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### Estimation of genetic variability parameters for yield and its components in bread wheat (*Triticumaestivum* L. em. Thell) genotypes

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**Abstract**

Ten diverse bread wheat genotypes namely, QLD 39, KAUZ/ALTAR84/3/MILAN/KAUZ/4/HUITES, UP 2762, KFA/2\*KACHU, RAJ 4419, PBW 729, WH 1187, HD 2967, DBW 50 and NIAW 1594 were crossed in half diallel fashion and 45 F<sub>1</sub>'s excluding reciprocals with their parents and checks were evaluated for genetic variability parameters including range, genotypic (GCV), phenotypic (PCV), environmental coefficient of variation (ECV), genetic advance, genetic advance % mean and heritability. The genotypes studied showed significant differences for all the traits. The estimates of PCV and GCV were high and recorded for grain yield/plant and biological yield/plant. This indicated that selection was effective for the improvement of these traits as the variability between genotypes for these traits was highly heritable. Greater effects of environment was predicted for number of productive tillers per plant owing to high estimates of both PCV and ECV. High estimates of heritability were observed for thousand grain weight, biological yield/plant and grain yield/plant. Grain yield/plant, biological yield/plant, number of grains/spike and number of productive tillers/plant showed high values of genetic advance % mean. The traits viz., grain yield/plant and biological yield/plant showed high estimates of genetic advance and heritability suggesting the predominance of additive gene effects in governing these traits. These traits can therefore be improved by means of direct selection.

**Keywords:** Variability parameters, heritability, wheat, genetic advance, yield

**Introduction**

Bread wheat (*Triticumaestivum* L. em. Thell), an allohexaploid (2n=6x=42, AABBDD), is an important cereal crop grown in the world. It originally belongs to the Levant region but presently is being grown across the world and is a member of tribe Triticeae (Hordeae) family Graminae (Poaceae) and genus *Triticum*. Caryopsis, the fruit of wheat is the only portion utilized for human consumption. Rest of the biomass including stalk is used as fodder for animals. Wheat is widely adapted to different agroclimatic conditions, therefore, it is grown almost throughout the world. Even though wheat is highly adapted to region between 30°-60°N and 27°-40°S latitude (Nuttonson, 1955) [17], it can be cultivated under wide range of climatic conditions from Arctic Circle to equator. It is cultivated in almost all the continents except Antarctica from 260 m below sea level in Jordan up to 4000 m in Tibet. Bread wheat can though be cultivated in a variety of climate and soil types however, dry to sub humid areas with 250-750 mm annual rainfall are most suitable. Although the optimum growing temperature of wheat is 25°C it can also be cultivated in areas where minimum and maximum temperatures during the growing period ranges from 3° to 4°C and 30° to 32°C, respectively (Briggle, 1980) [4]. In India three wheat species i.e., *Triticumaestivum*, *Triticum durum* and *Triticumdicoccum* are grown. *T. aestivum* also called as the common/bread wheat covers 95% area of the country. It is ideal for making bread, biscuit, chapatti, cookies, noodles, cakes etc. *T. aestivum* is grown in all the agroclimatic zones of India including Northern Hill Zone (NHZ), North Western Plains Zone (NWPZ), North Eastern Plains Zone (NEPZ), Central Zone (CZ), Peninsular Zone (PZ) and Southern Hill Zone (SHZ). *T. durum* also called as macaroni wheat is grown in 4% area of the country. It is adapted to Central and Peninsular Zone and used for production of macaroni, vermicelli and spaghetti. *T. dicoccum* covers only

1% area of India and is grown only in Peninsular Zone of the country and is used for making chapatti, macaroni, spaghetti and also has medicinal value. The largest producer of wheat in world is China followed by India. In India wheat covers an area of 30.23 million hectare, with 93.50 million tonne production and 3093 kg/ha productivity. The major wheat producing states in India are Uttar Pradesh (26.9 million tonne), Punjab (16.11 million tonne) and Haryana (11.14 million tonne). Wheat has 30% contribution to food basket of India (Anonymous, 2016) [3]. Wheat is central to human advancement and has played a critical role in feeding a hungry world thereby ensuring global food security (Shiferaw *et al.*, 2013) [19] and (Tabassum *et al.*, 2017) [24]. There is a need to develop high yielding varieties of wheat in order to satisfy the demand of continuously rising population with the area under wheat cultivation remaining constant and in some instances also decreasing.

The production of varieties with high yield requires the estimation of variability prominently of genetic nature which can be exploited by selection. Heritability being the proportion of phenotypic variance that is due to genotype of the plant plays a predictive function in breeding of crops (Songsri *et al.*, 2008) [23]. Heritability is used to compute the genetic advance which indicates the degree of gain in a character obtained under a particular selection pressure (Eid, 2009) [6]. Therefore, genetic advance is yet another vital selection parameter that helps breeder in a selection program (Shukla *et al.*, 2004) [21]. High Heritability estimates along with high genetic advance indicates preponderance of additive gene effects and therefore, direct selection is effective for improvement of these traits (Harshwardhan *et al.*, 2016) [7]. The present investigation was, therefore, conducted to compute heritability, genetic variability, genetic advance and genetic advance % mean for yield and yield contributing traits in wheat.

### Materials and Methods

The research was undertaken at Norman E. Borlaug Crop Research Centre, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, India. The material for research was produced in Rabi 2015-16 and progenies produced were assessed in Rabi 2016-17. Ten parents were crossed in diallel fashion excluding the reciprocals and 45 crosses were produced. The parental lines namely, KAUZ/ALTAR84/3/MILAN/KAUZ/4/HUITES, QLD 39, UP 2762, KFA/2\*KACHU, RAJ 4419, PBW 729, WH 1187, HD 2967, DBW 50 and NIAW 1594 along with 45 F<sub>1</sub>'s and 2 checks (UP 2628 and WH 1105) were planted in randomized block design in three replications with spacing between rows was 20 cm and between plant spacing was 10 cm. Each entry was planted in one plot having 2 rows of 1 m in each replication. Observations were taken on five competitive plants selected randomly from each plot for characters as flag leaf area (cm<sup>2</sup>), plant height at maturity (cm), number of productive tillers/plant, spike length (cm), number of grains/spike, number of spikelets/spike, thousand grain weight, grain yield/plant, biological yield/plant, and harvest index. The average value of five plants was calculated and used for analysis. While for characters days to 75 % heading and days to maturity observations were taken on whole plot basis.

In order to test the significance of genotypic differences between the genotypes, analysis of variance for randomized block design (RBD) was conducted according to steps given by Panse and Sukhatme (1969) [18]. Thereafter, various

variability parameters were estimated for each of the twelve traits studied. The formula given by Singh and Chaudhary (1985) [22] was used to calculate phenotypic, genotypic and environmental coefficient of variation. Broad sense heritability and genetic advance for various traits were computed as suggested by Allard (1960) [2]. Genetic advance % mean was assessed as proposed by Johnson, Robinson and Comstock (1955) [8].

### Results and Discussion

Analysis of variance showed highly significant differences among genotypes for all the traits studied except for spike length for which the differences amongst genotypes were significant (Table 1 and 2). This revealed that variability was existent in the population for all the traits studied and that improvement in these traits was possible. Mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), environmental coefficient of variation (ECV), heritability, genetic advance and genetic advance % mean are presented in Table 3. As per Deshmukh *et al.* (1986) [5] PCV, GCV and ECV were characterised as high (>20%), medium (10-20%) and low (<10%). High GCV estimates were detected for number of productive tillers/plant (22.270%), biological yield/plant (25.281%) and grain yield/plant (25.678%), and moderate estimates were exhibited by flag leaf area (14.344%), number of grains/spike, (11.468%), thousand grain weight (10.417%) Low estimates of GCV were observed for all other traits. As PCV values were greater than the GCV values for all the traits studied there was effect of environment in the manifestation of all the traits. Number of productive tillers/plant (34.350 and 22.270), biological yield/plant (28.190 and 25.281) and grain yield/plant (29.618 and 25.678) showed high estimates of PCV and GCV, moderate estimates were recorded for number of grains/spike (13.466 and 11.466) and thousand grain weight (11.496 and 10.417). These findings are in general agreement with the results of Shoran (1955) [20], Makwana *et al.* (2009) [16], Kumar *et al.* (2014) [14], Kumar *et al.* (2015) [13] and Kumar *et al.* (2015) [10]. High ECV was observed for flag leaf area (21.985) and number of productive tillers/plant (26.146), hence the variation among genotypes is not heritable, so selection is ineffective in improvement of these traits. High or moderate PCV and GCV for number of grains/spike and thousand grain weight coupled with low ECV (7.056 and 4.860) indicated that these traits have less environmental influence suggesting the reliability of selection of genotypes on the basis of phenotypes for improvement of grain yield. Low PCV, GCV and ECV was observed for days to 75% heading, days to maturity, spike length and plant height. This shows that although these traits have less environmental influence on account of low ECV but improvement of these traits by selection is not possible as the heritable variation among genotypes is meagre. Flag leaf area on account of its low GCV (14.344%) with high PCV (26.251%) and ECV (21.985%) is more affected by the environment, hence trait enhancement by selection is not reasonable.

High heritability estimates ( $\geq 75\%$ ) were observed for thousand grain weight (82.122%), biological yield/plant (80.426%) and grain yield/plant (75.16%), moderate heritability estimates were observed for days to 75% heading (53.756%), days to maturity (60.049%), plant height (63.504%), number of grains/spike (72.537%) and harvest index (73.555%), while heritability estimates were low for flag leaf area (29.857%), number of productive tillers/plant

(42.061%), spike length (13.350%) and number of spikelets/spike (39.475%). Comparable results were also stated by Ali *et al.* (2008) [1], Kumar *et al.* (2014) [15], Kumar *et al.* (2015) [12] and Kumar *et al.* (2015) [11]. High and moderate estimates of heritability indicated that there is greater proportion of genotypic variance in the total phenotypic variance. However, low estimates of heritability indicated that the variability in the genotypes is mainly due to environmental influence and cannot be passed on to the next generation making the use of selection for trait improvement unrewarding.

Genetic advance as % mean (GAM) is classified as high (>20%), moderate (10-20%) and low (<10%) by Deshmukh *et al.* (1986) [5]. High GAM was perceived for number of productive tillers/plant (29.763%), number of grains/spike (20.12%), biological yield/plant (46.704%), grain yield/plant (45.85%) and harvest index (16.332%). Flag leaf area (16.146%), plant height (10.296%), thousand grain weight (19.448%) showed moderate GAM while GAM was low for days to 75% heading (3.401%), days to maturity (2.366%), spike length (2.294%), and number of spikelets/spike (9.232%). These findings are in general agreement with findings of Kumar *et al.* (2014) [15].

Genetic advance and heritability are together used as an important parameters for selection of genotypes (Joshi *et al.*, 2018) [9]. Estimates of heritability along with genetic advance are normally more reliable in predicting the gain under selection than heritability estimates alone (Johnson *et al.*, 1955) [8]. High heritability along with high genetic advance indicated that the trait is mainly governed by additive gene effects and this relationship was seen for biological yield/plant and grain yield/plant. Thus, selection can be used for improvement of these traits. High heritability along with low genetic advance indicated the preponderance of heritable but non additive gene effects. Such variability can be exploited by means of hybrid development and was observed for none of the traits. Low heritability accompanied with low genetic advance was perceived for spike length and number of spikelets/spike showing greater effect of environment in the manifestation of these traits so selection will be ineffective for the improvement of these traits.

### Conclusion

The main aim of any crop improvement programme is to attain higher yield. As grain yield is a complex trait improvement can be attained only when genotypes are selected or improved for yield contributing traits. For this purpose information regarding coefficient of variation, heritability and genetic advance is required. In the present study significant differences were observed among genotypes for all the traits showing possibility of improvement of these

traits. High PCV and GCV was observed for number of productive tillers/plant, biological yield/plant and grain yield/plant showing scope of improvement of these traits by selection. Biological yield/plant and grain yield/plant showed high heritability along with high genetic advance indicating that these characters were governed by additive gene effects and therefore, improvement can be achieved by direct selection.

**Table 1:** Analysis of variance (Mean squares) for different characters

Character(s)	Replication (df=2)	Treatment (df=54)	Error (df=108)
Days to 75% heading	13.927	17.703**	3.945
Days to maturity	2.579	15.856**	2.878
Flag leaf area (cm <sup>2</sup> )	39.599	84.940**	37.303
Number of productive tillers/plant	80.712	110.809**	34.868
Plant height (cm)	210.734	107.466**	17.277
Spike length (cm)	5.562	1.452*	0.993
Number of spikelets/spike	14.555	11.741**	3.971
Number of grains/spike	12.838	170.685**	19.126
Thousand grain weight (g)	19.534	69.974**	4.734
Biological yield/plant (g)	332.472	2685.043**	201.478
Grain yield/plant (g)	46.082	458.665**	45.505
Harvest index (%)	0.348	46.516**	4.978

\*, \*\* significant at 5% and 1% levels, respectively.

**Table 2:** Analysis of genotypes for yield and yield contributing traits

S. No.	Character(s)	GM	CV	CD at 1%	CD at 5%	SEM±
1.	Days to 75% heading	95.078	2.089	4.253	3.214	1.146
2.	Days to maturity	140.290	1.209	3.632	2.745	0.979
3.	Flag leaf area (cm <sup>2</sup> )	27.780	21.985	13.077	9.885	3.526
4.	Productive tillers/plant	22.584	26.246	12.643	9.556	3.409
5.	Plant height (cm)	87.414	4.755	8.899	6.727	2.399
6.	Spike length (cm)	12.832	7.768	2.134	1.613	0.575
7.	Number of spikelets/spike	22.562	8.832	4.266	3.225	1.150
8.	Number of grains/spike	61.973	7.056	9.363	7.078	2.524
9.	1000 grain weight (g)	44.767	4.860	4.658	3.521	1.256
10.	Biological yield/plant (g)	113.810	12.471	30.391	22.973	8.195
11.	Grain yield/plant (g)	45.701	14.760	14.443	10.917	3.894
12.	Harvest index (%)	40.252	5.542	4.777	3.611	1.288

GM: General mean, CV: Coefficient of variation, CD: Critical difference, SEM: Standard error mean

**Table 3:** Range, coefficient of variance, heritability and genetic advance for various characters

Character(s)	Range	PCV (%)	GCV (%)	ECV (%)	Heritability (%)	Genetic advance	Genetic advance % mean
Days to 75% heading	90-104	3.071	2.252	2.089	53.756	3.234	3.401
Days to maturity	134-146	1.913	1.482	1.209	60.049	3.320	2.366
Flag leaf area	13.98-48.87	26.251	14.344	21.985	29.857	4.485	16.146
Productive tillers/plant	4-46.6	34.350	22.270	26.146	42.061	6.721	29.763
Plant height	65-108	7.871	6.272	4.755	63.504	9.00	10.296
Spike length	9.5-17	8.342	3.048	7.765	13.350	0.294	2.294
Number of spikelets/spike	12.26-27.35	11.352	7.133	8.830	39.475	2.082	9.232
Number of grains/spike	33.8-81.6	13.466	11.468	7.056	72.537	12.470	20.12

1000 grain weight	30.6-58.6	11.496	10.417	4.860	82.122	8.705	19.448
Biological yield/plant	21.3-174.9	28.190	25.281	12.471	80.426	53.15	46.704
Grain yield/plant	9-76	29.618	25.678	14.760	75.16	20.957	45.85
Harvest index	27.95-52.85	10.778	9.244	5.542	73.555	6.574	16.332

PCV: Phenotypic coefficient of variance, GCV: Genotypic coefficient of variance, ECV: Environmental coefficient of variance

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