



Genetic architecture for grain yield parameter in bread wheat (*Triticum aestivum* L.) genotypes

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ABSTRACT

The overall objective was to study the extent of genetic variation and association among grain yield and yield related traits. Nine late sown genotype of bread wheat with their parents were evaluated in the year of 2017-18, using Randomized Block Design with four replications. Thus there was a high magnitude of genotypic variability for all the characters under study among the bread wheat genotypes. The value of phenotypic coefficients of variation was higher than genotypic coefficients of variation. The range for heritability was observed medium to high and the range for genetic advance as percent of mean was observed low to high. For days to heading and days to maturity moderate Heritability and low genetic advance as percent of mean was observed, high heritability with Low genetic advance as percent of mean observed for harvest index and biological yield, moderate heritability with Moderate genetic advance as percent of mean was observed for plant height, tiller per plant, spike length, grain yield per plant and biological yield, high heritability with moderate genetic advance as percent of mean was observed for test weight, high heritability with high genetic advance as percent of mean was observed for grain per spike. The overall genetic variability within the trait found to be low that indicated low chances of selection. Based on these result, we cannot reach to the final decision. But it can be used as a bench mark for further study. Therefore, it needs additional study over several years.

Key words: Wheat, GCV, PCV, Heritability, Variation

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INTRODUCTION

Globally wheat cultivation occupies the first position in the world, in India it cover 30.72million hectare area with 97.44 metric tons production. Wheat was traditionally cultivated in Gujarat an area of raging from 5 - 7 lakh hectares. Develop new varieties along with better yield and good performance in adverse climatic condition was the prime objective of breeders. Creation of variability by artificial crossing with estimation of genetic components range, mean value, genotypic variability, phenotypic variability, genotypic coefficient of variance, phenotypic coefficient of variance, heritability, genetic advance with genetic advance percent mean values are the important components to develop new variety. For information of the genetic variability, relationships and pattern of inheritance of concern trait is the key task in genetic improvement of crop plants. The knowledge of heritability is very important to predict the behaviour of the succeeding generation for making desirable selections. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program. Genetic advance is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection [5, 6]. The genetic variation for the trait under selection and a higher heritability are necessary to have response to selection [5]. Breeding programs depend on the knowledge of key traits, genetic systems controlling their inheritance, genetic and environmental factors that influence their expression [8, 1]. The study of statistical parameters like mean, variance, habitability and genetic advance is a measure to evaluate genetic potential, variability and stability performance of any genotype for effective selection of particular traits in that genotype.

MATERIAL AND METHODS

Experiment was conducted at the Lokbharti Wheat Research Centre, Sanosara Bhavnagar Gujarat. Geographically Sanosara is located at latitude of 23.00N, longitude of 72.00E in saurashtra region of Gujarat. It has an average elevation of 67 meter. Crop was grown at wheat research farm during the Rabi season of 2017-18. Experiment was carried in randomized block design (RBD) with four replications and plot was 5 m x 2 m size. Seeds were sown according to require seed rate with 10 rows per genotype per replication. Recommended package and practice was following to raise the crop. Nine genotypes were evaluated along with three checks. Data was recorded on the five plants per replication per genotypes. Data were recorded for ten following characters.

Heading days was calculated from date of sowing when 75% ear comes out side from flag leaf. The number of effective tillers per meter row length was counted at maturity stage. Spike length was taken in centimeter from primary spike sat maturity stages. Height was measured in centimeter from above soil surface to the top of the ear excluding awns at maturity stage. Average number of grains was calculated from random 10 well developed spikes to observe number of grain per spikes. 1000 grain weight was recorded in grams for test weight. Recorded the date when 75% of the plants show complete senescence and calculate days from the date of sowing for maturity days. Threshed grains weight was recorded in kg per genotype per replication and quintal per hectare yield was calculated. Harvest index was calculated by the formula of grain yield divided by biological yield.

Obtain data were subjected to the biometrical analysis that include analysis of variance, range, mean, genotypic variance, phenotypic variance, genotypic coefficient of variance, phenotypic coefficient of variance, heritability, genetic advance, genetic advance mean percent value were estimated by the formula suggested by Singh and Chaudhary [11] and using software agristat (V.6.2003).

RESULT

The results of ANOVA indicated that mean sum of squares due to replications were significant for harvest index, tiller per meter and plant height at 5% level of significance while days to maturity was significant at 1% level of significance (Table 1). This indicated that significant variation existed among the replications for harvest index, tiller per meter, plant height and days to maturity. The mean sum of squares due to genotype was significant at 1 % level of significance for grain yield, harvest index, biological yield, spike length, grain per spike, test weight, tiller per plant, plant height, days to heading and days to maturity. This revealed that there was considerable magnitude of genotypic variability for all the characters under study among wheat genotypes.

Table 1: ANOVA of nine bread wheat genotypes for yield and yield attributes

Source of Variation	df	Mean square									
		YLD	HI	BLY	SPLN	GPS	TG	TPM	PH	DH	DM
Replicate	3	3.4	7.1*	9.4	0.2	8.037	0.9	79.1*	35.1*	0.7	6.2**
Treatments	8	51**	16.8**	51**	2.1**	146.7**	84.7**	266.6**	127.3**	26.1**	30.9**
Error	24	5.0	1.8	5.0	0.2	4.6	2.8	25.8	8.7	0.5	1.1

*, **significant difference at $p < 0.05$, $p < 0.01$ respectively, ANOVA: Analysis of variance DF: Degree of freedom, YLD: Grain yield, HI: Harvest index, BLY: Biological yield, SPLN: Spike lengths, GPS: Grain per spike, TG: Test weight, TPM: Tillers per meter, PH: Plant height, DH: Days to heading, DM: Days to maturity

Grain yield (YLD)

The range for grain yield was 39 to 44.7 quintal per hectare. The mean value for grain yield was 42.6 ± 1.1 quintal per hectare (Table 2 & 3). The magnitude of genotypic coefficient of variance (7.9 %) while phenotypic coefficient of variance (9.5 %). The heritability in broad sense (69.5 %) and genetic advance genetic advance (5.8) with genetic advance mean percent value was 13.6 %.

Harvest index (HI)

The range for harvest index was from 37.7 to 47.7 percent. The mean value for harvest index was 41.9 ± 0.7 percent (Table 2 & 3). The magnitude of genotypic coefficient of variance (4.6 %) while phenotypic coefficient of variance (5.6 %). The heritability in broad sense (68.1 %) and genetic advance genetic advance (3.3) with genetic advance mean percent value was 7.9 %.

Biological yield (BLY)

The range for biological yield was from 96.7 to 106.7 quintal per hectare. The mean value for biological yield was 101.6 ± 1.1 quintal per hectare (Table 2 & 3). The magnitude of genotypic coefficient of variance

(3.3 %) while phenotypic coefficient of variance (4 %). The heritability in broad sense (69.5 %) and genetic advance genetic advance (1.2) with genetic advance mean percent value was 15 %.

Spike length (SPLN)

The range for spike length was from 6.9 to 9.4 centimeter. The mean value for spike length was 8.1±0.2 centimeter (Table 2 &3). The magnitude of genotypic coefficient of variance (8.5 %) while phenotypic coefficient of variance (9.9 %). The heritability in broad sense (74.3 %) and genetic advance (1.2) with genetic advance mean percent value was 15.1 %.

Grain per spike (GPS)

The range for grain per spike in numbers was from 28 to 46.5. The mean value for grain per spike was 35.2±0.1 (Table 2 &3). The magnitude of genotypic coefficient of variance (16.9 %) while phenotypic coefficient of variance (18 %). The heritability in broad sense (88.6 %) and genetic advance (11.6) with genetic advance mean percent value was 32.8 %.

Test weight (TG)

The range for test weight was from 41.7 to 52.5 grams. The mean value for test weight was 47.6±0.8 grams (Table 2 &3). The magnitude of genotypic coefficient of variance (9.5 %) while phenotypic coefficient of variance (10.1 %). The heritability in broad sense (88.2 %) and genetic advance genetic advance (8.8) with genetic advance mean percent value was 18.4 %.

Tiller per meter (TPM)

The range for test weight was from 77 to 99.2. The mean value for test weight was 88.1± 2.5 (Table 2 &3). The magnitude of genotypic coefficient of variance (8.8 %) while phenotypic coefficient of variance (10.5 %). The heritability in broad sense (70 %) and genetic advance genetic advance (13.4) with genetic advance mean percent value was 15.2 %.

Plant Height (PH)

The range for plant height was from 77.5 to 95 centimeter. The mean value for plant height was 85± 1.5 centimeter (Table 2 &3). The magnitude of genotypic coefficient of variance (6.4 %) while phenotypic coefficient of variance (7.3 %). The heritability in broad sense (77.3 %) and genetic advance genetic advance (9.9) with genetic advance mean percent value was 11.6 %.

Days to heading (DH)

The range for days to heading was from 47 to 55 days. The mean value for days to heading was 51.2±0.4 days (Table 2 &3). The magnitude of GCV (4.9 %) while PCV (5.1 %). The heritability in broad sense (92.5 %) and genetic advance (5.0) with genetic advance mean percent value was 9.8 %.

Days to Maturity (DM)

The range for days to maturity was from 84.5 to 92.5 days. The mean value for days to heading was 88.3±0.5 days (Table 2 &3). The magnitude of genotypic coefficient of variance (3.1 %) while phenotypic coefficient of variance (3.3 %). The heritability in broad sense (87.3 %) and genetic advance (5.3) with genetic advance mean percent value was 5.9 %.

Table 2: Mean performance of various wheat genotypes with respect to various characters.

Genotype	YLD	HI	BLY	SPLN	GPS	TG	TPM	PH	DH	DM
GW 499	40	40.4	99	7.7	28	50	85	81.7	51	92.5
GW 509	37.7	39	96.7	7.8	29	52.5	78.5	80.5	50.5	90
GW 510	45	43.2	104	8.3	37.7	41.7	77	84.2	55	88.5
GW 511	38.5	39.4	97.5	6.9	30.7	51.5	80.7	95	47	86.5
LOK 74	46.5	44.1	105.5	9.4	46.5	49.7	93	92.5	51.7	88.5
GW 173	42.5	41.8	101.5	7.6	37	45.5	99.2	77.5	49	84.5
GW 11	47.7	44.7	106.7	7.9	41	45.2	93	85.5	55	86.5
HD 2864	41.2	41.2	100.2	8.6	31.7	40.3	97	82	51.3	92
LOK 1	45	43.3	104	8.1	35.7	52.3	89.7	86.2	51	85.7

Table 3. Mean, range, genotypic coefficient of variance, phenotypic coefficient of variance, heritability in broad sense, genetic advance and genetic advance value % means.

Traits	Range	Mean ± SE	GCV	PCV	h ² (b)	GA	GA value % means
YLD	37.7 - 47.7	42.6 ± 1.1	7.9	9.5	69.5	5.8	13.6
HI	39 - 44.7	41.9 ± 0.7	4.6	5.6	68.1	3.3	7.9
BLY	96.7 - 106.7	101.6 ± 1.1	3.3	4.0	69.5	5.8	5.7
SPLN	6.9 - 9.4	8.1 ± 0.2	8.5	9.9	74.3	1.2	15.1
GPS	28 - 46.5	35.2 ± 1	16.9	18.0	88.6	11.6	32.8
TG	41.7 - 52.5	47.6 ± 0.8	9.5	10.1	88.2	8.8	18.4
TPM	77 - 99.2	88.1 ± 2.5	8.8	10.5	70.0	13.4	15.2
PH	77.5 - 95	85 ± 1.5	6.4	7.3	77.3	9.9	11.6
DH	47 - 55	51.2 ± 0.4	4.9	5.1	92.5	5.0	9.8
DM	84.5 - 92.5	88.3 ± 0.5	3.1	3.3	87.3	5.3	5.9

*GCV= Genotypic Coefficient of Variation, * PCV= Phenotypic Coefficient of Variation, *h²(b)= Heritability (Broad Sense) *GA = Genetic Advance

DISCUSSION

According to Deshmukh *et al.* [4], phenotypic and genotypic coefficient of variance were classified in to three categories low when (<10%), moderate when (10 – 20 %) and high when (>20%). In this study phenotypic and genotypic coefficient of variance tends to low to moderate for all the traits. Grain per spike, test weight and tiller per meter show moderate phenotypic and genotypic coefficient of variance while grain yield, harvest index, biological yield, spike length, plant height, days to heading, days to maturity were show low phenotypic and genotypic coefficient of variance. The phenotypic coefficient of variance was relatively grater then the genotypic coefficient of variance for all the traits which indicated that traits were influenced by environmental factor. The magnitude of difference for phenotypic and genotypic coefficient of variance was 0.2 to 1.7 percent. Phenotypic and genotypic coefficient of variance was nearly similar for days to heading, days to maturity; test weight, biological yield and plant height which indicated that these traits were less influenced by environmental factors and selection computed for these traits are very effective for trait improvement. While magnitude difference of phenotypic and genotypic coefficient of variance for grain per spike, tiller per meter, grain yield, harvest index, biological yield and spike length were high which indicated that traits were much influenced by environmental factors, selection for these traits may be delay for subsequent generations.

Heritability of trait is considered high when the value is more than 80%, moderate when it ranges 40% to 80% and low when below 40%. The magnitude of heritability for all the traits was 68.1% to 92.5% which means the range for heritability was moderate to high. High heritability was found for days to heading, grain per spike, test weight and days to maturity which was indicated that the traits were less influenced by environment and selection computed for these traits was effective for trait improvement. High heritability was also found by Mesele *et al.*[9] for days to heading, days to maturity, test weight, grain per spike. While rest of the traits like grain yield, harvest index, biological yield, spike length, tiller per meter and plant height show Moderate heritability which was indicated that the traits were more influenced by environmental factors and selection for these traits may be computed in advance generation. Moderate heritability was also found by [9, 2, 3] for spike length, tiller per meter, plant height, harvest index and grain yield.

Genetic advance percent mean value Range was observed 5.7 % to 32.8 %, Deshmukh *et al.* [4] classified genetic advance as percent of mean value is low when < 10%, moderate when 10 – 20 %, and high when >20 %. High genetic advance percent mean value was observed for grain per spike which was indicated the trait may be expressed by additive gene action. Moderate genetic advance percent mean value was observed for grain yield, spike length, test weight, tiller per meter and plant height. Low genetic advance percent mean value was observed for harvest index, biological yield, days to heading and days to maturity. Yaqoob [12] also found similar result for spike length, test weight, tiller per meter, plant height, days to heading and days to maturity. Estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic traits. High values of genetic advance are indication of additive gene action whereas low values are indication of non-additive gene action [11].

Important to consider heritability and genetic advance mean percent value simultaneously [7]. Grain per spike show high heritability with high genetic advance mean percent value. High heritability with genetic advance mean percent value indicated that traits are less influenced by the environment and expressed by additive gene action, selection for best performing genotypes may be possible for trait improvement most likely the heritability of these traits is due to additive gene action and selection may be effective for these traits [1], while grain yield, spike length, test weight, tiller per meter, plant height show moderate heritability with moderate genetic advance value percent mean value on the other hand harvest index, biological yield, days to heading and days to maturity show moderate heritability with low genetic advance mean percent value. Moderate and low heritability indicates that selection for those traits may be commutated in advanced generation.

CONCLUSION

Selection of a genotype for improvement of any trait with additive component was the aim of breeders from ancient breeding scenario. Probability for Additive component was increased by high heritability with high genetic advance mean percent values [10]. In this study High heritability (88.6%) along with high genetic advance percent mean value (32.8) was observed for grain per spike. Therefore, selection is effective using grain per spike trait for improving grain yield, which is highest for LOK 74 (46.5) along with highest grain yield (46.5 q/ha), harvest index (44.1 %), biological yield (105.5q/ha) and spike length (9.4 cm) within all the five test entries. Lok 74 achieve 46.5 q/ha grain yield (table 2) that was highest over three checks GW 173, HD 2864 and LOK 1 42.5 q/ha, 41.2 q/ha and 45q/ha accordingly.

REFERENCES

1. Ali, Y., Atta, B. M., Akhter, J., Monneveux, P. and Lateef.(2008). Genetic variability, association and diversity studies in wheat (*triticumaestivumL.*) germplasm.*Pak. J. Bot.***40**: 2087-2097.
2. Demelash, A., Desalegn, T. and Alemayehu, G. (2013). Participatory Varietal Selection of Bread Wheat (*Triticumaestivum L.*) Genotypes at MarwoldK ebele, Womberma Woreda, West Gojam, Ethiopia. *International Journal of Agronomy and Plant Production*.**4**: 3543-3550.
3. Desheva, G. and Cholakov, T. (2014). Variability, heritability and genetic progress for some yield components in common winter wheat genotypes (*Triticum aestivum L.*). *Journal of Genetics and Plant Physiology*.**4**:191-200.
4. Deshmukh, S. N., Basu,M. S., and Reddy,P. S., (2006). Genetic variability characters association and path coefficient analysis of quantitative traits on Virginia bunch varieties of groundnut. *Indian J. Agric. Sci***56**:816-821.
5. Falconer, D. S. and Mackay, T. F. C. (1996). Introduction to Quantitative Genetics (4th ed.), Longman, Essex, UK.
6. Hamdi, A. (1992). Heritability and combining ability of root characters in lentil (*Lens culinaris Medik*), Egypt. *J of Agri. Res*.**70**: 247-255.
7. Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Estimation of genetic and environmental variability in soybean.*Agronomy Journal*.**47**:314-318.
8. Kashif,M., Ahmad, J., Chowdhry, M. A. and Perveen, K. (2003). Study of Genetic Architecture of Some Important agronomic Traits in durum wheat (*Triticum durum Desf.*).in: <http://www.ansijournals.com/ajps/2003/708-712.pdf>*Asian J Plant Sci*.**2**: 708-717.
9. Mesele, A. (2016).Estimation of Heritability and Genetic Advance of Yield and Yield Related Traits in Bread Wheat (*Triticum aestivum L.*)Genotypes at ofla District, Northern Ethiopia. *International Journal of Plant Breeding and Genetics*. **10**:31-37.
10. Singh, P. and Narayanan, S. S. (1993).Biometrical techniques in plant breeding, New Delhi.
11. Singh, R. K. and Chaudhary, B. D. (1985).Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi.
12. Yaqoob, M. (2016). Estimation of Genetic variability, heritability and genetic advance for yield and yield related traits in wheat under rained conditions. *J Agric. Res*. **54**:1-14.

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