Genetic Diversity Evaluation of Some Upland Cotton Genotypes (*Gossypium hirsutum* L.) By Cluster Analysis

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Received: 18/4/2023
Accepted: 10/5/2023
Published: 05/12/2023

Abstract

The study included ten genotypes of upland cotton, in 2022 at Rahmaniyah (Mosul) using a randomized complete block design with three replications, it was analyzed statistically to identify the nature of the differences between the genotypes. The stages of the cluster analysis showed that the genotypes were distributed in eight groups, the first, second, fourth, fifth, sixth and seventh included one genotype for each of them, respectively COKER310, MONTANA, SPERO, LACHATA, CANDIA and EDESSA, indicating the variation between it and the other genotypes, which is due to the variation in their genetic origin, which was thus reflected on their performance, while the other groups included two genotypes each. It is concluded from the results of the cluster analysis that there is a strong convergence between the pairs of genotypes W888 with IK259, and FLASH with BA440, because they have the least Euclidean distances, and this necessitates avoiding crossing between them, while the highest distance between the genotypes COKER310 and FLASH, was an indication of high genetic variation between them and other genotypes, that may be due to the difference in their genetic origin or to their possession of preferred main genes that the other genotypes lack, which encourages their inclusion in crosses with genotypes that showed distinguished genetic heterogeneity, to take advantage of the phenomenon of heterosis and the segregations that result from it.

Keywords: Cotton, Varieties, Cluster, Diversity.

INTRODUCTION

Upland cotton belongs to the Gossypium genus, which is primarily found in tropical and subtropical regions of the world and has 45 diploid species and five allotetraploid species. In the past, natural cross-breeding was crucial to the evolution of contemporary farmed cotton. (Ameer et al.,, 2019). Potential production of cotton in the future depends on the development of varieties of the crop that are characterized by a higher production capacity of seed cotton and good quality characteristics, in addition to their resistance to biotic and abiotic factors. Little attention has been given over the past few decades to expanding the genetic base of cotton germplasm. Only a small portion of the germplasm that is available to crop breeders is used for variety breeding; the majority of contemporary varieties have been created through re-

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Part of PH. D. Thesis for the first researcher

selection, which has caused a sharp decline in genetic diversity (Guang and Ming, 2006 and Rathinavel, 2017). It was expected that the reason for the decrease in yield and fiber characteristics is due to the narrow genetic base of cotton germplasm (Rathinavel, 2017). Molecular studies of genetic diversity in Upland cotton also confirmed its low genetic diversity (Shakeel et al., 2015). Although natural upland cotton contains wide genetic variance that is useful in cultivar improvement (Govindaraj et al, 2015), breeders have used closely related ancestors with few economic traits in approved breeding programs with minimal gains in yield. For this reason, Principal Components Analysis and Cluster Analysis were adopted to evaluate and

compare the genetic diversity that can be found across genotypes that originated in different eras and which might be useful in choosing parents for a productive breeding program. Any crop breeding program's capacity to succeed depends on its ability to gather data and the availability of genetic variants that may be used to implement an effective selection strategy. (Boopathi et al., 2008). Cluster analysis is one of the good and useful tools for plant breeders to use in evaluating genetic divergence with molecular indicators, in addition to not needing to make certain assumptions about the nature of data distribution (Hamdallah, 2011). For their important quantitative characteristics depending on the similarity of their responses to environmental conditions, as it depends on determining distances that reflect the amount of this divergence and the distribution of genotypes in groups according to their performance and genetic origins, and that estimates of similarity or genetic divergence or through In order to conserve genetic variety in the breeding program and to classify germplasm into hybrid groups for the breeding of hybrid crops, the genetic distance between genotypes is useful when picking parental groups to establish isolated populations. (Ali et al., 2008). Numerous studies have been conducted on the classification of cotton genotypes into homogeneous groups, including those carried out by, Boopathi et al. (2008), Ahmed et al. (2012), Noormohammadi et al. (2013), Abd El-Moghny et al. (2015), Mahmood et al. (2020) and Sarwar et al, (2020).

The aim of the current study was to evaluate to genotypes of cotton according to the characteristics of seed cotton yield, its components of other traits and fiber specifications, to estimate the degree of genetic variation between its genes, and to classify them into groups of parents to benefit from them in cross-breeding programs.

MATERIALS AND METHODS

The experimental materials included requirements to study the effect of two factors, the first is ten genotypes of medium-staple (*Gossypium hirsutum* L.) obtained from Dr. Jassim Muhammad Aziz, a professor at the College of Agriculture at the University of Tikrit, including (COKER310 and LACHATA) approved for cultivation in Iraq. Table (1) shows the names of these genotypes and their origins, and the second is four levels of nanofertilizer, where the ten varieties were cultivated at the levels (0. 1, 2 and 3 gm/liter) of nano-chelated NPK 20-20-20, sprayed on the leaves at the beginning of boll formation. Cultivation was in the Rahmaniyah area adjacent to the University of Mosul at 43.14 longitude and 36.37 latitude on April 22 and 23, 2022. The cultivation relied on a rows of 3 m length, and the distance between the rows is 0.75 m, and in holes on the top of the row, the distance between

Table 1: The studied cotton genotypes and their origins.

Sq	Name	Origin	Notes
1	BA440	American	Introduced by private sector agricultural companies 2018
2	FLASH	Turkish	Introduced by private sector agricultural companies 2018
3	EDESSA	Turkish	Introduced by private sector agricultural companies 2018
4	LACHATA	Spanish	Registered and certified in Iraq
5	SPERO	Greek	Introduced that and previously used in experiments in Iraq
6	IK259	Greek	Introduced and was widely used in experiments in Iraq
7	W888	American	previously entered into a preliminary comparison experiment by the Ministry of Agriculture in 1990, and in several experiments after that
8	COKER310	American	Registered and certified in Iraq
9	MONTANA	American	Introduced and tested in many experiments, especially within the cotton cultivation develop program in Iraq
10	CANDIA	South African	Introduced by the private sector, and it is of the varieties that follow a mid-late growing group

them is 0.25 m, and under the conditions of drip irrigation, after plowing the soil (clay loam soil) twice perpendicularly by means of the moldboard plow, then smoothing and leveling it and establishing the rows. The compound fertilizer (DIAMMONTUM PHSPHATE 18-46-0 (Jordanian dab) was added at a rate of 200 kg/ha after plowing and before establishment of the rows, and urea (46%) at a rate of 150 kg/ha at the beginning of flowering on June 20, 2022. Acta Super (Al-Thiamethoxam 14.1%+lambda-cyhalothrin 10.6% Sc) was used at a concentration of 50 ml / 100 liters of water to control the cotton boll worm on June 18, 2022 and the white fly on September 3, 2022. The two-factors experiment was carried out using a randomized complete block design with three replications, each block contained 40 experimental units, the factorial treatments (combination between genotypes and levels of nano-fertilizer) were randomly distributed to it, and each experimental unit contained three rows. All crop service procedures were carried out as needed during the crop growth and maturity period. Seed cotton was taken from five randomly selected plants from each experimental unit twice, the first on October 1, 2022 and the second on November 1, 2022. Data were recorded on the traits: number of days to first boll opens (NDFB), plant height in cm (PH), number of fruiting branches (NFB), number of bolls per plant (NOB), average weight of the boll in gm (BW), seed index in gm (SI), ginning outturn% (GOT), lint index in gm (LI), earliness (ER), seed cotton yield per plant in gm (SCY), 50% span length in mm (50%SL), 2.5% span length in mm (2.5%SL), fiber length uniformity% (LU), lint fineness in micronair (LF), lint strength (LS) in gm/tex and lint elongation% (LE).

After collecting the data for the different traits and tabulating them, the statistical analysis was conducted according to the experimental design method used to identify the nature of the differences between each of the levels of nano-fertilization and genotypes (Al-Zubaidy and Al-Falahy, 2016). Depending on the means of genotypes for the traits of the seed cotton yield, its components, and the fiber properties, a cluster analysis was conducted with the aim of placing the genotypes into groups according to the response pattern (Sneath and Sokai, 1973). The study was conducted in two stages: the principal components approach was used in the first stage, and multiple steps were involved in the cluster analysis, which began with the creation of a similarity matrix between the genotypes. (Proximities Matrix), after which the Dendogram is created using the UPGMA technique (Sneath and Sokai, 1973), whereby distances are calculated that represent how similar the averages are to one another. of the aggregates of the indicated matrix. The available programs SAS (Statistical Analysis System) and SPSS were used to implement the statistical procedures.

RESULTS AND DISCUSSION

Table (2) shows the analysis of variance results for the traits of seed cotton yield, its components, and fiber properties of, in which it is noted that the mean squares of the nano-fertilizer levels were quite significant for every traits but for LU (significant at 5% probability level), and for SI, 50% SL and 2.5% SL (not significant), and these results agree with Kanjana (2020) who found that there are significant differences between levels of nano-fertilizer for most traits he studied, and his results clearly revealed that application of

Table 2: Analysis of variance results for yield, its components, and fiber properties.

Source	df	Mean square for traits					
		NDFB	PH	NFB	NOB	BW	SI
Reps.	2	11.108	3.820	0.438	1.212	0.096	0.139
Nano-fertilizer	3	3.756**	23.526**	22.133**	8.542**	0.382**	0.091
genotypes	9	0.737	3010.905**	4.217**	39.880**	0.701**	1.768**
NF x Gen.	27	0.922**	326.439**	2.981**	14.049**	0.418**	0.500**
Error	78	0.4929	2.324	0.279	0.965	0.039	0.143
		GOT	LI	ER	SCY	50% SL	2.5% SL
Reps.	2	0.209	0.155	0.00001	21.018	0.684	2.675
Nano-fertilizer	3	78.568**	4.146**	0.019**	302.26**	0.914	0.509

genotypes	9	257.38**	11.845**	0.010**	390.08**	1.457**	7.549**
NF x Gen.	27	52.459**	2.390**	0.003**	308.39**	0.573	3.794**
Error	78	1.532	0.146	0.00007	8.159	0.361	1.686
		LU	LF	LS	LE		
Reps.	2	0.2979	0.215	0.157	0.191		
Nano-fertilizer	3	16.712*	1.046**	7.078**	5.075**		
genotypes	9	8.906	0.465**	11.281**	5.868**		
NF x Gen.	27	7.725	0.218	6.591**	4.338**		
Error	78	5.042	0.181	0.174	0.129		

(**) and (*) significant at 1% and 5% probability level respectively.

recommended dose of nano-fertilizers significantly increased seed cotton yield. As for the genotypes' mean squares, which are significant in the current investigation

for all traits except for NDFB and LU, and this is an indication of the existence of genetic differences between them. These results are consistent with the findings of Abd El-Moghny et al. (2015), Mahmood et al. (2020), Amein et al. (2020) and Balcha et al. (2022). It is noted that the interaction of genotypes with the levels of fertilization was highly significant for all traits except 50% SL, LU and LF. Hamdallah (2011) showed that genetic interaction with the environment lowers the rate of genetic improvement and impacts the precision of selection, necessitating the use of statistical methods (such as cluster analysis) to solve this issue. The means of nano-fertilization levels are shown in Table (3), and it is noted that the level of 3 gm/L is surpassed with highest means for the traits NDFB, PH, NFB, NOB, SI, SCY, and 2.5%SL, and the level of 2 gm/L gave highest means for the traits

Table 3: Means of nano-fertilizer levels for yield, its components and fiber properties.

Fertilizer levels	Traits							
	NDFB	PH	NFB	NOB	BW	SI	GOT	LI
0	104.100bc	105.593a	9.073 c	17.183a	4.394 c	9.943a	31.079c	4.514c
1 gm/L	104.333ab	104.213b	10.300b	16.937b	4.514 b	9.944a	31.339c	4.686c
2 gm/L	103.833 c	104.047b	10.513b	16.983b	4.646 a	9.834a	34.399a	5.373a
3 gm/L	104.667 a	105.720a	11.120a	18.080a	4.609ab	9.871a	33.451b	4.897b
	ER	SCY	50% SL	2.5%SL	LU	LF	LS	LE
0	0.879 c	76.759 c	12.787b	27.467a	46.571b	4.06bc	16.303a	6.760a
1 gm/L	0.915 b	77.495 c	12.86ab	27.417a	46.932b	4.22ab	15.700c	6.127b
2 gm/L	0.931 a	79.453 b	13.153a	27.340a	48.301a	4.34 a	15.177d	5.787c
3 gm/L	0.882 c	83.829 a	13.08ab	27.647a	47.36ab	3.913c	16.037b	6.063b

- Means followed by the same letter did not significantly different.

of BW, GOT, LI, ER, 50% SL, LU and LF, while for LS and LE the highest means were 16.303 gm/tex and 6.760% when fertilizer was not used. In general, it is clear that level 3 gm/L of the fertilizer gave good performance means for most traits, including seed cotton yield, followed by level 2 bm/L. These results indicate the importance of using this type of fertilizer to achieve positive results that are reflected in the seed cotton yield and its components. Table (4) shows the mean performance of the genotypes for the different traits, and it is noted that the best performance was in the genotype BA440 for NFM, GOT, LI and ER, FLASH for NOB, SCY, 50% SL and 2.5% SL, LACHATA for LU and LF, SPERO for NDFB, W888 for SI and LE, COKER310 for PH and BW, and CANDIA for LS. In general, it

Table 4: Means of cotton genotypes for yield, its components, and fiber properties.

genotypes	Traits							
	NDFB	PH	NFB	NOB	BW	SI	GOT	LI
BA440	104.1ab	88.917i	10.917a	18.792bc	4.253 c	9.633c	39.22a	6.549a
FLASH	104.4ab	91.150h	10.300bc	19.833 a	4.347 c	9.506c	37.62b	5.968b

EDESSA	104.4ab	97.533g	10.050cd	18.292cd	4.391 c	9.426c	38.45ab	5.509c
LACHATA	104.1ab	123.667b	10.850a	17.900 d	4.678 b	10.01b	30.49e	4.936d
SPERO	103.83b	111.883c	9.717 d	16.092fg	4.777ab	10.21b	27.93fg	4.009e
IK259	104.3ab	102.633f	10.617ab	16.325ef	4.613 b	10.18b	28.57f	4.305e
W888	104.1ab	105.633e	10.083cd	15.450 g	4.767ab	10.55a	28.87f	4.237e
COKER310	104.58a	134.733a	9.000 e	14.058 h	4.929 a	9.557c	27.27g	3.344f
MONTANA	104.0ab	109.000d	10.18bcd	17.042 e	4.257 c	9.691c	32.42d	4.337e
CANDIA	104.5ab	83.783 j	10.800 a	19.175ab	4.398 c	10.22b	34.84c	5.574c
	ER	SCY	50%SL	2.5%SL	LU	LF	LS	LE
BA440	0.929 a	80.66 cd	13.267ab	27.875ab	47.6abc	3.733c	16.042c	6.183c
FLASH	0.919bc	87.574a	13.650a	28.508 a	47.91ab	4.03bc	14.733e	5.375e
EDESSA	0.924ab	81.204 c	12.98bcd	28.492 a	46.62 c	4.13ab	16.583b	6.758b
LACHATA	0.918bc	84.757 b	12.72bcd	26.175 d	48.63 a	4.483a	15.875c	6.11cd
SPERO	0.903 d	78.74de	12.642cd	26.550cd	47.6abc	4.07bc	15.292d	6.04cd
IK259	0.912 c	76.424ef	12.73bcd	27.46abc	46.41bc	4.23ab	14.308f	5.200e
W888	0.872 e	74.709 f	13.225ab	27.892ab	47.4abc	4.13ab	16.992a	7.200a
COKER310	0.832 f	70.262 g	12.72bcd	26.72bcd	47.6abc	4.33ab	15.117d	5.542d
MONTANA	0.905 d	74.118 f	12.592 d	27.28bcd	46.6abc	4.13ab	15.792c	5.867d
CANDIA	0.902 d	85.995ab	13.18abc	27.733ab	47.6abc	4.08bc	17.308a	7.067a

- Means followed by the same letter did not significantly different.

seems that the CANDIA genotype showed good performance means for the largest number of traits, which reached ten, including the seed cotton yield, followed by W888, with good means performance for nine traits, and these findings suggest that cross-breeding initiatives should benefit from these two genotypes in order to convey the good characteristics of yield, its components and fiber properties to the locally approved varieties. The scheme shown in Figure illustrates how the genetic differences were represented through cluster analysis. (1), where the genotypes were distributed in eight groups (Table 5) and also included nine stages (Table 6). Table (5) indicates that the genotypes of Montana, Lachata, Chrip-AM53 and IK347 (Groups 2, 3, 7 and 10) varied from all other genotypes in that each one stood for a distinct group on its own, and this indicates that they have a large genetic difference from the genotypes the other, and this is confirmed by its high Euclidean distances with the other structures shown in Table (8). It is noted from Table (6) that the genotypes COKER310, MONTANA, SPERO, LACHATA, CANDIA, and EDESSA (Groups 1, 2, 4, 5, 6, and 7) differed from all other genotypes, as each of them represented an independent group

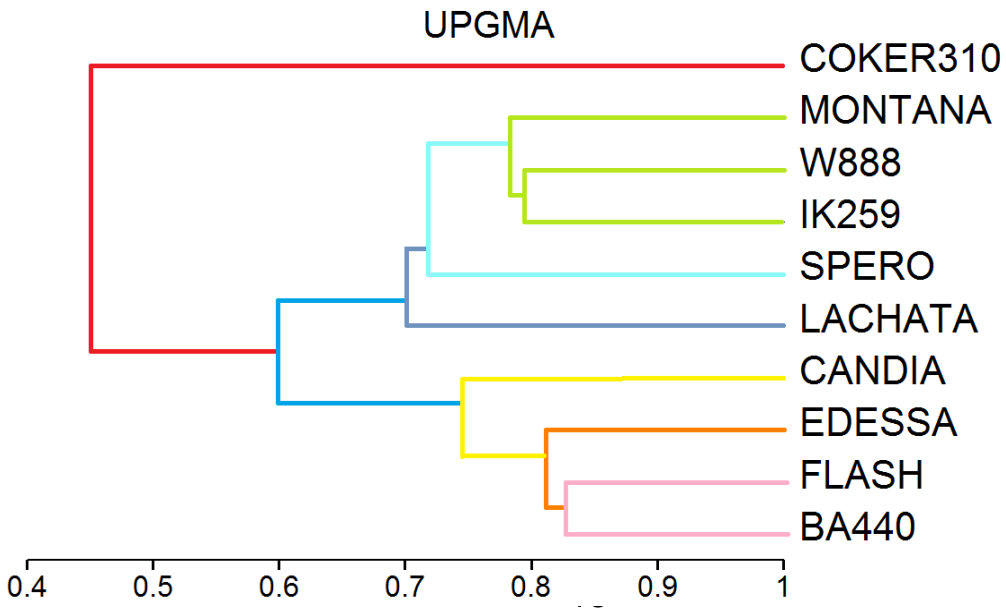

Figure 1: Cotton genotypes groups and

the genetic distance between them

Table (5): The genotypes were included in the groups that were created using cluster analysis..

Groups	Number of genotypes	Names of genotypes
1	1	COKER 310
2	1	MONTANA
3	2	W888 and IK259
4	1	SPERO
5	1	LACHATA
6	1	CANDIA
7	1	EDESSA
8	2	FLASH and BA440

Table 6: The distances between groups based on the cluster analysis stages.

Node	Group 1	Group 2	Similarity	Objects in group
1	BA440	FLASH	0.827	2
2	Node 1	EDESSA	0.813	3
3	IK259	W888	0.794	2
4	Node 3	MONTANA	0.783	3
5	Node 2	CANDIA	0.745	4
6	SPERO	Node 4	0.719	4
7	LACHATA	Node 6	0.7	5
8	Node 5	Node 7	0.599	9
9	Node 8	COKER310	0.451	10

by itself, and this indicates, it has a great genetic difference from each other and from all other genotypes, and this is confirmed by its large Euclidean distances (less resemblance) to other genotypes, as demonstrated in Table (7), which shows that the highest genetic distance (least similarity) was 0.27 between the two genotypes COKER310 and FLASH, then 0.304 and 0.326 between (COKER310 and BA440) and (COKER310 and CANDIA), respectively. As for the remaining third and eighth groups, each of them contained two genotypes, which are respectively (W888 and IK259) and (FLASH and BA440), with a high degree of similarity between the genotypes in the two groups, 0.794 and 0.827 respectively. These results indicate the potential for establishing a wide genetic base that gives isolated generations the chance to acquire genetic crossing over through cross-breeding across genotypes from genetically distinct groups. As for the results presented in Table (7), and based on Figure (1), it shows the stages of cluster shape formation, as the first stage began merging

Table 7: Matrix of distances between genotypes (Similarity matric).

genotypes	BA440	FLASH	EDESSA	LACHATA	SPERO	IK259	W888	COKER310	MONTANA	CANDIA
BA440	1									
FLASH	0.827	1								
EDESSA	0.818	0.808	1							
LACHATA	0.69	0.662	0.696	1						
SPERO	0.443	0.409	0.505	0.655	1					
IK259	0.621	0.566	0.694	0.755	0.715	1				
W888	0.501	0.467	0.56	0.695	0.763	0.794	1			
COKER310	0.304	0.27	0.44	0.457	0.491	0.609	0.603	1		

MONTANA	0.684	0.629	0.713	0.698	0.679	0.79	0.777	0.558	1	
CANDIA	0.712	0.769	0.754	0.734	0.539	0.67	0.563	0.326	0.638	1
	BA440	FLASH	EDESSA	LACHATA	SPERO	IK259	W888	COKER310	MONTANA	CANDIA

BA440 with FLASH due to their smallest Euclidean distance, they belong to the same group (high similarity) of 0.827. It is noted that in the second stage, the genotypes of the first stage (BA440 and FLASH) and EDESSA genotype with a Euclidean distance of 0.813 separated them after merging. These separations progressively get bigger with the progression of the stages, to reach in the last stage to 0.451, in which the genotypes of the 8th stage (Node 5 and Node 7) were combined with the genotype COKER310. It is concluded from the foregoing that the less Euclidean distances indicate a strong relationship or close genetic similarity between the genotypes, as is the case between pairs of genotype W888 with IK259, and FLASH with BA440 (Table 5), which in this case necessitates avoiding interbreeding between them, and the highest distance between the two genotypes, COKER310 and BA440, amounted to (0.304), indicating their genetic difference with the rest of the other genotypes, which may be due to their difference in genetic origin or to their possession of Their favorable performance for many of the qualities under study was attributed to specific genes that are absent from other genotypes; as a result, crossing any of them with any other genotype may produce a desired heterosis. Table (8) shows the means of the eight cluster analysis groups for the studied traits, and it is noted that the highest significant performance was achieved in the first group for the two traits of PH and BW, and the third group for SI, and the fourth group for NDFB, the fifth group for the traits of NFB, LU and LF the sixth group for the traits of NOB, SCY, LS and LE, the seventh group for the two traits GOT and 2.5% SL, and finally the eighth group for the traits of LI, ER and 50% SL. Due to the fact that having separate genetic structures with significant genetic differences is essential for the success of any breeding and improvement program, these groupings may be adopted in cross-breeding programs to transfer distinct features the desired alleles can be collected and access to diverse types, each with unique requirements for quality and productivity. These findings suggest that these populations should be used in cross-breeding initiatives to impart unique features, as having unique genotypes with significant genetic variations is a crucial

Table 8: Means of the constituent groups according to cluster analysis for yield, its components, and fiber properties.

genotypes groups	Traits							
	NDFB	PH	NFB	NOB	BW	SI	GOT	LI
1 2	104.58a	134.73a	9.000b	14.058b	4.756 a	9.557bc	27.270c	3.344 c
2	104.00a	109.00c	10.18ab	17.04ab	4.339 a	9.691bc	33.09abc	4.337bc
3 1	104.21a	104.13d	10.27ab	15.89ab	4.712 a	10.365a	28.675 c	4.271bc
4 1	103.83a	111.88c	9.717ab	16.09ab	4.723 a	10.206a	27.929 c	4.176bc
5 3	104.08a	123.67b	10.85 a	17.90 a	4.716 a	10.01ab	30.497bc	5.019ab
6 4	104.58a	83.78 g	10.80 a	19.175a	4.339 a	10.223a	35.006ab	5.813 a
7 2	104.50a	97.53 e	10.05ab	18.292a	4.421 a	9.426 c	38.279 a	5.592 a
8 3	104.29a	89.77 f	10.608a	19.029a	4.378 a	9.600bc	37.563 a	6.089 a
	ER	SCY	50% SL	2.5%SL	LU	LF	LS	LE
1	0.832 d	70.262a	12.72bc	16.72bc	47.61ab	4.333ab	15.117e	5.842 e
2	0.905bc	74.118a	12.592c	27.28abc	46.56ab	4.133abc	15.792c	5.867de
3	0.893 c	75.266a	12.98abc	27.68ab	46.91ab	4.179abc	15.650c	6.200 c
4	0.903bc	78.740a	12.64bc	26.55bc	47.63ab	4.067bc	15.29de	6.042cd
5	0.919ab	84.924a	12.72bc	26.175c	48.63 a	4.483a	15.875c	6.108 c
6	0.902bc	86.162a	13.18ab	27.73ab	47.56ab	4.075bc	17.308a	7.267 a
7	0.924 a	81.204a	12.98abc	28.492a	45.62b	4.125abc	16.583b	6.758 b
8	0.927 a	83.571a	13.338a	28.246a	47.25ab	3.883 c	15.354d	5.750 e

- Means followed by the same letter did not significantly different.

determinant of any breeding and development program's success, allowing for the collection of the appropriate alleles and access to unique varieties with their own qualities and productivity requirements.

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تقييم التنوع الجيني لبعض التراكيب الوراثية للقطن الابلند (Gossypium hirsutum L.)
عن طريق التحليل العنقودي

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الخلاصة

تضمنت الدراسة عشرة تراكيب وراثية من القطن الابلند، زرعت بذورها عند أربعة مستويات من السماد النانوي NPK 20-20-20 ، (صفر و1 و 2 و3 غم/لتر) في عام 2022 في الرحمانية (الموصل) باستخدام تصميم القطاعات العشوائية الكاملة بثلاثة مكررات. تم تسجيل البيانات عن صفات عدد الايام لتفتح اول جوزة وارتفاع النبات وعدد الأفرع الثمرية وعدد الجوز بالنبات ومتوسط وزن الجوزة ودليل البذور وتصافي الحليج ودليل التيلة والتبكير بالنضج وحاصل القطن الزهر بالنبات وطول التيلة عند 50٪ وطول التيلة عند 2.5٪ وانتظام طول التيلة طول ونعومة التيلة ومتانتها واستطالتها، ثم تم تحليلها إحصائيا للتعرف على طبيعة الاختلافات بين التراكيب الوراثية. تم إجراء التحليل العنقودي بهدف تجميع الأنماط الجينية المتشابهة في مجموعات متجانسة وتقدير درجة الاختلاف الجيني بينها من خلال استخدام تقنية التجميع الهرمي التي تتضمن تكوين مصفوفة درجة التشابه وتقدير المسافات بين مجموعات التراكيب الوراثية المتكونة. أظهرت النتائج أن متوسط مربعات التراكيب الوراثية كان معنوياً لجميع الصفات باستثناء عدد الأيام لفتح اول جوزة. أظهرت مراحل التحليل العنقودي أن التراكيب الوراثية توزعت في ثماني مجموعات، الأولى والثانية والرابعة والخامسة والسادسة والسابعة تضمنت تركيبًا وراثيًا واحدًا لكل منها، وهي على التوالي COKER310 و MONTANA و SPERO و LACHATA و CANDIA و EDESSA، مما يشير إلى الاختلاف بينها وبين التراكيب الوراثية الأخرى، والذي يرجع إلى الاختلاف في أصلها الوراثي، مما انعكس على أدائها، بينما تضمنت المجموعات الأخرى تركيبين وراثيين لكل منهما. ويستنتج من نتائج التحليل العنقودي أن هناك تقارب قوي بين أزواج التراكيب الوراثية W888 مع IK259 و FLASH مع BA440، لأنهما يمتلكان أقل المسافات الاقليدية، وهذا يستلزم تجنب التهجين بينهما، بينما كانت أعلى مسافة بين التركيبين الوراثيين COKER310 و FLASH، وهو مؤشر على وجود تباين جيني عالي بينهما ومع التراكيب الجينية الأخرى، والذي قد يكون بسبب الاختلاف في الاصل الوراثي أو امتلاكها للجينات الرئيسية المفضلة التي تفتقر إليها التراكيب الجينية الأخرى، مما يشجع على ادخالها في تهجينات مع التراكيب الجينية التي أظهرت تباينًا جينيًا مميزًا، للاستفادة من ظاهرة قوة الهجين والانعزالات التي تنتج عنها.

الكلمات المفتاحية: القطن، الأصناف، العنقود، التنوع.