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Assessment of Genetic Variability, Diveristy and Association in Fifteen Bread Wheat Genotypes

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ABSTRACT

The present work was conducted at Nubaria Research Station Farm to assess the genetic behavior of fifteen bread wheat genotypes during the two growing seasons of 2013/2014 and 2014/2015. The experimental design used was a randomized complete block design, with three replicates. The Analysis of variance and covariance were computed to estimate broad sense heritability (h^2). Also, genotypic and phenotypic correlation coefficients and path analysis were computed between grain yield and its related characters, as well as cluster analysis was automated to identify the interrelationships among the tested genotypes.

Results showed significant differences among wheat genotypes for all studied characters in the first and second seasons and across the two seasons. Genotypes No. 2, 6 and 11 outyielded the average grain yield of the three check cultivars (Giza 168, Sids 12 and Misr 1) by 25, 6.07 and 12.35 %, respectively, indicating their magnitude as promising genotypes that could be recommended for release. Large values of h^2 couple yield. Highly significant and positive correlation coefficients were detected between grain yield and each of number of spikes/m^2 followed by number of kernels/spike at the genotypic and phenotypic levels. Also, path analysis showed that number of spikes/m^2 and number of kernels/spike gave the maximum influence directly and indirectly upon grain yield in wheat crop. As a result, the above mentioned characters could be used as selection criteria in wheat breeding program. The cluster analysis classified the tested genotypes into four main different groups (clusters), where each group contained the genotypes which showed similar phenotypic performance. It is clear that the second cluster included the maximum number of items (seven out of fifteen genotypes), followed by the third cluster (four genotypes) and the first cluster (three genotypes) and finally the fourth (two genotypes).

Accordingly, the results exhibited the presence of considerable genetic diversity among the tested genotypes, which gave a good chance to achieve sufficient steps for genotypic improvement of wheat through the hybridization among genotypes, taken from divergent clusters.

Key words: Correlation coefficient, Path analysis, Wheat.

INTRODUCTION

Bread wheat (Triticum aestivum L.) is one of the most important crops in Egypt, where its planted area ranged about 1.26 million hectares (3.00 million feddans). The local production is about 8.1 million tons, however it covers less than half of the local consumption. Increasing wheat productivity is a national target in Egypt to reduce the gap between wheat consumption and production.

properties.

The production of wheat can be increased either by increasing the planted area or by increasing crop yield productivity per unit area. Currently, it is difficult to increase the planted area of wheat crop due to competition with other winter crops and because each of restricted reclaimed lands and water shortage, etc. Therefore, the only alternative strategic solution is to increase its productivity per feddan (4200 m^2) by applying the better crop management techniques and introducing high yielding cultivars characterized by tolerance against biotic and abiotic stresses.

Knowledge on heritability and genetic advance is a basic step to identify the characters amenable to genetic improvement through selection. Tammam *et al*. (2000), Kashif and Khaliq (2004), Ali *et al*. (2008), Abd El-Mohsen *et al.* (2012), Baloch *et al*. (2013) emphasized that, without considering genetic advance, the heritability values (h^2) would not be practically useful in breeding program, depending on visual selection.

Improvement of a complex and low heritable character, like grain yield, may be more successful and fast using selection through its more heritable components, which showed significant positive association with it.

Information, obtained from correlation coefficients, can be augmented by partitioning the correlations into direct and indirect effects for a given set of causal interrelationships. In such situations, the correlation coefficients may be confounded with indirect effects due to common association inherent in trait interrelationships. So, path coefficient analysis has proven useful in providing additional information that describes the casual relationships such as grain yield and its components.

Therefore, the information about interrelationships among grain yield and its components have received considerable attention from many researchers in wheat crop, among them, Tammam et al. (2000), Kashif and Khaliq (2004), Ali et al. (2008), Ashmawy et al. (2010), Abd El-Mohsen et al. (2012), Baloch et al. (2013), Abd El-kreem (2014), Abd El-Mohsen and Abd El-Shafi (2014), Mostafa and Omar (2014) who confirmed that the breeder must be more aware about the important associations among grain yield and its components to design more successful selection program.

The presence of genetic diversity, among plant materials, represents the corner stone for designing a useful breeding program. Since, the information about the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization.

Cluster analysis is a valuable biometrical tool, aimed to quantify the degree of genetic divergence among tested genotypes, based on their performance and their contributing characters. Genetic divergence among wheat genotypes, using cluster analysis also was reported by Singh and Dwivedi (2002), Khodadadi *et al.* (2011), Savii and Nedelea (2012), Azam *et al*. (2013), Verma *et al*. (2013), Sheykhi *et al*. (2014).

Therefore, the present work was planned to investigate the estimates of heritability (h^2) using the yield data of twelve newly promising inbred lines and three check cultivars. Also, the study aimed to identify the interrelationships among grain yield and its related characters, using correlation and path analysis at both genotypic and phenotypic levels, as well as to assess the possibility to classify the tested wheat genotypes, using cluster analysis procedure. The results may be helpful to plan appropriate selection strategies for improving grain yield of wheat crop in Egypt.

MATERIALS AND METHODS

Plant materials and experimental design

The present work was carried out at the Nubaria Research Station Farm during the two successive winter seasons of 2013/2014 and 2014/2015 to evaluate the yield performance of fifteen bread wheat genotypes (representing a wide genetic background). The tested genotypes comprised three released Egyptian cultivars (Giza 168, Sids 12 and Misr 1) and twelve newly promising inbred lines, selected from Wheat Breeding Program of Agricultural Research Center. A detailed description of the code and pedigree of the tested genotypes are presented in Table (1).

In each season, the plant materials were laid out in a randomized complete block design, with three replications.

Table 1: The name and pedigree of the fifteen bread wheat genotypes used.

Code	Pedigree
G1	MILAN/S87230// BAV92
G2	SAKHA 94 / 5/ BLl133 /3/ CMH 79A.955*2/ CNO 79// CMH 79A.955 / BOW"s" /4/ GIZA 164 /SAKHA 6l
G3	MAI "S" / PJ // ENU"S" /3/ KITO / POTO.19//MO/JUP/ 4 / Kl34(60) /VEE /7/ KAUZ / 6/ ATL66 /H567.71// ATL66 / 5 // PMN5//S9 48.AL/4*CNO67 /3/ PMNS /4/ CMH 75 A.66
G4	SAKHA 12 / 5/ KVZ // CNO 67 / PJ 62 /3/YD "S" / BLO "S" /4/ K134 (60) I VEE /61 HUBARA-I
G5	SUNCO/2*PASTOR.
G6	KAMBI*2/ KIRITATI.
G7	GIZA 168 /5/ MAI "S" /FJ//ENU'S'/3/ KITO/ POTO l9// MO / JUP / 4/ K l34 (60) VEE.
G8	IRENA / I WL 7060I TURACO.
G9	SERI.1B*2/ 3/ KAUZ*2/ BOW // KAUZ / 4/ PBW343* TIUKURU/5/C80.1/3*BATAVIA//2*WBLLI
G10	WBLLI *2/KIRITATI
G11	WHEAR/SOKOLL
G12	WHEAR//2 *PRL/2 *PASTOR
Giza 168	MRL/BUC//SERI CM93046-8M-0Y-0M-2Y-0B-0GZ
Sids 12	BUS//7C//ALD/5/MAYA74/ON//1160.147/3/BB/GLL/4/CHAT"S"/6/MAYA/VUL//CMH74 A.630/4*SX. SD720096-4SD-1SD-1SD-0SD
Misr 1	OASIS/SKAUZ//4*BCN/3/2*PASTOR. CMSSOOYO 1881T-050M-030Y-030M-030WGY-33M-0Y-0S

The experimental plot area was 4.2 m^2. Each plot consisted of six rows, 3.5 m long and 0.2 m apart while the distance between plants was 0.02 m. Sowing dates were 20 and 23 November in the two successive seasons, respectively. The experiment was subjected to the recommended package of agronomic and protection practices at the proper time to obtain a healthy crop.

Data collection:

During the two seasons the following data were recorded: At harvest time, the central four rows of each plot, with four meters long, were harvested and the data were recorded for grain yield and its components, as follows:

Plant height (cm), data of number of days to 50% heading (DH) and number of days to 50% maturity (DM) were recorded on plot basis. At harvest, data on grain yield and its attributes were recorded on plants, randomly chosen from the inner rows as follows:

1. Number of spikes/m² was estimated as the number of fertile spikes of guarded square meter within each plot before harvesting.
2. 1000-kernel weight (g) was recorded as the average of random samples of 1000 kernels from clean grains each plot.
3. Number of kernels/spike was estimated as the average of ten spikes taken randomly from each plot.
4. Grain yield (GY) was determined from the central area of the plot (3.2 m^2), then converted to the unit of (ardab/fad).

Statistical procedures:

Data were subjected to individual and combined analysis of variance (ANOVA) of randomized complete block design for each one of the two seasons and over them (Steel *et al.*, 1997). Levene test (1960) was run prior to the combined analysis to test the homogeneity of individual error terms. Least significant difference (LSD) test was used to detect the significant differences among genotype means. The genotypic and phenotypic variances and their corresponding coefficients of variations were estimated, using the pertinent mean square expectations, according to the method, suggested by Johnson *et al.* (1955). Broad sense heritability (h^2) was estimated as described by Allard (1999).

The interrelationships, among grain yield (as a resultant variable) and its related characters (as casual variables) were studied at the genotypic and phenotypic levels, using the following methodologies:

1. Simple correlation coefficients between all pairs of the studied traits as suggested by Steel *et al.* (1997).
2. Path analysis methodology was primarily proposed by Wright (1921 and 1934), that was rediscovered and used by Dewey and Lu (1959) in the agricultural research. A BASIC program (Atia, 2007) was used to automate the computations of genetic parameters, as well as genotypic and phenotypic correlations and path analyses.

Also, the model of Cluster analysis was performed on genotypes “r” matrix, using a measure of Euclidean distance. It is the most commonly used measure of similarity between two objects. Essentially, it is a measure of the length of a straight line drawns between two objects. Genotypes were clustered using un-weighted pair group method, using arithmetic average as outlined by Kovach (1995).

RESULTS AND DISCUSSION

Mean performance:

The mean values of grain yield and its related characters for the fifteen wheat genotypes, evaluated in two seasons, are given in Table (2). The results of Levene test (1960) proved the homogeneity of separate variances for all studied traits that permits to apply combined analysis. The mean values and significance among the aimed genotypes for all studied characters, in individual and combined analyses over the two seasons, are presented in Tables (2 and 3).

The results, shown in Table (2), revealed the presence of highly significant differences among genotypes, seasons and their interaction for three agronomic characters, except for plant height, where the effect of seasons was insignificant.

Results showed that genotype No. 7 was the earliest heading one in the first and second seasons (70.67 and 94.67 days), followed by genotype No. 8 recording 72 and 95 days, respectively. In addition, the two genotypes were the earliest across the two seasons, having an average of 82.67 and 83.50 days, respectively. On the other hand, genotype No. 12 headed later in the first and second seasons and over the two seasons, having averages of 90, 104 and 97 days, respectively. Generally, the wheat genotypes headed in the second season (98.60 days), later than the first one (81.13 days), which may be returned to the environmental effects. Thus, there was a highly significant difference between the two seasons.

Regarding the number of days to 50% maturity, results in (Table 2) appeared that genotypes No. 7 and Misr 1(G15) were the earliest in maturity, in the first season, and across the two seasons, recording (137.33 and 137 days), and (141.17 and 141.33 days), respectively. Giza 168 was the latest one in maturity in the first season, recording an average of 149 days. Plants of genotypes No. 9 and 12 were early maturing than the others in the second season,

Table 2: Mean performance of fifteen wheat genotypes for three agronomic characters during 2013/2014 and 2014/2015 winter seasons and their combined data.

Genotypes		Number of days to heading			Number of days to maturity			Plant height (cm)		
		1st S	2nd S	Comb.	1st S	2nd S	Comb.	1st S	2nd S	Comb.
G1		74.33	95.00	84.67	137.67	146.33	142.00	103.33	93.33	98.33
G2		84.67	100.67	92.67	141.00	144.67	142.83	98.33	91.67	95.00
G3		72.00	95.33	83.67	139.00	145.00	142.00	103.33	103.33	103.33
G4		73.00	94.33	83.67	138.67	145.33	142.00	101.67	101.67	101.67
G5		88.33	103.00	95.67	146.33	145.00	145.66	103.33	96.67	100.00
G6		81.67	96.00	88.83	144.00	145.00	144.50	106.67	108.33	107.50
G7		70.67	94.67	82.67	137.33	145.00	141.17	98.33	106.67	102.50
G8		72.00	95.00	83.50	141.33	146.33	143.83	108.33	116.67	112.50
G9		86.00	100.33	93.17	146.00	144.33	145.17	108.33	101.67	105.00
G10		88.33	101.67	95.00	145.67	148.67	147.17	106.67	111.67	109.17
G11		86.67	100.33	93.50	145.00	144.67	144.83	110.00	103.33	106.67
G12		90.00	104.00	97.00	138.33	144.33	141.33	103.33	91.67	97.50
G13		84.00	100.33	92.17	149.00	144.67	146.83	101.67	103.33	102.50
G14		78.67	99.33	89.00	141.33	144.67	143.00	100.00	101.67	100.83
G15		86.67	99.00	92.83	137.00	145.67	141.33	108.33	108.33	108.33
Mean		81.13	98.60	-	141.84	145.31	-	104.11	102.67	-
LSD at (0.01)	Genotype (G)	1.60	1.34	1.02	2.11	1.52	1.26	4.57	4.76	3.22
	Season (S)	-	-	**	-	-	**	-	-	NS
	S x G	-	-	1.44	-	-	1.79	-	-	4.55

**= Significant of 0. 01 level, according to LSD (0. 01).
NS= Not significant.

recording 144.33 days whereas genotype No. 10 was the latest one in maturity in the second season and over the two seasons, recording 148.67 and 147.17 days, respectively. The considerable variability, among the assessed genotypes in heading and maturity, provides a good chance to improve the early characters of wheat crop.

Concerning plant height, Genotype No.11 had the tallest plants (110 cm) in the first season, followed by genotypes No. 8, 9 and Misr 1, recording 108.33 cm without significant differences among them. However, genotypes No. 2 and 7 had the shortest plants recording 98.33 cm. In the second season, results revealed that the tallest plants were recorded by the genotypes No. 8 (116.67 cm), No. 10 (111.67 cm) and No. 6 and Giza 168 (108.33 cm). As combined data, genotypes No. 8, 10 and Misr 1 gave the highest plant length, recording 112.50, 109.17 and 108.33 cm, respectively, while, genotypes No. 1, 2 and 12 had the shortest plants, recording 98.33, 95 and 97.50 cm. These results are in agreement with those obtained by Mohamed *et al.* (2005), Afiah *et al.* (2007), Ashmawy (2010), Abd El-Kreem and Ahmed (2013), El-Sarag and Ismaeil (2013) and who found significant differences among the tested genotypes for most studied agronomic characters. Results, shown in Table (3), appeared that the grain yield and its related characters (number of kernels/spike, number of spikes/m^2. and 1000-grain weight) were highly significantly affected by genotypes and their interaction with seasons. But, the effect of season was insignificant for the studied characters, except for the number of spikes per m^2.

Table (3) elucidates that genotype No. 2 gave the maximum number of kernels per spike (54.83 kernels) in the first season, and ranked the first over all tested genotypes, followed by genotypes No. 1, 11 and 12, recording 53.63, 54 and 53.33 kernels, respectively, without significant differences among them. In the second season, the highest number of kernels per spike was obtained by Sids 12(G14) (64 kernels), followed by genotypes No. 2, 3 and 4, recording 59, 57.50 and 57 kernels. With regard to the average over the two seasons, it is obvious that Sids 12 and genotype No. 2 produced the highest number of kernels per spike recording 57.67 and 56.92 kernels, respectively, without significant differences among them.

For the number of spikes/m^2 (Table 3), the mean of the second season (339.96 spikes) was dramatically less than its corresponding value in the first season (422.67 spikes), which may be attributed to the influence of environmental conditions. In the first season, genotypes No. 5, 11 and 12 significantly surpassed all tested genotypes, recording 526.67, 511.33 and 535.33 spikes, while genotype No. 2 had the highest average in the second season and as combined across the two seasons, recording 441.67 and 430.83 spikes, respectively.

However, the heaviest weights of 1000 grains were obtained by genotype No. 3 in the first and second seasons and the combined across the two seasons, recording 63, 55.17 and 59.08 g, respectively, followed by genotype no. 10, recording 55.80, 56.33 and 56.07g, respectively.

The results, in Table (3), farther revealed that genotypes No. 5, 11 and 12 outyielded the maximum grain yield in the first season recording 23, 24.75 and 24.72 (ardab/fad), respectively. In the second season, the highest grain yield values were obtained by genotypes No. 2, 4, 6 and Giza 168, recording 25.50, 19.83, 21.25 and 19.53 (ardab/fad), respectively. As average overall the two seasons, it is clear that genotype No. 2, 6 and 11 gave the profuse grain yield having averages being 22.25, 19.88 and 20.03 (ardab/fad), respectively. The aforementioned genotypes outyielded the average grain yield of the three check cultivars (17.80 ardab/fad) by 25, 6.07 and 12.53%, respectively, indicating their magnitude as promising genotypes that may be used in breeding programs of wheat. The current results are similar to the findings obtained by Mohamed *et al.* (2005), Afiah *et al*. (2007), Ashmawy (2010), Abd El-Kreem and Ahmed (2013), Baloch *et al.* (2013) and El-Sarag and Ismaeil (2013).

Genetic parameters:

Estimates of genotypic (GCV) and phenotypic (PhCV) coefficients of variation, broad sense heritability (h^2), and genetic advance (GA), expressed as percent of grand mean (at 5% and 10% selection intensity), are presented in Table (4). Generally, the values of (PhCV) were slightly higher than their corresponding values of (GCV) for all studied characters, which reflectal that the variations among tested genotypes were mostly returned to genetic makeup rather than to environmental effect. High estimates of genotypic (GCV) and phenotypic (PhCV) coefficients of variation were obtained by grain yield (19.26 and 21.71) and number of spikes/m^2 (18.46 and 19.82), respectively, indicating a wide pattern of genotypic variation among tested genotypes considering the previous two characters. In accordance, the selection among the tested genotypes would be successful and effective to improve these traits. Meanwhile, moderate values of (GCV and PhCV) were observed with number of kernels/spike (15.41 and 16.74) and number of days to 50% heading (11.53 and 11.57), respectively. On the other hand, the low estimates of GCV and PhCV were recorded by plant height (5.28 and 5.94) and number of days to 50% maturity (2.26 and 2.40), respectively.

It is important to emphasize that, without considering genetic advance (GA), the heritability values (h^2) would not be practically valuable in the selection depends on phenotypic appearance. Johnson *et al*. (1955) confirmed that heritability estimates, in conjunction with genetic advance would give more reliable index of selection value.

In the present investigation, the h^2 values ranged from 66.51, for weight of 1000 grains, and 99.20 for number of days to 50% heading while the values of GA % ranged between 4.41 and 35.43 at 5% and 3.77 and 30.27 at 10% selection intensity for number of days to 50% maturity and number of spikes/m^2, respectively. The high values of heritability ($h^2 \geq 75$) coupled with high values of genetic advance (%), both at 5% and 10% selection intensity ($GA \geq 25$), were recorded by number of kernels/spike, number of spikes/m^2 and grain yield. Such results indicated the importance of the additive gene effects, so, selection would be effective in early generations for these traits. Also, number of days to 50% heading recorded the highest heritability value (99.20), but a it was accompanied with moderate genetic advance value (20.21 and 16.68 at 5% and 10% selection intensity). Number of days to 50% maturity and plant height exhibited high values of broad sense heritability (h^2), but coupled with low genetic advance values. The smallest heritability value jointed with low genetic advance value was recorded by the weight of 1000 grains. From there results, it is obvious the limited scope for improvement of these traits among the tested genotypes. The current conclusions are supported by Tammam *et al* (2000), Kashif and Khaliq (2004), Ali *et al*. (2008), Balooch *et al*. (2013) who confirmed that plant breeders could safely make their selection when they took in consideration the high values of heritability and genetic advance.

Genotypic and phenotypic correlation matrix:

Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients, for all possible paired combinations of studied characters, estimated over two seasons, are given in Table (5).

Generally, there was a clear agreement between all genotypic and its related phenotypic correlation coefficients (above and below diagonal) in direction (positive or negative). But, it is obvious that the absolute values of most correlation coefficients at the genotypic level, were higher than their corresponding values at the phenotypic level, indicating that the observed associations among most characters might be attributed to the genetic effects.

Results, in Table (5), showed that the most effective relationships to wheat breeder were those between grain yield and each of number of spikes/m^2 (0.777 and 0.772**), followed by number of kernels/spike (0.603 and 0.664**) at the genotypic and phenotypic levels, respectively.

Table 4: Genetic parameters of grain yield and its related characters computed from fifteen wheat genotypes evaluated over two seasons.

Characters	Genetic parameters					
	Grand mean	G CV	Ph CV	h^2	GA (%)	
					at 0.05	at 0.10
Number of days to heading	89.87	11.53	11.57	99.20	23.65	20.21
Number of days to maturity	143.58	2.26	2.40	89.30	4.41	3.77
Plant height	103.39	5.28	5.94	79.13	9.68	8.27
Number of kernels/spike	48.29	15.41	16.74	84.75	29.23	25.00
Number of spikes/m^2	381.21	18.46	19.82	86.80	35.43	30.27
1000 Kernel weight (g)	51.76	8.42	10.32	66.51	14.15	12.09
Grain yield (ardab/fad)	18.31	19.26	21.71	78.73	35.21	30.08

Table 5: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among grain yield and its related characters computed from fifteen wheat genotypes evaluated over two seasons.

Characters	DH	DM	PH	NK/S	NS/m2	1000 GW	GY
DH	1	0.649	-0.121	0.254	-0.336	-0.454	0.087
DM	0.627**	1	0.136	0.157	-0.134	-0.468	0.054
PH	-0.100	0.132	1	-0.273	0.233	0.165	0.131
NK/S	0.236	0.173	-0.203	1	0.390	-0.404	0.603
NS/m^2	-0.307	-0.114	0.195	0.452**	1	-0.177	0.777
1000 GW	-0.305	-0.338	0.189	-0.280	-0.132	1	-0.356
GY	0.083	0.119	0.144	0.644**	0.772**	-0.210	1

Abbreviations: DH: number of days to heading, DM: number of days to maturity, PH: plant height, NK/S: no. kernels/spike, NS/m^2: no. spikes/m^2, 1000 GW: weight 1000 kernel, G Y: Grain yield.
*, ** Significant at 0.05 and 0.01 level, respectively.

The highly significant positive genotypic correlation between the aforementioned two characters and the grain yield confirmed that the breeder can obtain high yielding wheat genotypes through selection program for one or both characters, especially if they proved to be more contributors to grain yield variation, as lately shown by path analysis. However, the weight of 1000 grains showed negative and significant correlation coefficient (-0.356) with grain yield at the genotypic level, while, its corresponding association at the phenotypic level (-0.210) was insignificant. These results are in harmony with those reported by Abd El-Mohsen *et al.* (2012), Baloch *et al.* (2013), Abd El-Mohsen and Abd El-Shafi (2014). On the other hand, the grain yield attributes exhibited various trends of associations among themselves.

There was positive and highly significant genotypic and phenotypic association between number of days to 50% heading and number of days to 50% maturity (0.649** and 0.627**). The associations between the weight of 1000 grains and each of number of days to 50% heading and number of days to 50% maturity were negative and highly significant (-0.454** and -0.468**) only at the genotypic level. Such result indicated that the earlier wheat plants had heaviest weight of 1000 grains and vice versa. Using the present materials, no significant genotypic or phenotypic association was obtained between plant height and any one of the other grain yield characters, indicating its independent inheritance.

Number of kernels/spike was significantly and negatively correlated with the weight of 1000 grains (-0.404) at the genotypic level, indicating the compensatory effects between the two characters. Also, number of kernels/spike showed a highly significant and positive association with number of spikes/m^2 (0.452**) at the phenotypic level. On the other hand, the remaining correlation coefficients, among the studied traits, were negligible and insignificant. These findings are in agreement with those obtained by Tammam *et al.* (2000), Kashif and Khaliq (2004), Ali *et al.* (2008), Ashmawy *et al.* (2010), Abd El-Mohsen *et al.* (2012), Baloch *et al.* (2013), Abd El-kreem (2014), Abd El-Mohsen and Abd El-Shafi (2014), Mostafa and omar (2014) .

In fact, selection decisions, based only on correlation coefficients may not always be effective because they measure the mutual association between a pair of traits, neglecting the complicated interrelationships among all traits (Kang, 1994).Therefore, the correlation procedure may not provide a deep imagine about the importance of each component in the structure of grain yield. The path analysis can efficiently play this vital role.

Path analysis:

In the present investigation, the resultant variable was grain yield while, the remaining characters represented the casual variables. The matrix of direct and joint effects, for the six yield characters on grain yield at the genotypic and phenotypic levels, are shown in Table (6).

Table 6: The relative importance (RI %) for six predictor characters on grain yield at genotypic and phenotypic levels computed from fifteen wheat genotypes evaluated over two seasons.

Characters		RI (%)	
		Genotypic level	Phenotypic
Number of Days to heading (X$_1$)		8.54	5.18
Number of Days to maturity (X$_2$)		1.57	0.02
Plant height (X$_3$)		0.58	0.59
Number of kernels/spike (X$_4$)		3.80	6.63
Number of spikes/m^2 (X$_5$)		34.94	38.06
Weight of 1000 kernel (X$_6$)		0.12	0.10
Number of Days to heading (X$_1$) *Via*	X$_2$	4.75	0.35
	X$_3$	0.54	0.35
	X$_4$	2.89	2.77
	X$_5$	11.61	8.62
	X$_6$	0.91	0.49
Number of Days to maturity (X$_2$) *Via*	X$_3$	0.26	0.025
	X$_4$	0.77	0.11
	X$_5$	1.98	0.17
	X$_6$	0.40	0.02
Plant height (X$_3$) *Via*	X$_4$	0.81	0.80
	X$_5$	2.10	1.84
	X$_6$	0.08	0.09
Number of kernels/spike (X$_4$) *via*	X$_5$	8.98	14.36
	X$_6$	0.54	0.45
Number of spikes/m^2 (X$_5$) *via*	X$_6$	0.72	0.50
Total (direct + indirect)		86.91	81.51
Residuals		13.09	18.49
TOTAL		100	100

- The bold and underline cells indicate the direct effects.

- Abbreviations: DH: number of days to heading, DM: number of days to maturity, PH: plant height, NK/S: no. kernels/spike, NS/m^2: no. spikes/m^2, 1000 GW: weight of 1000 kernel, GY: Grain yield.

Positive direct effects were recorded for all yield characters, considering the genotypic and the phenotypic levels, except for the number of days to 50% maturity, which had negative genotypic and phenotypic path coefficients as well as the weight of 1000 grains, but only at the genotypic level.

The maximum direct effects were obtained by the number of spikes/m^2 (0.753 and 0.705), followed by the number of days to 50% heading (0.372 and 0.260) and the number of kernels/spike (0.248 and 0.294) at the genotypic and phenotypic levels, respectively. However, the three characters recorded small indirect effects on grain yield, compared to their large direct effects. Accordingly, the high positive direct effects of the three mentioned characters, on grain yield, indicated that the indirect selection through these characters would be effective for wheat improvement. On the other hand, the direct effects of the other three yield characters were very small and of low magnitude at the genotypic or phenotypic levels.

With respect to the considerable components of the indirect effects, it is noted that each of the number of days to 50% heading (-0.253 and -0.216), the number of days to 50% maturity (-0.101 and -0.080) and the weight of 1000 grains (-0.133 and -0.093) had large negative indirect effects on grain yield through their genotypic and phenotypic associations with the number of spikes/m^2, respectively. Meanwhile, a strong positive influence on grain yield was indirectly recorded by each of plant height and number of kernels/spike *via* number of spikes/m^2, whether at the genotypic (0.176 and 0.294) or phenotypic (0.137 and 0.319) levels, respectively. The other indirect effects values were less important and negligible.

The current results showed the positive relationship between number of spikes/m^2 and the number of kernels/spike, but, on the contrary, it confirmed the above mentioned conclusion about the compensatory relationships between each one of the number of spikes/m^2 and the number of kernels/spike, on one side, and the weight of 1000 grains on the other side. In the light of the previous results, it is worthy to note that the wheat breeder must be fully aware with genotypically and phenotypically inter-relationships among their studied characters to construct an effective selection program.

Table 7: Summary of cluster analysis showed the included genotypes, similarity level and cluster means of the fifteen wheat genotypes using the studied yield characters.

Cluster no.	Included genotypes	Similarity level	Cluster average						
			DH	**DM**	**PH**	**NK/S**	**NS/m2**	**1000 GW**	**GY**
1	1, 14, 4	69.66	85.78	142.33	100.28	53.88	370.70	53.30	17.97
2	6, 8, 9, 10, 11,15	59.06	91.14	144.47	108.19	45.51	390.80	52.53	18.59
3	2, 5, 12, 13	54.56	94.38	144.17	98.75	51.96	406.40	47.36	20.38
4	3, 7	65.20	83.17	141.58	102.92	40.88	317.75	55.97	13.86

- Abbreviations: DH: number of days to heading, DM: number of days to maturity, PH: plant height, NK/S: no. of kernels/spike, NS/m^2: no. of spikes/m^2, 1000 GW: weight of 1000 kernel, GY: Grain yield.

The relative importance (RI %), according to genotypic and phenotypic path analysis, was presented in Table (6). It is evident that the most grain yield variation (genotypic and phenotypic) was explained by the direct effects for number of spikes/m^2 (34.94 and 38.06), followed by the number of days to 50% heading (8.54 and 5.18) and the number of kernels/spike (3.80 and 6.63).

On the other hand, the great components of joint effects on grain yield were expressed by the number of days to 50% heading *via* the number of spikes/m^2 (11.61 and 8.62) and the number of kernels/spike also through the number of spikes/m^2 (8.98 and 14.36) at the genotypic and phenotypic levels, respectively. Trivial values of relative importance were observed for the other direct and indirect effects.

Totally, the studied six yield characters explained 86.91 and 81.51 % of grain yield variation at the genotypic and phenotypic levels, respectively. In accordance, the residual part may be attributed to unknown variation (random error), committing of errors during measuring the studied characters and/or some other traits that were not incorporated in the present investigation.

An overall view on the results of path analysis, it is revealed that the two yield components, *i.e.*, the number of spikes/m^2 and the number of kernels/spike gave the maximum influence directly and indirectly upon grain yield in wheat crop. But, the number of spikes/m^2 is more interesting to the plant breeder because it is relatively easy to visually selected in the field. In addition it is more heritable than grain yield itself. The current results are in harmony with those obtained by Ali *et al.* (2008), Ashmawy *et al.* (2010), Abd El-Mohsen *et al.* (2012), Baloch *et al.* (2013), Abd El-kreem (2014), Abd El-Mohsen and Abd El-Shafi (2014), Moustafa and omar (2014) who confirmed that the two characters were found among the main determinants of grain yield in wheat.

Cluster analysis:

The cluster analysis was used as an efficient procedure to emerge the structural relationships among tested genotypes and provides a hierarchical classification of them. In the present work, the similarity levels of the 15 wheat genotypes were estimated based on grain yield and its related characters. These genotypes were classified into four main groups (clusters) where each group contained the genotypes that showed similar phenotypic performance. The clustering pattern of these genotypes is tabulated in Table (7) and diagrammatically displayed as dendrogram graph in Figure (1).

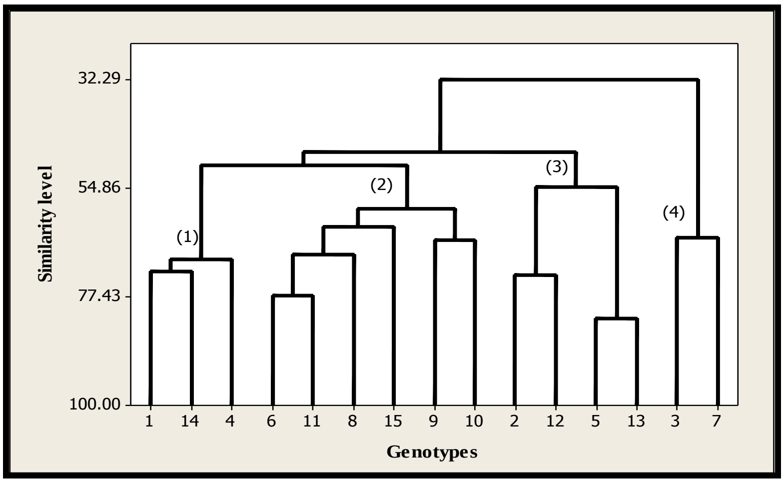

Fig. 1: Linkage dendrogram showing the similarity among fifteen wheat genotypes, based on grain yield and its related characters.

Results showed that the main clusters also divided into sub clusters except the fourth cluster which consisted of only two genotypes (G3 and G7). It is clear that the 2nd cluster included the maximum number of items (6 out of 15 genotypes) followed by the 3rd cluster (4 genotypes) and 1st cluster (3 genotypes) and finally 4th (2 genotypes).

The first cluster aggregated the genotypes that had the highest number of kernels per spike (Table 7) while the second cluster contained the genotypes that had the latest maturating and tallest plants. The third cluster consisted of the genotypes that had the shortest plants and the lightest weigh of 1000 grains but characterized by late heading and maturity and attained maximum values of number spikes/m^2 and grain yield. The fourth cluster included the genotypes that had the heaviest weight of 1000 grains but their plants were the earlier in heading and maturity and gave the minimum values of number of spikes/m^2, kernel number per spike and grain yield.

In the light of previous results that exhibited the presence of considerable genetic diversity among the tested genotypes, it gave a good chance to achieve sufficient scope for genotypic improvement of wheat through the hybridization among genotypes taken from divergent clusters (Savii and Nedelea 2012, Azam *et al*. 2013 Verma et al. 2013 and Sheykhi *et al*. 2014.

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الملخص العربى

تقدير التباين والتباعد الوراثي والارتباط في خمسة عشر تركيبا وراثيا من قمح الخبز

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أجري هذا البحث بمحطة البحوث الزراعية بالنوبارية خلال موسمي الزراعة الشتويين ٢٠١٤/٢٠١٣ و٢٠١٥/٢٠١٤ لدراسة السلوك الوراثي لخمسة عشر تركيبا وراثيا من القمح تمت زراعتها في تصميم القطاعات الكاملة العشوائية في ثلاث مكررات، وكذا تقدير التصنيفات الوراثية والمظهرية وذلك باستخدام مكونات التباين المتوقع. كما تهدف الدراسة أيضا إلى تقدير كل من الارتباط البسيط الوراثي والمظهري وكذا تحليل معامل المرور بين محصول الحبوب ومكوناته، بالإضافة إلى تحديد مدى التقارب والتباعد بين التراكيب الوراثية المختبرة باستخدام التحليل العنقودي.

وتتلخص أهم النتائج المتحصل عليها فيما يلي:

أظهرت النتائج وجود فروق معنوية بين التراكيب الوراثية المختبرة فى كلا الموسمين وكذا للتحليل المشترك لجميع الصفات تحت الدراسة حيث أعطت التراكيب الوراثية رقم ٢، ٦، ١١ أعلى قيم لمحصول الحبوب (أردب/فدان) متفوقة بذلك على متوسط أصناف المقارنة المستخدمة (جيزة ١٦٨، سدس ١٢، مصر ١) بنسب ٢٥، ٦,٠٧، ١٢,٣٥% على التوالي مما يشير إلى تفوقها وكونها من التراكيب الوراثية المبشرة التي يمكن التوسع في استخدامها خلال برامج تربية محصول القمح.

وأشارت الدراسة إلى أهمية الجمع بين نتائج درجة التوريث بمعناها الواسع وبين التحسن الوراثي المتوقع (% المتوسط) وذلك في الحكم على مدى إمكانية الانتخاب للصفات المختلفة بناء على الشكل الظاهري، حيث تبين أن أعلى قيم من درجة التوريث مصحوبة بأعلى قيم للتحسن الوراثي المتوقع قد تم الحصول عليها لصفات عدد السنابل/م^{٢}وعدد الحبوب/السنبلة وكذا محصول الحبوب مما يظهر إمكانية تحسين هذه الصفات عند الانتخاب لها على أساس الشكل الظاهري في الأجيال المبكرة.

كما أظهرت النتائج وجود علاقة ارتباط موجبة عالية المعنوية بين محصول الحبوب وكل من صفتي عدد السنابل/م^{٢} وعدد حبوب/السنبلة وذلك على المستوى الوراثي أو المظهري، كما أكدت نتائج تحليل معامل المرور أيضا أن كلا الصفتين كانتا الأكثر إسهاما في محصول الحبوب سواء عن طريق التأثير المباشر أو غير المباشر (وراثيا ومظهريا) مما يشير إلى أهمية وضع هاتين الصفتين فئ الاعتبار من قبل المربى عند وضع برامج التربية لتحسين محصول القمح.

واتضح من نتائج التحليل العنقودي أن التراكيب الوراثية المختبرة أمكن تقسيمها إلى أربع مجموعات متباينة فيما بينها وذلك تبعا للصفات تحت الدراسة حيث احتوت المجموعة الثانية على سبعة تراكيب وراثية تليها المجموعة الثالثة(أربعة) ثم الأولى (ثلاثة) فالمجموعة الرابعة أشتملت على تركيبين وراثيين فقط. ويظهر من الدراسة أن التحليل العنقودي يمكن أن يساهم بشكل كبير في برامج تحسين محصول القمح وذلك عن طريق التهجين بين التراكيب الوراثية ذات الصفات المرغوبة من مجموعات متباينة.