

Study of genetic variability parameters in advance breeding lines of bread wheat (*Triticum aestivum* L.)

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ABSTRACT

A field study was carried out under irrigated conditions during *Rabi* 2016-17 to study the genetic variability, heritability and expected genetic advance for eight traits in 40 advance breeding lines in bread wheat. The genotypes exhibited wide range of variation for all the traits except for number of tillers per meter indicating the presence of enough genetic variability in the study material. Genetic coefficient of variation ranged from 2.25 for days to maturity to 19.61 for number of grain per spike. PCV values were higher than GCV values for all the traits which reflect the influence of environment on the expression of traits. All the traits exhibited high heritability except number of tillers per meter and grain yield per plot. However, very high values of heritability were observed for days to heading (92.78%), spike length (90.76%) and days to maturity (89.45%). High heritability coupled with high genetic advance as percent of mean was observed for spike length and number of grain per spike suggesting selection for these traits would give good response. Thus, these characters may be effective as selection indices during breeding programme for improving grain yield.

Key words: *Triticum aestivum*, PCV, GCV, Heritability, Genetic advance

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). The development of high yielding wheat cultivars is the main objective of any breeding programs in the world (Ehdaie and Waines, 1989).

Generating information about the genetic variability, relationships and mechanisms of inheritance of the genetic traits involved is the key task in genetic improvement of any crop plant. The knowledge of heritability helps the plant breeder in predicting the behaviour of the succeeding generation and making desirable selections. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program. Genetic advance has considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi, 1992)

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Thus, the present study was designed to evaluate genetic variability and heritability parameters of yield and its component traits in advance breeding lines of bread wheat.

MATERIALS AND METHODS

Description of the study area

The advance breeding lines were tested at Wheat Research Station, Vijapur (altitude 23.350 N and longitude 072.550 E) in *rabi* season of 2016-17. The annual average maximum and minimum temperature of the study area was 31.8°C and 15.9°C, *respectively*. The soil type classified as sandy loam soil with a pH of 7.74.

Experimental Materials

The experimental materials were consisted of 40 advance breeding lines of bread wheat (*Triticum aestivum* L.) including five varieties (GW 496, GW 322, GW 366, GW 451 and HI 1544).

Experimental Design and Trial Management

The experiment was carried out in a Randomized Block Design (RBD) with two replications. Each genotype was sown in six rows of 6.0 meter length and 20 cm apart, with seed rate of 120 kg/ha. Weeds were controlled manually. Planting was done by hand drilling in November-2016. Recommended fertilizer rate of 120-60-40 N-P-K Kg/ha in the forms of Urea, DAP and Muriate of potash was applied in each plot in the shallow furrow depths.

Five plants were selected randomly from each genotype per replication for recording agronomic data and observations on days to heading and days to maturity were recorded on plot basis. The data obtained were subjected to the biometrical analysis that included analysis of variance, heritability and genetic advance. Genotypic coefficient of variation (GCV%), phenotypic coefficient of variation (PCV%), broad sense heritability (h^2 (bs)%) and genetic advance in percent mean (GAPM) were estimated by the formula suggested by Singh and Chaudhary

(1985). The estimate of GCV and PCV were classified as low, medium and high (Sivasubramanian and Madhavamenon, 1973). The heritability was categorized as suggested by Robinson *et al.* (1949). Again, genetic advance was classified by adopting the method of Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Highly significant mean squares due to genotypes for all the characters except number of tillers per meter in forty advance breeding lines revealed the presence of enough genetic variability in the material under study (Table 1). The results pertaining to mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2 bs) and expected genetic advance as percent of mean (GAPM) for all the characters studied are furnished in (Table 2). Variability is essential for wide adaptability and resistance to biotic and abiotic factors and hence, an insight into the magnitude of genetic variability present in a population is of paramount importance to a plant breeder for starting a judicious breeding programme. The magnitude of genetic variability for plant height was ranged from 62.30 to 92.90 cm with the mean value of 78.49 cm and for number of tillers per meter 64.00 to 102.00 with the mean value of 84.24. Variability of number of grain per spike ranged from 23.00 to 58.00 with the mean value of 38.56 and for thousand grain weight varied from 37.40 to 58.20g with the mean value of 47.06g. Thus, these results indicate the presence of wide range of genetic variability in the material studied.

The PCV values were higher than GCV values for all the traits which reflect the influence of environment in expression of traits. The genotypic coefficient of variation (GCV) ranged from 2.25 percent to 19.61 percent and phenotypic coefficient of variation (PCV) ranged from 2.38 percent to 20.85 percent (Table 2). The result of genotypic and phenotypic coefficient of

variation revealed that number of grain per spike and grain yield per plot exhibited the highest genotypic coefficient of variation of 19.61 percent and 14.27 percent, respectively and the highest phenotypic coefficient of variation of 20.85 percent and 20.38 percent, respectively. The high PCV and moderate GCV observed are evident from their high variability that in turn offers good scope for selection (Table 2). The lowest GCV and PCV were recorded for days to maturity (2.25% and 2.38%, respectively) and days to heading (5.94% and 6.16%, respectively) indicating difficulty of improvement for these traits through selection (Table 2). These findings were in agreement with those of Kumar *et al.* (2014) and Desheva and Kyosev (2015).

Heritability is a useful quantitative parameter, which considers the role of heredity and environment determining the expression of a trait (Allard 1960). Effective selection can be achieved only when additive effects are substantial and environmental effects are small. Heritability estimates ranged from 14.90 (for number of tillers per meter) to 92.78 percent (for days to heading). Spike length (90.76%), days to maturity (89.45%), number of grain per spike (88.45%), plant height (87.18) and thousand grain weight (74.72%) also, exhibited higher broad sense heritability values emphasizing that the additive genetic variation was the major component of genetic variation in the inheritance of these traits and the effectiveness of selection in the early segregating generations in improving these traits (Panse 1957). High heritability estimates for plant height (Tripathi *et al.* 2011), days to heading (Baranwal *et al.* 2012), thousand kernel weight (Ashraf *et al.* 2002) and spike length (Ali *et al.* 2008), were also reported.

Expected genetic advance as percent of mean indicates the expected genetic progress for particular trait under selection cycle and measures the extent of its stability under selection pressure. The higher value was recorded for number of grain per spike; spike length and grain yield per plot and lower for days

to maturity and number of tillers per meter. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone in selecting best individuals (Johnson *et al.* 1955).

High heritability along with high genetic advance percent of mean was noticed for spike length and number of grain per spike suggesting predominance of additive genetic effects and selection could be effective in early segregating generations for these traits and the possibility of improving bread wheat grain yield through direct selection for grain yield related traits (Table. 2).

High heritability along with moderate genetic advance percent of mean was noticed for days to heading, plant height and thousand grain weight suggesting predominance of additive and non-additive gene action in the expression of this trait. Therefore, these traits can be improved by mass selection (Table. 2). High heritability accompanied by low genetic advance for days to maturity indicates predominance of non-additive genetic source of variation and improvement of the trait through selection may not be effective in this population, which could be exploited through heterosis breeding. Low heritability coupled with low genetic advance was found for number of tillers per meter this indicate that this trait was highly influenced by environment and selection would be ineffective for this character.

Naik *et al.* (2015) reported that high genotypic coefficient of variation along with high heritability and genetic advance provide better information than other parameters alone. In the present study, number of grain per spike and spike length showed high genetic advance in conjunction with high heritability and moderate genotypic coefficient of variation (Table 2). These traits are the most important quantitative traits to be taken into consideration for effective selection in wheat. Similar results have been reported by Ali *et al.* (2008), Sharma and Garg (2002). From the present study, it is evident that genotypes studied may provide good source of material for

further breeding program. On the basis of results as summarized above, it is concluded that traits like spike length and number of grain per spike can be considered as suitable selection criteria for the development of high yielding bread wheat varieties.

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Table 1 Analysis of variance for morphological characters in bread wheat

Source of variation	d.f.	Days to heading	Days to maturity	Plant height (cm)	Number of tillers/m	Spike length (cm)	Number of grain/spike	Thousand grain weight (g)	Grain yield/ plot (Kg)
Replication	1	4.05	3.61	21.44	1015.31	0.004	32.51	0.02	0.08
Treatments	39	21.86**	11.46**	72.01**	179.82	2.38**	121.80**	32.45**	0.09**
Error	39	0.82	0.64	4.94	133.18	0.115	7.46	4.68	0.03

** Indicate Significant at 5% and 1% levels of significance

Table 2 Genetic parameters for yield and its attributing characters in bread wheat

Variability parameters	Mean	Range		PCV (%)	GCV (%)	H ² bs (%)	GA	GAPM (%)
		Min.	Max.					
Days to heading	54.62	50.00	61.00	6.16	5.94	92.78	6.44	11.78
Days to maturity	103.21	100.00	108.00	2.38	2.25	89.45	4.53	4.39
Plant height (cm)	78.49	62.30	92.90	7.90	7.38	87.18	11.14	14.19
Number of tillers/m	84.24	64.00	102.00	14.85	5.73	14.90	3.84	4.56
Spike length (cm)	8.89	7.00	11.10	12.55	11.96	90.76	2.09	23.48
Number of grain/spike	38.56	23.00	58.00	20.85	19.61	88.45	14.65	37.99
Thousand grain weight (g)	47.06	37.40	58.20	9.16	7.92	74.72	6.64	14.11
Grain yield/ plot (Kg)	1.20	0.81	1.59	20.38	14.27	49.05	0.25	20.59