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Genetic variability and character association studies in advanced backcross generation of rice (*Oryza sativa* L.)

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Abstract

An experiment was designed to know the genetic variability, heritability, genetic advance and character association among the lines homozygous dominant for gall midge resistance genes *Gm1* and *Gm4* in the genetic background of ADT 38 variety of rice in advanced backcrossed (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 heritability coupled with high genetic advance as percent of mean was registered for character like hundred grain weight. 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. Positive direct effect was exhibited by number of tillers, number of filled grains per panicle and hundred grain weight towards single plant yield. These characters will be useful for further breeding.

Keywords: phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2), genetic advance (GA), correlation, direct effect

Introduction

Rice (*Oryza sativa* L.) being the most important cereal food crops in the world which forms the staple diet of 2.7 billion people (Tannidi *et al.*, 2016) [29]. Around 32- 59% of the dietary energy and 25-44% of the dietary protein was obtained from rice in more than 39 countries (Prabhu *et al.*, 2017) [22]. Rice crop losses due to biotic stresses are estimated at 1 to 85 per cent (Rola and Widawsky, 1998) [23]. India has about 433.88 lakh hectare 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 millions tonnes of rice by 2030 to feed its projected one and half billion plus population by then (Adhya 2011) [1]. The Asian 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) [5]. Genetic parameter such as heritability offers the information of transmissibility of characters from one generation to consecutive generations (Bello *et al.*, 2012) [4]. High heritability with high genetic advance (%) of mean is used to predict the performance of genotype/progeny for yield and yield contributing traits (Singh *et al.*, 2011 and Govintharaj *et al.*, 2016) [27, 10].

Material and Methods

The present investigation comprised of evaluation of BC_1F_5 population having gall midge resistance genes *Gm1* and *Gm4* in the background of ADT 38 variety of rice along with unpyramided ADT 38 as check. The seed material for the present study was obtained from plants homozygous dominant for *Gm1* and *Gm4* in the BC_1F_4 population of the ADT 38. Previously the gene pyramiding being done into ADT 38 background where Kavya and Abhaya being the donor for *Gm1* and *Gm4* gall midge resistance gene respectively. The pyramided ADT 38 (*Gm1*+ *Gm4*) 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 – EXCEL

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and 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) [13]. Broad sense heritability and genetic advance as percent of mean was estimated as suggested by Johnson *et al* (1955) [13]. The genotypic correlation coefficient for all character combinations were calculated by following formula given by Millar *et al* (1985) [17]. The direct and indirect contribution of various characters to yields were calculated through path coefficient analysis suggested by Wright (1921) [30] and elaborated by Dewey and Lu (1959) [8].

Result 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 and single plant yield indicating the environmental influence in expression of these characters. High GCV was exhibited by number of productive tillers, hundred grain weight and 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. Characters like number of filled grain exhibited moderate GCV where as low GCV value was recorded for days to 50% flowering, plant height, number of tillers, panicle length, grain length, grain width and grain length/grain width ratio. The low GCV values give an indication of less variability among lines in BC₁F₅ generation with *Gm1 + 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) [6], Laxuman *et al* (2010) [14] and Shiva Prasad *et al* (2011) [26].

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 estimates provides the assessment of amount of transmissible genetic variability to total variability, happens to be the most important basic component that determines the genetic improvement or response to selection. However, the degree of improvement attained through selection is not only dependent on heritability but also on the amount of genetic variation present in the breeding population and the extent of selection pressure applied by the breeder. High heritability estimate was recorded for days to 50% flowering (67.29), grain length (96.64), grain width (95.33), grain length/grain width ratio (93.58), hundred grain weight (90.12) and single plant yield (67.11) (Table 1). However among rest of the characters moderate level of heritability was exhibited by number of productive tillers (46.02), panicle length (39.99), number of filled grain (49.92) and low magnitude of heritability was recorded for plant height (11.17) and number of tillers (8.06).

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 high genetic advance as percent of mean (36.26) was registered for character like hundred grain weight (Govintharaj *et al.*, 2016) [10] (Table 1). High heritability along with high genetic advance indicates that mostly the heritability is due to the additive gene effects and selection may be effective. High heritability coupled with low genetic advance was found in characters like days to fifty per cent flowering (Lingaiah *et al.*, 2014) [16], grain length and grain width. High heritability coupled with low genetic advance is the 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 with low genetic advance was recorded in case of plant height and number of 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) [20]. The mean performances of all the yield attributing characters are presented in table 4.

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 ($r = 0.640^{**}$), number of productive tillers ($r = 0.569^{**}$) and number of filled grain per panicle ($r = 0.665^{**}$). 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) [2], Sabesan *et al* (2009) [24], Jayasudha and Sharma (2010) [12], Selvaraj *et al* (2011b) [25] Augustina *et al* (2013) [3] and Minnie *et al* (2013) [18]. 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 hundred grain weight is associated positively with single plant yield but not significantly (Guru *et al.*, 2016) [11]. Traits like days to 50% flowering and grain length had negative association with yield (Lingaiah *et al.*, 2014) [16].

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) [8]. 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 tillers (0.854), number of filled grains per panicle (0.658) (Mohankumar *et al.*, 2011) [19] and hundred grain weight (0.533) (Chakraborty *et al.*, 2010) [7] (Mohammad *et al.*, 2013) [21]. However plant height and grain width expressed negative direct effect on single plant yield. The result of negative direct effect indicated that these characters had low association and selection based on these characters would not be effective.

Lenka and Mishra (1973) [15] 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 0.53 – 0.85.

Hence, the contribution of the above characters to single plant yield is evidently high and hence, they can be potentially help for direct selection for increased yield. Similar types of results

were also reported by Gawai *et al* (2006)^[9] and Jayasudha and Sharma (2010)^[12] for number of tillers per plants and number of filled grains per panicle.

Table 1: Variability parameters of advanced backcross generation (BC₁F₅ lines) with gall midge resistance gene (*Gm1Gm1 Gm4Gm4*) involving ADT 38 as a recurrent parent

Characters	RANGE	MEAN	PCV	GCV	h ² _(bs) (in %)	GA (%) of mean
DFE (days)	87.40 – 91.40	90.15	2.04	1.68	67.29	1.58
PH (cm)	77.10 – 84.80	80.75	5.64	1.89	11.17	1.30
NT (no.)	12.00 – 16.00	13.90	27.80	7.89	8.06	2.30
NPT (no.)	10.60 – 15.40	12.65	31.86	21.61	46.02	12.89
PL (cm)	17.00 – 21.20	18.85	14.83	9.38	39.99	6.43
NFG (no.)	89.40 – 117.00	101.90	21.25	15.01	49.92	3.95
GL (mm)	145.80 – 162.20	156.40	4.59	4.51	96.64	1.46
GW (mm)	50.60 – 58.40	54.60	5.65	5.52	95.33	2.94
GL/GW	2.78 – 2.93	2.87	3.90	3.77	93.58	11.32
HGW (gm)	1.36 – 2.42	1.90	23.00	21.83	90.12	36.26
SPY (gm)	17.43 – 28.42	20.78	51.41	42.11	67.11	16.47

Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) (h²), Genetic advance (GA)

Table 2: Genotypic correlation between different pair of traits in advanced backcross generation (BC₁F₅) with gall midge resistance gene (*Gm1Gm1 Gm4Gm4*) involving ADT 38 as a recurrent parent

Characters	DFE	PH	NT	NPT	PL	NFG	GL	GW	GL/GW	HGW	SPY
DFE	1.000	-0.136	0.172	0.263	-0.118	-0.368	-0.586**	-0.683**	0.290	-0.772**	-0.317
PH		1.000	0.208	0.138	0.389*	-0.073	0.369	0.299	0.001	0.201	0.134
NT			1.000	0.957**	-0.104	0.063	-0.463*	-0.101	-0.406*	-0.338	0.640**
NPT				1.000	-0.136	0.017	-0.523**	-0.207	-0.327	-0.400*	0.569**
PL					1.000	0.063	0.334	0.426*	-0.222	0.306	0.095
NFG						1.000	-0.022	0.375	-0.559**	0.144	0.665**
GL							1.000	0.733**	0.127	0.770**	-0.032
GW								1.000	-0.581**	0.754**	0.427*
GL/GW									1.000	-0.175	-0.650**
HGW										1.000	0.232
SPY											1.000

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

Table 3: Path analysis showing direct and indirect effects of different traits on yield in advanced backcross generation (BC₁F₅ lines) with gall midge resistance gene (*Gm1Gm1Gm4Gm4*) involving ADT 38 as a recurrent parent.

Characters	DFE	PH	NT	NPT	PL	NFG	GL	GW	GL/GW	HGW	SPY
DFE	0.224	0.019	0.147	0.005	-0.004	-0.241	-0.081	0.002	0.026	-0.412	-0.317
PH	-0.030	-0.139	0.177	0.002	0.014	-0.048	0.051	-0.001	0.000	0.107	0.134
NT	0.038	-0.029	0.854	0.019	-0.004	0.041	-0.064	0.001	-0.036	-0.180	0.640
NPT	0.059	-0.019	0.817	0.020	-0.005	0.011	-0.073	0.000	-0.029	-0.213	0.569
PL	-0.026	-0.054	-0.088	-0.002	0.036	0.041	0.046	-0.001	-0.019	0.163	0.095
NFG	-0.082	0.010	0.053	0.001	0.002	0.658	-0.003	-0.001	-0.049	0.077	0.665
GL	-0.131	-0.051	-0.395	-0.010	0.012	-0.015	0.139	-0.002	0.011	0.410	-0.032
GW	-0.152	-0.042	-0.086	-0.004	0.015	0.247	0.102	-0.002	-0.052	0.402	0.427
GL/GW	0.065	-0.001	-0.346	-0.007	-0.008	-0.368	0.018	0.001	0.089	-0.093	-0.650
HGW	-0.173	-0.028	-0.288	-0.008	0.011	0.095	0.107	-0.002	-0.017	0.533	0.232

Residual effect = 0.176, Diagonal values indicate the direct effects

Table 4: Mean performance of yield attributing traits of advanced backcross generation (BC₁F₅ lines) with gall midge resistance gene (*Gm1Gm1Gm4Gm4*) involving ADT 38 as a recurrent parent.

Genotypes	DFE (Days)	PH (cm)	NT (no.)	NPT (no.)	PL (cm)	NFG (no.)	GL (mm)	GW (mm)	GL/GW	HGW (gm)	SPY (gm)
ADT 38	90.20	79.50	14.60	13.60	18.70	126.00	159.40	54.00	2.95	1.82	25.27
Kavya	85.20	80.70	11.40	9.70	27.40	148.60	149.40	52.40	2.85	2.38	17.68
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	87.40	80.90	13.40	11.80	19.60	117.00	162.20	58.40	2.78	2.42	28.42
Line 2	90.80	84.80	12.00	10.60	21.20	102.80	158.60	54.20	2.93	1.94	17.43
Line 3	91.00	80.20	14.20	12.80	17.60	89.40	159.00	55.20	2.88	1.86	18.86
Line 4	91.40	77.10	16.00	15.40	17.00	98.40	145.80	50.60	2.88	1.36	18.39
Mean of line 1- line 4	90.15	80.75	13.90	12.65	18.85	101.90	156.40	54.60	2.87	1.90	20.78

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