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**RESEARCH PAPER**

# Genetic parameters for yield and yield components traits of some wheat genotypes grown in newly reclaimed soils

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## Abstract

A field experiment was carried out at the experimental farm of the Faculty of Agriculture, Fayoum University, Egypt, during 2012-2013 and 2013-2014 seasons, in order to estimate genetic parameters for yield of 40 wheat genotypes arranged in design of randomized complete block with three replications. Results showed highly significant differences for all the traits among genotypes and genotypes × year interactions. Heading date (95.22 and 93.05), days to maturity (39.92 nd 38.85) and spike density (0.3 and 0.2) exhibited mostly equal values for phenotypic (Vp) and genotypic (Vg) variation, respectively. The estimates of Vpfor other traits were higher than Vg. Both Vp and Vg surpassed the corresponding environmental variance. A wide range of phenotypic (PCV) and genotypic (GCV) coefficients of variation were observed for all the traits. High PCV and moderate GCV were recorded for grains weight spike$^{-1}$(29.00 and 23.31), grain yield /fed (34.46 and 27.41), number of spikes m$^{-2}$ (27.06 and 22.84), biological yield (29.76 and 20.28), straw yield (33.91 and 23.18) and harvest index (28.66 and 21.36) respectively. Moderate values of GCV and PCV were recorded for plant height and number of tillers plant$^{-1}$. Moderate PCV and low GCV was observed for number of grains spike$^{-1}$. Low values of GCV and PCV were observed for days to maturity, heading date, spike density, spike length, number of spikelets spike$^{-1}$ and 1000-grain weight. High heritability accompanied with high genetic advance as percentage of mean was observed in case of heading date, plant height (84.7 and 21.16) and 1000-grains weight (80.76 ad 20.90) respectively. But, moderate values of heritability with high genetic advance as percentage of mean were obtained for grain yield, number of spike/m², grains weight/spike and number of grains/ spike.

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## Introduction

Bread wheat (*Triticum aestivum* L.) is one of the most important crops in Egypt and its cultivated area is about 1.303 milionhectare. The local production is about 9.5 million ton however; it covers less than 60% of local consumption (FAO, 2013). An intended objective of the Egyptian policy is consequently to reduce the dependence on imported wheat by enhancing grain yield average and production. Increasing wheat productivity is a national target in Egypt to fill the gap between wheat consumption and production. Cereals and its products play an important role for food, comprising more than half of the daily energy consumption. Wheat grain contains 10-15% proteins which are mostly present in the endosperm, many proteins in the mature grains have either metabolic or structural role, still the vast majority of grain proteins are storage proteins that function as a nitrogen reserves for germinating embryo (Shewry *et al.*, 1995).

The Study of statistical parameters like mean, variance, phenotypic, genotypic and environmental coefficients of variation, heritability and genetic advance is helpful to evaluate the performance of any particular genotype and service in determining the effectiveness of selection for a particular trait in that genotype. Heritability isolates the amount of genotypic variation from phenotypic one. The utility of heritability, therefore, increases when it is used to calculate genetic advance, which indicates the degree of gain in the traits obtained under a particular selection pressure. Thus the genetic advance is then another important selection parameter that aids breeder in a selection program. Similar to the present study results, several authors estimated various genetic variability for grain yield and its component traits in bread wheat and reported moderate to high heritability and genetic advance (Welsh 1981; Ferdous *et al.,* 2011; Ahmadi *et al.,* 2012; Singh *et al.,* 2014; Tewodros *et al.,* 2014 and Ghuttai *et al.,* 2015). However, Kumar *et al.,* 2009; Kumar *et al.,* 2013 and Salman *et al.,* 2014, estimated high to moderate heritability and genetic advance values for grain yield.

The objectives of this research work were to estimate various genetic parameters for grain yield and some yield component traits and to identify superior genotypes for further breeding programs suitable for growing in newly reclaimed soils.

## Materials and methods

### Experimental site

The present investigation was carried out at the experimental farm (Demo, new reclaimed sandy loamy soil) of the Faculty of Agriculture, Fayoum University, Egypt, during the two successive growing seasons, 2012/2013 and 2013/2014. This work aimed to evaluate 40 breed wheat genotypes to determine the relationship between vegetative growth traits and reproductive ones in the different tested genotypes. These genotypes consisted of 36 genotypes of hybrid origin in their F4 generation resulted from a prior study (Ghallab, 2006) and 4 commercial parental cultivars. Pedigree of the genotypes is presented in Table 1.

### Experimental design and layout

The experiments were designed in a randomized complete block design with three replications. Each replicate of forty plots included 36 genotypes together with the four cultivars. Grains of each were hand sown in five rows. Each row was of 3.0 m long, with a row to row distance of 0.25 m while distance between plants was 0.05 m. The experimental plot area was 10.5 m². Sowing at the grain rate of 70 grain 0.75 m$^{-2}$ was done on 23$^{th}$ and 19$^{th}$ of November in the two seasons, respectively. Six flooding irrigations were added during growth season. Total nitrogen fertilization was applied at the rate of 140 kg feddan$^{-1}$ N as Urea (46.5%) in two equal doses, before the first and second irrigations. The crop was subjected to recommended package of agronomic and plant protection practices to obtain a healthy crop.

### Harvesting and Observations recorded

At harvest, ten guarded plants were randomly taken from the inner rows of each plot to measure the plant height (cm), number of tillers plant$^{-1}$, spike length (cm),

number of spikelets spike[-1], number of grains spike[-1], grains weight spike[-1], 1000- grain weight (g), spike density and grain yield plant[-1]. In addition, the following traits were also determined on plot basis; number of spikes m[-2], grain yield, biological yield (t/fed), straw yield (t/fed) and harvest index.

**Table 1.** List of genotypes with pedigree used in the present investigation.

| No | Name of Genotypes | Pedigree | No | Name of Genotypes | Pedigree |
|---|---|---|---|---|---|
| 1 | 96*42 2 | Sakha93 * Gimmeiza5- 2 | 21 | 95*15 8 | Sids1 * Giza168- 8 |
| 2 | 96*42 3 | Sakha93 * Gimmeiza5-3 | 22 | 95*15 10 | Sids1 * Giza168-10 |
| 3 | 96*42 4 | Sakha93 * Gimmeiza5-4 | 23 | 96*95 1 | Sakha93* Sids1-1 |
| 4 | 96*42 5 | Sakha93 * Gimmeiza5-5 | 24 | 96*95 2 | Sakha93* Sids1- 2 |
| 5 | 96*42 6 | Sakha93 * Gimmeiza5-6 | 25 | 96*95 3 | Sakha93* Sids1-3 |
| 6 | 96*42 7 | Sakha93 * Gimmeiza5-7 | 26 | 96*95 4 | Sakha93* Sids1- 4 |
| 7 | 96*42 9 | Sakha93 * Gimmeiza5-9 | 27 | 96*95 5 | Sakha93* Sids1-5 |
| 8 | 42*15 1 | Gimmeiza5 * Giza168-1 | 28 | 96*95 7 | Sakha93* Sids1-7 |
| 9 | 42*15 4 | Gimmeiza5 * Giza168-4 | 29 | 96*95 8 | Sakha93* Sids1-8 |
| 10 | 42*15 5 | Gimmeiza5 * Giza168-5 | 30 | 96*95 9 | Sakha93* Sids1-9 |
| 11 | 42*15 7 | Gimmeiza5 * Giza168-7 | 31 | 96*15 1 | Sakha93* Sids1-6 |
| 12 | 42*15 9 | Gimmeiza5 * Giza168-9 | 32 | 96*15 4 | Sakha93* Giza168-1 |
| 13 | 42*15 10 | Gimmeiza5 * Giza168-10 | 33 | 96*15 6 | Sakha93* Giza168-4 |
| 14 | 95*42 7 | Sids1 * Gimmeiza5-7 | 34 | 96*15 7 | Sakha93* Giza168-7 |
| 15 | 95*42 8 | Sids1 * Gimmeiza5-8 | 35 | 96*15 8 | Sakha93* Giza168-8 |
| 16 | 95*15 2 | Sids1 * Giza168-2 | 36 | 96*15 10 | Sakha93* Giza168-10 |
| 17 | 95*15 3 | Sids1 * Giza168-3 | 37 | Sids 1 | HD2172/Pavon"S"//1158.27/Maya74"S"Sd46-4Sd-2Sd-1Sd-0sd |
| 18 | 95*15 4 | Sids1 * Giza168-4 | 38 | Sakha 93 | Sakha 92/TR 810328 S 8871- 1S-2S-0S |
| 19 | 95*15 6 | Sids1 * Giza168-6 | 39 | Giza 168 | MIL/BUC//Seri CM93046 – 8M-0Y-0M-2Y-0B |
| 20 | 95*15 7 | Sids1 * Giza168-7 | 40 | Gemmeiza5 | Vee "S"/SWM 6525 CGM 4017-1GM-6GM-3GM-0GM |

*Data analysis*

The data collected during the two years were subject to analysis of variance using GENSTAT 12th Edition software package to determine least significant difference (LSD) test at 1% and 5% probability level among our genotypes. The variability present in the genotypes was estimated by simple measure, namely: range, mean and standard error. The phenotypic and genotypic variance and coefficient of variation were estimated according to the methods suggested by Burton and Devane (1953). Heritability (h[2]) in broad sense and genetic advance (GA) for selection intensity (K) at 5% were computed using the formula adopted by Allard (1960). Genetic advance mean (GAM) was computed to compare the extent of predicted genetic advance of different traits under selection using the following formula: $GAM= \frac{GA}{X} * 100,$ Shukla *et al.,* 2006.

**Results and discussion**

Mean squares for the studied traits are presented in Tables 2. It was noticed that, except grains weight spike[-1] and number of spikes m[-2], all other traits exhibited highly significant differences among genotypes. Due to years (Y), indicating that the two expectations were lesser influenced by seasonal fluctuations compared to the rest of traits. Results showed highly significant differences for all the traits under the study among 40 genotypes in both seasons. The mean squares suggested that the tested genotypes were genetically variable and considerable amount of variability were existed among them, revealing that successful selection for these traits would be effective for wheat improvement. Similar results were reported by several investigators (Khan *et al.,* 2011; Abd El-mohsen *et al.,* 2012; Baloch *et al.,* 2013;

Abd El-mohsen and Abd El-shafi, 2014; Khan *et al.*, 2015; Raza *et al.*, 2015 and Bhutto *et al.*, 2016). However, the present results are in contrary to the findings of Khan *et al.*, 2013 who observed non-significant differences among bread wheat genotypes for days to maturity, spike length, number of spikelets spike[-1], number of grains spike[-1] and grain yield. It is worth to mention that genotypes × years (Y×G) interactions were highly significant for all studied traits, except heading date and days to maturity, indicating that great environmental

effects on the expression of the former ones. Coefficient of variation (CV) values showed another clue for trait variation among the tested genotypes. Straw yield had the highest CV values (32.11) followed by the three traits which calculated on plot bases. Grains weight spike[-1] showed also high CV value (21.06) followed by tillers number plant[-1] (16.15). The remainder traits showed low to moderate CV values, ranged from 4.26 (days to maturity) to 12.41 (plant height). These results reflected different magnitudes of the traits variation.

**Table 2.** Mean squares from analysis of variance for the 15 yield and yield components traits of forty bread wheat genotypes over two seasons.

| S.V Traits | Year(Y) | Error | Genotypes (G) | Y*G | Error (b) | CV |
|---|---|---|---|---|---|---|
| Heading date | 336.067** | 6.129 | 560.96** | 1.195[ns] | 2.65 | 9.887 |
| Days maturity (days) | 230.104** | 1.408 | 234.446** | 0.591[ns] | 1.297 | 4.260 |
| Plant height (cm) | 6280.19** | 4.54 | 986.65** | 84.08** | 2.42 | 12.41 |
| No .of tillers plant[-1] | 24.37** | 0.01 | 1.00** | 0.60** | 0.04 | 16.15 |
| Spike length (cm) | 6.399** | 0.02 | 5.53** | 1.41** | 0.06 | 8.45 |
| Spike density | 0.333** | 0.00 | 0.07** | 0.03** | 0.00 | 7.82 |
| No. of spikelets spike[-1] | 11.792** | 0.51 | 11.74** | 3.77** | 0.30 | 7.55 |
| No. of grains spike[-1] | 161.65** | 1.34 | 199.97** | 86.70** | 4.56 | 12.33 |
| Grains weight spike[-1](g) | 0.203[ns] | 0.11 | 1.31** | 0.61** | 0.04 | 21.06 |
| 1000 - grains weight (g) | 216.6** | 4.53 | 87.50** | 16.89** | 1.77 | 9.24 |
| No. of spikes m[-2] | 2030[ns] | 523.70 | 10946.8** | 4568.6** | 222.50 | 19.82 |
| Straw yield (t/fed) | 445.55** | 0.57 | 8.36** | 7.32** | 0.72 | 32.11 |
| Biological yield (t/fed) | 487.80** | 0.47 | 11.18** | 10.27** | 0.84 | 26.97 |
| Grain yield (ardab/fed) | 42.514** | 0.43 | 53.20** | 26.19** | 1.80 | 25.06 |
| Harvest index | 3159.22** | 21.47 | 100.76** | 54.36** | 9.39 | 25.97 |

*and **, significant at P<0.05 and P<0.01, respectively. ardab = 150 Kg.

Estimates of phenotypic (Vp) and genotypic (Vg) variances; phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) of the studied traits are presented in Table 3. The detected results of traits ranges and standard error of means, confirmed the previously results of mean square and CV. Where the ranges and standard error (SE) values of the traits calculated on the plot bases, in addition to heading and maturity as well as plant height and grains spike[-1] showed greater values than other traits. In the present investigation, heading date, days to maturity and spike density exhibited mostly equal

values for phenotypic (Vp) and genotypic (Vg) of variation, indicating their less influenced by environmental factors. On the contrary, other trait estimates of phenotypic coefficient of variation were higher than their corresponding genotypic coefficient of variation, indicating the presence of environmental influences on the expression of these traits. Both Vp and Vg surpassed the corresponding environmental variance values. Phenotypic variance ranged from 0.02for spike density to 3458.58 for number of spikes m[-2]. Values of genotypic variances ranged from 0.01 to 1787.38 for the same two traits, respectively.

Environmental variance ranged from 0.001to 222.50for the same two traits, respectively over two seasons. A wide range of phenotypic and genotypic coefficients of variation (PCV and GCV) were observed for all the traits which ranged from (4.25&4.19 %) for days to maturity to (33.91 & 23.18) and (34.46 & 27.41%) for straw yield and grain yield, respectively. High PCV and moderate GCV were recorded for grains weight spike$^{-1}$, grain yield /fed, number of spikes m$^{-2}$, biological yield, straw yield and harvest index. Moderate values of GCV and PCV were observed for plant height, and number of tillers plant$^{-1}$. Moderate PCV and low GCV are observed for number of grains spike$^{-1}$. Low values of GCV and PCV were observed for days to maturity, heading date, spike density, spike length, number of spikelets spike$^{-1}$ and 1000- grains weight (Table 3). Regarding heading date and may be days to maturity GCV were higher or equal to PCV estimates, revealing again their less influences by environment and their variation was mainly due to genetic factors. Whereas, the other studied traits showed PCV higher than the corresponding GCV values, revealing the importance of environmental influences on their expression. Similar results were also observed by Gulnaz *et al.* (2012) and Maurya *et al.* (2014). However, the results were not agreed with those of Ferdous *et al.* (2010) who found moderate PCV and GCV for harvest index whereas, Singh and Upadhyay (2013) reported high PCV and GCV for days to 50% maturity.

Heritability is a significant parameter for selecting an efficient population improvement method. Heritability estimate for the traits under study are presented in Tables 3. High heritability in heading date (97.73%) followed by days to maturity (97.34%), plant height (84.70%) and1000- grains weight (80.14%). Moderate values of heritability were observed for spike length followed by number of spikelets/spike, number of grains/spike, spike density, grains weight/spike and grain yield/fed, while it was low values for other traits. Similar results were reported by Gulnaz *et al.* (2012); Kalimullah *et al.* (2012); Singh *et al.* (2012); Singh and Upadhyay (2013); Yahaya (2014); Desheva and Kyosev (2015) and Kyosev and Desheva (2015).

The genetic advance as a percentage of mean was ranged from 8.31 for days to maturity to 44.92% for grain yield/fed. This result indicated that selecting the top 5% of the genotypes could be result in an advance of 8.31% to 44.92% over the respective population mean. The traits had highest genetic advance as percentage of mean in the current study were grain yield, number of spikes m$^{-2}$, harvest index, grains weight spike$^{-1}$, number of tillers plant$^{-1}$, straw yield, biological yield, number of grain spike$^{-1}$ and plant height. But, the traits revealed moderate genetic advance as percentage of mean were 1000- grains weight (20.90%), spike length (18.95%), heading date (21.00%) and spike density (13.91%). while days to maturity showed low values. Similar results were reported by Khokhar *et al.* (2010) and Desheva and Kyosev (2015), while Majumder *et al.* (2008) reported high of genetic advance for days to maturity.

High heritability accompanied with high genetic advance was observed in case of heading date, plant height and 1000-grains weight. But, moderate values of heritability with high genetic advance as percentage of mean were obtained for grain yield, number of spike/m$^2$, grains weight/spike and number of grains/spike. This indicated that most likely the heritability of these traits is due to additive gene effects and selection may be effective for these traits**.**

**Conclusion**

In conclusion, significant differences among genotypes and their interaction with environment are detect, indicating the effective influences on the environment. The Vp for other traits were higher than Vg. Both Vp and Vg surpassed the corresponding environmental variance. A wide range of phenotypic (PCV) and genotypic (GCV) coefficients of variation were observed for all the traits. High heritability accompanied with high genetic advance as percent of mean was observed in case of heading date, plant height and 1000-grains weight respectively. But, moderate values of heritability with high genetic advance as percent of mean were obtained for grain yield, number of spike/m$^2$, grains weight/spike and number of grains/spike.

**Table 3**. Range, mean, variance, genotypic and phenotypic coefficients of variability, broad sense heritability and genetic advance as percent of mean for the yield and 15 yield components of bread wheat genotypes over two seasons.

| Parameter Traits | Range | Mean± S.E | Vg | Ve | Vp | PCV% | GCV% | h²ᵦ% | GA | GAM% |
|---|---|---|---|---|---|---|---|---|---|---|
| Heading date (day) | 81.3-118.33 | 98.57±0.629 | 93.05 | 2.65 | 95.22 | 9.90 | 9.79 | 79.73 | 20.70 | 21.00 |
| Days to maturity (day) | 141-161 | 148.812±0.409 | 38.85 | 1.297 | 39.92 | 4.25 | 4.19 | 97.32 | 12.67 | 8.51 |
| Plant height (cm) | 90.92-149.79 | 114.73±0.919 | 164.04 | 2.42 | 193.68 | 12.13 | 11.16 | 84.70 | 24.28 | 21.16 |
| No .of tillers plant⁻¹ | 3.08-5.07 | 3.86±0.040 | 0.32 | 0.04 | 0.55 | 19.21 | 14.66 | 58.18 | 0.89 | 23.03 |
| Spike length (cm) | 10.75-15.20 | 12.96±0.070 | 1.82 | 0.06 | 2.33 | 11.78 | 10.41 | 78.11 | 2.46 | 18.95 |
| Spike density (spikelets/cm) | 1.52-1.99 | 1.71±0.008 | 0.02 | 0.00 | 0.03 | 10.13 | 8.27 | 66.67 | 0.24 | 13.91 |
| No. of spikelets spike⁻¹ | 19.4-24.73 | 22.11±0.108 | 3.81 | 0.30 | 5.27 | 10.38 | 8.83 | 72.30 | 3.42 | 15.46 |
| No. of grains spike⁻¹ | 46.25-70.12 | 57.63±0.458 | 65.14 | 4.56 | 97.08 | 17.10 | 14.00 | 67.10 | 13.62 | 23.63 |
| Grains weight spike⁻¹ (g) | 2.13-3.96 | 2.78±0.037 | 0.42 | 0.04 | 0.65 | 29.00 | 23.31 | 64.62 | 1.07 | 38.60 |
| 1000 - grains weight (g) | 39.83-56 | 47.35±0.283 | 28.58 | 1.77 | 35.39 | 12.56 | 11.29 | 80.76 | 9.90 | 20.90 |
| No. of spikes m⁻² | 184.5-392.67 | 261.82±3.351 | 3574.77 | 222.50 | 5245.97 | 27.66 | 22.84 | 68.14 | 101.67 | 38.83 |
| Straw yield (t/fed) | 4.71-8.92 | 6.89±0.143 | 2.55 | 0.72 | 5.46 | 33.91 | 23.18 | 46.70 | 2.25 | 32.63 |
| Biological yield (t/fed) | 6.05-11.78 | 9.16±0.159 | 3.45 | 0.84 | 7.43 | 29.76 | 20.28 | 46.43 | 2.61 | 28.46 |
| Grain yield (ardab/fed) | 8.87-21.61 | 15.10±0.244 | 17.13 | 1.80 | 27.07 | 34.46 | 27.41 | 63.28 | 6.78 | 44.92 |
| Harvest index % | 18.22-34.42 | 25.84±0.433 | 30.46 | 9.39 | 54.84 | 28.66 | 21.36 | 55.54 | 8.47 | 32.79 |

Where: SE = Standard error of mean, Vp = Phenotypic variance, Vg = Genotypic variance, Ve = environmental variance, PCV = phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, h²bs = Broad sense heritability, GA= genetic advance, GAM (%) = Genetic advance as percent of mean.

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