (Karim *et al.,* 2016; Singh *et al.,* 2018), for panicle length (Singh *et al.,* 2018) and for length/breadth ratio of grain (Behera *et al.,* 2018). These results revealed that less variability present among the segregants for these characters hence breeder could not get any improvement in these traits by selection in such type of population.

Heritability and Genetic advance

In present study high broad sense heritability was observed for all the character studied which ranged from minimum in area under disease progress curve (93.35) to maximum in panicle length (99.95) followed by test weight (99.75). Generally, in variability study a wide range of variation in heritability for the characters is expected but in present study, environmental influence observed exceptionally low hence difference between genetic and phenotypic variance was found low which resulted in high heritability in all the characters studied. High heritability for test weight and panicle length was observed by Khare *et al.,* (2014); Behera *et al.,* (2018); Panigrahi *et al.,* (2018); Singh *et al.,* (2018); Kalaiselvan *et al.,* (2019). High heritability like present study was earlier reported for days to 50% flowering (Behera *et al.,* 2018; Panigrahi *et al.,* 2018; Kalaiselvan *et al.,* 2019), for days to maturity (Adhikari *et al.,* 2018), for plant height, number of effective tillers, panicle length, spikelet fertility % and grain yield per plant (Behera *et al.,* 2018; Goswami 2018; Kalaiselvan *et al.,* 2019), for weight of panicle (Singh *et al.,* 2018), for number of filled grains per panicle (Behera *et al.,* 2018; Panigrahi *et al.,* 2018) and for number of unfilled grains per panicle, respectively. Reports of high heritability for all the characters under study are available except for two blast disease related traits- disease severity percent and area under disease progress curve.

Although broad sense heritability is an important measure to determine the response to selection but the heritability estimates with genetic advance will be more effective and reliable measure (Johnson *et al.*, 1955). In present study four traits- number of filled grains per panicle, number of unfilled grains per panicle, spikelet fertility percent and area under disease progress curve were showed high heritability with high genetic advance. Hence, additive gene effects are responsible for these traits and selection for these traits are highly effective.

Table 2: Genetic variability parameters for fourteen blast disease related and yield traits under blast disease condition

****Para-meters**	**Range**		**Mean**	**V_g**	**V_p**	**GCV**	**PCV**	**h^2 (%)**	**GA (%)**
	Min	**Max**							
#DOF	73.00	97.00	84.89	26.25	27.71	6.03 (L)	6.20 (L)	94.75 (H)	10.27 (M)
DOM	103.33	127.33	115.26	26.52	28.18	4.47 (L)	4.60 (L)	94.08 (H)	10.29 (M)
PH	87.33	92.00	89.90	64.38	65.43	8.93 (L)	8.99 (L)	98.39 (H)	16.39 (M)
NET	9.00	19.33	9.90	12.83	13.45	36.18 (H)	37.04 (H)	95.39 (H)	7.20 (L)
PL	20.67	23.67	20.99	4.37	4.37	9.96 (L)	9.96 (L)	99.95 (H)	4.31 (L)
WP	2.09	2.65	2.49	0.38	0.40	24.88 (H)	25.24 (H)	97.13 (H)	1.26 (L)
NFG	74.20	138.33	125.25	1088.11	1095.32	26.34 (H)	26.42 (H)	99.34 (H)	67.72 (H)
NUG	48.13	67.47	63.10	620.63	660.79	39.48(H)	40.73 (H)	93.92 (H)	49.74 (H)
SFP	52.38	74.18	66.72	152.89	157.09	18.53 (M)	18.78 (M)	97.33 (H)	25.13 (H)
TW	15.89	19.51	15.95	3.41	3.42	11.58 (M)	11.60 (M)	99.75 (H)	3.80 (L)
GY	12.76	27.12	15.42	77.76	80.62	57.18 (H)	58.23(H)	96.45 (H)	17.84 (M)
L/B ratio	3.78	4.65	3.86	0.143	0.145	9.81 (L)	9.88 (L)	98.62 (H)	0.77 (L)
DSP	19.21	43.46	34.22	78.32	80.72	25.86 (H)	26.25 (H)	97.03 (H)	17.96 (M)
AUDPC	259.16	611.85	477.51	16147.83	17298.07	26.61 (H)	27.54 (H)	93.35 (H)	252.92 (H)

*Alphabets in the parenthesis indicates: H = High; M = Moderate; L = Low

**Vg = Genotypic variance, Vp = Phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, h^2 = Heritability (Broad sense), GA = Genetic advance

#(DOF) Days to 50 per cent flowering, (DOM) days to maturity, (PH) plant height, (NET) number of effective tillers per plant, (PL) panicle length,(WP) weight of panicle, (NFG) number of filled grains per panicle, (NUG) number of unfilled grains per panicle, (SFP) spikelet fertility per cent, (TW) test weight, (GY) grain yield per plant, (L/B ratio) length breadth ratio of grain, (DSP) disease severity per cent and (AUDPC)area under disease progress curve

Table 3: Phenotypic correlation coefficients among fourteen blast disease related and yield traits under blast disease condition

	DOF	DOM	PH	NET	PL	WP	NFG	NUG	SFP	TW	L/B	DSP	AUDPC	GY
#DOF	1													
DOM	0.989**	1												
PH	-0.018	-0.030	1											
NET	-0.028	-0.014	0.210	1										
PL	-0.233	-0.2043	0.338**	0.096	1									
WP	0.169	0.143	-0.048	0.029	-0.021	1								
NFG	0.129	0.088	0.119	0.023	-0.037	0.849**	1							
NUG	-0.005	0.019	-0.146	0.094	0.155	-0.260*	-0.380**	1						
SFP	0.075	0.036	0.165	-0.088	-0.155	0.548**	0.726**	-0.896**	1					
TW	-0.084	-0.096	0.331**	0.050	0.385**	0.352**	0.158	-0.344**	0.276*	1				
L/B Ratio	-0.183	-0.162	-0.287*	0.174	0.021	-0.328**	-0.353**	0.357**	-0.417**	-0.395**	1			
DSP	0.086	0.066	-0.398**	-0.169	-0.262*	-0.034	-0.078	0.276*	-0.222	-0.386**	0.276*	1		
AUDPC	0.089	0.069	-0.394**	-0.162	-0.259*	-0.039	-0.079	0.275*	-0.223	-0.388**	0.275*	0.999**	1	
GY	-0.010	-0.017	0.385**	0.775**	0.224	0.254*	0.403**	-0.187	0.309**	0.219	-0.123	-0.279*	-0.267*	1

*Significance at 5% level of significance, **Significance at 1% level of significance

(DOF) Days to 50 per cent flowering, (DOM) days to maturity, (PH) plant height, (NET) number of effective tillers per plant, (PL) panicle length,(WP) weight of panicle, (NFG) number of filled grains per panicle, (NUG) number of unfilled grains per panicle, (SFP) spikelet fertility per cent, (TW) test weight, (GY) grain yield per plant, (L/B ratio) length breadth ratio of grain, (DSP) disease severity per cent and (AUDPC)area under disease progress curve

Similar findings were earlier reported for spikelet fertility percent and number of grains per panicle (Goswami 2018; Singh *et al.,* 2018). High heritability associated with moderate genetic advance was observed for days to 50% flowering, days to maturity, plant height, grain yield per plant and disease severity. This reveals greater role of non-additive gene action in inheritance of these traits for which heterosis breeding recommended. Similar results were reported for days to 50% flowering (Adhikari *et al.,* 2018); for grain yield per plant (Kalaiselvan *et al.,* 2019). High heritability associated with low genetic advance was observed for number of effective tillers, panicle length, weight of panicle, test weight and length/breadth ratio. Similar results were reported for number of effective tillers (Goswami 2018); for panicle length (Panigrahi *et al.,* 2018) and for test weight (Singh *et al.,* 2018), respectively.

Association between traits

Correlation studies on association of studied traits with grain yield per plant and blast related traits, revealed that significant highest positive phenotypic correlation was observed between area under disease progress curve and disease severity % (0.999) followed by between days to 50% flowering and days to maturity (0.989). Significant highest negative phenotypic correlation was observed between number of unfilled grains per panicle and spikelet fertility % (-0.896) followed by between disease severity % and plant height (-0.398). Grain yield per plant was observed to show significant highest positive correlation with number of effective tillers per plant (0.775) followed by number of filled grains per panicle (0.403), plant height (0.385), spikelet fertility %. Hence, positive selection for above mention traits resulted in improvement of grain yield per plant under blast disease condition. Similar results were earlier reported in literature (Khare *et al.,* 2014; Devi *et al.,* 2017; Gour *et al.,* 2017; Panigrahi *et al.,* 2018; Saha *et al.,* 2019).

Significant highest negative correlation with grain yield per plant was showed by both blast disease related traits- disease severity % (-0.279) and area under disease progress curve (-0.267) followed by number of unfilled grains per panicle. Results clearly revealed that grain yield per plant was tremendously decreased when plant is affected with blast disease, result indicate that leaf blast infection causes significant decrease in grain yield per plant. Both blast related traits were also showed significant highest positive correlation with number of unfilled grains per panicle and length/breadth ratio. Hence, blast disease infection increases the number of unfilled grains per panicle as well as increase in length/breadth ratio of the grains. Significant highest negative correlation with both the blast related traits was found in plant height followed by test weight and panicle length, revealing that test weight will be decreased if blast disease incidence occurs in field that also affect plant height and panicle length, respectively.

Conclusion

Results of present investigation indicated that enough variability present in the population. Role of environmental factors were found very less in present study and the characters studied were reported predominantly influenced by genetic factors only. Higher value for both GCV and PCV were observed for number of effective tillers per plant, weight of panicle, number of filled grains per panicle, grain yield per plant, disease severity per cent and area under disease progress curve. High heritability with high genetic advance observed for number of filled grains per panicle, number of unfilled grains per panicle, spikelet fertility percent and area under disease progress curve which indicates involvement of additive gene effect and effectiveness of selection for these traits. Association studies revealed that number of effective tillers per plant, number of filled grains per panicle, plant height and spikelet fertility % positively corelated with grain yield per plant thus performing selection for these traits will be resulted into improvement of grain yield per plant. Leaf blast infection revealed causing significant decrease in grain yield per plant because both blast disease related traits in the study showed significant negative correlation with grain yield per plant. Significant negative correlation with both the blast related traits was also showed by plant height, test weight and panicle length, revealing that test weight will be decreased if blast disease present in the field as well as plant height and panicle length, respectively.

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