

## Yield Potential and Genetic Relationships of Some Doubled Haploid Lines in Wheat

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### ABSTRACT

The objectives of the present study are to determine the performance of six promising (DH) lines wheat compared the two check varieties for yield stability and analysis of genetic diversity using agronomic traits under different environmental conditions. Multivariate analysis (factor analysis and cluster analysis) were used to assess the relative importance of plant characters contributing to the grain yield. Field experiments were conducted at two locations over two seasons. Results indicated that significant variations were observed among different wheat genotypes in respect of all yield attributes. The Kafr El-Sheikh location during season 2013/14 gave superior to yield and other characters as compared to the other environments. Three DH lines yielded significantly better than the higher-yielding check variety Gemmeiza-11 over the four environments. The dendrogram generated from standardized agronomic data separated the eight wheat genotypes into three main groups, which diverged at similarity index of 0.40. The average genetic similarity among the eight wheat genotypes was 0.68, with value ranging from 0.33 to 0.90. The G7\*164-DHL29 and G168\*164-DHL2 genotypes showed a very high degree of similarity (0.90). Pooled analysis of variance and stability analysis of grain yield were highly significant for all sources studied. Wide range of stability statistics was observed among genotypes for all the stability parameters. The large variation in mean grain yield, phenotypic variance ( $\sigma_p^2$ ), coefficient of variation (C.V. %), regression coefficient ( $b_i$ ) and regression deviation ( $S^2_d$ ) indicates different responses of genotypes to environmental changes. The line G7\*164-DHL29 was the most stable for grain yield ( $\bar{X}=25.07$ ,  $b_i=1.26$  and  $S^2_d=0.45$ ). Factor analysis and cluster analysis indicated that grain filling rate and 1000-kernel weight were the most responsible attributes for grain yield and could therefore considered as selection criteria in wheat breeding programme

**Key words:** Wheat, yield stability, genetic diversity, factor analysis and cluster analysis..

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### Introduction

Wheat is one of the most important global food crops. To meet the food demands of the increasing world population, it is estimated that about 40 % increases in wheat production is required before 2020 (Borlaug and Dowsell, 1997). Grain yield stability is one of the most important goals of agriculture research, the ideal wheat genotype should be high yielding under any environmental conditions, but as genetic effects are not independent of environmental effects, most genotypes do not perform satisfactorily in all environments (Carvalho *et al.*, 1983). When interaction between genotype and environment occur, the relative ranking of cultivars for yield often differs when genotypes are compared over a series of environments and/or years.

The breeding strategies adopted during the last decades have contributed to reduce the interaction of genotypes with environments selecting genotypes with better stability across a wide range of locations and years and modern genotypes out performed the old ones in all test environments with a strong adaptability to improved fertility. Genotype  $\times$  Environment (G $\times$ E) interaction results in genotype rank changes from an environment to another, a difference in scale among environments, or a combination of these two situations (Aycicek and Yildirim, 2006). G $\times$ E interactions are of major importance, because they provide information about the effect of different environments on cultivar performance and have a key role for assessment of performance stability of the breeding materials (Moldovan *et al.*, 2000).

In a breeding program, knowledge of the degree of genetic diversity among parental materials for key selection traits will facilitate the development of high yielding under any environmental conditions. Morphological analysis is among the most used tool for the estimation of genetic distances within a group of genotypes. This poses a serious problem for selecting genotypes significantly superior in grain yield (Stafford, 1982). Various statistical techniques have been developed to identify systematic variation in individual genotypic responses. Among these, Eberhart and Russell (1966) model has been widely used in studies of adaptability and stability of plant materials (Rharrabi *et al.*, 2003). Therefore, the choice of an adequate model to measure the stability of different genotypes is a question to be resolved by researchers. According to Crossa *et al.* (1988) the

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selection of superior genotypes in a plant breeding program is based mainly on their yield potential and stable. The regression coefficient ( $b_i$ ) and the average departure from regression line ( $S^2_d$ ) are two mathematical indices for the assessment of stability (Eberhart and Russell, 1966). Finlay and Wilkinson (1963) regarded those genotypes with a  $b_i$  near 1.0 and high mean yield as being well adapted to all environments.

The relationships between grain yield and the related traits under environmental conditions evaluated using two multivariate analyses, including factor analysis and cluster analysis. Factor analysis assumed that each of the variables measured depends upon the underlying factors but is also subject to the random errors. The principal factor analysis method was followed in the extraction of the factor loadings (Tadesse and Bekele, 2001). The cluster analysis as a method for classification of varieties under a similar condition with respect to set of variables has gained increased interest in the recent years (Vural and Karasu, 2007)

The objectives of the study are (1) to determine the potential of promising bread wheat genotypes for yield stability under different environmental conditions (2) to estimate the genetic diversity using agronomic performance and (3) to discuss the interrelationships among the examined agronomic traits

## Material and methods

### *Field trials and traits evaluation*

Eight genotypes of bread wheat (*Triticum aestivum* L.) representing a wide range of diversity for several traits were selected in this study. These included the two check cultivars viz., Gemmeiza-9, Gemmeiza-11 as well as six doubled haploid (DH) lines namely; G7\*164-DHL34, G7\*115-DHL23, G168\*164-DHL2, G7\*164-DHL29, G7\*164-DHL30 and G7\*115-DHL19 were obtained from Dr. I. M. Al-Ashkar, Agronomy Dept., Fac. of Agric., Al-Azhar Univ., (2011). These lines were derived from another culture technique. They were evaluated phenotypically for stability in two locations (Kafr El-Sheikh and Cairo), over two seasons (2012 /13 and 2013 /14) to expose wheat genotypes to different environment of yield stability. The layout of the experiment was a split-plot design with three replications. The two locations were assigned to the main plots, while the eight genotypes were allocated to the sub plots. Seven agronomic traits were scored for the bread wheat genotypes. These are heading date (HD), grain filling period (GFP), grain filling rate (GFR), spike number per  $m^2$  (NS/ $m^2$ ), number of grains /spike (NG/S), 1000- kernel weight (KW) and grain yield (GY). Grain yield was determined from the central rows and converted to grain yield per ard. Spike number was determined by counting the number of grain-bearing tillers in an area of 50×50 cm and converted to number per  $m^2$ . Kernels per spike was determined in spikes of 10 random tillers which were hand threshed and number of kernels were counted and recorded as the average number of kernels per spike. Filling period was calculated by subtracting the number of heading date to from the number of maturity date. Grain filling rate was estimated as the ratio between grain yield per  $m^2$  and grain filling period (g/ day).

### *Statistical analysis*

The data were subjected to analysis of variance (Steel *et al.*, 1996) to determine the significant differences among genotypes. To determine a data matrix of pairwise similarities between genotypes, the standardized traits mean values (mean of each traits was subtracted from the data values and the result divided by the standard deviation) were used, according to Jaccard coefficient (Jaccard, 1908). All matrices based on agronomic traits were used to obtain the respective dendrograms using the algorithm UPGMA (Unweighed Pair Group Method with Arithmetic Average). The correlation coefficients between the Jaccard distance matrix based on agronomic traits and genetic distance matrix obtained were analyzed according to Mantel (Mantel, 1967) using NTSYS-pc. Yield stability, each combination of year and location was considered as one distinct environment. Genotype means for the four environments were subjected to stability index analysis, as given by Eberhart and Russell (1966). The stability analysis of variance and stability parameters: phenotypic variance ( $\sigma^2_p$ ), coefficient of variance (C.V. %), linear regression coefficient ( $b_i$ ) and deviation from regression ( $S^2_d$ ) of genotype means across environments index were computed as suggested by Eberhart and Russell (1966). For the regression analysis of variance, the residuals from the combined analysis of variance were used as a pooled error. Factor analysis, the array of commonality, the amount of the variance of a variable accounted by the common factors together, was estimated by the highest correlation coefficient in each array as suggested by Seiller and Stafford (1985). The number of factors was estimated using the principal component analysis. The varimax rotation method (an orthogonal rotation) was used in order to make each factor uniquely defined as a distinct cluster of inter-correlated variables. The factor loadings of the rotated matrix, the percentage of variability explained by each factor and the commonalities for each variable were determined.

## Results and Discussion

### Field evaluation

There was highly significant effect of location, seasons and genotypes for all agronomic traits (Table 1). The first order interactions were highly significant for all agronomic traits except heading date and 1000 kernel weight for (locations  $\times$  seasons), grain filling period and number per spikes/m<sup>2</sup> for (seasons  $\times$  genotypes). The second order interactions were insignificant for all agronomic traits except number of grains /spike and 1000 kernel weight which were highly significant. The effect of location on the relative grain yield of genotypes was of greater magnitude than the effect of season. These results indicated that the wheat genotypes under investigation were responded differently to the various environmental conditions, suggesting the importance of the assessment of genotypes under different environments in order to identify the best genetic make up for a particular environment.

The significance of variances due to genotypes, environments and their interactions was attributed to variations in different climatic and edaphic conditions at different locations, indicating the necessity of testing at multiple locations over time for accurate characterization of genotypic performance across divergent regions (Afzal Arain, *et al.*, 2001). Ülker, *et al.* (2006) reported that, the results indicated that there were significant variances due to interactions among genotypes, locations and seasons. Combined analysis of variance revealed significant differences among locations, seasons, genotype  $\times$  seasons and location  $\times$  seasons interactions (Parveen, *et al.*, 2010). Koumber, *et al.* (2011) using analysis of variance showed that all sources of variation were highly significant for grain yield and other traits mean squares.

**Table 1:** The combined analysis of variance for the effect of seasons, locations and genotypes on yield and agronomic traits of wheat.

S.O.V	HD	GFP	GFR	NS/m <sup>2</sup>	NG/S	KW	GY
Seasons (S)	**	**	ns	**	**	**	**
Location (L)	**	**	**	**	**	**	**
S $\times$ L	ns	**	**	**	**	ns	**
Genotypes (G)	**	**	**	**	**	**	**
L $\times$ G	**	**	**	**	**	**	**
S $\times$ G	**	ns	**	ns	**	**	**
S $\times$ L $\times$ G	ns	ns	ns	ns	**	**	ns

*n.s*, \*\* indicate not significant and significant at 0.01 levels of probability, respectively; HD= heading date; GFP= grain filling period; FPR =grain filling rate. NS/m<sup>2</sup>= No. of spikes/m<sup>2</sup>; NG/S=No. of grains /spike; KW=1000-kernel weight (gm); GY=grain yield (ard/ fed).

Means of the four environments (two locations and two seasons) averaged over eight bread wheat genotypes, for the agronomic traits under study are presented in (Table 2). All traits varied considerably among environments for yields and other characters at Kafr El-Sheikh 2013/14 location which being superior to the other environments. This superiority could have been due to the moderate temperatures in this season especially during the tillering and grain filling stages. This was reflected on the most agronomic traits (Table 3). The differences between locations and seasons in grain yield were mainly due number of spikes/m<sup>2</sup> and 1000- kernel weight and these are temperature, edaphic condition and consequently would be expected to give high grain yield.

**Table 2:** Environment means for the agronomic traits averaged over genotypes.

Locations	HD	GFP	GFR	NS/m <sup>2</sup>	NG/S	KW	GY
Kafr El-Sheikh 2012/13	79.29	40.33	19.35	614.79	51.59	38.15	21.07
Kafr El-Sheikh 2013/14	81.29	44.00	20.46	676.17	41.44	43.85	24.36
Cairo 2012/13	74.79	36.79	17.94	558.42	46.22	33.58	17.87
Cairo 2013/14	77.13	38.79	17.46	685.42	39.63	37.58	18.32
L.S.D. 5%	0.83	0.69	0.70	17.56	1.66	1.12	0.71
L.S.D. 1%	1.08	0.76	0.91	22.83	2.16	1.45	0.93

The mean performance of DH lines and the check varieties for the agronomic traits over four environments is presented in Table (3). Results indicated that there were highly significant differences in all agronomic traits among six DH wheat lines. Heading date ranged from 70.17 to 85.67 days in DH lines compared to the two check varieties (Gemmeiza-9 and Gemmeiza-11), which gives 90.58 and 76.33 days, respectively. Four DH line were significantly earlier in heading than the earlier check variety Gemmeiza-11. For grain filling period, all DH lines were ranged from 37.67 to 42.50 days, which significantly taller than the short period check variety (Gemmeiza-9), while three DH lines only were significantly taller than the tall period check variety (Gemmeiza-11). Regarding grain filling rate, four DH lines exhibited a significant increase in this trait than the better the check variety (Gemmeiza-9) and ranging from 19.16 to 22.21 gram/m<sup>2</sup>/day.

Number of spikes /m<sup>2</sup> ranged from 526.42 to 733.08 spikes in the DH lines compared to the better check (Gemmeiza-9), which gave 762.67 spikes. Furthermore, no DH lines had significantly superior number of spikes /m<sup>2</sup> than the best check variety Gemmeiza-9. Concerning number of grains per spike, two DH lines exhibited a significant increase in this trait than the better check variety Gemmeiza-9. Weight of 1000-kernel was significantly heavier than the better check in three DH lines ranging from 40.64 to 42.22 g compared to the better check variety Gemmeiza-11, which was 36.96 g. Regarding grain yield (arb/ fed.), the mean values of DH lines ranged from 17.22 to 25.07 (arb/ fed.) compared to the check varieties (Gemmeiza-9 and Gemmeiza-11), which gives 16.66 and 18.08 (arb/ fed.), respectively. Only three DH lines had higher grain yield than the better check variety. From these results, it can be observed that some DH lines performed well and gave high grain yield and its components comparing with the better and the check variety. In this respect, Mahmood and Baenziger (2008) and El-Hennawy, *et al.* (2011) found that similar results. Ülker, *et al.* (2006) and Koumber, *et al.* (2011) also found differences in grain yields and other traits of different wheat genotypes in response to different environmental conditions.

**Table 3:** Means of agronomic traits for eight wheat genotypes over four environments.

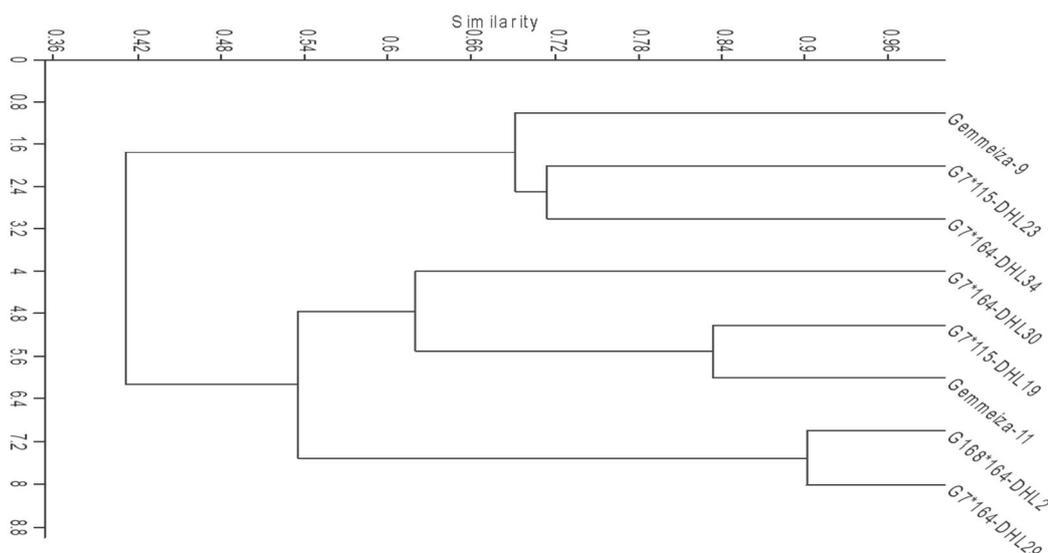
Genotypes	HD	GFP	GFR	NS/m <sup>2</sup>	NG/S	KW	GY
G7*164-DHL34	82.92	39.50	21.66	733.08	41.85	37.47	23.40
G7*115-DHL23	85.67	37.67	19.16	526.42	41.52	35.29	19.66
G168*164-DHL2	71.00	41.83	20.92	622.67	47.85	40.64	23.67
G7*164-DHL29	73.67	41.58	22.21	634.50	46.81	42.22	25.07
G7*164-DHL30	70.17	42.25	17.03	608.67	41.62	41.64	19.48
G7*115-DHL19	74.67	42.50	14.92	638.92	50.82	37.64	17.22
Gemmeiza-9	90.58	33.67	18.22	762.67	41.47	34.45	16.66
Gemmeiza-11	76.33	40.83	16.31	542.67	45.83	36.96	18.08
L.S.D. 5%	0.48	0.77	0.70	17.560	1.66	1.12	1.43
L.S.D. 1%	0.62	1.00	0.91	22.83	2.16	1.45	1.86

### Diversity analysis based on agronomic traits

Genetic diversity, relatedness and structure of parental germplasm are important for breeders to design strategy in breeding programme. Diversity analysis is important for deciphering genetic relationship including parentage and for the efficient management of germplasm and thereby, use in breeding of improved varieties. Establishing the identity of crop variety using diversity study has assumed greater importance for protecting plant breeders' and farmers' rights (Al-Doss, *et al.* 2011).

A dendrogram generated from the standardized morph-agronomic data is presented in Figure 1. The UPGMA dendrogram separated the eight wheat genotypes into three main clusters, which diverged at similarity index of 0.40. The first cluster contained two wheat lines (G7\*164-DHL29 and G168\*164-DHL2). These lines had one parent was Giza-164 and characterized as different environments adapted. The other parent for G7\*164-DHL29 was Gemmeiza-7 and characterized as high yielding cultivars. The second cluster consisted of the two wheat lines (G7\*164-DHL30 and G7\*115-DHL19) and the commercial Egyptian wheat Gemmeiza-11. The third cluster consisted of the two wheat lines (G7\*164-DHL34 and G7\*115-DHL23) and the commercial Egyptian wheat Gemmeiza-9 (Figure 1).

The average genetic similarity among the eight wheat genotypes was 0.68, with value ranging from 0.33 to 0.90. The G7\*164-DHL29 and G168\*164-DHL2 genotypes showed a very high degree of similarity (0.90) indicating that, these two genotypes had similar agronomic traits under different environments. On the other hand, G7\*164-DHL34 and G7\*164-DHL30 genotypes showed a low degree of similarity (0.33) which indicated that this pair is not closely related genotypes and had different agronomic traits under different environments. Similar results were reported by several investigators (Barakat, *et al.*, 2010 and Al-Doss, *et al.*, 2011).



**Fig. 1:** Dendrogram based on Jaccard similarity coefficient of eight wheat genotypes, generated by seven agronomic traits over two seasons at two locations.

### Yield stability

The pooled analysis of variance of grain yield indicated that there were highly significant variances due to both genotypes (G), environments (E) and genotype by environment ( $G \times E$ ) (Table 4) and revealing the presence of variability among genotypes as well as environments. The stability analysis of grain yield in wheat genotypes at four environments suggested by Eberhart and Russell (1966) showed significance for genotypes (G), environments (linear) and genotype by environment ( $G \times E$ ) linear interaction in Table (5). The significant  $G \times E$  (linear) interactions in all combined analyses indicated that the linear grain yield response of genotypes was not the same at various environments. The pooled deviations were also highly significant when tested against the pooled experimental error (Table 5). These results are in agreement with those found by several investigators (Boggini, *et al.*, 1997 and Koumber, *et al.*, 2011).

The average of grain yield, phenotypic variance ( $\sigma_p^2$ ), coefficient variation (C.V. %), regression coefficient ( $b_i$ ) and regression deviation ( $S_d^2$ ) of the eight wheat genotypes are given in (6). Results showed that for the eight genotypes over the four environments ranged from 16.66 ard/ fed. (Gemmeiza-9) to 25.07 ard/ fed. (G7\*164-DHL29) with an average of 20.40 ard/ fed. for grain yield. The values of  $\sigma_p^2$  ranged from 8.00 (G7\*164-DHL30) to 90.00 (G7\*164-DHL34) with an average of 35.08. The C.V. % ranged from 9.24 for the G168\*164-DHL2 to 22.41 for the G7\*164-DHL34 with an average of 15.52. The highest value for  $b_i$  was (G7\*164-DHL34) which gave 1.80, while the lowest genotype was (G7\*164-DHL30) which value 0.49 with an average of 1.00. The genotype G7\*164-DHL29 was the highest  $S_d^2$  (1.79) while the genotype G7\*115-DHL23 was the lowest one (0.27) with an average of 0.85. Three genotypes in mean (grain yield,  $\sigma_p^2$ , and  $S_d^2$ ) and four genotypes in C.V. % gave higher values than the mean value for these corresponding stability parameters.

The large variation in mean grain yield,  $\sigma_p^2$ , C.V. %,  $b_i$  and  $S_d^2$  indicated different responses of genotypes to environmental changes (Akcura, *et al.*, 2005). These parameters were studied separately for each genotype in groups of environments. According to the Eberhart and Russell (1966) model, a stable cultivar is one with a high mean yield, unit regression coefficient ( $b_i=1$ ) and deviation from regression as small as possible ( $S_d^2=0$ ). These results are in agreement with those found by several investigators (Kakar, *et al.*, 2003; Akcura, *et al.*, 2005; Al-Doss *et al.*, 2010). In the analysis of four environments, the genotype G7\*164-DHL29 was the most productive and stable genotype in all groups of environments, followed by G7\*164-DHL2 and G7\*164-DHL34 genotypes. The highest values of phenotypic variation across environments were recorded for lines G7\*164-DHL34, G7\*115-DHL23 and G7\*164-DHL29, although some genotypes with very close average yield had different phenotypic variances. This closer magnitude suggested that the greater role of variability is due to the environment conditions. All genotypes had lower C.V. %. Mustateal, *et al.* (2009) stated that, plotting C.V.'s against average yield proved to be the most useful tool identifying cultivars with high and stable yield.

The regression coefficient ( $b_i$ ) values of the eight genotypes used in this study exhibited no genotype with  $b_i$ -values equal to 1.00 or near unity. Three genotypes had regression coefficients above unity, while five genotypes expressed  $b_i$  values below unity. Regression values above 1.00 describe genotypes with higher sensitivity to environmental change and greater specificity of adaptability to high yielding environments. DH

lines G7\*164-DHL34, G7\*164-DHL2 and G7\*164-DHL29 had regression coefficient values of 1.80, 0.62 and 1.26, respectively, with high grain yield. Baker (1988) considered deviation from regression ( $S^2_d$ ) to be the most appropriate criterion for measuring phenotypic stability in an agronomic sense, because this parameter measures the predictability of genotypic reaction to environment; with high and desirable per se performance of a variety across environments is also a positive point to rate the variety as a better and highly stable genotype. Three genotypes, G7\*164-DHL29, G7\*164-DHL23 and G7\*164-DHL30 gave low  $S^2_d$  values which show better stability and specific adaptation to favorable environments. Four genotypes, G7\*164-DHL2, G7\*164-DHL34, Gemmeiza-9 and Gemmeiza-11 had high  $S^2_d$ , indicating less stability and indicating sensitivity to environments changes. Due to the high values of  $S^2_d$ , these genotypes are expected to give good yield under favorable environmental conditions. Deviation from regression as small as possible is the measure of genotypic stability across a set of environments (Koumber, *et al.*, 2011).

Accordingly, the line G7\*164-DHL29 ( $\bar{X}=25.07$ ,  $b_i=1.26$  and  $S^2_d=0.45$ ) was the most stable for grain yield because their regression coefficient was the highest,  $b_i$  value near unity and it had lower deviations from regression. Therefore, the G7\*164-DHL 29 would be recommended as promising variety and need further testing in the Central Region and upper of Egypt. Genotypes with a high mean yield, unit regression coefficient ( $b_i=1$ ) and deviation from regression as small as possible ( $S^2_d=0$ ) are considered stable (Finaly and Wilkinson, 1963 and Eberhart and Russell, 1966). Al-Doss, *et al.* (2010) considered that a desirable genotype with stability and above average grain yield should have a regression line with a positive intercept and slope equal to 1.00 and lower deviation from regression.

**Table 4:** Pooled analysis of variance for grain yield in eight wheat genotypes grown in four environments.

Source of variation	d.f	Mean squares	F
Genotypes (G)	7	124.21**	41.34
Environments (E)	3	214.68**	71.45
V X E	21	7.32**	2.44
Error	64	3.00	

\*\* Indicate significant at 0.01 levels of probability

**Table 5:** Stability analysis of grain yield in eight wheat genotypes grown in four environments.

Source of variation	d.f	Mean squares
Genotypes (G)	7	41.40**
Environment + (G X E)	24	11.08**
Environment (Linear)	1	214.68**
G X E (Linear)	7	5.19**
Pooled Deviation	16	2.5**
Pooled error	64	1.00

\*\* Indicate significant at 0.01 levels of probability.

**Table 6:** Mean grain yield for eight wheat genotypes under two locations and their stability statistics.

Genotypes	Location		Over all mean	Stability statistics			
	Kafr El-Sheikh	Cairo		$\sigma^2_p$	C.V. %	$b_i$	$S^2_d$
G7*164-DHL34	27.73	19.08	23.40	90.00	22.41	1.80	1.79
G7*115-DHL23	22.79	16.52	19.66	53.00	19.70	1.37	0.27
G168*164-DHL2	25.51	21.83	23.67	15.20	9.24	0.62	1.39
G7*164-DHL29	27.61	22.53	25.07	48.41	16.16	1.26	0.45
G7*164-DHL30	20.78	18.18	19.48	8.00	11.93	0.49	-0.18
G7*115-DHL19	18.97	15.46	17.22	21.00	15.90	0.81	0.61
Gemmeiza-9	18.51	14.80	16.66	23.00	15.08	0.82	1.43
Gemmeiza-11	19.81	16.35	18.08	22.00	14.75	0.82	1.02
Mean	22.71	18.09	20.40	35.08	15.64	1.00	0.85

### Multivariate analysis of yield and some agronomic traits

#### Factor analysis

The factor analysis technique divided the six traits of yield components and early traits into three independent groups or factors which explained 64.84 % of the total variability in the dependence structure. The factors were constructed by applying the principal component approach to establish the dependent relationship between grain yield attributes in wheat. Bramel, *et al.* (1984) in factors analysis most researchers emphasized on estimating the yield with including it in the other traits. While in factors analysis did not consider the grain yield (Damania and Jackson, 1986).

Based on the results, standard of (KMO) Kaiser-Meyer-Olkin is less than 0.5, which was (0.44). A summary of the composition of variables of the three extracted factors with loading are given in Table (7). This rotation accentuated the larger loadings in the extracted factors and suppressed the minor loadings thus improving the opportunity of achieving meaningful interpretation of factors. The factor which made the largest contribution accounted for 35.51% of the total variation and was composed of the some components of grain yield including grain filling period, grain filling rate, 1000- kernel weight and grain yield (Table 7). The three variables had communality with first factor would be the most effective way of increasing yield.

All variables had positive loadings in the first factor. Therefore, this factor may be called grain filling. The second factor, which accounted for 20.74 % of the total variation, the two variables were heading date and number of grain per spike. The sign of loading values indicates the direction of the relationship between the factor and its related traits. So, the negative sign of the number of grain per spike indicate to their negative correlation coefficients with heading date. This factor may be called growth. The third factor was responsible for 8.59 % of the total variability in the dependence structure. It included only one variable viz., number of spikes /m<sup>2</sup>. It contains the variable regarded as a spikes factor.

Factor analysis is suitable multivariate technique in identify and determination of independent factors that are effective on plant traits separately. Varimax rotation maximizes variance between factors since factors that accounted for higher variations between traits are more important than others. Because of that, traits effective in every factor were identified and factors also entitled based on traits having loading factor greater than 0.5. Therefore, factor analysis help breeders to genetic improvement traits such as yield that have low heritability specifically in early generations via indirect selection for traits effective in this study (Chowdhry, *et al.*, 1999; Leilah and Al-Khateeb, 2005; Beheshtizadeh, *et al.*, 2013). The indirect selection via traits grain filling period , grain filling rate, 1000- kernel weight which have higher heritability than grain yield especially in early generations and strongly associated with these traits are emphasized in this study for genetic improvement of grain yield. Several investigators had been reported similar results (Golparvar, *et al.*, 2006; Zarei, *et al.*, 2013) for breeding these important traits in bread wheat genotypes.

**Table 7:** Principal factor matrix after varimax rotation for traits of bread wheat genotypes.

Variables	Factors			Communality
	I	II	III	
DH	-0.13	<b>0.60</b>	-0.25	0.437
GFP	<b>0.74</b>	-0.62	-0.23	0.985
GFR	<b>0.74</b>	0.59	0.33	0.995
NS/m <sup>2</sup>	0.19	0.40	<b>-0.51</b>	0.434
NG/S	0.01	<b>-0.31</b>	0.25	0.163
KW	<b>0.64</b>	-0.25	-0.23	0.527
GY	<b>0.99</b>	0.20	0.15	0.997
Eigenvalue	2.49	1.45	0.60	4.54
Variability (%)	35.51	20.74	8.59	
Cumulative %	35.51	56.24	64.84	

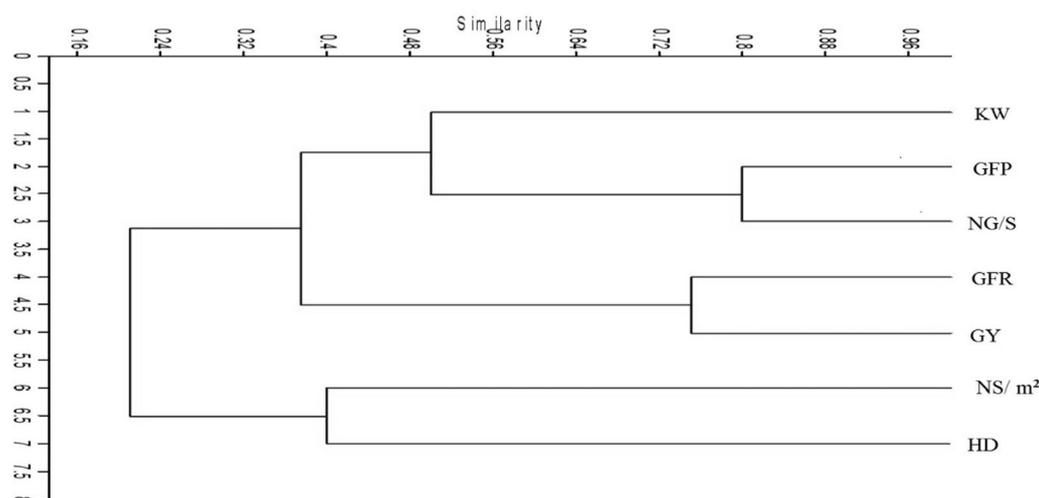
Extraction method: Principal factor analysis  
 KMO=0.44

Rotation method: varimax with Kaiser normalization

#### Cluster analysis

Cluster analysis creates groups of samples based on their distances. It seeks objects groups of the same properties which differ at the same time from the next objects group (Švec, *et al.*, 2007). Cluster analysis was chosen to express the reciprocal relations between the effects studied. A dendrogram generated from the standardized genotypes data is presented in Figure 2. The UPGMA dendrogram separated the seven agronomic

traits of wheat into three main clusters, which diverged at similarity index of 0.20. Cluster first included NS/m<sup>2</sup> and HD, while cluster second contained GY and GFR and cluster third comprised GFP, NG/S and KW. Our data reflected the tendency of each grouped variables in one cluster to express their close relationships. The GFP and NG/S traits showed a very high degree of similarity (0.80). Results showed high degree of similarity between GY and each of GFR (0.75) and KW (0.50). Cluster analysis results proved that the GFR and KW were the variables most closely related to GY. This result completely confirmed the result of factor analysis (Zarei, *et al.*, 2013).



**Fig. 2:** Dendrogram based on Jaccard similarity coefficient of seven agronomic traits, generated by ght wheat genotypes over two seasons and environments conditions.

In conclusion, it could be recommended from the previous results that, the important traits for two statistical procedures of analysis were the grain filling rate and 1000- kernel weight mainly contributed to a better grain yield in wheat under different environment conditions. The result obtained from this study could be useful for wheat breeders and grain producers in order to increase grain yield in different conditions. It should be taken into consideration that all the investigated traits are quantitative characters and are affected by environmental conditions to a great extent; therefore, the result may be changed from environment to environment (Zarei, *et al.*, 2013).

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