# Research paper

# Genetic Variability, Heritability and Genetic Advance in Bread Wheat (*Triticum aestivum* L.)

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## ABSTRACT

Genetic variability is important for crop improvement. This study aimed to determine genetic variability, heritability and genetic advance for yield and other agronomic traits of bread wheat. Each experiment was laid out in a randomized complete block with three replications. The analysis of variance showed significant variation among the genotypes for all tested characters. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were highest for number of spikes per $m^2$ and plant height. High heritability was recorded on plant height and 1000 – grain weight.

*Key words:* Agronomic traits, genotypic variation, phenotypic variability.

# التباين الوراثي والتوريث والتقدم الوراثي في قمح الخبز

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التباين الوراثي مهم لتحسين المحاصيل. هدفت هذه الدراسة الي تحديد التباين الوراثي والتوريث والتقدم الوراثي للإنتاجية وبعض الصفات الحقلية الأخرى لقمح الخبز. تم استخدام تصميم القطاعات العشوائية الكاملة بثلاث مكررات لتنفيذ كل تجربه. اوضح تحليل التباين وجود اختلافات معنويه بين اصناف القمح في كل الصفات المدروسة اعطي معامل التغير الوراثي ومعامل التغير المظهري اعلى نسبه لعدد السنابل في المتر المربع وطول النبات. التوريث العالي المتقدم سجل في طول النبات ووزن ال 1000 حبه.

**الكلمات المفتاحية:** الصفات الحقلية، التباين الوراثي، الاختلاف المظهري

**Introduction**

Wheat (*Triticum aestivum* L.) is one of the most widely grown cereal crops, contributing to the global food supply and economic security. Globally, the total cultivated area is 221.61 million ha producing739.53 million tones with an average yield of 3289 kg per hectare (FAOSTAT, 2018). The enhancement in wheat productivity and the development of improved crop management technologies played crucial roles in its expansion to new non-traditional and less favorable areas. For instance, wheat yield was estimated to be 30.2kg/ha/year during the period from 1960 to 1990 (Tahir *et al.,* 2000). The growing season of wheat in Sudan is short (about 100-110 days from mid-November to early March) leading to heat stress being one of the major factors that affect wheat grain yield and quality (Ishag and Ageeb, 1991; Elahmadi, 1996; Tahir *et al*, 2006). Genetic variation is required to achieve genetic gains in a breeding program. Estimation of genetic variation among genotypes can be based on qualitative and quantitative traits (Souza and Sorrells, 1991; Barbosa-Neto *et al.*, 1996; Cao *et al.*, 1998; Fahima *et al.*, 1999). Demand of wheat is increasing by population growth and always be felt new method which can select high yielding varieties fast and accurate. Selection of genotypes based on high value of heritability and forecasted genetic conditions would be an effective method (Ghandorah and El -Shawaf, 1993). Heritability estimates need to be considered together with genetic advance, which is more important than heritability alone to predict the resulting effect of selecting the best individuals. It had been generally believed that the higher the heritability estimates of given traits, the simpler the selection procedure and the better would be the response to selection (Baloch, 2004).

A number of researchers in their studies have reported the presence of high heritability and genetic progress in different yield related attributes in wheat; Afiah *et al.*, (2000); Ashraf *et al.*, (2002); Arshad and Chowdhry (2003); Baloch *et al.* (2003); Khalil and Afridi (2004); Shabana *et al.* (2007) and Kumar *et al*. (2014).

The present study was carried out to estimate genetic variation, heritability and genetic advance in 24 bread wheat genotypes for utilization in selection programs aimed at productivity increase of future genotypes.

## Materials and methods

### Area of experiment, genetic material and cultural practices

Two experiments were conducted during the winter seasons of 2013/14 and 2014/15 at Merowe Research Station Farm (M.R.S.F), Northern State, Sudan (Latitude: 18° 27' 0" N, Longitude: 31° 49' 59" E, Elevation: 258 meters). The geotypes used in the experiments included 24 advanced breeding lines and varieties of wheat (*Triticum aestivum* L.), which were selected from the national wheat breeding program of the Agricultural Research Corporation (ARC), Sudan. Twenty genotypes were advanced breeding lines and the others were released varieties namely; Wadi El Neel, Debeira, Imam and El Nielain. Pedigree of the pracices as advanced genotypes used in the study were given in Table (1). All cultural practices were recommended by Agricultural Research Corporation (ARC), Sudan. Each plot consisted of seven rows, each row was 5 m in length and the distance between rows was 20 cm apart at a seed rate of 120 kg/ha.

### Statistical analysis

The collected data were subjected to standard procedure of analysis of variance and means separated using Duncan's Multiple Range Test (DMRT) method as described by Gomez and Gomez (1984) using MSTAT C software package.

### Estimation of genetic variability, heritability and genetic advance

Heritability in broad sense (H²) was estimated according to Falconer (1989) as follows:

$$\text{Heritability (H}^2) = (\sigma^2 g \, / \, \delta^2 ph) \times 100$$

H²: Heritability; $\delta^2 g$: genotypic variance and $\delta^2 ph$: phenotypic variance. Genotypic ($\delta^2 g$) and phenotypic variances ($\delta^2 ph$) were obtained from the analysis of variance Table according to Comstock and Robinson (1952) as follows:

$$\delta^2 g = (MS1 - MS2) \, / \, r \times s$$
$$\delta^2 ph = (MS1) \, / \, r \times s$$

Where:

r: replication, s: season, MS1: Mean square for cultivar, MS2: Mean square for genotype × season.

**Table (1): Twenty four bread wheat advanced genotypes used in the study**

| Entry no. | Cultivar / line |
|---|---|
| 1 | Wadi  El Neel (released commercial cultivar) |
| 2 | Debeira (released commercial cultivar) |
| 3 | Imam (released commercial cultivar) |
| 4 | El Nielain (released commercial cultivar) |
| 5 | TRCH*2//PFAU/WEAVER |
| 6 | SERI.IB*2/3/KAUZ*2/BOW//KAUZ/4/PBW343*2/… |
| 7 | HUAYUN-INIA |
| 8 | CHUM18/7*BCN |
| 9 | HUBARA-2/QAFZAH-21//DOVIN-2 |
| 10 | KAUZ'S'/FLORKWA-1//GOUMRIA-3 |
| 11 | PBW343*2/KUKUNA//KIRITATI |
| 12 | KAUZ'S'/SERI/3/KAUZ//KAUZ/STAR |
| 13 | BAJ #1/3/KIRITATI//ATTILA*2/PASTOR |
| 14 | WBLL1/KUKUNA//TACUPETO F2001/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1 |
| 15 | ATTILA/3*BCN//BAV92/3/PASTOR/4/TACUPETO F2001*2/BRAMBLING/5/PAURAQ |
| 16 | SOMAMA-9/ICARDA-SRRL-2 |
| 17 | ATTILA 50Y//ATTILA/BCN /3/STAR*3/MUSK-3 |
| 18 | KAUZ'S'/SERI/3/KAUZ//KAUZ/STAR |
| 19 | YAV_3/SCO//JO69/CRA/3/YAV79/4/AE.SQUARROSA(498)/5/LINE 1073/6/KAUZ*2/4/CAR//KAL/BB/3/NAC/5/KAUZ/7/KRONSTAD F2004/8/KAUZ/PASTOR//PBW343 |
| 20 | Kavir |
| 21 | Kauz //Trap # 1 / Bow |
| 22 | KAUZ'S'/SERI/3/TEVEES"S'// CROW/VEES |
| 23 | Panar |
| 24 | RUSHI |

The mean values were used for genetic analyses to determine phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), according to Singh and Chaudhury (1985) as follow:

Phenotypic coefficient of variation (PCV) = $(\sqrt{\delta^2 g} / \bar{x})$ x100

Genotypic coefficient of variation (GCV) = $(\sqrt{\delta^2 ph} / \bar{x})$ x 100

Where:

$\delta^2 g$ = genotypic variance.

$\delta^2 ph$ = phenotypic variance.

$\bar{x}$ = sample mean.

Genetic advance (GA) was calculated with the method suggested by Allard (1960); Singh and Chaudhury (1985) as follows:

GA = K. σph.   H²

Where:

GA: genetic advance, K: constant = 2.06 at 5% selection intensity, σph: square root of phenotypic variance, H²: Heritability.

GA as % of mean (GAM) = (GA / mean value) x 100

## Results and discussion

## Analysis of variance and genotypes mean performance

Results on Table 2 revealed that the studied genotypes showed highly significantly variation (p ≤ 0.001) for all the traits in combined analyses. This provides evidence for sufficient variability and selection on the basis of these traits can be useful. The result was inconformity with the results reported by many authors, Garcia Del-Moral *et al.* (2003) reported significant differences between genotypes for grain yield, number of grains per spike and grain weight. Also, Ahmadizadeh *et al.* (2011b) in studying genetic diversity of durum wheat landraces from Iran and Azerbaijan reported highly significant differences among the genotypes in all of the morphological traits. Furthermore, Mollasadeghi *et al.* (2011); Molasadeghi and Shahryari, (2011) and Ahmadizadeh *et al.* (2011a) reported similar results.

The results showed that the mean square of environments (seasons) and genotypes x environments interaction were significant for all characters measured except the genotypes x environments interaction were not significant in the plant height, number of spikes per m², number of grains per spike and 1000 - grain weight.

## Yield related characters

Results in Table 3 showed the number of days to 50% heading, days to 90% maturity and plant height combined over two seasons. Number of days to 50% heading of the twenty four genotypes ranged from 53 to 62 days whereas number of days to 90% maturity ranged from 85 to 95 days. The earliest genotype combined over the two seasons in heading and maturity was entry no. 22 (85 days), whereas the latest one was entry no. 5 and the cultivar El Nielain (95 days). The tallest genotype (89 cm) was entry no. 19 whereas the shortest one (66 cm) was entry no. 12. Results in table 4 showed highly significant differences (p ≤ 0.001) for average number of spikes per m², number of grains per spike 1000 – grain weight and harvest index (%). Comparison of genotypic means showed that entries no. 16, 10, 19 and 18 had the highest number of spikes per m² (Table

4). The highest number of grains per spike (49.30) was recorded for entries no. 21 and 7 whereas, the lowest number (34) was scored for entry no. 19. Entries no. 22 and 23 had the maximum harvest index (%). Whereas, the entry no. 11 recorded the lowest harvest index (Table 4).

**Grain yield**

Table 4 shows the average grain yield (tons ha$^{-1}$) of the tested genotypes combined over two seasons. Highly significant differences were detected among the tested genotypes for this character. Grain yield productivity among wheat genotypes tested ranged from 5.06 tons/ha (Entry no. 23) to 3.74 tons/ha (Entry no.9) with a grand average yield of 4.40 tons/ha. Grain yields in generally high for experimental plots. The top yielder was obtained by the entries no. 23, 21, 17 and 18. These entries gave higher yielded than the three checks Wadi El Neel, Debeira and El Nielain. Also these entries out - yielded the check wadi El Neel by about 22, 20, 18.3 and 16.6%, respectively (Table 4). Eleven of the tested genotypes had yield exceeding the overall mean of the trial.

**Genetic characters**

Combined analysis revealed a wide range of genetic variability for all the tested traits. The genotypic variance, Phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance and genetic advance as percentage of mean are given in table 5. The maximum phenotypic variance value of 2107.92 was noticed for number of spikes per m$^2$ and 19.83 for plant height. The genotypic variance for these characters were also high, indicating that the genotype was reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) ranged from 11.31% (harvest index) to 333.50% (number of spikes per m$^2$) and 5.69% (harvest index) to 191.30% (number of spikes per m$^2$), respectively. Generally, the PCV values were higher than GCV values for all the traits studied that reflect the influence of environment on the expression of all traits. Results on genetic characters have similarity with Singh *et al.* (2006) and Sharma and Garg (2002).

The heritability indicates that number of spikes per m$^2$, number of grains per spike, 1000 - grain weight and plant height were highly low (Table 5). Only spikes per m$^2$ and harvest index were moderately low indicating that the characters were more influenced by environment. Although high heritability estimate have been found to be effective in the selection for superior

genotypes on the basis of phenotypic performance. Johnson *et al*. (1955) suggested that heritability estimates along with genetic advance will be more useful in predicting the effect for selecting the best individual.

The high heritability estimates along with low genetic advance indicates that genotype - environment interaction plays a significant role in the expression of the trait as observed in days to 90% maturity in the present study. Genetic advance expressed as percentage of mean was high for number of spikes per $m^2$ (9.89%) followed by number of grains per spike (9.59%), 1000 – grain weight (9.27%) and plant height (8.77%). The high genetic advance accompanied with high estimate of heritability observed for plant height and 1000 – grain weight indicates that heritability is mainly due to additive gene effect and selection may be effective to improve the traits.

**Conclusion**

Results indicated that the following conclusion could be drawn:

Sufficient genetic variability for yield and its components existed among the genotypes under study. These plant materials could be successively used production in different environmental conditions, as they have a good perspective from various aspects. Our data have isolated a nine candidate genotypes that out – yielded the check varieties. These lines included; entries no.23, 21, 17, 18, 22, 16, 19, 5 and 20. High genotypic coefficients of variation (191.30%) were observed for number of spikes per $m^2$ followed by plant height (18.55%). Genotypic coefficients of variation (GCV) values were lower than phenotypic coefficients of variation (PCV) values for all the traits which reflect the influence of environment on the expression of traits. High heritability estimates were recorded for days to 90% maturity (80.7%) followed by days to 50% heading (55.4%), plant height (52.9%) and 1000 – grain weight (51.1%).

**Authors contribution**

In this research, all authors contributed effectively. Fatih E. A. Hamza designed and achieved experiments and wrote the paper; Hussein A. Yagoub performed research, Galal A. El Toum analyzed the data and performed data interpretation.

**Table (2): Mean squares of the different characters in 24 bread wheat advanced genotypes grown during two seasons 2013/14 and 2014/15**

| Characters | Season (d.f = 1) | Genotype (d.f = 23) | Seas. X geno. (d.f = 23) | Pooled error (d.f = 92) |
|---|---|---|---|---|
| Days to 50 % heading | 269.507*** | 36.376*** | 10.116*** | 0.917 |
| Days to 90 % maturity | 171.174*** | 42.497*** | 4.536*** | 0.046 |
| Plant height (cm) | 1058.418* | 151.495*** | 32.490n.s | 40.897 |
| No. of spikes/$m^2$ | 232203.516* | 21489.543*** | 8842.019n.s | 8108.159 |
| No. of grains/spike | 1599.333** | 81.646*** | 27.984n.s | 22.182 |
| 1000 – grain weight (g) | 448.028* | 43.722*** | 11.178n.s | 8.812 |
| Harvest index (%) | 1324.353** | 24.526*** | 13.250* | 6.591 |
| Grain yield (kg ha$^{-1}$) | 448447576.694** | 766077.883*** | 952266.057*** | 219568.847 |

*, ** and *** Significant at 0.05, 0.01 and 0.001 levels of probability, respectively
n.s indicates not significant at 0.05 level of probability.

**Table (3): Mean performance of 24 genotypes for some vegetative characters in wheat**

| Entry no. | DH | DM | PH | Entry no. | DH | DM | PH |
|---|---|---|---|---|---|---|---|
| 1 | 54 | 93 | 78 | 15 | 56 | 87 | 80 |
| 2 | 54 | 89 | 73 | 16 | 59 | 94 | 78 |
| 3 | 59 | 90 | 76 | 17 | 60 | 90 | 74 |
| 4 | 56 | 95 | 84 | 18 | 60 | 91 | 73 |
| 5 | 60 | 95 | 80 | 19 | 62 | 93 | 89 |
| 6 | 57 | 90 | 76 | 20 | 53 | 92 | 78 |
| 7 | 59 | 91 | 69 | 21 | 60 | 92 | 76 |
| 8 | 57 | 89 | 71 | 22 | 54 | 85 | 74 |
| 9 | 60 | 94 | 76 | 23 | 55 | 88 | 71 |
| 10 | 62 | 92 | 73 | 24 | 60 | 92 | 78 |
| 11 | 59 | 92 | 82 | Mean | 58 | 91 | 76 |
| 12 | 58 | 87 | 66 | S.E+ | 0.39 | 0.41 | 2.61 |
| 13 | 56 | 88 | 78 | C.V (%) | 1.6 | 1.1 | 8.3 |
| 14 | 57 | 90 | 80 | | | | |

DH: Days to 50 % heading, DM: Days to 90 % maturity, PH: Plant height (cm)

**Table (4): Mean performance of 24 genotypes for yield and yield components characters in wheat**

| Entry no. | G.Y | NS/ m² | NGS | 1000-g.w | HI (%) | Entry no. | G.Y | NS/ m² | NGS | 1000-g.w | HI (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 4.15 | 583 | 38 | 34 | 36 | 15 | 3.98 | 525 | 43 | 41 | 34 |
| 2 | 4.20 | 545 | 40 | 39 | 36 | 16 | 4.47 | 659 | 40 | 34 | 33 |
| 3 | 4.41 | 582 | 40 | 36 | 34 | 17 | 4.91 | 549 | 38 | 36 | 33 |
| 4 | 4.23 | 467 | 38 | 39 | 35 | 18 | 4.84 | 606 | 43 | 33 | 36 |
| 5 | 4.44 | 544 | 41 | 39 | 33 | 19 | 4.47 | 612 | 34 | 38 | 34 |
| 6 | 4.15 | 504 | 42 | 41 | 37 | 20 | 4.43 | 551 | 47 | 34 | 37 |
| 7 | 4.00 | 516 | 48 | 32 | 36 | 21 | 4.98 | 427 | 49 | 37 | 37 |
| 8 | 4.29 | 494 | 45 | 35 | 36 | 22 | 4.72 | 507 | 40 | 37 | 40 |
| 9 | 3.74 | 598 | 40 | 38 | 34 | 23 | 5.06 | 547 | 42 | 36 | 40 |
| 10 | 4.41 | 649 | 38 | 34 | 35 | 24 | 4.30 | 557 | 37 | 38 | 35 |
| 11 | 4.12 | 585 | 41 | 36 | 32 | Mean | 4348 | 548 | 41 | 37 | 35 |
| 12 | 4.29 | 510 | 47 | 32 | 38 | S.E± | 191.3 | 36.76 | 1.92 | 1.21 | 1.04 |
| 13 | 3.75 | 508 | 41 | 40 | 37 | C.V(%) | 10.7 | 16.4 | 11.2 | 8.0 | 7.1 |
| 14 | 4.01 | 428 | 41 | 40 | 34 | | | | | | |

GY: grain yield (tons ha$^{-1}$), NS/ m²: Number of spikes per meter square, NGS: Number of grains per spike, 1000-g.w:Thousand grain weight (g), HI: Harvest index (%).

**Table (5): Genotypic, phenotypic variance, coefficient of variability, heritability (broad sense) and genetic advance for seven characters in wheat.**

| Characters | δ²ph | δ²g | GCV (%) | PCV (%) | H² (%) | GA | GAM (%) |
|---|---|---|---|---|---|---|---|
| **Days to heading** | 7.89 | 4.37 | 8.71 | 11.70 | 55.4 | 3.21 | 5.53 |
| **Days to maturity** | 7.83 | 6.32 | 10.47 | 11.65 | 80.7 | 4.66 | 5.12 |
| **Plant height** | 37.47 | 19.83 | 18.55 | 25.50 | 52.9 | 6.67 | 8.77 |
| **Spikes/m²** | 6406.60 | 2107.92 | 191.30 | 333.50 | 32.9 | 54.25 | 9.89 |
| **Grains/ spike** | 21.95 | 8.94 | 12.45 | 19.52 | 40.7 | 3.93 | 9.58 |
| **1000-grain weight** | 10.61 | 5.42 | 9.70 | 13.57 | 51.1 | 3.43 | 9.27 |
| **Harvest index** | 7.38 | 1.87 | 5.69 | 11.31 | 25.3 | 1.42 | 4.05 |

(δ2ph): phenotypic variation, (δ2g) genotypic variation, (GCV) genotypic coefficient of variation, (PCV) phenotypic coefficient of variation, (H²) broad sense heritability, (GA) genetic advance, (GAM) genetic advance as a percentage of the mean.

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