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# GROUPING OF SOME EGYPTIAN WHEAT GENOTYPES WITH CLUSTER ANALYSIS

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## ABSTRACT

Two field experiments were carried out during the two winter seasons of 2011/12 and 2012/13 at the Farm of Research and Production Station, National Research Centre, Al Emam Malek Village, Nubaria District, Al Behaira Governorate, Egypt. The investigation was carried out with 8 bread wheat genotypes to assess the variability of the genotypes or the genetic diversity based on agronomic parameters using cluster analysis. The results revealed that the genotypes significantly differed from each other in the studied characters. Regarding the, number of days to 50% heading cultivars Gemmeiza 10 and 7 recorded the highest values, respectively; however, the cultivar Giza 168 recorded the lowest one. The cultivar Sids 12 recorded the highest number of spikelets/spike, number of grain/spike and grain weight/spike; however, the cultivars Sakha 94, Gemmeiza 9, Giza 168 and Gemmeiza 10 recorded the lowest values, respectively. Cultivar Sids 12 recorded the highest spikes number/m<sup>2</sup>; while, Sids 1 recorded the lowest value on the other hand, cultivar Sids 1 recorded the highest seed index, while Sids 12 recorded the lowest value. The cultivar Sids 12 recorded the highest value of grain yield/ha, however, the cultivar Sids 1 recorded the lowest value. Due to Cluster analysis: the 7 studied characters were used to construct a similarity matrix using the Jaccard coefficient and used to generate, phenogram showing similarity among all the variety.

**Key Words:** Wheat- Diversity – Variation- Agronomic – Cluster analysis

## 1. INTRODUCTION

World food supply stated that world population will reach over than 8 million by 2030 that supplying food for this population requires more attention in science and agriculture. Despite remarkable progress in the past three decades, the annual consumption of food has only increased by about 20%. According to the estimates in 2030, the value of food production in developing countries should be 70% more than current production to be able to progress along with population growth and meet their needs (Asghari, 2011). Egypt, like other developing countries, suffers from food shortage problem as a result for a huge increment of population and the big loss of agricultural soils. This situation makes



the problem of food production and human nutrition more acute. To meet our present and future food production goals, high yielding and disease resistant varieties, application of balance fertilizers, improved agricultural practices and application of suitable plant protection measures must be adopted. However, maintenance of soil fertility/productivity is becoming more difficult because of intensive production of food crops, excessive tillage, and depletion of soil organic matter and increase soil salinity.

The genetic diversity between plant species is huge as observed by the large differences in many traits. However also within species substantial genetic variation is present in nature or has been generated by breeders and researchers. For a successful breeding program, the presence of genetic diversity and variability plays a vital role. Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production. The presence of genetic diversity and genetic relationships among genotypes is a prerequisite and paramount important for successful wheat breeding program. Developing hybrid wheat varieties with desirable traits require a thorough knowledge about the existing genetic variability (Maniee et al., 2009; Kahrizi et al., 2010). Germplasm improvement and genetic diversity is a key to reliable and sustainable production of the food crops. For effective evaluation and utilization of germplasm, measure of extent of available genetic diversity is of most importance (Zubair et al., 2007). The use of multivariate statistical algorithms is an important strategy for classification of germplasm and analysis of genetic relationships among breeding material (Mohammadi and Prasanna, 2003). For a successful breeding program, the presence of genetic diversity and variability play a vital role. Genetic diversity is essential to meet the diversified goals of plant breeding such as breeding for increasing yield, wider adaptation, desirable quality and pest and disease resistance. Genetic divergence analysis estimates the extent of diversity existed among selected genotypes (Mondal, 2003). Estimation of genetic distance is one of appropriate tools for parental selection in wheat hybridization programs. Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase (Islam, 2004). Some appropriate methods, like cluster analysis for genetic diversity identification, parental selection, tracing the pathway to evolution of crops, centre of origin and diversity, and study interaction between the environment are currently available (Mohammadi and Prasanna, 2003; Eivazi et al., 2007).

The use of cluster analysis algorithms is an important strategy for classifying germplasm, ordering variability for a large number of accessions, or analyzing genetic relationships among materials. The cluster analysis is an appropriate method for determining family relationships (Mellingers, 1972). This statistical analysis has several advantages (Peters et al., 1989), it allows mixing of both qualitative and quantitative data and therefore all the available information on the sample can be utilized cluster analysis had been used in widely different fields (Murphy, 1986), it can serve as a tool of selection and data reduction via similarity coefficient, similar genotypes may consider one genotype in the second test of performance provided that they have genetic diversity among them to avoid inbreeding effect. Also, it provides useful information about genetic diversity in crops. The cluster analysis was used to see whether the genotypes fell into groups or clusters analysis. Fang et al. (1996) clustered 120 genotypes of durum wheat into five groups based on maturity date, plant height, spike length, number of grain per spike, 100-grain weight and spike grain yield. Fufa et al., (2005) clustered hard red winter wheat genotypes on the basis of pedigree information, morphological characters, end-use quality traits and molecular markers to estimate genetic diversity. Seventy wheat genotypes were evaluated for variability parameter including cluster analysis for eight traits by Ali et al. (2008). Aharizad et al. (2012) applied cluster analysis using Wards algorithm and squared Euclidean distances and assigned 94 bread wheat inbred lines into three groups. The level of variation was higher for peduncle length, flag leaf area, number of spikes and grain yield. El kramany et al. (2009) reported that cluster analysis of the 40 triticale lines estimated where, 9 studied characters were used to construct a similarity matrix using the Jaccard coefficient, and used to generate phenogram showing similarity among all the genotypes. Some genotypes were most similar to each other with similarity coefficient of 1.00; this may suggest that these genotypes could be originated from a single colony. The present investigation was carried out to assess the performance of 8 wheat genotypes under sandy soils conditions.



## 2. MATERIALS AND METHODS

### Plant materials

Numerous of Egyptian wheat genotypes (Sids1, Sids 12, Sakha 93, Sakha 94, Giza 168, Gemmeiza 7, Gemmeiza 9 and Gemmeiza 10) introduced by Central Administration for Seed Production, Ministry of Agricultural and Land Reclamation were subjected to the investigation under reclaimed sandy soils

### Field experiments

Two field experiments were conducted at the farm of the National Research Center at Nubria district Al Behira Governorate, Egypt in 2011/2012 and 2012/2013 successive winter seasons to assess the performance and the variability of wheat genotypes, based on agronomic parameters using cluster analysis. The experimental soil was analyzed according to the method described by (Chapman and Pratt, 1978). Soil texture was sandy and having the following characteristics: Sand 93.7%; pH 7.8; organic matter 0.65%; CaCO<sub>3</sub> 1.30%; EC 0.50 dS/m; total N 8.1 ppm, P 3.60 ppm and K 23.5 ppm, varieties were arranged in randomized complete block design with four replicates where the plot area was 10.5 m<sup>2</sup>, wheat grains were sown in mid November in both seasons. The experiment was fertilized with ammonium nitrate (33.5 %) at the rate of 135 kg N/ha, the dose of N was applied in 10% was added before sowing as activation dose, 50% in the tillering stage and 40 % before heading stage. Calcium superphosphate was added during the preparation of grain bed at the rate of 35 kg P<sub>2</sub>O<sub>5</sub>/ha. Sprinkler irrigation was applied as plants needed. Normal cultural practices of growing wheat conducted in the usual manner followed by the farmers of this district.

### Evaluation parameters

Number of days to 50% heading was determined by count of spikes/plants and compared to the total plants of the two central rows in each plot. At harvest stage, ten plants from the two central rows were harvested and the following characters: Number of spikelets/spike, number of grain/spike, grain weight/spike (g), number of spikes/m<sup>2</sup>, seed index and grain yield (kg/ha).

### Statistical analysis

Data collected for yield and yield attributes were subjected to the statistical analysis according to (Snedecor, 1982) and all means were compared at 5% level of probability. The cluster analysis was performed using the Program SAS v.9.1.3 (SAS Institute Inc., 2002). That adopts Euclidian distance as a measure of dissimilarity and the Ward's method as the clustering algorithm (Ward, 1963): Before computing the distance between varieties, our data were standardized as recommended by (Fox et al.,1982)

## 3. RESULTS AND DISCUSSIONS:

**Table 1.** Analysis of variance of agronomic characters of 8 wheat varieties (combined analysis).

variety	No. Days to 50% heading	Number of spikelets/spike	Number of grain/spike	Grain weight/spike, g	Number of spikes/m <sup>2</sup>	Seed index	Grain yield, Kg/ha
Sids1	83.07 d	20.01 c	59.72 b	2.99 b	327.66 e	51.70 a	5317.80 f
Sids12	83.46 d	23.66 a	67.75 a	3.15 a	445.33 a	47.85 e	6554.09 a



Sakha93	85.16 c	18.94 cd	55.01 d	2.88 c	419.00 ab	50.20 c	6017.10 c
Sakha94	84.26 cd	17.76 d	55.62 cd	2.73 d	428.33 a	50.53 bc	6182.84 b
Giza168	83.00 d	20.30 bc	54.94 d	2.65 e	412.66 b	49.78 d	6084.74 c
Gemmeiza7	92.70 a	19.31 c	60.61 b	2.93 c	362.66 c	49.81 d	5592.30 e
Gemmeiza9	89.59 b	19.53 c	53.38 e	2.72 d	409.66 b	50.64 b	5945.10 d
Gemmeiza10	91.48 a	21.66 b	56.68 c	2.65 e	413.00 b	48.16 e	6114.15 b

Data presented in Table (1) revealed that wheat varieties significantly differed for all studied characters. There were wide variations among all varieties for all studied characters.

#### **Number of days from sowing to 50% heading:**

Data showed in Table (1) revealed that significant differences among wheat genotypes were observed at 5% probability level, where the cultivar Giza168 was the earliest one it takes 83 days from sowing to 50% heading with no significant differences between this variety and Sids 1 and Sids 12, while the cultivars Gemmeiza7 and Gemmeiza10 were the tallest period from sowing to 50% heading where they take about 92.70 and 91.48 days from sowing to 50% heading, respectively and found wide variations between test varieties.

#### **Number of spikelets/spike:**

Data presented in Table (1) showed that the cultivar Sids12 produced the highest number of spikelets/spike (23.66), followed by cultivar Gemmeiza 10 (21.66) while, the cultivar Sakha94 produced the lowest one (17.76), which represents about 75% of the highest value of the trait; with no significant differences between this cultivar and Sakha 93 (18.94), respectively, this reflects a wide diversity among the genotypes in that trait.

#### **Number of grain/spike:**

Data presented in Table (1) illustrate that the cultivar Sids12 produced the highest number of grain/spike (67.75), followed by the cultivar Gemmeiza 7 (60.61) and Sids1 (59.72), while, the cultivars Gemmeiza9 and Giza 168 produced the lowest values where they record (53.38) and (54.94), respectively. Number of grain/spike recorded by cultivar Gemmeiza9 represents about 79% of the highest value of the trait, this reflects a wide diversity among the variety in that trait.

#### **Grain weight/spike:**

A significant differences among the tested variety were detected in Table (1) where the cultivar Sids12 produced the highest grain weight/spike (3.15 g), followed by cultivar Sids 1 (2.99), while, the cultivars Giza168 and Gemmeiza10 produced the lowest one, (2.65 and 2.65g) respectively, the lowest grain weight/spike represented about 84% of the highest grain weight/spike (3.15 g) this demonstrated the wide diversity among the tested variety.

#### **Number of spikes/m<sup>2</sup>:**

Data presented in Table (1) showed that the cultivar Sids 12 produced the highest number of spikes/m<sup>2</sup> (445.33), followed by Sakha 94 (428.33) and Sakha 93 (419.00) with no significant differences between them, while, the cultivar Sids1 the lowest one (327.66), which represents about 73% of the highest value of the trait (445.33), this reflects a wide diversity among the variety in that trait.



### Seed index:

Table (1) showed significant differences among varieties where, the cultivar Sids1 recorded the highest seed index (51.70 g), followed by Gemmeiza 9 (50.64 g) and Sakha 94 (50.53 g), respectively. However, the cultivar Sids12 which produced the lowest seed index (47.85g), and it represents about 92% of the highest value.

### Grain yield/ha

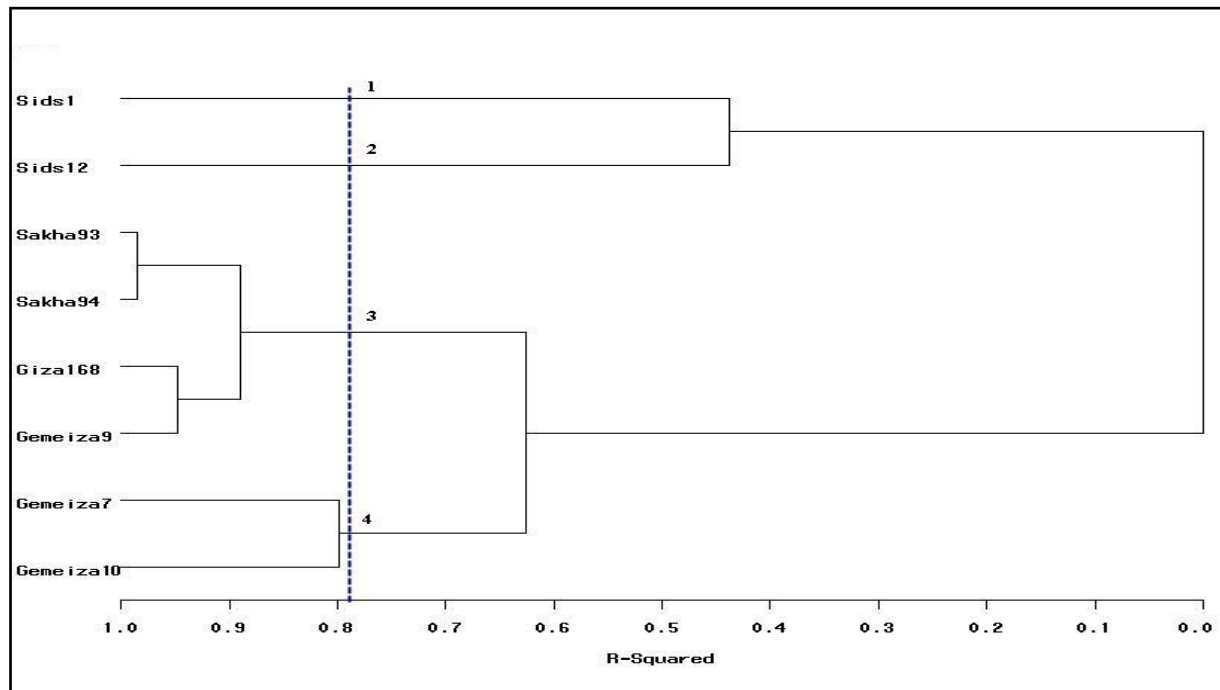
Data presented in Table (1) illustrate the tested varieties significantly differed from each other, where the cultivar Sids 12 records the highest grain yield/ha (6554.09 kg/ha), followed by Sakha 94 (6182.84 kg/ha) and Gemmeiza 10 (6114.15 kg/ha), respectively with no significant differences between them. While, the cultivars Sids1 and Gemmeiza 7 produced the lowest values of grain yield/ha (5317 and 5592.30 kg/ha, respectively), the lowest grain yield represented about 81% of the highest grain yield; this demonstrated the wide diversity among the tested variety. The increment in grain yield of Sids 12 may be resultant from the increment in number of spikelets/spike, number of grain/spike, grain weight/spike and number of spikes/m<sup>2</sup>

### Cluster analysis:

The average of all the studied characters of the two seasons was used to construct a distance Matrix using the Euclidian coefficient, Table (2) and used to generate the dendrogram show similarity among all variety (Ward 1963) figure 1. In this investigation to cluster studied genotypes we used cluster analysis based on standardized data and WARD method. In a breeding program, the more parents are genetically far from each other, their offspring will be more aggressive, the main objective of cluster analysis is to determine the extent of genetic affinity or distance of genotypes from each other so the researcher could get an ideal genotype by accident rather append energy and time to a host of hybridization, he first cluster studied genotypes based on cluster analysis and then selects limited blocks of hybrid by choosing a hybrid of the best from far cluster considering desirable traits. So by hybrid between genotypes which have been chosen from far cluster, the possibility of getting favorable results increases. On the basis of results obtained from the present study high degree of genetic divergence was observed. It is evident as more number of cluster (three) formed by the 8 wheat genotypes and high rang of values of inter and intra cluster distance. The more diversity of parents, the greater chance of obtaining high heterosis (Zaman et al., 2005). Amongst three clusters formed (Figure 1), cluster II was largest number of genotypes (4 genotypes, Sakha 93, Sakha 94, Giza 168 and Gemmeiza 9) and cluster I (Sids 1 and Sids 12) with a characteristics feature of lowest number of days to 50% to heading, high number of spikelets/spike, number of grains/spike, weight of grain/spike and number of spikes/m<sup>2</sup> and cluster III (Gemmeiza 7 and Gemmeiza 10) were smallest with two genotypes only. The maximum inter cluster distance was observed between cluster I and cluster III, which exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization program. All the 8 bread wheat genotypes were divided into three clusters by non-hierarchical Euclidian cluster analysis (Figure 1). Maximum number of genotypes (4) grouped in cluster 2 and minimum (2) genotypes in each of cluster 1 and 3 (Table 1). The relative association among the different genotypes is presented in the form of Wards Minimum Variance Dendrogram which was prepared using the rescaled distance. The resemblance coefficient between two genotypes is the value at which their branches join. The dendrogram elaborate the relative magnitude of resemblance among the genotypes as well as the clusters. Similar type of result was also found by Garg and Gautam (1997) in their experiment. The result showed that geographical and genetic diversity exhibited no correspondence between them as genotypes from one and different geographic reason are grouped together, which might be due to free exchange of genetic material from different regions. Sharma et al. (2002) and Sharma et al. (2008) have also revealed that the pattern of distribution of genotypes within various clusters was random and independent of geographical isolation. So there is no association between the geographical distribution and genetic diversity.



Figure 1. Dendrogram showing cluster analysis (Ward method) of 8 wheat varieties.



The average of all the studied characters of the two seasons in (Table 1) was used to construct a distance matrix using the Euclidian coefficient (Table 2) and the data from the distance matrix was used to generate the dendrogram showing dissimilarity among all the varieties (Ward, 1963), figure 1. The varieties Sakha 93 and Sakha 94 were the most similar to each other with distance coefficient of 1.19, this may suggest that these varieties could be originated from a single source. On contrast, the varieties Sids 12 and Sakha 94 were the most dissimilar varieties with dissimilarity coefficient of 5.88.

Table 2. Distance matrix based on Euclidian coefficient for the 8 wheat varieties. using data from the two seasons.

	Sids1	Sids12	Sakha93	Sakha94	Giza168	Gemeiza7	Gemeiza9	Gemeiza10
Sids1	0.00							
Sids12	4.29	0.00						
Sakha93	4.37	5.25	0.00					
Sakha94	4.52	5.88	1.19	0.00				
Giza168	3.98	4.96	2.01	1.89	0.00			
Gemeiza7	3.23	4.18	3.36	3.68	3.51	0.00		
Gemeiza9	3.88	5.50	2.08	2.10	1.92	2.55	0.00	
Gemeiza10	5.10	4.73	3.22	3.52	2.60	3.00	2.47	0.00



#### 4. Conclusion

There is significant genetic variability among the tested wheat genotypes that indicates the presence of excellent opportunities to bring about improvement through wide hybridization by crossing genotypes with high genetic distance. The information obtained from this study can be used to plan crosses and maximized the use of genetic diversity and expression of heterosis

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