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Evaluation of Genetic Variability of Bread Wheat Genotypes under Normal Irrigation and Water Stress Conditions Using Multivariate Analysis

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ABSTRACT

The data collected were used to study the genetic diversity in 24 bread wheat genotypes originating from genotypes (22) from Bahteem Gene Bank, Genetic Resources Research Department, Agricultural Research Center, Giza, Egypt, and two check varieties (Sakha 94 and Giza 168). An experiment arranged on a randomized complete block design with three replications was performed in normal irrigation and drought stress conditions. Variance analysis indicated highly significant differences among the genotypes in all traits. Also, there is considerable variability among genotypes in all traits. The presence of genetic diversity among genotypes was recorded in our study. Percent decrease due to drought stress was a positive value for all traits, except chlorophyll content. Broad sense heritability values were very high under normal irrigation for days to heading, days to anthesis, days to maturity and grain yield per faddan. In both conditions, spike per m² had direct positive effects with 0.487 and 0.363 while days to heading showed more negative effects with (-0.408) and (-0.562) respectively. The cluster analysis divided the genotypes into five groups under different (normal or stress) conditions, genetic divergence has been found related to several genetic and non-genetic conditions like the extent of genotype x environment interaction and components of genetic variation. Accordingly, results give a good chance to achieve genotypic improvement of wheat through the hybridization among genotypes taken from different clusters. where, genotypes 14, 2, 11, 23, 17 and 20 had high yielding and divergent under water shortage stress conditions for yield improvement in bread wheat

Keywords: Wheat, genotypes, water deficit, genetic diversity.



INTRODUCTION

Triticum aestivum, commonly known as wheat, is one of the important cereal crops that depend on them for human food. Regarding global production, the world produces about 76,092,5831 tons during 2020 of a total harvested area of about 219,006,893 hectares with an average yield of 3,477 tons per hectare. The local production of Egypt is about 9,000,000 tons of the total cultivated area of 1,370,235 hectares (FAO., 2020).

Water deficit is one of the most important problems facing many countries of the world. Drought is major abiotic stress that adversely affects crop productivity and quality. It threatens the world Water deficit is the biggest environmental stress and causes severe damage to agricultural products in many countries around the world (Khan *et al.*, 2007).

Drought tolerance is a quantitative trait, and the development of high-yielding wheat cultivars is a major objective in breeding programs (Ehdaie and Waines, 1989), improve yield and its components under low water supply conditions is a very challenging task. The physiological approach can complement experimental optimization to improve the rate of performance improvement. Today's efforts are focused on improving the genotypes of crops in drought-prone areas. To achieve this goal, it is necessary to understand the mechanisms underlying drought tolerance, which can lead to the restoration of physiological function and hardening of plants under drought stress (Akbarian, *et al.*, 2011).

Plant breeding research is very important to produce new wheat and barley cultivars having a high degree of drought

tolerance. In addition, to improve drought tolerance, plant breeders must improve grain yield combined with high tolerance to drought. The first step is to select the potential germplasm that contains genotypic differences for drought tolerance (Baenziger, 2016). Selection for drought tolerance must be tested in more than one year or/and location in the target environments because drought tolerance usually has low heritability. Furthermore, drought tolerance measurements are often affected by spatial variation, so the trials need multiple replications. The efficiency of phenotypic selection is also affected by GE interaction if the environments are different (which is expected due to year-to-year or site-to-site variation). High levels of G×E can lead to no progress in drought tolerance because the environments require selecting different types of drought tolerance. Therefore, the G×E interaction is considered a major complication in breeding programs (Ahmed Sallam., *et al* 2019).

Cluster analysis is a valuable biometrical tool aimed to quantify the degree of genetic divergence among tested genotypes based on their performance and their contributing characteristics. But it was found that the run of cluster analysis depending on (STI's) parameters is useful to differentiate Wheat genotypes for salt tolerance, (Saad *et al.*, 2014).

The main objectives of this research were to: 1- Evaluate the influence of water stress on grain yield and its components of wheat genotypes. 2- performance of these genotypes under water stress conditions. 3-Study of genetic diversity and heritability for genotypes under normal irrigation and water deficit water

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MATERIALS AND METHODS

To study the genetic variability of some bread wheat genotypes (22) from Bahtem Gene Bank, Genetic Resources Research Department, Field Crop Research Institute, Agricultural Research Center, Giza, Egypt, and two check varieties (Sakha 94 and Giza 168) were shown in Table 1, to evaluate under normal irrigation and water stress conditions exposed after 50% flowering. A split plot in a randomized complete blocks design with three replications was used. Irrigation treatments were randomly arranged in the main plots, while wheat genotypes occupied the sub-plots. Planting dates were on 19th November and 25th November During the 2018/2019 and 2019/2020 growing seasons, respectively. At Bahtem farm, Gene Bank, Genetic Resources Research Department, Field Crop Research Institute, Agricultural Research Center, Giza, Egypt. Net plot size was 3.36 m² involving six rows, three meters long with 20 cm apart. All agriculture practices of wheat cultivation were done following standard recommendations. The studied characters were; days to heading, days to anthesis, days to maturity, plant height, spikes number per square mete, grains number per spike, 1000-grain weight, and grain yield. Total chlorophyll content (SPAD) which was measured using a chlorophyll meter (SPAD_502 Minolta Camera Co. Ltd; Japan) and canopy temperature depression was measured at three periods (at 5/2, 16/2 and 25/2).

Table 1. Location, pedigree, code and number of tested twenty-four Egyptian bread wheat genotypes.

Location	Pedigree	code	NO.
Aswan	5km E of Aneba along wadi kharit	217	1
Aswan	6km SE of Kom Ombo on the main road to wadi kharit	226	2
Aswan	13km SE of Kom Ombo on the road to wadi kharit	229	3
Aswan	38 km N of kalabsha ,by the main road	253	4
Assiut	Beni feez ,near sidfa	353	5
Assiut	14km W of Assiut	403	6
Assiut	25km N of Assiut	405	7
ASSIUT	Beni rafi	265	8
QENA	4km W of Qena in the road to Dandara Temple	293	9
QENA	17km W of Qena by the Nile left bank main road	322	10
QENA	14km E of Nag Hammadi	333	11
QENA	Nag hammadi	343	12
Fayoum	13km W of El Minya ,Nauara , near Gandir	352	13
Fayoum	Tamiya	369	14
New valley	El rashda, Daakhla	383	15
New valley	Budkhula ,Daakhla	388	16
Minia	12km S of El _ Minia	559	17
Minia	3 km S of Beni Mazar	585	18
Sohag	21km N of Griga	398	19
Sohag	19km N of sohag	305	20
Sohag	25km N of sohag	307	21
Beni suef	11KM S of Ihnasya El Madina	512	22
Egypt	OPATA/RAYON/3/JUP/BJY//URES	Sakha94	22
Egypt	MIL/BUC//SERI	Giza168	24

Table 2. Mean squares of components 24 bread wheat genotypes under normal irrigation and drought stress conditions.

S.o v	d.f.	DH	DA	DM	PH	spike per M ²	KS	1000-KW	GY Ton/F	CHIO-CON	CTD
Condition	1	352.5	653.65	212.94	6168.79	87616.00	753.05	771.45	11.30	103.70	181.58
Error	4	49.40	53.86	44.73	6.37	437.70	76.68	21.50	0.12	18.09	5.33
Genotypes	23	134.99	162.59	86.42	61.95	8349.10	44.54	45.89	0.69	27.94	2.18
Cond.*Geno	23	2.61	3.90	3.83	18.81	951.20	7.77	5.29	0.16	7.39	0.67
Error	92	2.23	2.99	4.56	8.81	692.50	9.04	5.10	0.04	5.93	0.67

Plant physio-morphological traits are very important for selection in a breeding program to improve drought tolerance due to their relation to the adaption for future climate scenarios (Bowne, 2012). The data in Table 4 shows that all traits have been affected by water deficit. Where, there was a decrease in the number of days to heading, days to anthesis and number of days to maturity for all genotypes. Genotypes 322 and 217 recorded the lowest days to heading

RESULTS AND DISCUSSION

Highly significant differences were found among 24 wheat genotypes, during the two growing seasons 2017/2018 and 2019/2020 under both normal and water stress conditions. Regarding the effects of irrigation treatments (normal irrigation and drought stress treatment), analysis of variance show clearly that the application of these treatments high significantly enhanced the days of anthesis and kernel per spike and significantly the plant height, spike per M², 1000 Kw, grain yield and canopy temperature parameters. Also, data in table 2 shows that there is considerable variability among genotypes in all of the traits, recording the presence of genetic diversity among genotypes in our study. The interaction (G*C) was not significant for all the traits except plant height and grain yield per faddan. This can enhance the plant breeder by focusing on the characteristic of plant height, yield and its components under water stress conditions.

The percent decrease due to drought stress was a positive value for all traits except chlorophyll content (table 3). Thus these traits can be used as selection criteria.

Broad sense heritability values were very high under normal irrigation for days to heading, days to anthesis, days to maturity and grain yield per faddan. While., it was high for plant height, spike per M² and 1000-kernel weight. And it was low for kernel per spike, chlorophyll content and canopy temperature depression .on the other hand, estimating broad sense heritability under stress conditions shows low values for days to heading, days to anthesis, days to maturity, spike per M² and 1000-kernel weight. While it was high for other treats. (Table 3). Our results were similar to Tripathi *et al.* 2011., where, High heritability estimates for plant height and days to heading (Baranwal *et al.* 2012), thousand kernel weight (Ashraf *et al.* 2002) and spike length (Ali *et al.* 2008). Heritability is a part of the selection differential that can be exercised in efficiency to traits will be effective (Falconer and Mackay, 2005). Due to the higher appreciation of heritability, large selection benefits can be expected for the traits studied (Mehri *et al.*, 2009). However, the selection should be made with great care, as inheritance is measured in the broadest possible sense. K_g² for every trait and the percent of the variation of traits were computed by Golabadi *et al.* (2005). (K_g² = genetic variance of trait x in stress environment / genetic variance of trait x in non-stress environment)

(79.63 days), days to anthesis (83.33days) and the number of days to maturity (131.37 days), respectively., in the same conditions, genotype 293 heading and anthesis were the last with a mean (95.83 days) and (99.10) respectively. genotype 333 maturity was last with a mean (141.80 days). Under normal irrigation, genotype 217 heading was earliest with a mean of (83.13 days) days and days to anthesis with a mean (87.50 days). on the other side, in non-stress

conditions, the maturity of genotype 322 was earliest with a mean of (134.57 days) while the maturity of genotype 403 was the last (148.13 days). Under normal irrigation, The tallest plant was determined in genotype 8 with means

(114.57 cm) and the shortest length in genotype 403 with means (103.10cm). The 24 genotypes recorded higher heights compared to the other genotype with an average of (101.93 cm) under stress conditions.

Table 3. Range, mean, percentage decrease, and heritability in broad-sense and K^2_g under drought stress (out) compared with normal irrigation (with) conditions.

Traits	Condition	MIN	MAX	Range	Mean	SEM	decrease%	h^2_b %	K^2_g
DH	out	77.60	99.30	21.70	88.38	0.59	3.42	87.32	1.01
	with	79.70	101.10	21.40	91.51	0.59		94.66	
DA	out	80.80	101.30	20.50	91.64	0.61	4.44	85.81	1.28
	with	83.50	105.10	21.60	95.90	0.68		93.45	
DM	out	129.70	148.40	18.70	139.36	0.46	1.72	67.67	1.64
	with	132.50	150.50	18.00	141.79	0.56		79.92	
PH	out	83.90	103.60	19.70	95.27	0.54	12.08	50.08	0.94
	with	99.60	116.10	16.50	108.36	0.48		59.94	
SM ²	out	242.00	419.00	177.00	321.22	4.94	13.31	62.31	1.36
	with	269.00	486.00	217.00	370.56	5.50		68.20	
KS	out	44.90	63.60	18.70	53.36	0.41	7.89	40.62	1.33
	with	48.10	68.50	20.40	57.93	0.54		37.36	
1000-KW	out	33.60	50.60	17.00	41.70	0.38	9.99	43.06	1.95
	with	40.40	59.70	19.30	46.33	0.44		68.86	
GY Ton/F	out	1.49	3.15	1.66	2.28	0.04	19.72	64.36	2.00
	with	1.77	3.73	1.96	2.84	0.05		84.40	
CHIO -CON	out	41.80	58.60	16.80	49.86	0.40	-3.52	50.32	0.45
	with	41.30	54.80	13.50	48.16	0.35		27.06	
CTD	out	-7.50	-3.30	4.20	-5.32	0.11	29.69	26.71	1.12
	with	-10.20	-5.50	4.70	-7.57	0.13		27.94	

Data in the table (4) shows that sakha94 had the highest number of kernels per spike with 65.30 gm in non-stressed conditions. genotype 512 had the highest no. of kernel per spike with 57.33 gm in stress condition (Table 4).on the other site, sakha94 had the heaviest 1000-kernel weight 57.33 gm in non-stressed condition. Also, the heaviest 1000-kernel weight was recorded for the same genotype in normal irrigation conditions with a mean 48.00 gm. The highest grain yield was determined in genotype 369 with mean (3.52 tons) and (3.05 tons) in non-stress conditions and normal irrigation, respectively. In normal conditions, genotype 229 had the highest mean spike/m² with mean (459.00 spikes) and giza168 had the lowest mean Spike/m² of ((273.00 spikes)). In stress condition genotype 369 had a maximum mean spike/m² of (380.3 spikes) and genotype 265 had a minimum mean spike/m² of (259.33). We can say that the selection of genotypes with 1000-kernel weight, number of kernels per spike and grain yield from agronomic characteristics influences yield improvement under stress conditions, Similar to Badran, (2022) reported that the selection of drought tolerant genotypes leads to reconnaissance genotypes with high 1000 grain weight. The effect of drought stress on the yield and yield components generally causes a decrease in photosynthesis and growth. Where it was found to decrease in yield and yield components under stress conditions studied.

Plants grown under drought conditions have a lower stomatal conductance to conserve water. Consequently, CO₂ fixation is reduced and the photosynthetic rate decreases, resulting in less assimilate production for the growth and yield of plants. Diffusive resistance of the stomata to CO₂ entry probably is the main factor limiting photosynthesis under drought (Boyer. 1970). Also, severe drought stress inhibits the photosynthesis of plants by causing changes in chlorophyll content, affecting chlorophyll components and damaging the photosynthetic apparatus (Iturbe Ormaetxe *et*

al., 1998). Ommen *et al.* (1999) reported that leaf chlorophyll content decreases as a result of drought stress. In our study, chlorophyll content was affected by water deficit. genotype 585 was the most affected by water stress where recoded 45.80 while genotype 403 was the lowest affected by water stress where recorded 57.20.

Path analysis

Determination of associations between different traits especially grain yield and its components and also the determination of cause and effect relations between them allow breeders to select the most suitable lead to higher yield. In these types of studies to identify direct and indirect effects on components and entered traits into regression model path analysis by the method of (Dewey Wolve, 1959) was applied. The results of the path analysis to the normal and stress conditions are shown in Table 5. In both conditions spike per M² direct positive effects with 0.487 and 0.363 while days to heading showed more negative effects with (-0.408) and (-0.562) respectively. While spike per M² was the highest indirect positive effect on the yield in both conditions. Days to heading and canopy temperature was the highest indirect negative effect.

Cluster analysis

Cluster analysis was carried out on genotypes using the average grain yield traits to classify the measured genotypes for drought stress tolerance. Genotypes were clustered into hierarchical dendrograms based on Euclidean distance procedure using the un-weighted pair group method as described by Michael Eisen *et al.* (1998). Statistical analyses were performed using Minitab-16. Most studied traits revealed significant variation in respect of the genotypes under this investigation. There were observed differences exist at the genotypic level under normal and drought stress conditions. Euclidean cluster analysis of 24 bread wheat genotypes resulting concerning normal and drought stress conditions are presented in Tables 6 and 7. Cluster analysis method divided the

genotypes into five groups under different (normal or stress) conditions (Figures 1 and 2). In normal conditions, the cluster pattern revealed that cluster-1 concluding of 6 genotypes recorded the largest cluster average of grain yield (3.02 ton/fed) which was followed by cluster-2 (10 genotypes) with average (2.89 ton/fed) grain yield. Meanwhile, cluster 4 which contained only genotype no. 24 was the smallest cluster average (2.05 ton/fed).

Under water shortage stress conditions among the five clusters, cluster-1 had the largest cluster average (3.05 ton/fed) containing only genotype no. 14 followed by

cluster-3 consisting of (5 genotypes) scoring an average (2.43 ton/fed). On the other side, cluster-4 which consisted of (3 genotypes) was the smallest cluster average (1.95 ton/fed). The grouping pattern indicated little association of genetic divergence with yield traits of genotypes, suggesting that clustering and represents genetic diversity responding to stress conditions. These findings indicate that the resulting grouping containing favorable traits leads to discriminate clustering that may be developed mechanism directional selection pressure, especially under stress conditions.

Table 4. Mean-performance of yield components each genotype in normal irrigation (with) and drought stress (out) conditions

Entry		DH	DA	DM	PH	SM2	KS	1000-KW	GY Ton/F	CHIO-CON	CTD
217	Out	80.50	83.77	131.37	97.03	279.67	51.93	46.27	1.86	52.67	-4.93
	With	83.13	87.50	134.67	114.00	320.00	60.03	50.50	2.53	48.63	-7.17
226	Out	82.53	83.73	135.63	94.13	309.00	54.40	41.37	2.52	51.97	-4.97
	With	86.93	90.50	139.80	106.10	334.33	58.73	46.13	3.34	47.60	-8.07
229	Out	88.57	91.43	136.67	98.43	342.67	53.67	40.50	2.29	46.40	-5.43
	With	92.30	94.73	139.43	106.07	459.00	57.50	44.63	2.72	44.90	-7.67
253	Out	89.83	93.47	139.13	96.40	269.33	53.47	40.83	2.36	46.37	-5.77
	With	93.80	96.23	140.77	110.90	387.00	57.80	44.10	3.06	47.97	-7.73
353	Out	83.07	86.10	135.90	97.53	338.00	51.10	42.70	2.24	50.50	-5.13
	With	85.80	89.40	135.53	111.80	377.00	53.30	47.13	2.84	48.73	-6.67
403	Out	97.80	99.33	144.03	88.60	349.67	53.43	39.70	1.98	48.97	-5.93
	With	99.37	102.87	148.13	103.10	389.00	57.47	46.90	2.83	46.60	-8.00
405	Out	84.17	87.10	135.37	93.40	284.67	55.20	38.30	2.52	57.20	-5.27
	With	86.80	91.27	137.07	105.90	332.00	60.70	42.33	2.85	53.43	-6.60
265	Out	89.70	95.13	141.47	97.40	259.33	51.50	39.50	1.92	48.73	-4.73
	With	93.50	102.40	142.50	114.57	335.00	59.57	48.80	3.28	51.30	-7.87
293	Out	95.83	99.10	142.63	99.47	279.33	53.13	46.17	2.01	51.27	-6.13
	With	97.00	102.77	146.13	110.70	316.67	60.37	49.80	2.35	48.27	-7.63
322	Out	79.63	83.33	134.77	91.47	283.00	54.67	42.77	2.17	50.80	-4.37
	With	81.57	86.00	134.57	107.03	319.67	61.80	46.43	1.96	48.70	-6.00
333	Out	90.67	97.43	141.80	92.03	317.00	55.20	40.43	2.12	54.10	-5.63
	With	93.83	103.07	144.43	101.87	381.67	56.40	44.83	2.49	49.93	-7.07
343	Out	93.37	96.80	139.63	100.20	347.00	54.20	40.73	2.36	46.80	-6.23
	With	94.43	100.70	140.83	110.33	410.33	56.70	44.77	3.10	45.67	-7.93
352	Out	92.47	94.40	144.60	89.87	368.67	51.13	39.63	1.98	48.70	-5.77
	With	96.77	99.43	146.53	103.97	395.33	54.03	42.63	2.70	47.47	-8.50
369	Out	83.20	85.70	136.37	93.47	380.33	49.93	41.57	3.05	51.77	-4.80
	With	86.67	90.83	137.57	110.67	419.33	54.00	43.13	3.52	48.00	-7.33
383	Out	88.10	90.43	138.37	88.97	337.00	56.07	38.47	2.26	50.00	-6.30
	With	90.13	92.77	139.80	104.53	367.67	56.83	44.47	3.35	48.63	-7.77
388	Out	89.57	93.97	142.13	101.20	346.67	52.97	42.97	2.32	46.40	-5.97
	With	94.17	98.47	144.77	108.47	390.33	57.53	47.10	2.26	49.77	-7.30
559	Out	93.13	95.73	141.83	91.20	328.33	55.20	40.07	2.40	47.50	-5.30
	With	96.67	101.70	145.80	107.60	369.33	55.73	42.60	2.88	44.83	-8.57
585	Out	88.83	91.37	137.60	98.83	355.67	50.87	40.40	2.35	45.80	-5.77
	With	90.87	93.17	139.43	107.90	398.00	54.93	44.93	2.54	44.33	-8.03
398	Out	81.47	86.37	138.73	94.03	361.00	53.00	40.43	2.80	50.07	-4.03
	With	86.77	90.17	138.73	108.60	415.00	58.87	43.77	3.39	47.33	-7.20
305	Out	91.13	95.83	142.00	94.00	325.00	55.10	40.40	2.36	49.47	-6.00
	With	96.17	101.80	145.03	104.57	364.67	61.90	46.87	2.89	48.43	-8.80
307	Out	90.13	93.17	144.60	93.70	368.67	48.07	41.10	2.24	50.33	-3.83
	With	92.20	99.30	147.87	109.50	418.33	53.90	48.37	3.05	48.63	-6.70
512	Out	91.07	95.13	139.93	97.50	297.33	57.33	46.23	2.34	51.17	-5.50
	With	96.70	101.53	144.70	113.53	362.00	65.30	50.93	2.86	46.50	-8.23
Sakha94	Out	89.13	91.70	141.70	95.77	318.67	48.90	48.00	2.72	49.13	-5.00
	With	90.83	93.17	147.80	112.33	358.67	54.13	56.10	3.32	51.57	-8.03
Giza168	Out	87.20	88.77	138.43	101.93	263.33	60.13	42.33	1.56	50.43	-4.87
	With	89.80	91.80	141.17	106.70	273.00	62.83	44.70	2.05	48.57	-6.70

Generally, genetic divergence has been found related to several genetic and non-genetic conditions like extent of genotype x environment interaction and components of genetic variation. Therefore, selected parents for hybridization to get more heterotic and

desirable segregates based on genetic diversity. Therefore, a hybridization program may be initiated involving the genotypes belonging to diverse cluster-1 and cluster-2 under different conditions with high average values for grain yield traits.

From obvious results, mean performance of the genotypes 5, 15, 17, 20, 22 and 23 within the clusters recorded high yielding and divergent under condition

normal. Meanwhile, genotypes 14, 2, 11, 23, 17 and 20 had high yielding and divergent under water shortage stress conditions for yield improvement in bread wheat.

Table 5. The direct and indirect contribution of various traits to yield in bread wheat genotypes.

Trait		Direct effect		Indirect effect							Total effect
		DH	DA	DM	PH	SM2	KS	1000-KW	Chlo-con	CTD	
DH	out	-0.408	0.260	-0.147	0.003	0.065	-0.002	-0.010	-0.025	0.021	-0.244
	with	-0.562	0.169	0.099	-0.021	0.069	0.004	0.000	-0.029	0.300	0.030
DA	out	0.277	-0.382	-0.149	0.002	0.033	-0.002	-0.009	-0.024	0.019	-0.234
	with	0.184	-0.517	0.096	-0.017	0.046	0.003	0.001	-0.013	0.243	0.025
DM	out	-0.197	-0.305	0.210	0.009	0.126	0.006	-0.007	-0.021	0.009	-0.169
	with	0.128	-0.432	0.137	-0.023	0.022	0.021	0.004	-0.004	0.201	0.054
PH	out	-0.050	0.026	-0.012	0.037	-0.127	-0.007	0.022	-0.015	0.004	-0.123
	with	0.129	0.093	-0.024	-0.023	-0.014	-0.012	0.014	0.011	0.044	0.220
SM2	out	0.487	-0.054	0.019	-0.051	0.013		0.024	-0.014	-0.018	0.002
	with	0.363	-0.107	0.023	0.008	-0.005		0.034	-0.006	-0.045	0.066
KS	out	-0.079	-0.013	0.005	0.015	-0.005	-0.149		-0.003	0.008	0.009
	with	-0.115	0.018	-0.005	-0.023	0.013	-0.106		0.006	-0.007	0.077
KW	out	0.060	0.066	-0.043	0.022	-0.018	-0.117	0.003		0.008	-0.003
	with	0.031	0.002	0.004	0.019	0.061	-0.068	-0.023		0.024	0.020
CHIO-	out	0.095	0.109	-0.070	0.044	0.008	-0.092	-0.007	0.005		-0.005
	with	0.154	0.104	-0.016	-0.004	0.009	-0.107	0.005	0.005		-0.113
CTD-	out	-0.048	0.173	-0.111	0.037	0.004	-0.025	0.015	0.004	0.009	0.059
	with	-0.523	0.323	-0.085	-0.049	-0.011	-0.046	0.017	-0.001	0.033	-0.343

DIRECT = Out (27.562), With (30.92). INDIRECT = Out (36.492), With (44.67).

RI % = OUT 64.053, With (75.59). RES % = Out (35.947), with(24.42).

Table 6. Distribution of 24 bread wheat genotypes into five clusters based on similarity analysis under normal conditions and cluster average of grain yield.

Cluster number	No. of Genotype s	Similarity	Genotype s Number	Percentage %	Cluster mean
Cluster1	6	85.36	5, 15, 17, 20, 22 and 23	25.00	3.02
Cluster2	10	66.07	4, 16, 18, 6, 13, 11, 12, 21, 14 and 19	41.67	2.89
Cluster3	1	45.31	3	4.17	2.72
Cluster4	1	65.73	24	4.17	2.05
Cluster5	6	84.92	1, 10, 2, 7, 8 and 9	25.00	2.72

Table 7. Distribution of 24 bread wheat genotypes into five clusters based on similarity analysis under stress conditions and cluster average of grain yield.

Cluster number	No. of Genotype s	Similarity	Genotype s Number	Percentage %	Cluster mean
Cluster1	1	63.27	14	4.17	3.05
Cluster2	10	71.03	3, 12, 16, 5, 15, 6, 13, 21, 18 and 19	41.67	2.28
Cluster3	5	78.29	2, 11, 23, 17 and 20	20.83	2.43
Cluster4	3	89.04	4, 8 and 24	12.50	1.95
Cluster5	5	67.84	1, 10, 7, 9 and 22	20.83	2.18

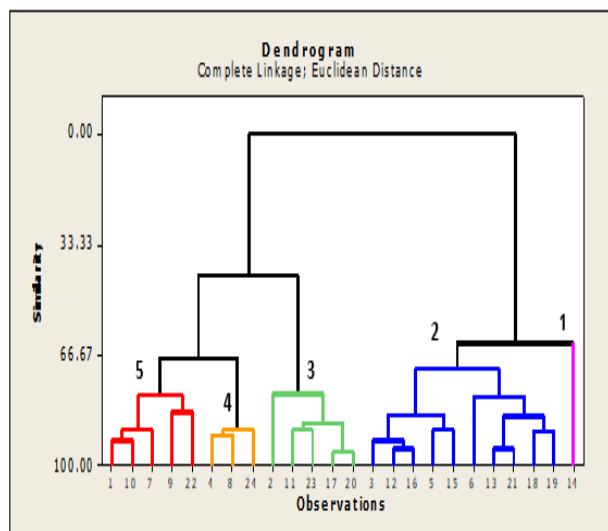


Fig. 1. Dendrogram showing the genetic relationship of 24 bread wheat genotypes, clustering based on similarity analysis under normal conditions.

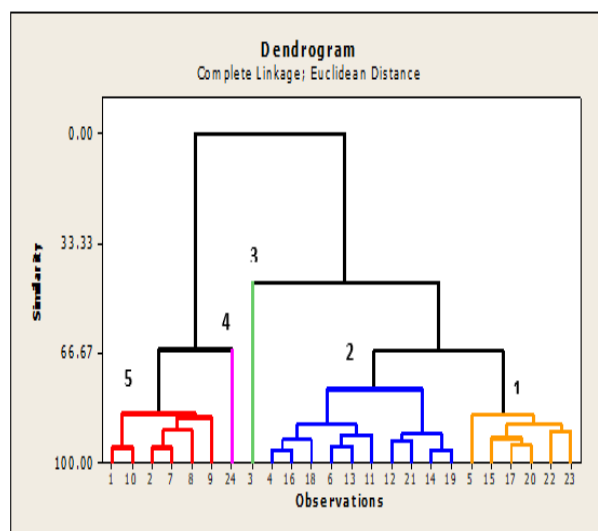


Fig. 2. Dendrogram showing the genetic relationship of 24 bread wheat genotypes, clustering based on similarity analysis under stress conditions.

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تقييم التنوع الوراثي لبعض التراكيب الوراثية لقمح الخبز تحت ظروف الري العادي الإجهاد المائي باستخدام تحليل متعدد المتغيرات

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المخلص

تم اجراء البحث لتقييم التنوع الوراثي لـ 24 تركيب وراثي للقمح، 22 من التراكيب الوراثية تم الحصول عليها من مركز البحوث الزراعية، الجيزة، مصر، وصنفان تجاريان هما؛ سخا 94 و جيزة 168. صممت التجربة في قطاعات منشقة كاملة العشوائية في ثلاث مكررات. سجل تحليل التباين فروقا عالية معنوية لجميع الصفات بين التراكيب الوراثية تحت ظروف الإجهاد المائي. وكان هناك تنوع وراثي بين التراكيب الوراثية لجميع الصفات. وظهرت النتائج نسبة انخفاض في قيمة الصفات لجميع التراكيب تحت ظروف الإجهاد المائي ما عدا صفة محتوى الكلوروفيل. كما سجلت درجة التوريث بعناها الضيق قيمة عالية لصفات عدد الايام حتى طرد السنابل وعدد الايام حتى النضج الفسيولوجي ومحصول الفدان. ايضا كان التأثير المباشر ايجابيا لصفة عدد السنابل لكل متر مربع في كلا المعاملتين حيث كانت النتائج كالتالي 0.784 و 0.383 على التوالي وبينما كان التأثير سلبيا لصفة عدد الايام حتى طرد السنابل بقيم 0.408 و -0.562 على التوالي. قسمت طريقة التحليل العنقودي الأنماط الجينية إلى خمس مجموعات تحت ظروف مختلفة (رى أو إجهاد)، وقد وجد أن الاختلاف الجيني له علاقة بحالات وراثية وغير وراثية مثل مدى تفاعل التراكيب الوراثية مع البيئة وكذلك مكونات التباين الجيني. تحت ظروف الإجهاد المائي بين المجموعات الخمس، كان المجموعة 1 أكبر متوسط في التحليل العنقودي (3.05 طن / فدان). هذه النتائج تعطي فرصة جيدة لتحقيق التحسين الوراثي للقمح من خلال التهجين بين التراكيب الوراثية عالية الإنتاجية العالية تحت ظروف الإجهاد مثل 14 و 2 و 11 و 23 و 17 و 20.