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Morphological Characterization of Advanced Backcross Population for Yield and Yield Attributing Character in Rice (*Oryza sativa* L.)

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A B S T R A C T

An experiment was framed to know the genetic variability, heritability, genetic advance and character association among the lines homozygous dominant for gall midge resistance gene *Gm4* in the genetic background of ADT 38 variety of rice in advanced backcross (BC_1F_5) generation of rice. The Phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters studied. High GCV coupled with high PCV was exhibited by single plant yield. This result creates scope for selection of superior segregants. Moderate heritability coupled with high genetic advance was recorded for hundred grain weight indicating that the selection could be done at later generation. Highly significant positive correlation with single plant yield was exhibited by traits like number of tillers, number of productive tillers and number of filled grain per panicle. The path coefficient analysis reveals that the traits like number of productive tillers, number of filled grains per panicle, grain width, grain length/grain width ratio and hundred grain weight has a positive direct effect towards single plant yield.

Introduction

Rice is the most important cereal food crop of the developing world and the staple food of more than half of the world's population, cultivated in an area of more than 150 million hectare. More than 90% of the world's rice output comes from Western and Eastern Asia, out of which China and India account for more than 33% (Pennisi, 2010). Worldwide, more than 3.5 billion people depend on rice for more than 27% of their daily dietary energy supply, 20% of dietary protein and 3% of dietary fat. India has about 433.88 lakh hactre of area under rice with an annual production of 104.32 million ton presently (GOI 2016-17). It is estimated that India needs to produce 120 million tonnes of rice by 2030 to feed its projected one and half billion plus population by then (Adhya, 2011).

Major constraints in Rice production are due to biotic stress which account of 1- 85% (Rola and Widawsky, 1998). TheAsian rice gall midge, *Orseolia oryzae* (Wood-Mason) (Diptera: Cecidomyiidae), a major pest of rice (*Oryza sativa* L.), forms leaf-sheath gall called 'silver shoot'. It is the third most economically important pest of rice in India causing an average annual yield loss worth US$ 80 million (Bentur *et al.*, 2003).

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Chaudhary *et al.*, 2004). Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm. Heritability is a good index of the transmission of character from one generation to consecutive generation (Falconer *et al.*, 1981; Bello *et al.*, 2012). Genetic advance is the measure of genetic gain under selection. The success of genetic advance under selection depends on genetic variability, heritability and selection intensity (Johnson *et al.*, 1955).

Materials and Methods

The present investigation comprised of evaluation of BC_1F_5 population having gall midge resistance gene *Gm4* in the background of ADT 38 variety of rice along with un-pyramided ADT 38 as check. The seed material for the present study was obtained from plants homozygous dominant for *Gm4*genein the BC_1F_4 population of the ADT 38. Previously the gene introgression being done into ADT 38 background where Abhaya served as a donor for*Gm4* gall midge resistance gene. The ADT 38 (*Gm4*) was backcrossed by taking ADT 38 as recurrent parent and selfed upto F_4 generation.

The field experiment was conducted in Randomized Design, with 5 replications by following a standard spacing of 20 cm x 20 cm. The standard agronomical practices were followed to grow healthy crop at wet lands, Tamil Nadu Agricultural University, Coimbatore during the growing season of 2013- 2014. The mean values of 5 replications were used for statistical analysis. The observation were recorded on eleven quantitative traits *viz.,* days to fifty per cent flowering (DFF), plant height (PH), number of tillers (NT), number of productive tillers (NPT), panicle length (PL), number of filled grains (NFG), grain length (GL), grain width (GW), grain length/grain width ratio (GL/GW), hundred grain weight (HGW) and single plant yield (SPY) The descriptive statistics were estimated for each trait studied with the help of MS – EXCELand for biometrical calculation GENRES software was used. The Phenotypic and genotypic coefficient of variation (PCV and GCV) were calculated as described by Johnson *et al.*, (1955). Broad sense heritability and genetic advance as percent of mean was estimated as suggested by Johnson *et al.*, (1955). The genotypic correlation coefficient for all character combinations were calculated by following formula given by Millar *et al.*, (1985). The direct and indirect contribution of various characters to yields were calculated through path coefficient analysis suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

Results and Discussion

The Phenotypic coefficient of variation (PCV) was higher than the Genotypic coefficient of variation (GCV) for all the characters, however large difference was recorded between PCV and GCV for character viz., number of tillers, number of productive tillers clearly indicating the environmental influence in expression of these characters. High GCV coupled with high PCV was exhibited by single plant yield. The high GCV gives an indication of justifiable variability among genotypes with respect to these characters and therefore gives scope for improvement through selection (Pandey *et al.*, 2010; Tiwari *et al.*, 2011). This finding was corroborated with Ukaoma *et al.,* (2013). High PCV and moderate GCV were observed for characters like number of tillers, number of productive tillers and number of filled grain per panicle. This result was in accordance with Prabhu *et al.,* (2017).

Moderate PCV and GCV were recorded for panicle length. However low PCV coupled with low GCV were exhibited by days to 50% flowering, plant height, grain length, grain width and grain length/grain width ratio. Moderate PCV along with low GCV was exhibited by hundred grain weight. The low GCV values give an indication of less variability among lines in BC_1F_5 generation with *Gm4* gene for maximum number of traits and hence it is inferred that those lines are stabilized for that trait. Similar results were reported by, Binse *et al.,* (2009), Laxuman *et al.,* (2010), Shiva Prasad *et al.,* (2011) and Seyoum *et al.,* (2012).

The quantitative characters are governed by many genes and are more influenced by environment. The phenotype observed is not transmitted entirely to next generation. Therefore, it is necessary to know the proportion of observed variability that is heritable.

Heritability of a trait is important in determining its response to selection. Genetic improvement of genotypes for quantitative traits requires reliable estimate of heritability for designing an efficient breeding program. The knowledge of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a character into subsequent generations (Sabesan *et al.,* 2009; Ullah *et al.,* 2011). High heritability estimate was recorded for number of filled grain per panicle (68.78), grain length (75.52), grain width (72.61), grain length/grain width ratio (83.07) and single plant yield (64.37) (Table 1). However moderate heritability was recorded for days to 50% flowering (55.87), panicle length (52.08) and hundred grain weight (51.55). For rest of the characters viz., plant height (21.36), number of tillers (30.36) and number of productive tillers (30.55) low heritability estimate was recorded.

Genetic advance as percentage of mean is more reliable index for understanding the effectiveness of selection in improving the traits because it's estimated value is derived by involvement of heritability, phenotypic standard deviation and intensity of selection (Sinha and Wagh, 2013). Thus genetic advance as percentage of mean along with heritability provides clear picture regarding the influences positively the effectiveness of selection for improving the plant characters. Estimation of heritability along with genetic gain is usually more useful in predicting the resultant effect from selecting the best individual.

High heritability coupled with moderate genetic advance was recorded for single plant yield. This result was also in accordance with Mohan lal and Chauhan (2011) and Prabhu *et al.,* (2017). High heritability coupled with low genetic advance was recorded for number of filed grain per panicle, grain length, grain width and grain length/grain width ratio. It is indication of the predominance of epistasis and dominant gene action (non - additive gene action) and selection for such traits may not be rewarding.

Low heritability coupled with low genetic advance was recorded for plant height, number of tillers and number of productive tillers. Low heritability coupled with low genetic advance indicates that the characters are highly influenced by environmental effects and selection would be ineffective (Nandarajan and Gunasekaran, 2005). The mean performances of all the yield attributing characters are presented in Table 4.

Table.1 Variability parameters of advanced backcross generation (BC_1F_5lines) with gall midge resistance gene (*Gm4Gm4*) involving ADT 38 as a recurrent parent

Characters	RANGE	MEAN	PCV	GCV	$h^2_{(bs)}$ (in %)	GA (%) of mean
DFF (days)	87.40 – 91.20	90.18	1.76	1.32	55.87	1.31
PH (cm)	77.00 – 83.60	80.26	4.87	2.25	21.36	2.14
NT (no.)	11.60 – 17.60	13.90	24.09	13.27	30.36	7.47
NPT (no.)	10.80 – 17.20	13.26	26.71	14.76	30.55	8.14
PL (cm)	16.20 – 21.00	18.88	16.57	11.96	52.08	8.36
NFG (no.)	91.80 – 147.40	116.68	23.50	19.49	68.78	4.75
GL (mm)	155.60 – 163.80	158.32	1.68	1.46	75.52	1.13
GW (mm)	52.00 – 55.20	53.64	2.37	2.02	72.61	2.28
GL/GW	2.89 – 3.04	2.95	2.33	2.13	83.07	9.76
HGW (gm)	1.68 – 2.12	1.90	10.38	7.46	51.55	20.73
SPY (gm)	19.84 – 35.96	27.89	36.79	29.52	64.37	11.77

Days to fifty per cent flowering (DFF), plant height (PH), number of tillers (NT), number of productive tillers (NPT), panicle length (PL), number of filled grains (NFG), grain length (GL), grain width (GW), grain length/grain width ratio (GL/GW), hundred grain weight (HGW) and single plant yield (SPY), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) (h^2), Genetic advance (GA).

Table.2 Genotypic correlation between different pair of traits in advanced backcross generation (BC_1F_5) with gall midge resistance gene (*Gm4Gm4*) involving ADT 38 as a recurrent parent

Characters	DFF	PH	NT	NPT	PL	NFG	GL	GW	GL/GW	HGW	SPY
DFF	1.000	0.078	-0.036	0.027	-0.090	0.032	0.179	-0.048	0.186	0.030	0.043
PH		1.000	0.137	0.126	0.420**	-0.175	0.213	0.080	0.068	0.078	0.015
NT			1.000	0.956**	0.005	0.105	0.035	-0.035	0.055	-0.075	0.735**
NPT				1.000	-0.023	0.104	0.098	0.003	0.062	-0.048	0.782**
PL					1.000	-0.117	-0.084	-0.055	-0.009	0.011	-0.132
NFG						1.000	0.330**	0.288**	-0.060	-0.605**	0.599**
GL							1.000	0.396**	0.308**	-0.153	0.285*
GW								1.000	-0.751**	-0.104	0.192
GL/GW									1.000	-0.002	0.007
HGW										1.000	-0.111
SPY											1.000

** Significant at 1% level, * Significant at 5% level

Days to fifty per cent flowering (DFF), plant height (PH), number of tillers (NT), number of productive tillers (NPT), panicle length (PL), number of filled grains (NFG), grain length (GL), grain width (GW), grain length/grain width ratio (GL/GW), hundred grain weight (HGW) and single plant yield (SPY),

Table.3 Path analysis showing direct and indirect effects of different traits on yield in advanced backcross generation (BC_1F_5 lines) with gall midge resistance gene (*Gm4Gm4*) involving ADT 38 as a recurrent parent

Characters	DFF	PH	NT	NPT	PL	NFG	GL	GW	GL/GW	HGW	SPY
DFF	**-0.019**	0.003	0.001	0.021	0.003	0.024	-0.286	-0.111	0.418	-0.011	0.043
PH	-0.001	**0.044**	-0.007	0.097	-0.016	-0.129	-0.340	0.186	0.152	0.029	0.015
NT	0.001	0.006	**-0.049**	0.740	-0.000	0.078	-0.056	-0.080	0.123	-0.027	0.735
NPT	-0.000	0.005	-0.047	**0.774**	0.001	0.077	-0.156	0.007	0.138	-0.017	0.782
PL	0.002	0.019	-0.000	-0.017	**-0.038**	-0.087	0.133	-0.127	-0.021	0.004	-0.132
NFG	-0.000	-0.008	-0.005	0.080	0.004	**0.742**	-0.527	0.669	-0.134	-0.222	0.599
GL	-0.003	0.009	-0.001	0.075	0.003	0.245	**-1.597**	0.919	0.690	-0.056	0.285
GW	0.001	0.003	0.001	0.002	0.002	0.214	-0.632	**2.321**	-1.683	-0.038	0.192
GL/GW	-0.003	0.003	-0.003	0.048	0.000	-0.044	-0.492	-1.743	**2.242**	-0.001	0.007
HGW	0.001	0.003	0.004	-0.037	-0.000	-0.449	0.245	-0.240	-0.005	**0.368**	-0.111

Residual effect: 0.127, Diagonal values indicate the direct effects

Days to fifty per cent flowering (DFF), plant height (PH), number of tillers (NT), number of productive tillers (NPT), panicle length (PL), number of filled grains (NFG), grain length (GL), grain width (GW), grain length/grain width ratio (GL/GW), hundred grain weight (HGW), single plant yield (SPY),

Table.4 Mean performance of yield attributing traits ofadvanced backcross generation (BC_1F_5 lines) with gall midge resistance gene (*Gm4Gm4*) involving ADT 38 as a recurrent parent

Genotypes	DFF (Days)	PH (cm)	NT (no.)	NPT (no.)	PL (cm)	NFG (no.)	GL (mm)	GW (mm)	GL/GW	HGW (g)	SPY (g)
ADT 38	90.20	79.50	14.60	13.60	18.70	126.00	159.40	54.00	2.95	1.82	25.27
Abhaya	83.20	90.20	13.20	10.60	27.60	102.40	157.60	48.00	3.28	2.49	22.06
Line 1	90.60	81.20	17.60	17.20	20.20	115.40	159.20	53.80	2.96	1.88	35.06
Line 2	91.00	79.40	14.40	14.20	16.20	106.80	158.00	52.00	3.04	1.88	27.83
Line 3	90.60	83.20	13.00	12.40	21.00	106.40	156.40	53.20	2.94	1.94	24.79
Line 4	91.20	81.60	15.00	14.00	20.00	106.00	155.60	53.00	2.94	1.86	24.80
Line 5	90.60	83.60	14.80	14.20	18.00	147.40	163.80	55.20	2.97	1.74	35.96
Line 6	91.20	77.00	11.60	11.60	17.20	129.80	158.00	54.60	2.89	1.90	28.66
Line 7	88.00	78.20	13.40	11.60	18.90	137.40	156.00	53.60	2.91	1.68	25.49
Line 8	87.40	79.40	12.00	10.80	18.70	91.80	157.20	54.20	2.90	2.12	19.84
Line 9	90.60	79.20	13.40	13.00	19.80	124.40	159.00	54.00	2.94	1.94	29.36
Line 10	90.60	79.80	13.80	13.60	18.80	101.40	160.00	52.80	3.03	2.02	27.09
Mean of line 1- line 10	**90.18**	**80.26**	**13.90**	**13.26**	**18.88**	**116.68**	**158.32**	**53.64**	**2.95**	**1.90**	**27.89**

The correlation coefficient estimates, the degree and direction of association between a pair of characters and proved to be useful for simultaneous improvement of the correlated traits through selection. The data obtained for genotypic correlation with analysis was mentioned in Table 2 which reveals that highly significant positive correlation with single plant yield was exhibited by traits like number of tillers (r = 0.735**), number of productive tillers (r = 0.782**) and number of filled grain per panicle (r = 0.599**). From the results it was evident that if the genotype is selected which possesses more number of tillers, productive tillers, number of filled grains per panicle then it will contribute to increased yield.

This was also in confirmation with the findings of Anbanandan *et al.,* (2009), Sabesan *et al.,* (2009), Jayasudha and Sharma (2010), Selvaraj *et al.,* (2011b), Augustina *et al.,* (2013) and Minnie *et al.,* (2013). Characters of the above which is having positive and significant correlation between them indicate the possibility of simultaneous improvement of those traits by selection.

The grain length has a significant and positive correlation with single plant yield. The hundred grain is negatively associated with single plant yield Similar type of result also reported by Sabesan *et al.,* (2009).

A path coefficient is simply a standardized partial regression coefficient and measures the direct influence of one variable upon another and permits the separation of the correlation coefficient into components of direct and indirect effects (Dewey and Lu, 1959).

The path coefficient analysis was used to partition the correlation coefficients of all the characters studied with single plant yield into direct and indirect effects. The results of various causes influencing single plant yield (direct and indirect effect) are shown in Table 3. The path coefficient analysis of different traits contributing towards single plant yield revealed that positive direct effect was exhibited by number of productive tillers, number of filled grains per panicle, grain width, grain length/grain width ratio and hundred grain weight.

Lenka and Mishra (1973) reported rating of the direct and indirect effect ranging from 0.30-1.00 as high and above 1.00 as very high. In this study the values of the direct and positive effect for the above characters were ranging from 0.36 – 2.32.

Hence, the contribution of the above characters to single plant yield is evidently high to very high hence, they can be potentially help for direct selection for increased yield. Similar types of results were also reported by Hossain *et al.,* (2015) and Devi *et al.,* (2017) for number of filled grains per panicle, Ramakrishnan *et al.,* (2006), Agahi *et al.,* (2007), Kole *et al.,* (2008), Satish Chandra *et al.,* (2009) and Chakraborty *et al.,* (2010) for hundred grain weight, Agahi *et al.,* (2007) for number of productive tillers.

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