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Genetic Variability, Principle Components and Cluster Analysis of Twenty-eight Egyptian Wheat Genotypes

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ABSTRACT

Wheat is Egypt's main cereal crop and the foundation of its food security. During two consecutive seasons (2018/2019 and 2019/2020), twenty-eight wheat landraces were cultivated on the farm of Bahteem Research Station, Giza, Egypt, to evaluate their genetic variability and to determine genetic relationships among these evaluated genotypes using cluster analysis and principal components analysis. Across the two seasons, the genotypes investigated differed significantly ($P \leq 0.0.01$) for all agronomic characteristics and high assessments of the broad sense heritability were noted for all traits. The data were classified into three major components using principal components analysis. The eigenvalues of the first two were greater than one. These three major components described 76.21% of the total variability in wheat genotypes, while the other five components described only 23.79% of the variation. The cluster analysis divided all genotypes into six groups. The first cluster had three genotypes, accounting for 10.71% of all genotypes. Six genotypes, accounting for 21.43% of all genotypes, were categorized as belonging to the second cluster. The third cluster was also assigned six genotypes, accounting for 21.43 percent of all genotypes. Only one genotype (G5), accounting for 3.57 percent of all genotypes, was identified as belonging to the fourth cluster. Seven genotypes were found in the fifth cluster whereas five genotypes were found in the sixth cluster. Clusters II and IV had the greatest distance between them, followed by Clusters III and IV. Crossing between these clusters may lead to more efficient and superior recombinant wheat improvement programs.

KEYWORDS: Cluster Analysis, Principal Component Analysis, Wheat

1. INTRODUCTION

Wheat is the most important cereal crop because of its domestication and significance as the world's primary staple food crop (Iqbal *et al*., 2021). Wheat is grown in forty-four countries throughout the world (Kumar *et al*., 2017). Wheat grains are consumed by humans, while straw is consumed by animals. Wheat currently controls the majority of arable land (38.8%) and has a greater grain protein content (12-15%) than other cereals, providing 20% of the world's calories (Shiferaw *et al*., 2013) but its productivity is still low (Loke *et al*., 2016).

Wheat (*Triticum aestivum* L.) is Egypt's most significant crop. Egypt is the world's biggest importer of wheat and consumes a considerable amount of bread. The difference between wheat productivity and consumption in Egypt is caused by a lack of farmed area and the availability of only one source of irrigation water, the Nile River (Abdelmageed *et al*., 2019). Egypt's national goal is to improve wheat productivity to close the gap between wheat consumption and production. According to Mujeeb *et al*., (2008), wheat contributes 40% of the protein and 37% of the calories in the Egyptian diet. There is an urgent need to bridge the gap between production and consumption by expanding in reclaimed regions, which represent the most promising fields for improving agricultural output and, as a result, alleviating food shortages and raising vertical output by producing new high-yielding cultivars (Abdellatif *et al*., 2012).

Genetic variability studies are critical for plant breeding because they provide information on breeders that allow for a high heterotic effect and higher segregation in recombinants when crossed, increasing the likelihood of superior genotypes appearing in progenies (Silva *et al*., 2008). The genetic variety accessible to breeders for producing genotypes highly adapted to different ecosystems and production methods is critical to the success of a breeding program (Hoisington *et al*., 1999). It is vital to investigate the relationships between genotype variation and yield components to make the best use of wheat genetic resources in breeding program initiatives. High-yielding genotypes are selected in proportion to the degree of genetic variation existing and the number of inherited characters (Scarano *et al*., 2014). The degree of genetic control related to some heritable significant features is referred to as heritability (Ayele, 2011). It displays how much of the genetic variation has a genetic basis and is useful for the selection method (Buratto *et al*., 2007).

Several authors have suggested the use of cluster and principal component analyses to study the genetic diversity and relationships of wheat genotypes (Adilova *et al*., 2020; Fouad, 2020; Khodadadi *et al*., 2011). Cluster analysis and principal component analysis (PCA) are two major genetic diversity analysis methods that differ in some ways. The benefit of cluster analysis is that cultivars or samples are grouped based on complex traits instead of single characteristics (Brown-Guedira *et al*., 2000). Principal component analysis can reduce a large number of potentially correlated variables to a smaller number of variables known as principal components (Mujaju and Chakauya, 2008). The main purposes of this investigation were to evaluate the genetic variability, and heritability of 28 Egyptian genotypes of wheat, and to use cluster analysis and principal components analysis to determine genetic relationships among evaluated genotypes.

2. MATERIALS AND METHODS

2.1. Plant Materials

In this study, twenty-eight Egyptian landraces collected from various agro-climatic regions and market centers in Egypt, as well as two check varieties (Giza 168 and Giza 171) were used (Table 1).

2.2. Field experiments and studied traits

The field experiment was conducted at the experimental farm of Bahteem Research Station, Genetic resources research department, field crop research institute, Agricultural Research Center, Giza, Egypt (30° 28″ N, 31°

Table 1. Origin and obtained location of the studied 28 wheat landraces.

NO	ORIGIN	LOCATION
G1	Aneba village, by wadi kharit	Aswan
G2	35km N of Idfu by Elsabaya village	Qena
G3	5km S of Kom Ombo on the main road to Aswan	Aswan
G4	18km S of Armant	Qena
G5	Beni Rafi	Assuit
G6	14Km E ofNag Hammadi	Qena
G7	Tamyia	Fayoum
G8	13Km W of ElMinya, Naura, near Grandir	Fayoum
G9	El Balyana	Sohag
G10	Girge	Sohag
G11	Tahta	Sohag
G12	9Km S of Sidfa	Sohag
G13	14Km W of Assiut	Assiut
G14	12Km W of El- Minia	Minia
G15	11 Km S of Ihnasya El Madina	Beni Suef
G16	3Km of El- Fayoum	Fayoum
G17	5Km E of Zagazig	Sharkia
G18	5Km W of MitGhamr	Dakahlia
G19	5Km E of Tanta	Gharbiya
G20	Assafena, Tukh center	Qalubiya
G21	Hurein	Minufiya
G22	Kafr Alim	Minufiya
G23	Amyut, 2Km N of Putur	Gharbiya
G24	Semile , 3/4Km of Sibirba	Gharbiya
G25	Biyala	Kafr El Sheikh
G26	5Km NW of Ibshan	Kafr El Sheikh
G27	Mil/buc//seri cm934046-8m-0y-0m-2y-0B	Giza168
G28	Sakha93/gemmiza9 s.6-1gz-4gz-1gz-2gz-0s	Giza171

11″ E),). Twenty-eight wheat landraces were sown during two consecutive seasons (2018/19 and 2019/20) to evaluate the genetic variability, heritability, genetic advance, and correlation between chosen agronomic traits of 28 Egyptian landraces of wheat. A randomized complete block design (RCBD) was used in the experiment, with three replications for each landrace.

For each plot, 10 plants were randomly selected/tagged from two central rows to estimate the following traits: (1) days to heading (DH), (2) days to anthesis (DA), (3) days to maturity (DM), (4) plant height (PH, cm), (5) number of Spikes/ m², (6) number of grains/spike, (7) thousand-grain weight (1000 KWT, g), and (8) grain yield (Ton/faddan) (GY).

2.3. Statistical analysis

2.3.1. Variance analysis

The studied traits were analyzed using ANOVA for the randomized complete block design (RCBD). To identify significant differences among the genotypes, the Least Significant Difference (LSD) test for means was used.

2.3.2. The phenotypic variation coefficient (PCV) and genotypic variation coefficient (GCV)

The phenotypic and genotypic coefficients of variation were estimated using the method provided by (Singh, and Chaudhary, 1979):

$PCV\ (\%) = (\sigma p / \bar{x}) \times 100$

$GCV\ (\%) = (\sigma g / \bar{x}) \times 100$

where σp denotes the phenotypic standard deviation, σg stands for the genotypic standard deviation, and $\bar{x}$ stands for the trait's grand mean.

2.3.3. Heritability

According to (Falconer and Mackay, 1981), it was calculated as the ratio of total genotypic variance to phenotypic variance:

$H^2 = GV/PV$

where H^2 refers to heritability in a broad sense, GV refers to the genetic variance and the total phenotypic variance is denoted by PV.

2.4. Clustering and principal components analysis (PCA)

NTSYS-pc software (version 2.1) was used to perform clustering and PCA to examine the associations between wheat landraces depending on data from agronomic characteristics (Rohlf, 1997). The data was evaluated using the Euclidian distance method and the dissimilarity coefficient. The genetic connections between wheat landraces were determined using the unweighted pair-group technique of arithmetic (UPGMA) average and SAHN clustering. The EIGEN module of the NTSYS-pc software was used to estimate principal component analysis (PCA). To display the wheat by trait two-way data in a biplot, the GT biplot method (Yan *et al*., 2001) was used. Yan and Rajcan, (2002) have detailed these statistical methods. The Gen-Stat package (Payne, 2009) was used to create all of the biplots in this study.

3. RESULTS AND DISCUSSIONS

3.1. Agronomic traits and genetic variability

The results showed that the genotypes studied differed significantly ($P \leq 0.01$) for all agronomic characteristics across the two seasons (Table 2). Days to heading, days to anthesis, days to maturity, plant height, number of spikes/m^2, no. of grains/spike, 1000 grain weight and grain yield in the first season ranged from 81.8 (G24) to 100.47 days (G7), 85.8 to 105.67 days (G13), 135.57 (G12) to 153.13 days (G7), 103 (G4) to 119.1 cm (G15), 330.1 (G18) to 451.4 (G5), 40.97 (G20) to 56.8 (G14), 42.25 (G4) to 58.97 g (G23) and 2.16 (G10) to 3.24 tons/faddan (G27), respectively, indicating that these traits are highly variable (Fig. 1A).

Table 2. Mean squares, heritability in the broad sense (H^2%), genotypic (GCV%) and phenotypic (PCV%) coefficients of variation of the studied traits in the first 2018/19 and second 2019/20 seasons.

Season	First season 2018/19							
Source of variation	**Replication**	**Genotypes**	**Error**	**Mean**	**LSD**	**H^2**	**GCV%**	**PCV%**
d.f.	2	27	54					
DH	176.48	80.87**	0.56	91.25	1.23	99.31	9.82	9.85
DA	266.52	90.22**	1.72	95.09	2.15	98.09	10.01	10.10
DM	237.31	45.03**	1.04	143.68	1.67	97.69	4.62	4.67
PH	113.72	64.23**	2.71	111.77	2.69	95.78	7.02	7.17
No. Spike/ m²	799.60	2874.20**	491.60	378.17	36.30	82.90	12.91	14.18
No. grains/ spike	157.28	62.75**	4.87	46.40	3.61	92.24	16.40	17.07
1000-KWT	83.95	53.56**	2.10	48.94	2.37	96.08	14.66	14.95
GY (Tons/faddan)	0.04	0.24**	0.01	2.79	0.19	94.24	17.05	17.57
			Second season 2019/20					
DH	217.9376	71.9562**	0.2026	88.47	0.74	99.72	9.58	9.59
DA	243.088	71.0635**	0.2022	92.22	0.74	99.72	9.13	9.14
DM	72.903	40.69**	4.441	140.44	3.45	89.09	4.29	4.54
PH	89.853	54.132**	3.353	109.58	3.00	93.81	6.50	6.71
No. Spike/ m²	1595.6	1662.5**	467.5	356.84	35.39	71.88	9.69	11.43
No. grains/ spike	102.922	47.82**	1.815	43.48	2.21	96.20	15.60	15.90
1000-KWT	33.678	26.535**	6.015	45.12	4.02	77.33	10.04	11.42
GY (Tons/faddan)	0.60561	0.26029**	0.01037	2.69	0.17	96.02	18.59	18.98

**: *significance at 0.01 level*

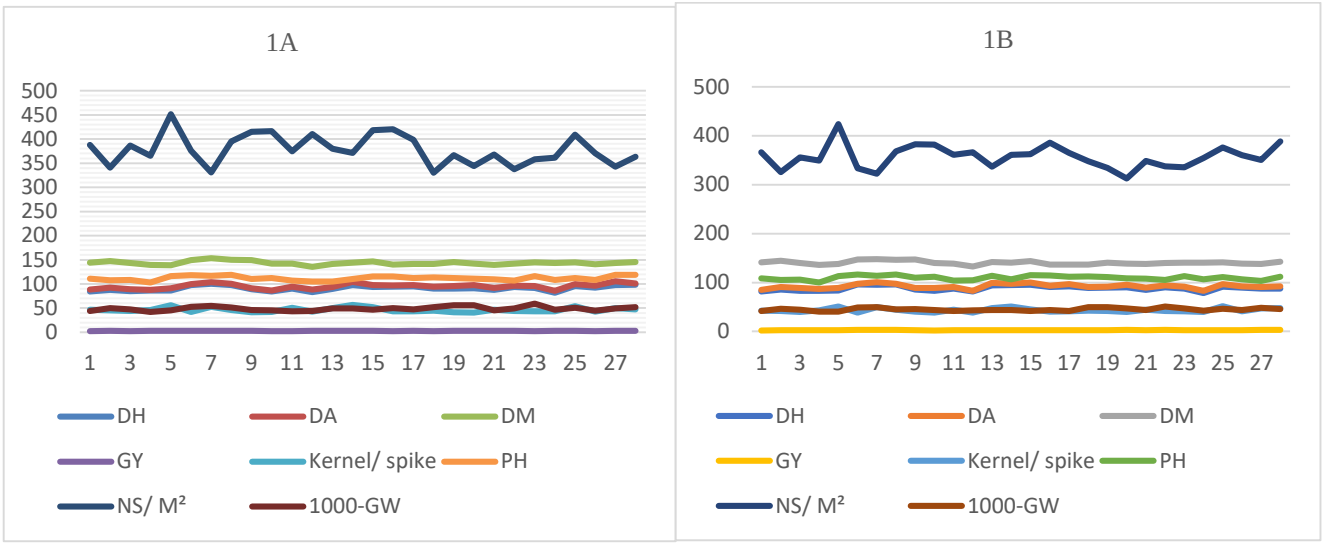

Fig. 1 The eight agronomic traits of the wheat genotypes across the first season (1A) and the second season (1B)

Whereas in the second season, the days to heading, days to anthesis, days to maturity, plant height, number of spikes/m2, no. of grains/spike, 1000 grain weight and grain yield traits ranged from 78.7 (G24) to 96.2 days (G6), 82.8 (G12) to 100.73 days (G7), 132.6 (G12) to 147.57 days (G7), 100.3 (G4) to 116.6 cm (G8), 312.67 (G20) to 423.43 (G5), 38.33 (G6) to 51.43 (G25), 40.28 (G4) to 50.78 g (G22) and 1.99 (G1) to 3.18 tons/faddan (G27), respectively (Fig. 1B).

In the first season, high assessments of heritability in the broad sense were noted for all traits, ranging from 82.90 % for the number of spikes/m2 to 99.31% for the days to heading. In the second season, all traits also had high heritability values ranging from 71.88 % for the number of spikes/ m 2 to 99.72 for the days to heading and days to anthesis traits. The majority of traits had high estimates of genotypic (GCV%) and phenotypic (PCV%) variation coefficients except for days to maturity, which had low estimates in both seasons. The lower GCV values compared to PCV values for all studied traits indicated that the environment had little impact on plant development.In our results, genotypic variations were found for all traits across the year and replication which were consistent with the findings of (Naif and Abdelghany, 2022). Singh, *et al*., (2017) also showed that the genotype's mean squares were significant for all attributes. Basic statistics for all the studied traits showed high heritability for all traits in both seasons. Results from summary statistics show that there was a wide range of diversity among genotypes based on estimated traits. Such a high variability plays a vital role in the breeding program to meet desired objectives of breeding such as breeding for high yield and high quality and will provide the chance for the development of cultivars with desirable properties.

3.2. Principal components analysis (PCA)

The principal components analysis classified the total variation into eight components. Three principal components were the major. The first two of them had eigenvalues greater than one. These three major components explained approximately 76.21% of the total variability whereas the other five components explained only 23.79% of the variation in wheat genotypes (Table 3). The first principal component had an eigenvalue of 3.60 and explained 44.99% of the variation. PC2 and PC3 attributed 18.77% and 12.44% of the variation, respectively, with eigenvalues of 1.5 and 0.99 (Table 3). All of the principal components explained 100% (as a cumulative percentage) of the overall variation. Traits with the highest absolute factor loading value close to one contribute more to PC variability than

Table 3. Eigenvalues, the proportion of variance, and cumulative values for investigated wheat characteristics.

Value	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8
Eigenvalue	3.600	1.502	0.995	0.780	0.561	0.375	0.172	0.015
% of Var.	44.996	18.774	12.441	9.752	7.010	4.692	2.153	0.182
Cum. %	44.996	63.770	76.211	85.963	92.973	97.665	99.818	100.000

characteristics with the lowest absolute factor loading value near zero. The first component had the highest factor loading for days to anthesis (0.484) and days to heading (0.482) (Table 4). Correspondingly, in PC2, the most important characteristics were the number of spikes per square meter (0.633) and the number of grains per spike (0.546) (Table 4). The characteristics that contributed the greatest to PC3 variability were grain yield (tons/faddan) (0.594), plant height (-0.533), and the number of grains per spike (0.499) (Table 4).

The associations among the various factors and genotypes and their respective principal components are further described by principal component biplots, as shown in Fig. 3. Smaller angles between vectors pointing in the same direction indicate a higher correlation in principal component analysis. Genotypes with a greater value of a specific trait were arranged nearer to the vector line and further in the direction of that specific vector, frequently on the convex hull vertices (Fig. 3). Traits with narrower acute angles were more strongly associated, whereas characteristics with obtuse angles were inversely correlated. The leading positive relationship was among grain yield and hundred-grain weight and days to maturity, whereas was negatively associated with the number of spikes per meter square.

Genotypes such as 6, 7, 18, 19, 20, 22, and 23 ex celled in yield, owing primarily to high 1000 grai n weight and grain yield (tons/faddan) (Fig. 3). Genotypes such as G5, G9, G10, and G11 was associated with only one trait (number of spikes per square meter) and their performance were negatively in terms of grain yield and hundred-kernel weight traits.

Table 4. The first 3 principal components (PCs) analysis for 8 characters of 28 bread wheat genotypes.

Factor loading			
Trait	**PC1**	**PC2**	**PC3**
DH	0.482	0.129	0.042
DA	0.484	0.141	0.077
DM	0.366	-0.024	-0.270
PH	0.361	0.272	-0.533
No. Spike/ m²	-0.193	0.633	-0.166
No. grains/ spike	0.168	0.546	0.499
1000-KWT	0.376	-0.416	-0.079
GY (Tons/Faddan)	0.248	-0.132	0.594

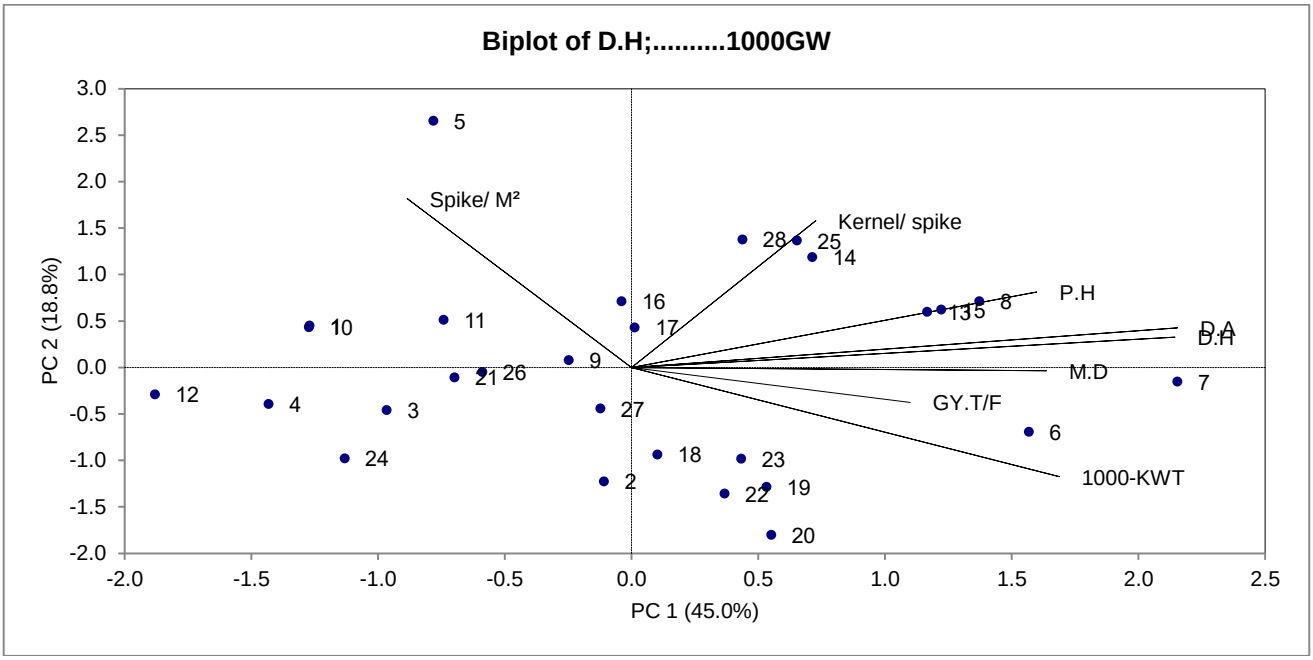

Fig. 3. PCA Biplot for the morphological traits with numbers indicating genotypes.

The principal component analysis was used to analyze the average data. It is a useful multivariate technique for identifying and determining independent principal components that have separate effects on plant characteristics. As a result, principal component analysis assists breeders in genetically improving traits with low heritability like yield, particularly in the early generations, through indirect selection for characteristics effective on this (Golparvar *et al*., 2006). The importance of the largest contributor to total variation along each axis of differentiation is reflected in the principal component analysis. The resulting eigenvalues are frequently used to decide how many factors to keep. Typically, the sum of the eigenvalues equals the variable's number (Khodadadi *et al*., 2011). The first three principal components of our study showed that landraces were dispersed across all four quarters, indicating a high level of genetic diversity in the genotypes tested which agrees with the findings of (Fouad, 2020). These landraces had a high level of diversity, which was beneficial in breeding programs (Qaseem *et al*., 2017). The first two components (PC1 and PC2) had eigenvalues greater than one, inferring that the assessed principal component weight values were reliable (Mohammadi and Prasanna, 2003) and that they were more informative than the original variable. Our findings showed that G6, G7, G18, G19, G20, G22, and G23 performed the best in terms of grain yield and hundred kernel weight agreeing with the findings of (Qaseem *et al*., 2017).

3.3. Cluster Analysis

The Cluster analysis was utilized to classify the 28 landraces into different classes. The cluster analysis for studied traits revealed diversity between wheat genotypes. The twenty-eight genotypes are divided into six groups. The first cluster contained three genotypes, accounting for 10.71% of all genotypes (Table 4). Six genotypes were classified as belonging to the second cluster, accounting for 21.43 percent of all genotypes (Table 4). Six genotypes were also assigned to the third cluster, accounting for 21.43 percent of all genotypes. Only one genotype (G5) was classified as belonging to the fourth cluster, accounting for 3.57 percent of all genotypes. The fifth cluster contained seven genotypes, accounting for 25% of all genotypes. The sixth cluster contained five genotypes, accounting for 17.86% of all genotypes (Table 4). The cluster analysis was represented graphically in a dendrogram, indicating their similarity (Fig. 5).

Table 4. Distribution of 28 bread wheat genotypes into observed clusters based on D^2 analysis

Cluster no.	No. of genotypes	Percentage (%)	Genotypes no.
1	3	10.71	1, 3 and 12
2	6	21.43	8, 17, 25, 9, 10, 15 and 16
3	6	21.43	2, 18, 22, 20, 7 and 27
4	1	3.57	5
5	7	25.00	4, 21, 24, 6, 19 and 23
6	5	17.86	11, 26, 13, 14 and 28

Clusters II and IV have the greatest inter-cluster distance (104.45), then clusters III and IV (84.2) and clusters IV and VI (72.89). Clusters III and VI had the shortest inter-cluster distance (14.04), followed by Clusters I and VI (19.41) and Cluster I and V (19.65) (Table 5). Cluster V had an intra-cluster distance of 11.80, then cluster III (9.75), Cluster II (9.16), Cluster I (8.03), Cluster VI (7.27), and Cluster IV (0.00) (Table5).

Table 5. Average Intra and inter-cluster distances for six clusters estimated

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	8.03	47.16**	25.80**	59.896**	19.65**	19.41**
Cluster 2		9.16	21.49**	104.45**	60.26**	31.81**
Cluster 3			9.75	84.20**	40.33**	14.04
Cluster 4				0.00	45.11**	72.89**
Cluster 5					11.80	29.02**
Cluster 6						7.27
Cluster 6						7.27

- **: *significance at 0.01 level.*
- *X^2= 14.07 at 5% probability level and X^2=18.48 at 1% probability level.*

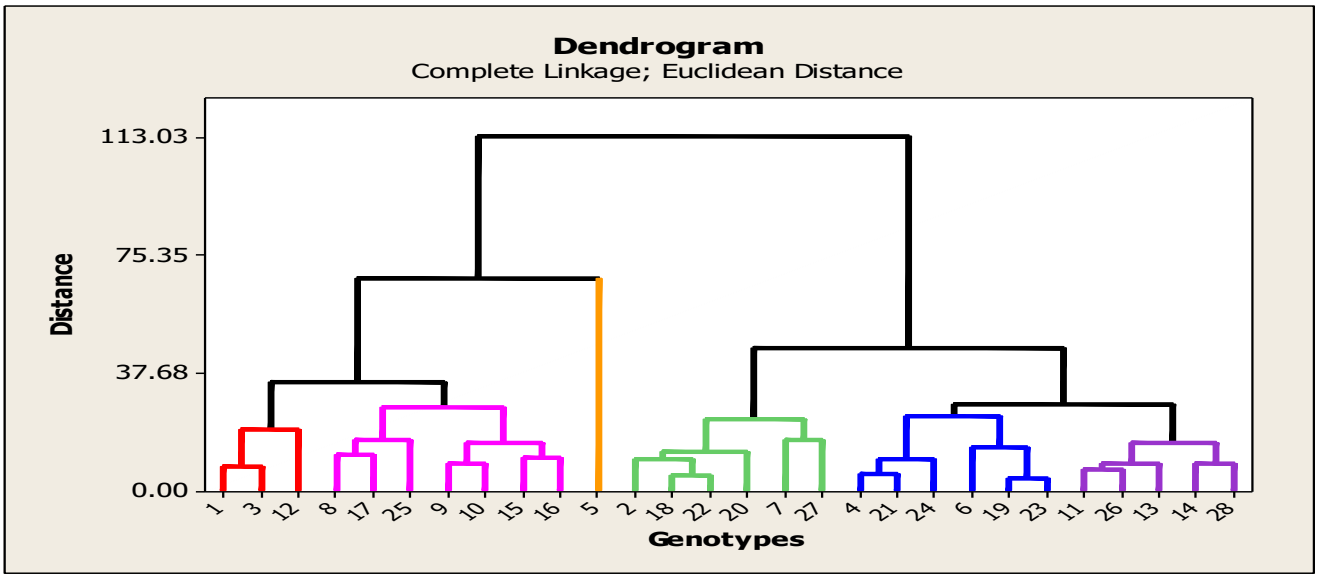

Fig. 5. A cluster dendrogram based on phenotypic related traits illustrates the distance between 28 wheat landraces.

Cluster analysis is commonly used to determine the extent of genetic diversity and to integrate organisms with similar parents into a single cluster (Mohammadi *et al*., 2015). Khodadadi *et al*., (2011) discovered that the outcomes of cluster analysis may be used in the planning and execution of future wheat breeding improvement strategies. The twenty-eight genotypes in this study are divided into six groups, revealing a high level of genetic diversity among the experimental material, as previously reported by (Arab *et al*., 2018; Baranwal *et al*., 2013). Using cluster analyses, (Adilova *et al*., 2020) investigated the relationship between yield and its components in wheat (*Triticum aestivum* L.). They classified all genotypes into three groups and revealed strong relationships between yield and other traits. Cluster V had the greatest intra-cluster distance, indicating the greatest genetic diversity between its constituents. Clusters II and IV have the greatest inter-cluster distance, then clusters III and IV and clusters IV and VI, indicating that the genotypes of clusters II, III, IV and VI are distantly related. It was discovered that genotypes with the greatest distance produced higher yields and increased the likelihood of obtaining transgressive segregants So, we can select the parents involved in the crossbreeding programs from the genotypes of these clusters. Also, this selection will be effective and sufficient. Clusters III and VI had the shortest inter-cluster distance, then Clusters I and VI and Cluster I and V, inferring that genotypes of clusters I, III, V, and VI have genes with a similar expression. As a result, these can be utilized in a backcross breeding program. This is in line with the results of (Jaiswal, 2015).

4. CONCLUSION

In this study, there was a wide range of variances for all of the studied traits in wheat genotypes, providing chances for genetic gain through selection or hybridization. As a result, enhancing one or more of the characteristics may lead to higher grain yield for the wheat variety. Based on PCA the promising genotypes for grain yield and hundred kernel weight traits were 6, 7, 18, 19, 20, 22, as well as 23. These genotypes may be considered high-yielding genotypes. Our results revealed that there were significant genetic information differences between landraces, providing new knowledge about the genetic relationships between Egyptian wheat, which is helpful for germplasm recognition and utilization in future wheat programs in various environments. Clusters II and IV had the greatest cluster distance, followed by Clusters III and IV. So crossing between these clusters' genotypes may result in better and superior recombinant wheat genotypes.

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الملخص العربي

التباين الوراثي وتحليل المكونات الأساسية والتحليل العنقودي لثمانية وعشرين تركيباً وراثيًا من القمح المصري

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القمح هو محصول الحبوب الرئيسي في مصر وأساس أمنها الغذائي. تمت زراعة ثمانية وعشرين سلالة من القمح (٢٦ سلالة بالإضافة إلى صنفين محليين هما جيزة ١٦٨ وجيزة ١٧١) في مزرعة بهتيم بمحطة أبحاث الجيزة ، مصر خلال موسمي (٢٠١٨/٢٠١٩ و ٢٠١٩/٢٠٢٠)، لتقييم تنوعها الجيني وتحديد العلاقات الجينية بين هذه السلالات المقيمة باستخدام التحليل العنقودي ، وتحليل المكون الرئيسي. خلال الموسمين ، اختلفت السلالات اختلافا معنويا ($P\leq0.0.01$) لجميع الصفات وكانت قيمة درجة التوريث بالمعنى الواسع مرتفعة لجميع الصفات. تم تقسيم البيانات إلى ثلاثة مكونات رئيسية باستخدام تحليل المكونات الرئيسية. وصفت هذه المكونات الثلاثة الرئيسية ٧٦,٢١٪ من التباين الكلي في االتراكيب الوراثية للقمح ، بينما وصفت المكونات الخمسة الأخرى ٢٣,٧٩٪ فقط من التباين. قسم التحليل العنقودي جميع التراكيب الوراثية إلى ست مجموعات. احتوت المجموعة الأولى على ثلاثة تراكيب وراثية تمثل ١٠,٧١٪ من جميع التراكيب الوراثية بينما تم تصنيف ستة تراكيب وراثية ، تمثل ٢١,٤٣٪ من جميع التراكيب الوراثية ، على أنها تنتمي إلى المجموعة الثانية. كما تم تخصيص ستة تراكيب وراثية للمجموعة الثالثة ، وهو ما يمثل ٢١,٤٣٪ من جميع التراكيب الوراثية. في حين تم تحديد تركيب وراثي واحد فقط (G5) ، يمثل ٣,٥٧ في المائة من جميع التراكيب الوراثية ، على أنه ينتمي إلى المجموعة الرابعة. تم تحديد سبعة تراكيب وراثية في المجموعة الخامسة بينما تم تحديد خمسة تراكيب وراثية في المجموعة السادسة. كان للمجموعة الثانية والرابعة في التحليل العنقودي أكبر مسافة بينهما ، تليهما المجموعتان الثالثة والرابعة. قد يؤدي التهجين بين التراكيب الوراثية لهذه المجموعات المتباعدة إلى تحسين محصول القمح.