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ESTIMATION OF GENETIC VARIATIONS AND CONTRIBUTION OF YIELD COMPONENTS IN GRAIN YIELD OF SOME BREAD WHEAT GENOTYPES

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ABSTRACT: This study was conducted to determine the genetic variations, correlation and factor analysis for grain yield and its components in eight wheat genotypes. The wheat genotypes showed significant differences for all the studied traits. Genotypes Sakha 95, Misr 1, Giza 171, Misr 1, and Misr 2 performed well in both seasons for grain yield and its components. Maximum phenotypic and genotypic variances were detected for number of spikes/m^2 and plant height in both seasons. The phenotypic coefficient of variation and genotypic one ranged from 48.72and 28.78% to 132.67and 74.73% and from 34.85and 21.42% to 182.98 and 117.17% for 1000 grains weight and the number of spikes/ m^2 in the 1st season and the 2nd one, respectively. The highest heritability was detected for plant height and flag leaf area in both seasons. Moderate heritability was observed for number of grains/ spikes in both seasons. Low heritability was detected for the remaining traits during both seasons. A high genetic advance was observed for number of spikes/m^2 (29.61) in the 2nd season. A significant positive correlation was registered between grain yield (ard./fed.) and each of flag leaf area, the number of spikes/plant and 1000 grains weight in both the 1st season and the 2nd one. The factor analysis method grouped the studied variants into two factors. These factors represented 79.424% in the 1st season and 84.255% in the 2nd one of the total variations of grain yield. The results of this study could be used to develop breeding programs for bread wheat improvement.

Kay words: Wheat, genetic variability, correlation, factor analysis.

INTRODUCTION

Wheat is the main food for people in Egypt and plays an important role in their agriculture. The yield of wheat grain can be improved by using the best farming practices and developing better varieties of wheat.

Grain yield is a complicated character that is affected by many factors. The successful selection of high-yielding varieties depends on the knowledge of genetic variations and the association of different morphological and agronomic traits with grain yield.

The main advantage of partitioning whole variation into its components *i.e.*, phenotypic variation, genotypic variation, and environmental variation is that it helps to assess the type of genetic variation present for different traits. This information can then be used to decide on a breeding program for the improvement of a character. Estimates of heritability measure the degree to which a trait is passed down from parents to offspring. The effectiveness of selection depends on the quantity of genetic variation present for a trait. Therefore, estimates of heritability combined with genetic advance are more useful for expecting the amount of genetic improvement that can be achieved through selection than heritability estimates alone.

The relationship between different yield components has been used to improve wheat grain yield. Correlation is a useful tool for measuring the degree to which different traits are related. By understanding these relationships, we can better utilize existing genetic resources

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and information to improve yield. Correlation studies with factor analysis can provide even more information about the association of various traits with grain yield. **Jan mohammadi *et al.* (2014) and Mahdy *et al.* (2022)** reported that genetic variance, heritability and genetic advance for wheat yield and its components were low to moderate. **Hossain *et al.* (2021), Seyoum and Sisay (2021) and Sewore *et al.* (2023)** showed that wheat genotypes revealed high variability in both phenotypic and genotypic for most of the yield and its components. **Tefera (2022) and Dragov *et al.* (2022)** detected significant correlations among most of the yield components. **Haleem *et al.* (2022)** showed that the number of spikes/m^2, number of grains/spike and 1000 grains weight were significantly correlated with grain yield.

Walton (1972) argued that correlation, multiple, and stepwise regression are not effective statistical techniques for identifying growth and plant characters related to yield in spring wheat. He suggested that factor analysis is a better technique for this purpose. According to factor analysis, the number of spikes/m^2, the number of grains/spike and 1000-grain weight were accounted the major contributing of grain yield (**Ibrahim *et al.*, 2022**).

This study aimed to determine the variations and the relations between yield and its components in bread wheat. This information could be used to improve this strategic crop by selecting for the traits that contribute most to grain yield.

MATERIALS AND METHODS

This study was performed at the experimental farm of the Faculty of Agriculture, Zagazig University, Egypt during the two winter growing seasons of 2020/2021 and 2021/2022. Eight wheat genotypes *i.e.*, Giza 171, Misr1, Misr 2, Sids 12, Sids 13, Sakha 95, Gemmeiza 11 and Gemmeiza 12 were used to estimate genetic variability, correlation, and factor analysis for wheat yield and its components, to improve wheat grain yield. The experimental design was a complete randomized block with three replications. The plot area was 3.6 m^2 (6 rows, 3 meters in length with 20 cm apart) and planted at a rate of 300 seed/m^2. The crop was grown using the recommended agricultural practices. At heading, plant height and flag leaf area were measured using ten plants from each genotype in each replicate. At harvest, the number of spikes /m^2, the number of grains/spikes, 1000 grains weight and grain yield (ard/fed.) were determined.

The data were analyzed statistically using analysis of variance (ANOVA), following the method described by **Steel *et al.* (1997)**. The least significant differences (LSD) at a significance level of 0.05 were calculated for the parameters that showed a significant effect.

To compare the mean values of the treatments, the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated following the method of **Burton (1952)** as follows:

$$\text{PCV}=\frac{\sqrt{\sigma 2P}}{\bar{x}}\ X\ 100$$

Where, σ^2 P = phenotypic variance and $\bar{x}$ = mean of the character being evaluated.

$$\text{GCV}=\frac{\sqrt{\sigma 2g}}{\bar{x}}\ X\ 100$$

Where, σ^2 g = phenotypic variance and $\bar{x}$ = mean of the character being evaluated.

Broad-sense heritability (h^2) was calculated as the ratio of the genotypic variance to the phenotypic variance according to **Singh and Ceccarelli (1996)** as follows:

$$h^2 = \frac{\sigma 2g}{\sigma 2p}\ X100$$

Where, H= heritability in the broad sense, σ^2 g = genotypic variance and σ^2 P = phenotypic variance.

Genetic advance (GA) assuming the selection of the superior 10% of the genotypes was also estimated following the procedure elaborated by **Singh and Chaudhary (2004)** as follows**.**

$$GA = K \text{ x } \sigma P \text{ x } h^2$$

RESULTS AND DISCUSSION

Mean Performance

The mean performance of wheat genotypes for yield and its components characters in both seasons is shown in Table 1. The results showed that there were significant differences between the genotypes for all the studied characters in

Table 1. Plant height, flag leaf area and grain yield as well as its components mean performance for the studied genotypes during the two seasons

Characters Genotypes	Plant height (cm)		Flag leaf area (cm^2)		Number of spikes /m^2		Number of grains /spike		1000 grain weight (g)		Grain yield (ard./fad.)	
	2020-21	2021-22	2020-21	2021-22	2020-21	2021-22	2020-21	2021-22	2020-21	2021-22	2020-21	2021-22
Giza 171	124.33	123.33	34.27	37.67	331.7	403.52	49.6	48	41.23	50.57	21.35	25.51
Misr 1	116.67	121.67	44.67	41.49	375.0	390.08	53.8	47.53	46.00	48.46	24.06	24.61
Misr 2	105.33	108.67	43.90	41.54	341.0	355.16	58.33	53.00	48.10	50.10	23.45	23.95
Sids 12	108.33	114.00	36.00	36.15	356.7	355.06	51	48.00	44.37	45.51	19.15	20.80
Sids 13	101.00	103.00	42.17	36.66	365.0	327.09	51.83	49.17	45.30	46.00	18.67	18.70
Sakha 95	107.33	109.33	45.83	46.22	390.0	396.78	51.6	55.57	49.57	47.89	26.80	25.53
Gemmeiza 11	103.00	105.00	43.90	38.14	353.3	347.70	60.07	52.77	45.67	47.46	20.46	21.63
Gemmeiza 12	94.33	97.67	37.00	42.68	352.0	352.48	52.65	50.33	45.60	46.45	22.39	21.98
Mean	107.54	110.33	40.97	40.07	358.08	365.98	53.61	50.55	45.73	47.8	22.04	22.84
LSD $_{0.05}$	5.86	3.38	2.17	2.08	29.11	37.73	4.15	3.67	2.21	2.67	3.84	3.46

both seasons. This indicates that there is a high degree of genetic variability among the studied wheat genotypes, which is useful for selecting and breeding new high-yielding cultivars. According to Table 1, wheat genotypes Sakha 95, Misr 1, Giza 171, Misr 1, and Misr 2 performed well in both seasons for yield and its component characters.

Phenotypic and Genotypic Coefficients of Variation, Heritability and Genetic Advance

The values of variance, Phenotypic and genotypic coefficients of variation, heritability and genetic advance for all six traits are shown in Table 2. The phenotypic coefficients of variation were similar to their corresponding genotypic coefficients, indicating that the environment had little impact on the expression of these traits. However, there was a strong correlation between the genotypic and phenotypic coefficients of variation for all the traits in both seasons. Number of spikes /m^2 and plant height registered maximum phenotypic and genotypic variances in both seasons. The small difference between both genotypic variance and phenotypic one and the higher values of genotypic compared with the environmental ones for all the traits suggest that the genotypes variations were due to hereditary factors.

High phenotypic and genotypic coefficients of variation were observed for all traits in both the 1st and the 2nd one. The phenotypic coefficient of variation estimates were higher than the matched genotypic one in both seasons, indicating that the environment had a small impact on the expression of these traits. However, there was a good correlation between the genotypic and phenotypic coefficients of variation for all the traits.

Values of both PCV and GCV ranged from 48.72 and 28.78% to 132.67 and 74.73% and from 34.85 and 21.42% to 182.98 and 117.17 % for 1000 grains weight and number of spikes/ m^2 in the 1st season and the 2nd one, respectively. Similar results were reported by **Seyoum and Sisay (2021) and Sewore *et al*. (2023)** where the estimates of PCV and GCV were high for 1000 grains weight and number of spikes/m^2.

Heritability estimates ranged (31.73) for number of spikes/m^2 to (89.04%) for flag leaf area and from (37.77) for 1000 grains weight to (93.07%) for plant heightinthe1stseason and the 2nd one, respectively. The highest heritability was detected for flag leaf area (89.04%) and (88.05) and plant height (82.32 %) and (93.07%) under the 1stseason and the 2nd one, respectively. According to these values of heritability, the variation of those traits was indeed through heredity factors and was less influenced by the

Table 2. **Variances, phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV), heritability (h^2_b) and genetic advance (GA) for grain yield and its components of studied genotypes in the two seasons**

Characters	Plant height (cm)		Flag leaf area (cm^2)		Number of spikes /m^2		Number of grains /spike		1000 grain weight(g)		Grain yield (ard./fad.)	
Genetic parameters	**2020-21**	**2021-22**	**2020-21**	**2021-22**	**2020-21**	**2021-22**	**2020-21**	**2021-22**	**2020-21**	**2021-22**	**2020-21**	**2021-22**
Phenotypic Variance (σ^2p)	98.57	83.48	21.78	27.38	630.30	1225.43	19.40	13.16	10.85	5.81	12.34	4.01
Genotypic Variance (σ^2g)	81.14	77.69	19.39	24.11	199.98	502.45	10.67	6.31	3.79	2.19	4.85	10.08
Environmental Variance (σ^2e)	17.42	5.79	2.39	3.27	430.32	722.98	8.73	6.84	7.06	3.61	7.49	6.07
PCV (%)	95.74	86.98	72.91	83.54	132.67	182.98	60.15	51.02	48.72	34.85	74.83	66.44
GCV (%)	86.86	83.91	68.80	78.39	74.73	117.17	44.61	35.34	28.78	21.42	46.92	41.90
h^2_b (%)	82.32	93.07	89.04	88.05	31.73	41.00	54.99	47.98	34.90	37.77	39.31	39.77
GA	16.86	17.54	8.57	9.50	16.43	29.61	5.00	3.59	3.79	1.88	2.85	2.60

environment. This means that it is possible to improve these traits through selection, and that the improvement is likely to be stable over time. The high heritability of these traits is also likely to be due to the action of many genes (polygenes), which makes them more amenable to selection. This is good news for plant breeders, as it means that they can make effective choices when selecting for these traits. **Hossain *et al.* (2021)** also found that plant height and flag leaf area had high heritability values. Moderate heritability estimates were found for the number of grains per spike under both seasons. Low heritability estimates were found for the remaining traits under both seasons.

Heritability is not the only factor that determines the effectiveness of selection. Genetic advance (GA), which is the amount of genetic improvement that can be achieved through selection, is also important. Therefore, it is more useful to consider both heritability and GA when selecting for a particular trait. GA can be predicted from heritability, and the present study found that a high GA was observed for the number of spikes per square meter (29.61) in the second season. A comparison of heritability and genetic advance for different traits showed that plant height had high heritability and moderate genetic advance, suggesting that this trait is heritable and that selection for this trait could be effective in improving grain yield. The dominance of the additive gene can be attributed to the pressure of action, meaning that the genes that control plant height have a direct effect on the trait. This makes selection for plant height more effective, as the desired traits will be passed on to the offspring more reliably. However, grain yield and its components had low heritability and low genetic advance. This suggests that these traits are controlled by non-additive genes, such as dominance and epistasis. This means that the effects of these genes are not simply additive and that the expression of these traits is more influenced by the environment. Therefore, heterosis breeding, which is the breeding of two different genotypes to produce offspring with superior traits, could be used to improve these traits.

Correlation

Simple correlation coefficient values of grain yield with plant height, flag leaf area, number of spikes/m^2, number of grains/spike and 1000 grains weight are presented in Table 3. positive and significant correlation was registered between grain yield (ard./fad.) and each of flag leaf area, number of spikes/m^2 and 1000 grains weight in both the 1st season and the 2nd one. Furthermore, a positive and significant correlation was detected between flag leaf area and each of number of spikes/m^2 and number of grains/spike in both seasons and 1000 grains weight in the 1st one; number of spikes/m^2 and 1000 grains weight in both the 1st season and the 2nd one as well as between number of grains/spike and 1000 grains weight in the 1st season only. This indicates that a high in one trait leads to a high in another associated one. On the other hand, a negative and significant correlation was observed between plant height and 1000 grains weight in the 1st season and number of grains /spikes in the 2nd one.

Factor Analysis

Principal factor matrix after orthogonal rotations for the studied traits in two seasons is shown in Table 4. The factor analysis method grouped the variables into two factors. These

Table 3. Simple correlation coefficient between the studied traits in the two seasons

	Plant height (cm)		Flag leaf area (cm^2)		Number of spikes /m^2		Number of grains/spike		1000 grains weight (g)	
	2020-21	2021-22	2020-21	2021-22	2020-21	2021-22	2020-21	2021-22	2020-21	2021-22
Plant height (cm)	1	1								
Flag leaf area (cm^2)	-0.201	-0.164	1	1						
Number of spikes /m^2	-0.167	0.741**	0.635**	0.440*	1	1				
Number of grains /spike	-0.344	-0.463*	0.563*	0.644**	-0.145	0.007	1	1		
1000 grains weight(g)	-0.469*	0.549**	0.815**	0.232	0.642**	0.616**	0.403*	0.129	1	1
Grain yield (ard./fad.)	-0.264	0.589**	0.965**	0.945**	0.648**	0.918**	0.466*	0.249	0.957**	0.790**

Table 4. Principal factor matrix after orthogonal rotations for the studied traits in the two seasons

Variants	Common factors coefficients				Communality	
	Factor 1		Factor 2		%	
	2020-21	2021-22	2020-21	2021-22	2020-21	2021-22
Plant height (cm)	-0.526	0.828	0.395	-0.504	0.433	0.939
Flag leaf area (cm^2)	0.916	0.325	0.073	0.859	0.844	0.844
Number of spikes /m^2	0.576	0.938	0.695	0.093	0.940	0.889
Number of grains /spike	0.554	-0.046	-0.748	0.924	0.867	0.856
1000 grains weight(g)	0.937	0.82	0.091	0.114	0.887	0.685
Variance ratio	55.172	46.901	24.252	37.354	79.424	84.255

two factors represented about 79.424% and 84.255% of the total variance of grain yield in both the 1st season and the 2nd one, respectively.

Concerning the 1st season, the first factor included three variants and represented 55.172%. These variants were plant height (22.11%), flag leaf area (38.5%) and 1000 grains weight (39.39%). The second factor included two variants and represented24.252% of the total variation of grain yield. These variants were number of spikes/m^2 (48.16%) and number of grains/spike (51.84%).

Regarding the 2nd season, the first factor included three variants and represented 46.901%. These variants were plant height (32.02%), number of spikes/m^2 (36.27%) and 1000 grains weight (31.71%). The second factor included two variants and represented 37.354% of the total variation of grain yield. These variants were flag leaf area (48.18%) and number of grains/spike (51.82%). It is noticed to mention that these variants had high loading coefficients and share much more on the reliance structure. Most of these variants showed significant positive correlation with grain yield. **Ibrahim *et al.*, 2022** reported that number of spikes/m^2, number of grains/spike and 1000grains weight were represented the main contributing of grain yield.

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تقدير الاختلافات الوراثية ومساهمة مكونات المحصول في محصول الحبوب لبعض التراكيب الوراثية من قمح الخبز

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أقيمت تجربتين حقليتين خلال الموسمين 2021– 2020 و2022– 2021 بالمزرعة البحثية لكلية الزراعة، جامعة الزقازيق، الشرقية، مصر. بغرض دراسة الاختلافات الوراثية بين 8 تراكيب وراثية من قمح الخبز وذلك لدراسة الاختلافات الوراثية، الارتباط وتحليل العامل بين محصول الحبوب (أردب/الفدان) ومكوناته. أشارت النتائج إلى وجود اختلافات عالية المعنوية بين التراكيب الوراثية في جميع الصفات تحت الدراسة. تفوقت التراكيب الوراثية سلالة 2، مصر 1، جيزة 171، سدس 13 وسلالة 4 في محصول البذور ومعظم مكوناته. سجلت كل من صفتي عدد السنابل /م^{2}وارتفاع النبات أعلى تباين مظهري ووراثي خلال موسمى الزراعة. تراوحت قيم معامل الاختلاف المظهري ومعامل الاختلاف الوراثي من 48.72 و28.78% إلى 132.67 و74.73 ومن 34.85 و21.42% إلى 182.98 و117.17% لصفة وزن 1000 حبة وصفة عدد السنابل/م^2 تحت ظروف كل من الموسم الأول والموسم الثانى على التوالي. كانت قيم كفاءة التوريث مرتفعة لصفات ارتفاع النبات ومساحة ورقة العلم، بينما كانت متوسطة لصفة وزن الـ 1000حبة ومنخفضة لصفة محصول البذور (طن/الفدان) خلال موسمى الزراعة. كان هناك ارتباط موجب ومعنوي بين محصول الحبوب وكل من مساحة ورقة العلم، عدد السنابل/م^2، ووزن 1000حبة خلال موسمى الزراعة. أظهر تحليل العامل تقسيم الصفات تحت الدراسة الى عاملين رئيسيين مثلا حوالي79.424% و84.255 من الاختلافات في صفة المحصول خلال كل من الموسم الأول والثاني، على التوالى.

الكلمات الإسترشادية: قمح الخبز، التباين الوراثى ، الارتباط، تحليل العامل.

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