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Studies on Genetic Variability Parameter under Artificial Epiphytotic Condition for Leaf Rust in Bread Wheat (*Triticum aestivum* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Present investigation was conducted to study the genetic variability for grain yield, its component traits and slow rusting component in advanced backcross segregating lines of bread wheat at AICRP on wheat, MARS, UAS, Dharwad, Karnataka during *Rabi* season of 2015-2016. The study revealed highly significant differences for the yield, its component traits and for slow rusting components, indicating the presence of sufficient genetic variability in these lines which is basis for the effective selection in any breeding programme. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values coupled with high heritability and high genetic advance over mean were recorded for some of the studied traits such as grain yield per plant and no. of productive tillers per plant. Also high PCV and GCV along with high heritability and high genetic advance over mean (GAM) was found for the slow rusting components. The presence of

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sufficient variability along with high heritability for all these traits indicates that simple phenotypic selection for these traits may be effective for genetic improvement of these traits. Hence based on present findings it can be concluded that practicing selection considering the traits like productive tillers per plant, grain yield per plant along with slow rusting components will be more beneficial for achieving durable type of resistance in future breeding programme.

Keywords: Leaf rust; backcross; slow rusting; variability; heritability.

1. INTRODUCTION

Present day cultivated bread wheat (*Triticum aestivum* L.) has recently been estimated to have formed through rare hybridization events between diploid and tetraploid progenitors with domestication occurring approximately 10,000 years ago [1]. Among the all type of biotic stress, leaf rust caused by fungal pathogen *P. triticina* Eriks. is a severe problem which may account for yield losses of 40 per cent in bread wheat [2]. To overcome this problem in economic and sustainable way one approach may be development and deployment of cultivars with broad spectrum rust resistance. Deployment of single rust resistance gene leads to high selection pressure on the existing races as a result evolution of new races through mutation, migration and recombination is very frequent which leads to breakdown of resistance. An effective way to overcome this problem is to development of varieties having combinations of minor or slow rusting genes possesing adult plant resistance (APR). These APR genes when present alone do not posses adequate resistance especially under high disease pressure condition. Combining 4-5 such genes in any cultivar through marker assisted selection usually result in durable long lasting type of resistance. Presently, among the known genes *Lr34* [3], *Lr46* [4], *Lr67* [5] and [6] and *Lr68* [7] are most common genes that shows slow rusting type of resistance. These genes shows pleiotropic effects and when pyramided in one line provides durable type of adult plant resistance in a non-race specific manner to the existing races of all three types of rust [8]. Hence keeping these views in mind, the present investigation was carried out to improve GW 322, a very popular and widely accepted variety of peninsular zone of India by deploying two slow rusting genes, *Lr34* and *Lr68* by Marker assisted backcross breeding. It is the magnitude of genetic variability for a particular trait which decides either a selection will be effective or not in any breeding programe [9]. It is not just the magnitude of genetic variability but the extent of heritable variation present in any breeding material, that is of prime importance for advancing gains in any selection programme. In this context, partitioning total variability into heritable and non-heritable components to further compute heritability and genetic advances becomes necessary. Thus, the present study was conducted in advanced backcross segregating lines of bread wheat to evaluate it for genetic variability parameters of yield, its attributing traits along with slow rusting components.

2. MATERIALS AND METHODS

An experimental material comprising of one eighty lines of different advanced segregating generations of the cross GW322 X PARULA were sown in Augmented Block Design along with 4 checks viz., UAS304, HD2189, GW322 and Parula in artificial epiphytotic condition for leaf rust. These lines were sown in 6 blocks, each block consisting 30 lines keeping spacing of 20 x 20 cm. Five plants were randomly selected and tagged and observations for the traits like grain yield, its component traits along with slow rusting component were recorded.

Statistical analysis was carried out on the mean values of the five randomly selected plants. Different genetic parameters and the statistical methods adopted were as follows.

2.1 Statistical Analysis

Analysis of variance (ANOVA) for augmented design was carried out for each character as per Federer [10]. The components of variance GCV, PCV and heritability were calculated as per method suggested by Burton and De Vane [11] and Johnson et al. [12]. Mean, range, coefficients of variance, genotypic variance and phenotypic variances were determined based on mean and variance calculated by using data of unreplicated treatments. As per suggested by Sivasubramanian and Menon [13], GCV and PCV values were categorized into low, moderate and high. Broad sense heritability was computed for all the traits using the ratio genotypic variance to phenotypic variance and values were expressed in percentage as suggested by Lush [14] and Hanson et al. [15]. As per formula suggested by Johanson et al. [12] the expected genetic advance from selecting five per cent of the superior progeny was calculated.

2.2 Slow Rusting Components

1. Coefficient of infection

Coefficient of infection (CI) was determined by multiplying the per cent infection and response value, assigned to each infection type, as per Loegering scale [16].

2. Area Under Disease Progress Curve (AUDPC)

The AUDPC was computed by using the formula suggested by Wilcoxson [17].

$$\text{AUDPC value} = \sum_{I=1}^{k} \tfrac{1}{2}(S_i + S_{i-1}) \times d$$

Where,

S_i = Disease severity at the end of time I
K = Number of evaluations of disease
d = Interval between two evaluations.

3. Relative Area under Disease Progress Curve (rAUDPC)

rAUDPC was computed by using the following formula.

$$\text{rAUDPC} = \frac{\text{AUDPC of a genotype/cultivar}}{\text{AUDPC of a local or susceptible cultivar}} \times 100$$

3. RESULTS AND DISCUSSION

Analysis of variance for yield, its attributing traits along with component of slow rusting in backcross segregating generation of the cross GW 322 X PARULA was done under artificial epiphytotic condition and the results are presented in the Tables 1 and 2 and Figs. 1 and 2. From the augmented RBD ANOVA in epiphytotic condition for leaf rust it can be interpreted that treatments were significant for the traits like plant height, number of productive tillers per plant, days to fifty per cent flowering, spike length, number of seeds per spike, grain yield per plant, ACI, AUDPC and rAUDPC. Results from present study revealed high mean and presence of wide range of variation for different traits indicating sufficient variability existed in the present breeding material selected for the study and hence indicating superior segregants can be isolated in these populations.

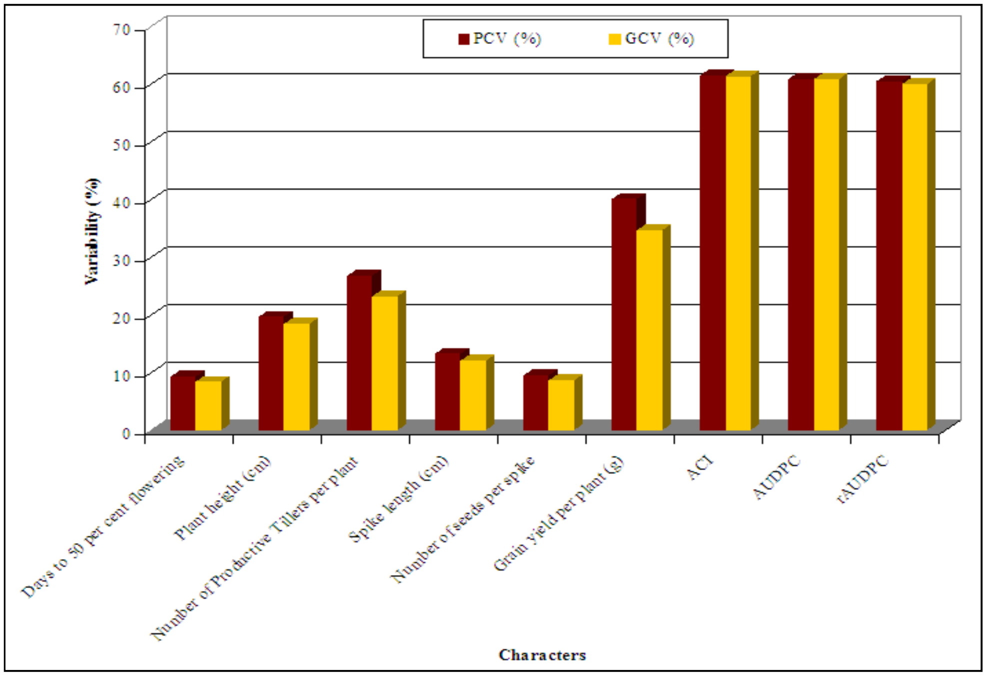

Fig. 1. Estimates of GCV and PCV for various traits in back cross segregating generation of bread wheat cross GW

Table 1. ANOVA for yield, its component traits and slow rusting component in advanced back cross segregating lines of the cross GW 322 x Parula in epiphytotic condition

Source	d.f.	Days to 50% flowering	Plant height (cm)	No. of tillers /plant	Spike length (cm)	No of seeds /spikelets	Grain yield/ plant (g)	ACI	AUDPC	rAUDPC
Treatment	183	26.77**	107.45**	1.38**	1.16**	16.44**	2.45**	74.04**	79217.16**	398.39**
Checks	3	42.15**	199.14**	2.04**	1.29**	14.31*	1.22	99.47**	165462.70**	506.97**
Checks + var. Vs var	180	26.51**	105.42**	1.37**	1.15**	16.48*	2.47**	74.64**	77779.73**	396.59**
Blocks (eliminating checks + var)	5	6.54	11.27	0.48	0.08	3.56	1.86	0.96	78.76	6.17
Enteries (ingnoring block)	183	35.17**	134.61**	1.56**	1.38**	18.61**	2.97**	103.33**	109583.90**	552.28**
Varieties	179	35.13**	131.84**	1.57**	1.39**	[illegible]	3.02**	95.64**	104900.90**	515.46**
Checks Vs varieties	1	21.06	424.64**	0.15	0.31	[illegible]	0.71	1490.84**	78023.10**	7278.10**
Error	15	5.78	8.79	0.35	0.22	3.97	0.69	0.44	50.76	7.61

**= significant at p=0.05, **= significant at 0.01*

Table 2. Estimates of components of variability for morphological traits along with slow rusting components in back cross segregating generations of bread wheat cross GW 322 X PARULA in epiphytotic condition

Characters	Mean	Range		PCV	GCV	h^2	GA	GAM (%)
		Min	Max					
Days to 50 per cent flowering	61.34	48.00	82.00	9.25	8.38	82.09	9.61	15.64
Plant height (cm)	57.90	36.00	62.00	19.64	18.38	92.68	20.92	36.46
Number of Productive Tillers per plant	4.51	2.00	18.00	26.73	23.20	75.31	1.86	41.48
Spike length (cm)	8.54	6.00	13.00	13.24	12.02	82.43	1.41	22.48
Number of seeds per spike	42.14	20.00	60.00	9.48	8.63	77.20	6.59	15.61
Grain yield per plant (g)	4.18	2.02	23.25	40.03	34.68	75.04	2.58	61.89
ACI	14.14	0.00	36.67	61.49	61.33	99.49	19.06	126.02
AUDPC	383.53	0.00	1540.00	60.84	60.83	99.95	634.05	125.27
rAUDPC (%)	33.54	0.00	87.30	60.47	59.97	98.37	43.77	122.53

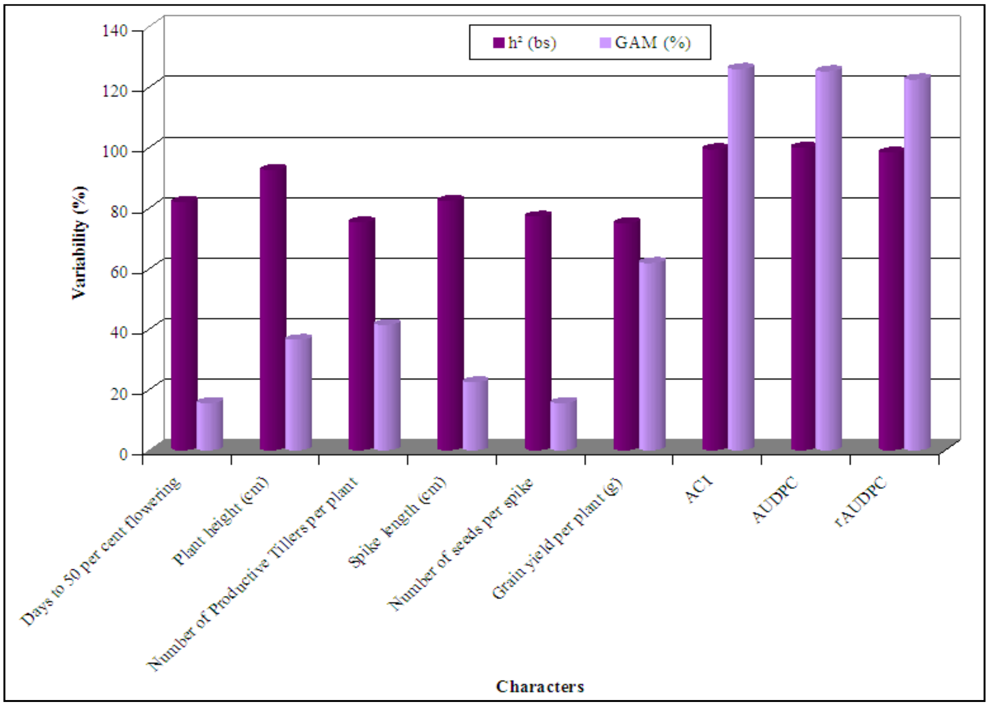

Fig. 2. Estimates of h^2 (bs) (%) and GAM for various traits in back cross segregating generation of bread wheat cross

The presence of genetic variability for economic traits is very important for improving the specific traits. The amount of variability present is of utmost importance for initiating a effective selection in any breeding program. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population. The estimation of phenotypic co-efficient of variance (PCV) and genotypic co-efficient of variance (GCV) was highest for average coefficient of infection (ACI) having a value of 61.49 and 61.33 respectively and found lowest for days to 50 percent flowering (9.25 and 8.38). Presence of narrow difference between PCV and GCV for all the characters except number of productive tillers per plant and grain yield per plant suggested low environmental influence in expression of these traits and the variability present for these traits were mainly due to genetic factors, hence greater effectiveness of selection and improvement to be expected while practicing selection for these traits in future breeding programme.

Magnitude of variation present in any breeding population may consist of both heritable and non-heritable component. Non heritable component mainly arises due to environmental influence on a particular phenotype and not passed onto progeny. It is only the extent of heritable variation arising mainly due to genetic values which are passed onto progeny , so heritable component of variation matters most for advancing gains in any selection programme. The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability. In present investigation heritability was found high for all the traits with a value ranging from 75.04 per cent for the trait grain yield per plant to 99.95 per cent for the AUDPC. The presence of high heritability may be mainly due to higher contribution of genotypic components on the expression of these traits and most likely due to additive genetic effects. Hence, direct selection for these traits may be rewarding in early segregating generation. Heritability estimates indicate effectiveness of selection for phenotypic performance but estimates of heritability alone is not enough to make sufficient improvement through selection. The high heritability estimates coupled with high genetic advance is more useful for the effective selection to take place.

High GCV and PCV values coupled with high heritability and high genetic advance over mean recorded for the traits such as no. of productive tillers per plant and grain yield per plant suggesting availability of sufficient variability for both traits and thus exhibited scope for genetic improvement for both traits through simple phenotypic selection for improving yield. Similar findings supporting higher magnitude of PCV and GCV for thousand grain weight, harvest index, spike length, grain yield per plant and no. of productive tillers per plan has been earlier reported by Arati et al. [18] and Navin et al. [19].

Moderate phenotypic and genotypic values coupled with high genetic advance over mean and high heritability was observed for this trait plant height and spike length. These results are in consonance with reports of Deepak et al., [20] who reported moderate PCV and low GCV for spike length and plant height.

For traits such as, no of seeds per spike and days to fifty per cent flowering low PCV and GCV values were recorded. Low values of PCV and GCV for these traits indicates expression of these traits are under the high influence of environmental condition, hence indicating genetic gain by practicing selection considering these traits will be of lower magnitude. These results are in accordance with Alemu Dabi et al. [21] who reported the lowest PCV and GCV values for traits like no. of kernels per spike, days to maturity, days to heading, no. of spikelets per spike and spikes length.

Slow rusting component like ACI, AUDPC and rAUDPC exhibited high PCV and high GCV coupled with high heritability and high GAM. High values of PCV and GCV for these component traits indicates presence of plenty variability and low environmental influence on the expression of these traits. The gain from selection for these traits is high in this population. These findings revealed high heritability for these traits is mainly due to the additive genetic effects and hence practicing selection considering these traits could be beneficial in early segregating generations. These results indicates the possibility of improving wheat grain yield along with leaf rust resistance through direct selection for grain yield related traits along with slow rusting components. These findings are in consonance with reports of Yashavantha [22].

4. CONCLUSION

Hence, present finding confirmed that plenty of variability for yield, its component traits and slow rusting component is present in the advanced backcrossed material generated in the present investigation which is the key for effective selection in any breeding programme. Traits like productive tillers per plant, grain yield per plant along with slow rusting components should be taken into consideration while selecting for superior high yielding plants having durable resistance in bread wheat.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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