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Principal Component and Cluster Analyses to Estimate Genetic Diversity in Bread Wheat (*Triticum aestivum* L.) Genotypes

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ABSTRACT

Analyze the genetic diversity of 22 bread wheat genotypes by principal component and cluster analyses were conducted at the Exper. Farm Fac. Agric., Minia Univ. Egypt during two seasons of 2017/18 and 2018/19. Principal component analysis (PCA) extracted three main components had eigenvalue >1 explained 79.59% of the total variation by 36.93% of PC1, 29.38% of PC2 and 13.28% of PC3. The most traits contributing in variation of first principal component were weight of spikes/plant, no. of grains/spike, weight of grains/spike, grain yield/plant, spike density and spikelet fertility. Cluster analysis divided the 22 bread wheat genotypes into five clusters. Each of them contained 8, 1, 3, 9 and 1 genotypes for cluster 1, 2, 3, 4 and 5, respectively. Average observed gain of cluster 1 showed positive increase for days to heading (DH), no. of spikelets/spike (NST/S) and spike density (SD) in percentage of mean overall genotypes. Cluster 3 had the highest yield potential. Nielain is separated in the second cluster and showed positive observed gain for plant height, NST/S and SD. Also, Genotype Emaral is separated in cluster 5 and showed high positive observed gain for the most traits in percentage of mean all genotypes. So, hybridization between Nielain of cluster 2 and Emaral of cluster 5 could give new recombination and transgressive segregations with long spike and high spike density in the progenies derived from their crossing.

Keywords: Eigenvalue, cluster, recombination, transgressive, segregations.



INTRODUCTION

Breeding wheat through hybridization, followed by selection for desirable individuals in the segregating generations depended on presence of genetic diversity between the crossed parents. The first step in breeding wheat program by hybridization is choice of parents.

Genetic diversity analysis of genetic resources is a prerequisite for their more efficient exploit in plant breeding program. Accurate determination of the genotype is very important during all the breeding program steps from parent choice for crossing to obtain new cultivars which utilize in crop production. Conversation the genetic diversity helps wheat breeders to find desired characters to improve wheat varieties and achieve high yield potential (Mwale *et al.*, 2016).

Estimation of genetic diversity based on genetic distance is useful for wheat breeding as one of tools for parental selection to enhance the new genetic recombination for increase yield Khodadadi *et al.* (2011) and Poudel *et al.* (2017).

Multivariate analysis by principal component and cluster analysis can be effective to determine genetic diversity and parental selection. Also, it used to identify components that are correlated with a certain traits which cause high variation and determine performance of genotypes and their effects on different traits. Principle component analysis (PCA) was used to classify a large number of traits into major components.

Euclidean distance used to estimate the genetic distance between parents to maximize the transgressive segregation. Babay *et al.* (2015) observed a high variation among the genotypes, as a result of wide range of Euclidean

distance among the genotypes. Poudel *et al.* (2017) revealed that selection of genotypes from cluster 2 would lead to selection of the superior genotypes used in breeding wheat. Rani *et al.* (2018) conducted cluster analysis with WARD method and Square Euclidean distance coefficient grouped 40 genotypes into 6 clusters. Cluster V had highest grain yield (1014.4 g), spikes/meter² (143.46) and second lowest plant height. Thus; the genotypes presence in clusters have excellent chances for improvement by wide hybridization. Pooja and Binewal (2018) revealed that results of cluster analysis could be exploited in planning and execution of future breeding improvement program in wheat. Kandel *et al.* (2018) identified superior genotypes after clustering them based on their genetic diversity in performance. Santosh *et al.* (2019) revealed that the genotypes bearing the desired traits from different clusters can be exploited in future breeding wheat program for the improving yield. Cluster analysis results showed that the cultivars were genetic different from each other could gave the farmers a wider range to choice from it Motlatsi and Mothibeli (2020). The objectives of the study were to analyze the genetic diversity of 22 bread wheat genotypes, determine the genetic relationships among different traits which contribute more towards grain yield and determine the promising excellent genotypes which could be parents in wheat breeding program.

MATERIALS AND METHODS

The experiment was conducted at Fac. Agric. Edu. Farm, Minia Univ., Egypt., 22 bread wheat genotypes included 10 F_{9:10} recombinant inbred lines (G1, G48, G62,

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G104, G124, G306, G352, G389, G395 and G463) from cross Giza168 x Sids4 were derived from the materials of Ph.D. study of the author, 11 varieties (Misr1, Misr2, Sids1, Sids4, Sids13, Giza168, Giza171, Gemmieza11, Gemmieza12, Sakha94 and Nielain) and long spike line Emaral. The 22 genotypes were sown in two seasons i.e.

2017/2018 and 2018/2019 on 20th Nov. A randomized complete block design of three replicates was used. The plot size was one row, 1.5 m long, 20 cm apart and 5 cm between grains within a row. The pedigree of the 12 bread wheat genotypes is given in (Table 1).

Table 1. The pedigree of the twelve bread wheat genotypes.

Genotypes	Pedigree
Misr1	OASIS/SKAUZ//4*BCN/3/2*PASTOR
Misr2	SKAUZ/BAV 92
Sids1	HD2172/Pavon“S”//1158/Maya74“S”
Sids4	Maya (S)/Man (S)//CMH 74A-592/3/Giza 157*2
Sids13	ALMAZ.19KAUZ“S”// TSI/ SNB“S”
Giza168	MIL/Buc//Seri CM93046-8M-04-0M-2Y-0B
Giza171	SAKHA 93 / GEMMEIZA 9 S.6-1GZ-4GZ-1GZ-2GZ-0S
Gemmieza11	BOW“S”/KVZ“S”//7C/SER182/3 /GIZA168/SAKHA 61
Gemmieza12	OTUS/3/SARA/THB//VEECMSS97Y00227S-5Y-010M-010Y-010M-2Y1M-0Y-0GM
Sakha94	OPATA/RAYON//KAUZCMBW90Y3180-0TOPM-3Y-010M-010M-010Y10M-015Y-0Y-0AP-0S
Nielain	S948.A1/7*SANTA ELENA (CMH72A.390-0SDN)
Emaral	Kindly provided by Prof. Dr. Ezzat Mahdy – Prof. of plant breeding in Agronomy Dept. – Fac. of Agriculture. Assiut Univ.

The following 12 studied traits were taken, days to 50% heading [DH], plant height [PH, cm], spike length [SL, cm], no. of spikes/plant [NS/P], weight of spike/plant [WS/P], no. of spikelets/spike [NST/S], no. of grains/spike [NG/S], weight of grains/spike [WG/S, g], grain yield/plant [GY/P, g], 1000-grain weight [1000-GW, g], spike density SD = [NST/SL], spikelet fertility SF = [NG/S] / [NST/S].

The monthly mean of air temperature and relative humidity during the experiment period of the two growing seasons are shown in Fig. 1.

Statistical procedures:

Data were subjected to proper statistical analysis of variance of RCBD according to Steel and Torrie (1980),

using MSTAT-C 2.1 software. Heritability in broad sense “H” was estimated according to Walker (1960). The phenotypic (PCV%) and genotypic (GCV%) coefficients of variability were calculated as outlined by Burton (1952). After standardization data, multivariate analysis performed on average the two growing seasons by principal component and cluster analyses using SPSS version 21 and XLSTAT software. Cluster analysis was carried out based on squared Euclidian distances by Ward’s method. The optimum number of clusters was determined by values of Pseudo F according to Calinski and Harabazs (1974).

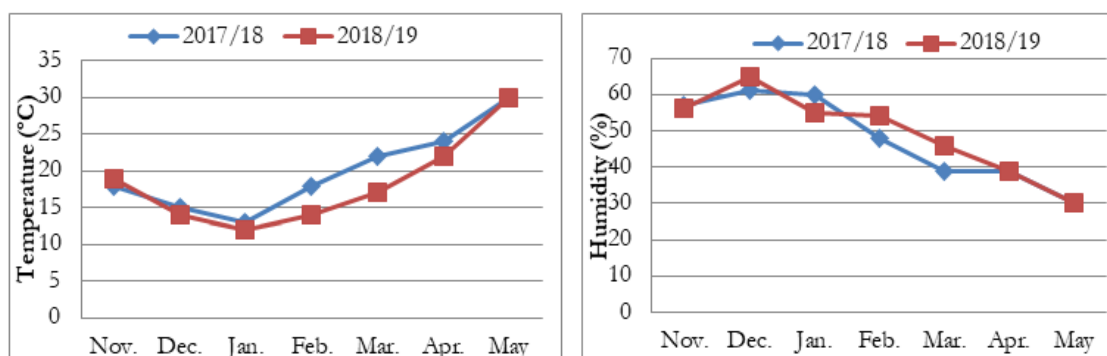


Fig.1. Monthly, mean of air temperature and relative humidity during the experiment period in first season 2017/18 and second season 2018/19. <https://www.timeanddate.com/weather/egypt>

RESULTS AND DISCUSSION

Significant differences ($P \leq 0.5$ or 0.01) were found for all the studied traits in the two seasons (Table 2). In 1st season high estimates of heritability in broad sense were observed for most traits with range from 78.03% for days to heading to 96.97% for plant height except moderate heritability were estimated for NG/S (68.17), WG/S (65.83) and SF (65.82%). In 2nd season, most of traits recorded high values of heritability with exception low values for weight of spike/plant (47.04) and grain yield/plant (43.083%) were observed. High estimates of genotypic (GCV%) and phenotypic (PCV%) coefficients of variation were found for

most of traits except low estimates were found for DH in first season 2017/18 and NST/S in second season 2018/19. Similar results were in agreement with Al-Ashkar *et al.* (2015), Birhanu *et al.* (2017) and Devesh *et al.* (2019).

Based on average of two seasons (Table 3) days to heading, plant height, spike length, weight of spikes/plant, no. of grains/spike, 1000 grain weight and grain yield/plant ranged from (92.17 to 108.33), (89.58 to 150.51 cm.), (10.22 to 22.18 cm.), (19.57 to 35.75 g.), (39.04 to 71.04), (50.62 to 69.18 g.) and (10.15 to 22.82g.) respectively, reflecting high variance of these traits.

Table 2. Mean squares, heritability in broad sense (H%), genotypic (GCV%) and phenotypic (PCV%) coefficients of variation of the studied traits in first 2017/18 and second 2018/19 seasons.

Season	First season 2017/18					
SV	Rep	Genotypes	Error	H%	GCV%	PCV%
df	2	21	42	-	-	-
DH	5.65	17.34**	3.81	78.03	2.25	2.55
PH	5.52	365.56**	11.07	96.97	11.71	11.89
SL	1.23	16.42**	1.57	90.43	16.26	17.1
NS/P	3.13	1.95**	0.32	83.49	16.62	18.18
WS/P	4.12	62.88**	4.72	92.5	21.52	22.38
NST/S	0.7	6.95**	1.1	84.12	6.23	6.8
NG/S	310.29	220.33**	70.12	68.17	14.24	17.25
WG/S	2.68	0.97**	0.33	65.83	15.52	19.13
1000GW	97.11	67.64**	19.89	70.6	6.64	7.9
GY/P	4.75	30.42**	2.97	90.24	20.62	21.71
SD	0.01	0.17**	0.02	88.13	13.42	14.29
SF	0.69	0.45**	0.15	65.82	14.06	17.33
				Second season 2018/19		
DH	67.56	207.57**	13.53	93.48	7.69	7.96
PH	10.29	586.85**	28.37	95.17	11.69	11.99
SL	4.26	15.63**	1.08	93.08	15.08	15.63
NS/P	4.27	7.07**	1.66	76.48	21.74	24.86
WS/P	64.43	87.13*	46.15	47.04	12.29	17.92
NST/S	1.72	6.6**	0.78	88.14	5.56	5.93
NG/S	116.29	146.49**	41.98	71.34	9.42	11.15
WG/S	0.52	0.89**	0.15	83.58	13.88	15.18
1000GW	24.2	130.61**	30.08	76.97	10.04	11.45
GY/P	28.83	43.95*	24.09	43.83	13.98	21.12
SD	0.02	0.17**	0.01	92.38	13.26	13.79
SF	0.1	0.15**	0.06	57.9	6.88	9.04

*and ** significant at 0.05 and 0.01 level of probability.

Table 3. Mean, minimum and maximum for the studied traits of 22 genotypes in first 2017/18, second 2018/19 and average of the two seasons.

Season	First season 2017/18			Second season 2018/19			Average		
	Min.	Max.	Mean	Min.	Max.	Mean	Min.	Max.	Mean
DH	87.67	98.67	94.38	91.33	120.00	104.56	92.17	108.33	99.47
PH; cm	74.90	134.02	92.86	90.00	167.00	116.70	89.58	150.51	104.78
SL; cm	9.80	22.53	13.68	10.63	21.83	14.60	10.22	22.18	14.14
NS/P	2.67	5.93	4.43	3.67	10.23	6.18	3.17	8.03	5.30
WS/P; g.	11.83	28.04	20.46	22.77	46.90	30.07	19.57	35.75	25.26
NST/S	20.63	27.57	22.40	22.70	29.37	25.04	21.90	28.47	23.72
NG/S	30.29	64.82	49.69	47.78	77.42	62.68	39.04	71.04	56.18
WG/S; g.	1.71	4.05	2.97	2.42	4.43	3.60	2.07	4.18	3.28
1000GW; g.	51.33	69.47	60.09	45.83	68.90	57.65	50.62	69.18	58.87
GY/P; g.	7.37	19.69	14.67	12.46	27.45	17.97	10.15	22.82	16.32
SD	1.23	2.47	1.67	1.34	2.42	1.75	1.29	2.45	1.71
SF	1.25	2.85	2.23	1.87	2.87	2.53	1.56	2.79	2.37

Principal component analysis (PCA) performed to indicate the traits which responsible for maximum variation amongst traits. Hence, PCA abbreviate a large number of variables to a small number of variables (traits) caused maximum variation. Principal component analysis extracted

12 components from the 12 studied traits (Fig. 2); the first three components of them had eigen values > one which explained 79.59% of the total variation by 36.93% of PC1, 29.38% of PC2 and 13.28% of PC3 (Table 4).

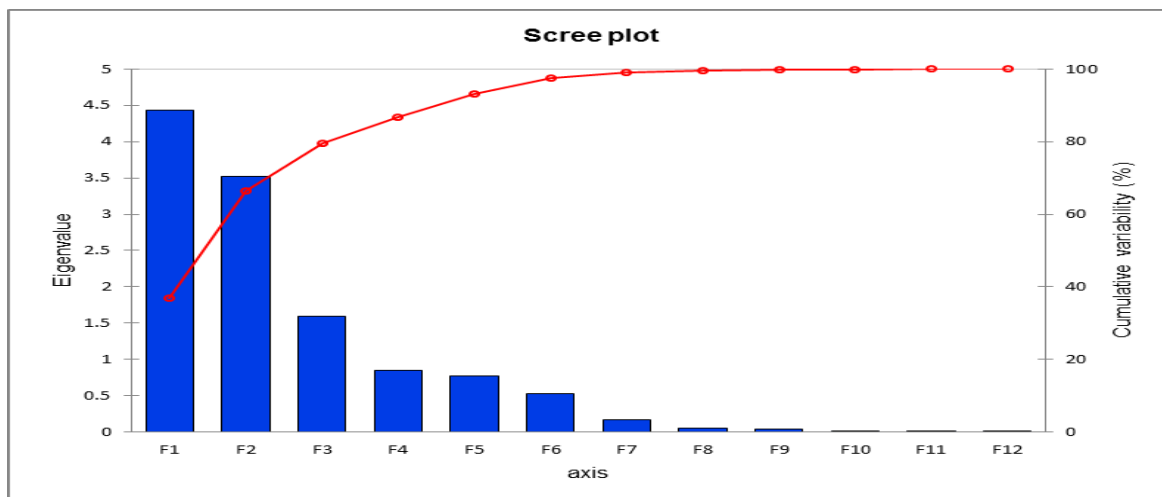


Figure 2. Scree plot of eigenvalue and cumulative variability (%) of 12 principal components extracted.

Table 4. Principal component analysis for the studied traits.

Trait/PC	Factor loadings		
	PC1	PC2	PC3
DH	-0.33	0.45	0.39
PH	-0.08	0.75	0.22
SL	0.42	0.80	0.26
NS/P	-0.09	-0.72	0.65
WS/P	0.64	-0.52	0.49
NST/S	-0.07	0.81	0.32
NG/S	0.82	0.40	0.15
WG/S	0.93	0.13	-0.23
1000GW	0.54	-0.20	-0.59
GY/P	0.66	-0.61	0.36
SD	-0.79	-0.32	0.01
SF	0.91	0.00	-0.02
Eigenvalue	4.43	3.53	1.59
Variability (%)	36.93	29.38	13.28
Cumulative %	36.93	66.30	79.59

According to values of factor loading of traits, the traits with highest absolute factor loading value close to one refer to high contribution of these traits in variation of the PC rather than traits close to zero. Hence, the most traits contributing in variation of PC1 were WS/P (0.64), NG/S (0.82), WG/S (0.93), GY/P (0.66), SD (-0.79) and SF (0.91) (Table 4). Their relative contributions in variation were 9.24, 15.19, 19.39, 9.7, 14.26 and 18.7%, respectively (Fig.3). Similarly, in PC2 the major traits contributing were DH (0.45), PH (0.75), SL (0.80), NS/P (-0.72) and NST/S (0.81) (Table 4). Their contributions in variation were 5.72, 15.79, 17.94, 14.64 and 18.52%, respectively (Fig. 3). Only 1000 GW (-0.59) represent the major contribution in variation of PC3. Boshev *et al.* (2016) and Devesh *et al.* (2019) revealed that the first three main principal components explained 71.39% of the total variation among the genotypes. PC1 explained 30.60% of the variation which reflects the genotype

yield potential. 5.22% and 15.49% of the total variance were attributed for PC2 and PC3, respectively.

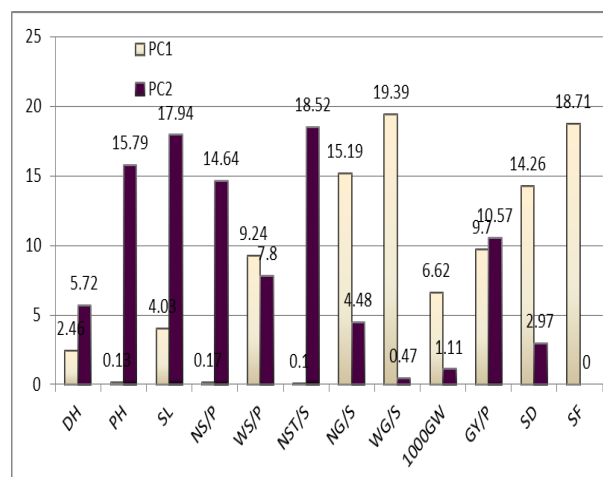


Figure 3. Contribution of the studied traits of the total variation in PC1 and PC2.

The first two principal components PC1 and PC2 explained 66.30% of the total variation. The factor loadings for 12 traits of these two PC were plotted on Fig. 4 to display the relationship between the 22 genotypes and their traits. The vectors of trait revealed angles between studied traits, angles < 90° refer to a positive correlation between traits, while angles > 90° refer to a negative correlation. Further, angles near 0° and 180° refer to increase in association intensity. Moreover, length of trait vector indicates the extent of variation caused by this trait in PCA (Boshev *et al.* (2016).

High significant (p<0.01) positive correlation was observed by acute angle (Fig. 4) between grain yield/plant and weight of spikes/plant (0.94), between no. of grains/spike with spikelet fertility (0.88) and weight of grains/spike (0.82) (Table 5).

Table 5. Simple correlation coefficients matrix for the studied traits.

Traits	DH	PH	SL	NS/P	WS/P	NST/S	NG/S	WG/S	1000GW	GY/P	SD
PH	0.18**										
SL	0.14	0.62**									
NS/P	-0.02	-0.36**	-0.43**								
WS/P	-0.32**	-0.23**	0.09	0.63**							
NST/S	0.46**	0.57**	0.56**	-0.42**	-0.27**						
NG/S	-0.05	0.14	0.73**	-0.30**	0.34**	0.37**					
WG/S	-0.25**	-0.11	0.52**	-0.34**	0.42**	0.05	0.82**				
1000GW	-0.33**	-0.27**	0.06	-0.24**	0.23**	-0.35**	0.12	0.64**			
GY/P	-0.34**	-0.42**	0	0.60**	0.94**	-0.37**	0.30**	0.46**	0.34**		
SD	0.09	-0.25**	-0.80**	0.24**	-0.31**	-0.01	-0.66**	-0.68**	-0.40**	-0.30**	
SF	-0.31	-0.15*	0.46**	-0.11	0.50**	-0.12	0.88**	0.85**	0.31**	0.51**	-0.69**

*and ** significant at 0.05 and 0.01 level of probability.

Furthermore, spike length showed significant (p<0.01) positive correlation with PH (0.62), NST/S (0.56), NG/S (0.73), WG/S (0.52) and SF (0.46). Also, significant (p<0.01) positive correlation was recorded between grain yield/plant with each NS/P, NG/S, WG/S and 1000GW. Similarly, significant (P<0.01) negative correlation was found by obtuse angles (Fig. 4) between spike density and spike length (-0.80) and between spikelet fertility and spike density (-0.69). Plant height gave significant (p<0.01) negative correlation with all traits except positive correlation with SL (0.62) and NG/S (0.14) (Table 5). Also, DH showed negative correlation with all traits except with PH, SL and NST/S and weak positive correlation with SD (0.09).

Strongest positive correlations >0.81 (Table 5) were revealed by acute angles among three traits, NG/S, WG/S and SF. One of them, WG/S, had highest effect on grain yield, where its vector was the tallest (Fig. 4). Boshev *et al.* (2016) revealed that biplot graph showed strongest positive association between tillers, weight of grains/spike and grain yield/plant. Genotypes with high values for specific traits will be included in the future breeding programs.

Location of the genotype is distance it from the biplot origin which refer to differ the genotype from a “average” genotype located at the biplot origin that has an average level for all traits Yan and Fregeau (2008). According to this, long vectors of the two genotypes Emaral

and Nielain showed that they possess high values for one or more studied traits. Furthermore, Emaral is concerned

superior genotype, where it is located in region with high positive values nearly for all studied traits (Fig. 4).

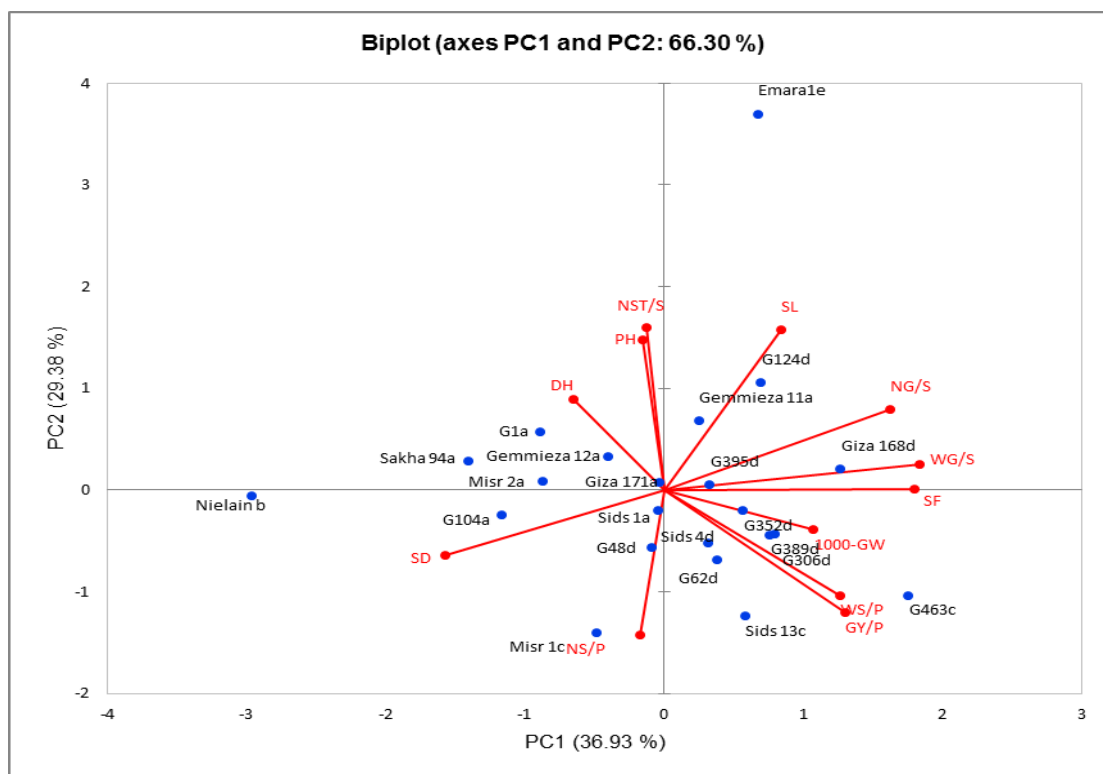


Figure 4. Biplot of PC1 and PC2 representing correlation between the 22 genotypes and traits. Small letters a, b, c, d, and e beside genotypes sign to cluster 1, 2, 3, 4 and 5, respectively.

Cluster analysis

The dendrogram generated from cluster analysis of the standardized data of the studied traits divided the 22 bread wheat genotypes into five clusters at cutting point distance 6 (Fig. 5).

The first cluster contained eight genotypes (36.36% of total genotypes); Giza171, Sids1, Gemmieza11, Gemmieza12, G1, Sakha94 and G104, Misr2, (Table 6).

Table 6. The five cluster grouping 22 bread wheat genotypes based on the studied traits.

Cluster	1	2	3	4	5
Frequency	8	1	3	9	1
Cluster membership	Giza 171 Sids 1 Gemmieza 11 Gemmieza 12 G1 Sakha 94 G104 Misr 2	Nielain	G463 Sids 13 Misr 1	G48 G62 G306 G389 G395 G352 G124 Sids 4	Emara 1

The average observed gain for the eight genotypes in cluster 1 showed positive increase for days to heading (4.01%), no. of spikelets/spike (1.57%) and spike density (4.19%) in percentage mean overall genotypes (Table 7). Nielain is separated in the second cluster (Table 6) and showed positive observed gain for PH (12.70%), NST/S (4.91%) and spike density (43.15%). The third cluster included 3 genotypes (13.64% of total genotypes); G463, Sids13 and Misr1 (Table 6). Average observed gain values of NS/P, WS/P, NG/S, WG/S, GY/P, SD and SF of this

cluster showed positive increase by 35.30, 29.64, 4.12, 1.27, 30.70, 0.42 and 6.55%, respectively in percentage of mean all genotypes (Table 7). The cluster three recorded the highest mean for no. of spikes/plant (7.18), weight of spikes/plant (32.75 g.) and grain yield/plant 21.33 g (Table 7). Cluster 3 had the highest yield potential compared to the others clusters. The fourth cluster represents 40.91% of total genotypes, including nine genotypes; G48, G62, G306, G389, G395, G352, G124, Sids4 and Giza168 (Table 6). Where, this cluster includes seven recombinant lines and their two original parents; Sids4 and Giza168. The average observed gain in percentage of mean all genotypes for the nine genotypes in cluster 4 showed positive increase in weight of spikes/plant, grains/spike, weight of grains/spike, 1000 grain weight, grain yield/plant and spikelet fertility by 1.65, 3.48, 8.87, 5.33, 3.10 and 7.03% respectively (Table 7). Furthermore, cluster 4 showed earliness in days to heading by -3.08% this attributed to the earlier variety Sids4 one of their two parents the seven genotypes included in cluster 4. Also, Genotype Emaral is solely separated in cluster five and showed high distance from the others genotypes due to its high values of the most studied traits, where it showed positive observed gain for PH (43.65%), SL (64.73%), NST/S (20.03%), NG/S (26.45%), WG/S (5.74%) and SF (5.48%) but it was late in days to heading by 5.06% in percentage mean all genotypes. Emaral had long spike (22.53 cm.) but its spike density was low (1.29). While, Nielain had short spike (9.80 cm.) and its spike density was high (2.45). So, hybridization between Nielain of cluster 2 and Emaral of cluster 5 could give new recombination and transgressive segregation with long spike and high spike density in the progenies. Birhanu *et al.*

(2017) revealed that cluster analysis grouped 64 genotypes into eight clusters. The crosses between genotypes selected from cluster-V with cluster-VIII and cluster V with cluster VII are expected to produce better genetic recombination and segregation in their progenies. Kabir *et al.* (2017) found that multivariate analysis of 16 lines and four commercial cultivars of bread wheat, 5 genotypes showed maximum divergence from others. They concluded that high genetic variation among the genotypes may help for further breeding and selection. Parents selected from clusters which had significant genetic distance for crossing and obtain genetic recombination and transgressive segregation in the following generations. Kandel *et al.* (2018) revealed that

cluster analysis of 41 wheat genotypes formed four clusters. Cluster 4 and 2 had highest value of spikes, spike length, grains/spike, 1000 grain weight, grain yield and days to heading. Cluster 3 had high days to heading, plant height, 1000 grain weight and grain yield. Santosh *et al.* (2019) revealed that cluster-II had maximum number of genotypes and clusters IV, V and VI each had single genotype only. Cluster-I exhibited highest cluster means for grains weight/spike and grain yield/plot. The genotypes bearing the desired values from different clusters can be exploited in future breeding program for the improving the wheat genotypes for yield.

Table 7. Means and observed gain of traits for each cluster in percentage of average all genotypes.

Cluster	1		2		3		4		5	
Trait	Mean	OG%	Mean	OG%	Mean	OG%	Mean	OG%	Mean	OG%
DH	103.46	4.01	96.33	-3.16	97.39	-2.09	96.41	-3.08	104.50	5.06
PH	101.65	-2.99	118.08	12.70	96.07	-8.31	103.90	-0.84	150.51	43.65
SL	13.49	-1.36	9.80	-28.35	13.01	-4.87	13.51	-1.21	22.53	64.73
NS/P	5.17	-2.57	5.19	-2.26	7.18	35.30	4.99	-5.97	3.75	-29.31
WS/P	22.98	-9.05	19.57	-22.56	32.75	29.64	25.68	1.65	23.04	-8.80
NST/S	24.09	1.57	24.89	4.91	23.13	-2.47	22.93	-3.35	28.47	20.03
NG/S	53.39	-4.96	39.04	-30.52	58.50	4.12	58.14	3.48	71.04	26.45
WG/S	3.07	-6.54	2.07	-37.07	3.32	1.27	3.57	8.87	3.47	5.74
1000GW	58.01	-1.46	51.83	-11.95	56.39	-4.22	62.01	5.33	51.96	-11.74
GY/P	15.10	-7.51	10.15	-37.81	21.33	30.70	16.83	3.10	12.71	-22.16
SD	1.78	4.19	2.45	43.15	1.72	0.42	1.61	-5.91	1.29	-24.77
SF	2.20	-6.79	1.56	-34.05	2.52	6.55	2.53	7.03	2.50	5.48

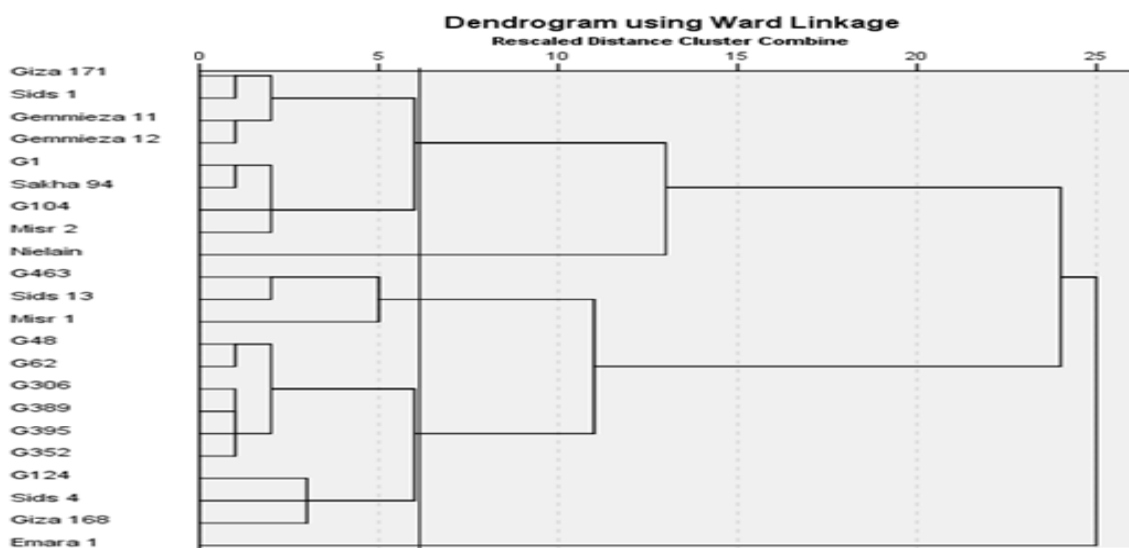


Figure 5. Dendrogram showing 22 bread wheat genotypes based on ward's method and squared Euclidean distance.

CONCLUSION

The most traits contributing in variation of the first principal component were weight of spikes/plant, no. of grains/spike, weight of grains/spike, grain yield/plant, spike density and spikelet fertility. Hybridization between Nielain of cluster 2 and Emara1 of cluster 5 could give new recombination and transgressive segregations in the progenies derived from their crossing.

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تحليل المكونات الأساسية والتحليل العنقودي لتقدير التنوع الوراثي في تراكيب وراثية لقمح الخبز

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اجرى تحليل التنوع الوراثي على ٢٢ تركيب وراثي من قمح الخبز باستخدام تحليل المكونات الأساسية والتحليل العنقودي. وزرعت التراكيب الوراثية في مزرعة التجارب بكلية الزراعة – جامعة المنيا – مصر خلال الموسمين ٢٠١٨/٢٠١٧ و ٢٠١٩/٢٠١٨ بتصميم القطاعات الكاملة العشوائية بثلاث مكررات، وأوضحت نتائج تحليل المكونات الأساسية وجود ثلاثة مكونات أساسية بقيم خاصة أكبر من ١ وهذه المكونات الثلاثة فسرت ٧٩,٥٩% من التباين الكلي بين الصفات الدراسية منها ٣٦,٩٣% للمكون الأساسي الأول و ٢٩,٣٨% للمكون الأساسي الثاني و ١٣,٢٨% للمكون الأساسي الثالث. وأكثر الصفات المساهمة في تباين المكون الأساسي الأول هي وزن سنابل النبات وعدد حبوب السنبل ووزن حبوب السنبل ومحصول الحبوب/نبات وكثافة السنبل وخصوبة السنبل. كما ادى التحليل العنقودي الى تقسيم ال ٢٢ تركيب وراثي لقمح الخبز الى ٥ عناقيد كل منهم احتوى على عدد ٨ ، ١ ، ٩ ، ١ تركيب وراثي للعنقود الأول والثاني والثالث والرابع والخامس على الترتيب، اظهرت النتائج ان متوسط التقدم المشاهد في العنقود الأول بالنسبة للمتوسط العام لكل التراكيب الوراثية زيادة موجبة في عدد ايام طرد السنابل وعدد سنبيلات السنبل وكثافة السنبل، كما اظهر العنقود الثالث اعلى قدرة محصولية، وقد انفرد الصنف نيلين بمفرده بالعنقود الثاني واظهر تقدم مشاهد موجب عالي لمعظم الصفات بالنسبة للمتوسط العام لكل التراكيب الوراثية، كما انفصل التركيب الوراثي عمارة ١ بمفرده في العنقود الخامس واظهر تقدم مشاهد موجب لطول النبات وعدد سنبيلات السنبل وكثافة السنبل، توصى الدراسة بالتهجين بين التراكيب الوراثية عمارة ١ للعنقود الخامس ونيلين للعنقود الثاني يمكن ان يعطى تراكيب جديدة وانعزالات متجاوزة للحدود في صفات السنبل الطويلة وكثافة السنبل العالية في الانسال الناتجة من تهجينهما.