



## Estimation of genotypic and phenotypic correlations for some growth traits and grain yield of Wheat genotypes

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Article published on May 29, 2017

**Key words:** Wheat, Growth traits, Phenotypic and genotypic correlation

### Abstract

Two field experiments were conducted in 2013/2014 and 2014/2015 growing seasons at the experimental farm of the Faculty of Agriculture, Fayoum University. Forty genotypes of bread wheat were planted in a randomized complete block design with three replications with aim to study the phenotypic and genotypic correlations for growth and grain yield traits. Data showed that genotypic correlation coefficients were higher than the corresponding phenotypic (rp) correlation coefficients in all studied traits except, 12 phenotypic ones at 105 days age and only three cases at 130 days age where phenotypic associations were higher than their corresponding genotypic (rg) correlation coefficients. These trait pairs of higher magnitude of rp than rg were; PLH with NT and each of NT, NLP and LA with both DWP and GYP as well as each of PLH and DWP with GYP in addition NT with GY (at 105 days). On the other hand, at 130 days age, rp values were higher than rg ones only for each PLH and DWP with EXT as well as DWP with GYP. The data led to conclude that GYP would be increased through good building of plant organs and total plant biomass that resulted in enough DWP and consequently improved grain yield.

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## Introduction

Wheat (*Triticum aestivum* L.) is one of the most imperative crop, extensively cultivated throughout the world, with main purpose of human consumption, supporting approximately 35% of the world's population and 95% of wheat grown today is hexaploid ( $2n=6x$ ), which is used in bread making and other bakery products (Debasis and Khurana, 2001). Since ages, wheat has been playing an important role in the economy of several countries (Singh *et al.* 2010). Increase production of wheat is necessary to provide food security in developing countries. Ways to sustain increasing productivity should be explored. It is now realized that sustaining as well as increasing productivity may be essential. The knowledge of factors responsible for high yields has been rendered difficult as yield is a genetically complex traits (Singh *et al.*, 2010).

Grain yield is a complex trait and highly influenced by many genetic factors and environmental fluctuations. They further added that in plant breeding programme, direct selection for yield as such could be misleading and successful selection depends upon the information on the genetic variability and association of morpho-agronomic traits with grain and yield (Sokoto *et al.*, 2012). Towards a clear understanding of the type of plant traits, correlation coefficient analysis is logical step. Correlation studies provide a better understanding of the association of different traits with grain yield. Phenotypic and genotypic correlations within genotypes are of value to indicate the degree to which various traits are associated with economic productivity (Abd El-Mohsen *et al.*, 2012). Correlation is a realistic technique to develop selection criteria, which is mostly based on phenotypic characters used for the improvement of yield through plant breeding program.

The aim of this study was to derive information on phenotypic and genotypic correlation effects of some growth traits and grain yield of different breed wheat genotypes. This may help wheat breeders in reshaping and improving future wheat breeding strategies.

## Materials and methods

### *Experimental Design and Field Management*

The present investigation was carried out at the experimental farm (Demo) of the Faculty of Agriculture, Fayoum University, Egypt, during the two successive growing seasons, 13/2014 and 14/2015. The study aim was to evaluated forty bread wheat genotypes in order to determine the relationship between some growth traits and grain yield in the tested genotypes grown under newly reclaimed land. As well as to determine the phenotypic and genotypic relationships among growth traits and grain yield to select the more desirable traits which may be contribute for wheat improvement. The experimental plant materials comprised of 40 bread wheat genotypes which were used as treatments and evaluated. These genotypes consisted of 36 genotypes of hybrid origin in their F<sub>4</sub> generation resulted from a prior study (Ghallab, 2006) and 4 commercial parental cultivars. Pedigree of the genotypes is presented in Table (1).

The experiments were designed in a randomized complete block design with three replications. Grains of each were hand sown in twelve rows. Each row was of 3.5m long, with a row to row distance of 0.25m while distance between plants was 0.05m. The experimental plot area was 10.5m<sup>2</sup>. Sowing at the grain rate of 70 grains in each row was done on 23<sup>th</sup> and 19<sup>th</sup> of November in the two seasons, respectively. The crop was subjected to recommended package of agronomic and plant protection practices to obtain a healthy crop.

### *Data collection*

At ages of 105 and 130 days, two vegetative samples of five guarded plants for each were randomly taken from inner rows plot<sup>-1</sup> and used to measure the average of the following traits: plant height, cm (PLH), number of tillers plant<sup>-1</sup> (NT), spike length, cm (SL), peduncle length, cm (PLS), extrusion peduncle, cm (EXT), number of leaves plant<sup>-1</sup> (NLP), flag leaf area, cm<sup>2</sup> (FLA), total leaf area (LA) and dry weight plant<sup>-1</sup>, g (DW) according Birch *et al.*, 1998. At the full-ripe stage of maturity of the tested genotypes. Ten guarded plants were randomly taken from the inner rows of each plot to measure the averages of grain yield plant<sup>-1</sup>, g (GYP) and grain yield, ardad/fed (GY).

**Table 1.** List and pedigree of the forty bread wheat genotypes including four check parental cultivars.

G	Pedigree	G	Pedigree
1	Sakha93 / Gimmeiza5 -2	21	Sids1 / Giza168 -8
2	Sakha93 / Gimmeiza5 -3	22	Sids1 / Giza168 -10
3	Sakha93 / Gimmeiza5 -4	23	Sakha93/ Sids1 -1
4	Sakha93 / Gimmeiza5 -5	24	Sakha93/ Sids1- 2
5	Sakha93 / Gimmeiza5 -6	25	Sakha93/ Sids1 - 3
6	Sakha93 / Gimmeiza5 -7	26	Sakha93/ Sids1 - 4
7	Sakha93 / Gimmeiza5 -9	27	Sakha93 /Sids1- 5
8	Gimmeiza5 / Giza168 -1	28	Sakha93/ Sids1 - 7
9	Gimmeiza5 / Giza168 -4	29	Sakha93/ Sids1 - 8
10	Gimmeiza5 / Giza168 -5	30	Sakha93/ Sids1 - 9
11	Gimmeiza5 / Giza168 -7	31	Sakha93/ Giza168 -1
12	Gimmeiza5 / Giza168 -9	32	Sakha93/ Giza168 -4
13	Gimmeiza5 / Giza168 -10	33	Sakha93/ Giza168 -6
14	Sids1 / Gimmeiza5 -7	34	Sakha93/ Giza168 -7
15	Sids1 / Gimmeiza5 -8	35	Sakha93/ Giza168 -8
16	Sids1 / Giza168 -2	36	Sakha93/ Giza168 -10
17	Sids1 / Giza168 - 3	37	HD2172/Pavon"S"//1158.27/Maya74"S"Sd46-4Sd-2Sd-1Sd-osd
18	Sids1 / Giza168 - 4	38	Sakha92/TR 810328 S 8871-1S-2S-1S-0S
19	Sids1 / Giza168 - 6	39	MIL/BUC//Seri CM93046 - 8M-oY-oM-2Y-oB
20	Sids1 / Giza168 -7	40	Vee "S"/SWM 6525 CGM 4017-1GM-6GM-3GM-oGM

G= Genotype

### Data Analysis

Analysis of variance and covariance for all studied traits was done according Gomez and Gomez (1984).

### Association of characters

Phenotypic (rp) and genotypic (rg) correlations between growth and yield traits were estimated using the method described by Miller, *et al.* (1958).

$$r_g = \frac{COV_g(x_1, x_2)}{\sqrt{V_g(x_1) \cdot V_g(x_2)}}$$

Where,  $COV_G(x_1, x_2)$  = Genetic covariance between  $x_1$  and  $x_2$  trait;  $V_g(x_1)$  = Genetic variance for  $x_1$ .  $V_g(x_2)$  = Genetic variance for  $x_2$ .

$$r_p = \frac{COV_p(x_1, x_2)}{\sqrt{V_p(x_1) \cdot V_p(x_2)}}$$

Where,  $COV_p(x_1, x_2)$  = Phenotypic covariance between  $x_1$  and  $x_2$  trait;  $V_p(x_1)$  = Phenotypic variance for  $x_1$  and  $V_p(x_2)$  = Phenotypic variance for  $x_2$ .

### Results and discussion

Among 55 correlation values, twelve phenotypic ones at 105 days age and only three cases at 130 days age, phenotypic (rp) associations were higher than the corresponding genotypic (rg) correlations (Tables 2& 3). Greater number of significant phenotypic cases at smaller age may be owing to the plants at young age were still in their developmental stage and marked environmental influences played an effective role in their variation.

At 105 days, rp values of PLH with NT and each of NT, NLP and LA with both DWP and GYP as well as each of PLH and DWP with GYP in addition NT with GY were higher than the corresponding rg values (Table 2). On the other hand, at 130 days age, rp values were higher than rg ones only for each PLH and DWP with EXT as well as DWP with GYP. This revealed that EXT and DWP were still developed and consequently partially influenced by environmental factors. In sum, rp values exceeded the corresponding rg ones in cases where the traits were in developmental stage and/or in activate state. Except for these cases, the significant rg values at each age were higher than their rp relationship. From breeding point of view, this result proved to be more important for selection practices, where the associations between the traits pairs under genetic control (Ashfaq *et al.*, 2003).

On the genotypic level, plant height (PLH) exhibited positive and highly significant rg with SPL, PLS, EXT and DWP in both 105 and 130 days ages, reflecting the importance of PLH as the main plant organ contributes in plant canopy, biomass and DWP. However, PLH showed contradicted rg with FLA and LA between the two ages where it had highly significant but negative rg with both traits at 105 days age and positive at 130 days age. This may be due to the clear difference between size and developmental stage of the two traits in the two plant ages.

Also, PLH showed positive and significant rg with NT at 130 days age and non-significant associations with GYP and GY in both ages. The same trend was previously reported by Khaliq *et al*, (2004) and Masood *et al*, (2014). Number of tillers plant<sup>-1</sup> showed positive and highly significant rg with NLP, FLA, LA and DWP at both 105 and 130 days ages and with SPL at the late age, indicating the importance of NT bases on their bearing NLP, FLA and LA in pholsynthesis process and consequently DWP (Sokoto *et al.*, 2012). Number of tillers plant<sup>-1</sup> had also positive highly significant rg with GYP and GY at 105 days age and SPL and positive significant with GY at 130 days age. The results were coincident with those reported by Masood *et al.* (2014). Spike length (SPL) was genotypic ally correlated positively and highly significant with PLS, LA, DWP and GYP at the both ages, and with GYP and GY at 130 days age, indicating its importance as productive organ. However, it had highly significant but negative rg with NLP and FLA at 105 age but positive rg with FLA at 130 days age, due to the difference in developmental stage of the traits in both ages. These results were in agreement with those reported by Masood *et al* (2014).

Extrusion length (EXT) exhibited negative and highly significant rg with NLP, FLA and LA at the both ages, indicating their independent actions. While it showed positive and highly significant and significant rg with DWP at 105 and 130 days ages, respectively. Revealing its importance for photosynsate and biomass formation.

However, at late age, it showed significantly negative rg with GYP (Fellahi *et al.*, 2013). Number of leaves plant<sup>-1</sup> (NLP) had highly significantly positive rg with both FLA and LA at the both stages and with DWP at the late age as well as with GYP and GY at 105 days age. These results may be that the good development of leaves is more important for yield at early stage than the late one which influenced by other productive traits.

Flag leaf area (FLA) showed positive and highly significant rg with LA at the both stages as well as DWP at late age and significant with GYP at 105 days age. Leaves area (LA) exhibited positive highly significant rg with GYP and GY at young age and with DWP at the late age. The results were coincident with those reported by Sokoto *et al*, 2012 and Nawaz *et al*, (2013). Dry weight plant<sup>-1</sup> (DWP) as the semifinal product, showed positive highly significant rg with both GYP (0.438\*\* & 0.297\*\*) and GY (0.266\*\* & 0.267\*\*) at the two ages, respectively, indicating its largest contribution to yield traits (Kalimullah *et al.*, 2012 and Sokoto *et al.*, 2012).

This advantage of DWP due to its strong positively highly significant rg with PLH (0.570\*\* & 0.288\*\*), NT (0.240\*\* & 0.548\*\*) and SPL (0.443\*\* & 0.596\*\*) and at the both ages, respectively and NLP (0.446\*\*), FLA (0.194\*\*) and LA (0.491\*\*) at late age and significant rg with EXL (0.165\*) at late age. Therefore, good building of plant organs and total plant biomass would be resulted in enough DWP and consequently improved yield.

**Table 2).** Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for nine growth traits after 105 days from sowing, grain yield plant-1 and grain yield /fed at harvesting of forty bread wheat genotypes in 2013/2014 and 2014/2015 (over two seasons).

Trait	PLH	NT	SPL	PLS	EXT	NLP	FLA	LA	DWP	GYP	GY
PLH		0.079	0.572**	0.603**	0.532**	-0.024	-0.188**	-0.415**	0.570**	0.038	0.015
NT	0.134*		-0.104	-0.108	-0.121	0.639**	0.239**	0.502**	0.240**	0.215**	0.240**
SPL	0.462**	0.005		0.907**	0.749**	-0.411**	-0.616**	0.562**	0.443**	0.108	-0.034
PLS	0.531**	-0.076	0.857**		0.951**	-0.518**	-0.660**	0.012	0.459**	0.008	-0.030
EXT	0.468**	-0.066	0.650**	0.924**		-0.522**	-0.639**	-0.672**	0.442**	-0.062	0.013
NLP	0.066	0.729**	-0.190**	-0.315**	-0.27**		0.368**	0.905**	0.109	0.189**	0.249**
FLA	-0.146*	0.222**	-0.498**	-0.542**	-0.52**	0.281**		0.640**	-0.017	0.114	0.088
LA	0.098	0.618**	0.462**	0.029	-0.47**	0.885**	0.450**		0.095	0.203**	0.182**
DWP	0.375**	0.449**	0.332**	0.338**	0.31**	0.394**	0.049	0.354**		0.438**	0.297**
GYP	0.134*	0.254**	0.108	0.033	-0.031	0.203**	0.121	0.235**	0.449**		0.563**
GY	0.051	0.206**	-0.005	-0.007	0.043	0.207**	-0.078	0.134*	0.189**	0.499**	

\*and \*\*, significant at P<0.05 and P<0.01, respectively.

Where, PLH= Plant height, NT = Number of tillers plant<sup>-1</sup>, SPL= Spike length, PLS= Peduncle length, EXT = Extrusion length, NLP= Number of leaves plant<sup>-1</sup>, FLA= Flag leaf area, LA=Total leaf area plant<sup>-1</sup>, DWP= Dry weight plant<sup>-1</sup>, GY= Grain yield/fed, GYP= Grain yield plant<sup>-1</sup>.

**Table 3.** Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for nine growth traits after 130 days from sowing, grain yield plant<sup>-1</sup> and grain yield/fed at harvesting of forty bread wheat genotypes in 2013/2014 and 2014/2015 (over two seasons).

Trait	PLH	NT	SPL	P LS	EXT	NLP	FLA	LA	DWP	GYP	GY
PLH		0.160*	0.570**	0.693**	0.296**	0.312**	0.464**	0.444**	0.228**	-0.009	0.107
NT	0.148*		0.387**	-0.003	-0.090	0.770**	0.362**	0.706**	0.548**	-0.005	0.152*
SPL	0.448**	0.335**		0.278**	-0.131	0.473**	0.597**	0.674**	0.593**	0.357**	0.234**
PLS	0.674**	-0.009	0.194**		0.795**	-0.087	0.226**	0.050	0.251**	-0.111	-0.099
EXT	0.347**	-0.024	-0.025	0.743**		-0.262**	-0.227**	-0.27**	0.165*	-0.146*	-0.034
NLP	0.288**	0.751**	0.411**	-0.050	-0.090		0.358**	0.905**	0.446**	-0.040	0.064
FLA	0.292**	0.232**	0.418**	0.192**	-0.172**	0.190**		0.648**	0.194**	0.094	0.032
LA	0.356**	0.698**	0.561**	-0.002	-0.141*	0.885**	0.441**		0.491**	-0.017	0.073
DWP	0.207**	0.532**	0.415**	0.218**	0.185**	0.490**	0.169**	0.245**		0.226**	0.267**
GYP	0.032	0.094	0.339**	-0.049	-0.072	0.015	0.088	0.062	0.268**		0.563**
GY	0.097	0.115	0.196**	-0.071	-0.048	0.080	0.022	0.041	0.160*	0.499**	

\*and \*\*, significant at P<0.05 and P<0.01, respectively.

Where, PLH= Plant height, NT = number of tillers plant<sup>-1</sup>, SPL= Spike length, P LS= Peduncle length, EXT = Extrusion length, NLP= Number of leaves plant<sup>-1</sup>, FLA= Flag leaf area, LA= Total leaf area plant<sup>-1</sup>, DWP= Dry weight plant<sup>-1</sup>, GY= Grain yield/fed, GYP= Grain yield plant<sup>-1</sup>.

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