Original Research Article

Studies on Genetic Variability and Heritability for Yield and Yield Attributing Traits in Advanced Backcross Segregating Populations in Bread Wheat (*Triticum aestivum* L.)

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Genetic variability was studied in backcross segregating generations of the cross GW322 X Parula in bread wheat during *Rabi* season of 2015-2016 at AICRP on wheat, MARS, UAS, Dharwad, Karnataka. The study revealed highly significant differences for all the yield and its contributing traits, indicating the presence of high genetic variability. The phenotypic and genotypic co-efficient of variation (PCV and GCV) was high for grain yield per plant followed no of productive tiller per plant and moderate for plant height, spike length and thousand grain weight. High heritability coupled with high GAM was found for the traits *viz*., plant height, no of productive tiller per plant, spike length, thousand grain weight and grain yield per plant indicating presence of substantial amount of variability for these traits which is key of practicing selection in any breeding programme.

Introduction

Wheat (*Triticum aestivum* L.) is the world's most staple food crop as well as most consumed cereal. It is known as "king of cereals" as its cultivation is easier, ecologically suitable and contain high amount of nutrients. It compares well with other cereals in nutritive value. In India, it is the staple diet in the northern and central regions. It is cultivated on 15.4% of the arable land in the world in almost all countries, except the humid and high-temperature areas in the tropics and high-latitude environments. Accounting for a fifth of humanity's food,

wheat is the second only to rice which provides 21% of the food calories and 20% of the protein for more than 4.5 billion people in 94 developing countries (Braun *et al.,* 2010).

It contributes 30% of the world's edible dry matter and 60% of the daily calorie intake in several developing countries (FAOSTAT, 2015).

The development of high yielding wheat cultivars is the main objective of any breeding programs in the world (Ehdaie and Waines,

1989). The prerequisite to achieve this goal is to find sufficient amount of variability. Identification of superior genotypes with desirable traits and their subsequent use in breeding program and establishment of suitable selection criterion can further help for successful varietal development programme.

It is necessary to partition the total variability into heritable and non-heritable components *viz.,* genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and further, to compute heritability and genetic advances for various metric traits of interest to the breeder.

The estimates of heritability are more advantageous when expressed in terms of genetic advance. Johnson *et al.,* (1955) suggested that without genetic advance the estimate of heritability will not be practical value and emphasized the concurrent use of genetic advance along with heritability.

Hanson (1963) stated that heritability and genetic advance are two complementary concepts.

Thus, the present study was designed to evaluate for genetic variability and heritability parameters of yield and its component traits in the populations of the cross GW322 x Parula *viz.,* BC_1F_3, BC_1F_4, BC_2F_3, BC_2F_4, BC_3F_3, BC_3F_4 and F_5.

Materials and Methods

The present investigation was conducted during *rabi* season 2015-16 at ICAR-All India Co-ordinated Wheat Improvement Project, Main Agricultural Research Station, University of Agricultural Science (UAS), Dharwad.

The materials of present experiment were comprised of 180 lines of different segregating populations of the cross GW322

X PARULA *viz.,* BC_1F_2, BC_1F_3, F_4, BC_2F_2, BC_3F_2, BC_3F_1, BC_4F_1.

These advanced backcross segregating lines were evaluated in Augmented Block Design. These lines were sown in 6 blocks, each block consist of 30 lines with 4 checks viz., UAS304, HD2189, GW322 and Parula having spacing of 20 x 20 cm. randomly five plants were selected and observations were recorded for the traits like plant height (cm), days to 50 per cent flowering, days to maturity, no of productive tillers per plant, spike length (cm), number of spikelet per spike, no of seeds per spike, thousand grain weight (g) and grain yield per plant (g).

Statistical analysis was done on the observation recorded on each individual plant in backcross segregating generation of the cross GW322 X PARULA for agronomic evaluation. Genetic parameters and the statistical methods adopted were as follows.

Statistical analysis

Analysis of variance (ANOVA) for augmented design as per Federer (1977) was carried out for each character.

The variance components, genetic coefficient of variation, phenotypic coefficient of variation and broad sense heritability were determined as suggested by Burton and De Vane (1953) and Johnson *et al.,* (1955).

Analysis of variance (ANOVA)

ANOVA for augmented design

Analysis of variance (ANOVA) for augmented design-II as per Federer (1977) was carried out for each character.

Where
b = Number of blocks
v = Number of genotypes

e = Number of entries
c = Number of checks

Estimation of genetic parameters

Mean, range, genotypic and phenotypic variances and coefficients of variance were computed based on mean and variance calculated by using data of unreplicated treatments.

General mean (X) =

$$\frac{\text{Sum of observations of all the plants for each genotype}}{\text{Number of plants}}$$

Range = The minimum and maximum values for each trait within population

Phenotypic variance

The individual observations made for each trait in backcross segregating generations of the cross GW 322 X PARULA is used for calculating the phenotypic variance.

Environmental variance

The average variance of parents is used as environmental variance for single crosses.

Environmental variance (σ^2_e) = (Var P_1 + Var P_2)/2

Where,
Var P_1 = Variance of P_1 parent
Var P_2 = Variance of P_2 parent

Genotypic variance

Genotypic variance ($\sigma^{2\,g}$) = σ^2_p - σ^2_e

Where,
σ^2_p = Phenotypic variance

σ^2_e = Environmental variance

Coefficient of variability (CV)

Both Phenotypic and genotypic coefficient of variability for all the characters were estimated using the formulae of Burton and De Vane (1953)

Genotypic coefficient of variability: GCV (%) = $\dfrac{\sigma_g}{\overline{X}}$ x 100

Phenotypic coefficient of variability: PCV (%) = $\dfrac{\sigma_p}{\overline{X}}$ x 100

Where,
σ_g = Genotypic standard deviation
σ_p = Phenotypic standard deviation
X = General mean of the characters

GCV and PCV values were categorized as low, moderate and high as indicated by Sivasubramanian and Menon (1973).

0-10 %: Low
10-20 %: Moderate
20 % and above: High

Heritability (Broad Sense)

Heritability in broad sense was estimated for all the characters as the ratio of genotypic variance to phenotypic variance expressed in percentage as suggested by Lush (1949) and Hanson *et al.,* (1956).

Heritability (h²) (%) = $\dfrac{\sigma^2_g}{\sigma^2_p}$ x 100

The heritability was categorized as low, moderate and high as given by Robinson *et al.,* (1951).
0-30 %: Low
30-60 %: Moderate
60 % and above: High

Genetic Advance (GA)

The extent of genetic advance to be expected from selecting five per cent of the superior progeny was calculated by using the following formula suggested by Johanson *et al.,* (1955).

Genetic advance (GA) = $ih^2 \sigma_p$

Results and Discussion

Treatments were significant for all yield and its component traits. The estimation of genotypic co-efficient of variance (GCV) was high for grain yield per plant (37.36) followed by no of productive tiller per plant (32.81), moderate for thousand grain weight (17.86) followed by plant height (14.50) and spike length (11.29) and low for days to 50 percent flowering (7.95), no of spikelets per spike (8.08) and no of seeds per spike (8.67). Phenotypic co-efficient of variance (PCV) was high for grain yield per plant (40.16) followed by no of productive tiller per plant (34.76) and moderate for thousand grain weight (19.16) followed by plant height (15.02) and spike length (11.94) (Table 2).

Low GCV and PCV values for the traits such as, days to fifty percent flowering, days to maturity, spikelets per spike and number of seeds per spike were recorded indicating less scope for selection as they are under the influence of environment. These results were in accordance with Yousaf *et al.,* (2008) who reported low PCV and GCV for traits like fifty percent flowering and days to maturity.

The moderate value of phenotypic coefficient of variance and genotypic coefficient of variance were obtained for plant height, spike length and thousand grain weight. These results were in accordance with reports of Yousaf ali *et al.,* (2008), who reported moderate PCV and GCV for the traits such as spike length*,* seeds per spike and thousand grain weight (Table 1).

ANOVA for augmented design

Sl. No.	Sources of variation	Df	S.S	M.S.S
1	Block (eliminating Check + Var.)	b-1	bSS	bMS
2	Entries	e-1	eSS	eMS
3	Checks	c-1	cSS	cMS
4	Varieties	v-1	vSS	vMS
5	Checks vs. Varieties	1	cvSS	cvMS
6	Error	(c-1) (b-1)	ESS	EMS

Table.1 Analysis of variance for yield and its contributing traits in back cross segregating generations of the cross GW322 x PARULA in natural condition

Source	d.f.	Days to 50% flowering	Plant height (cm)	No. of tillers /plant	Spike length (cm)	No of spikelets/ spike	No of seeds /spikelets	Thousand grain weight (g)	Grain yield/ plant (g)
Treatment	183	26.83**	62.07*	3.63**	0.74**	1.79**	14.45**	35.07**	8.30**
Checks	3	30.83*	108.35**	16.68**	0.742**	0.53	3.31	103.14**	29.30**
Checks + var. Vs var	180	26.79**	61.305**	3.41**	0.745**	1.81**	14.64**	33.93**	7.95**
Blocks (eliminating checks + var)	5	14.66	4.53	0.109	0.71**	0.85	2.33	4.07	0.64
Enteries (ingnoring block)	183	35.14*	79.80**	4.69**	1.036**	2.43**	21.52**	36.89**	10.97**
Varieties	179	35.13**	79.65**	4.51**	1.04**	2.46**	21.62**	35.13**	10.60**
Checks Vs varieties	1	50.15*	21.15	2.23*	0.20	1.30	58.90**	152.14**	21.38**
Error	15	6.93	4.97	0.449	0.10	0.45	58.90**	4.23	1.12

Table.2 Estimates of components of variability for morphological traits in back cross segregating generations of bread wheat cross GW322 X PARULA in natural condition

Characters	Mean	Range		PCV	GCV	h^2	GA	GAM (%)
		Min	Max					
Days to 50 per cent flowering	63.27	49.00	78.00	8.97	7.95	78.61	9.22	14.53
Plant height (cm)	56.53	26.00	90.00	15.02	14.50	93.14	16.33	28.83
Number of Productive Tillers per plant	5.87	2.00	23.00	34.76	32.81	89.10	3.72	63.81
Spike length (cm)	8.20	6.00	13.00	11.94	11.29	89.36	1.80	21.98
Number of spikelet's per spike	16.72	9.00	23.00	9.03	8.08	80.11	2.48	14.90
Number of seeds per spike	47.01	22.00	66.00	9.52	8.67	83.03	7.62	16.28
Thousand grain weight (g)	29.90	9.25	53.25	19.16	17.86	86.85	10.14	34.29
Grain yield per plant (g)	7.87	2.27	32.02	40.16	37.36	88.41	5.67	73.15
Days to maturity	113.25	105.00	134.00	2.43	2.03	70.10	3.97	3.51

The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability (Lush, 1945). Heritability estimates indicate effectiveness of selection for phenotypic performance but it is alone not enough to make sufficient improvement through selection. The high heritability estimates coupled with high genetic advance is more useful for the selection (Johnson *et al.,* 1995). 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 and thus exhibited scope for genetic improvement through selection for all these traits. These indicates predominance of additive gene action in the inheritance of these traits selection may be effective in early generations for these traits. These findings were agreement with the results of Tarekenge *et al.,* (1994) and Bhusan *et al.,* (2013) who reported high PCV and GCV values for grain yield, biomass, harvest index, 1000 grain weight and plant height in wheat.

High heritability coupled with moderate genetic advance was recorded for the traits days to 50 per cent flowering and number of spikelets per spike, indicated predominance non-additive gene action in the expression of these characters therefore these characters can be improved by mass selection and other breeding methods based on progeny testing. Direct selection may or may not be effective for these traits. Similar results in wheat were also reported by Kisana *et al.,* (1982) and Prasad *et al.,* (2006).

Hence, from the present finding it is concluded that the advanced wheat backcrossed material generated and used in the present study has plenty of variability for most of the traits and these traits should be taken into account while selecting superior plants for further improvement of yield and yield attributing traits in bread wheat.

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