PLANT SCIENCE TODAY
ISSN 2348-1900 (online)
Vol x(x): xx–xx
https://doi.org/10.14719/pst.1909

HORIZON
e-Publishing Group
HePG

RESEARCH ARTICLE

Assessment of genotype by year interaction for yield components and physiological traits in cotton under drought stress using multivariate analysis and genetic parameters

Waleed Mohamed Bassuny Yehia[1], Essam Fathy El-Hashash[*2], Salem Mesfir Al-Qahtani[3] & Nadi Awad Al-Harbi[3]

[1]Cotton Research Institute, Agriculture Research Center, Giza 12619, Egypt
[2]Department of Agronomy, Faculty of Agriculture, Al-Azhar University, Cairo 11651, Egypt
[3]Biology Department, University College of Tayma, University of Tabuk, P.O. Box 741, Tabuk, Saudi Arabia

*Email:dressamelhashash@azhar.edu.eg

OPEN ACCESS

ARTICLE HISTORY
Received: 22 May 2022
Accepted: 5 September 2022

Available online
Version 1.0 : 24 December 2022

Check for updates

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information is available at https://horizonepublishing.com/journals/index.php/PST/open_access_policy

Publisher's Note: Horizon e-Publishing Group remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS etc.
See https://horizonepublishing.com/journals/index.php/PST/indexing_abstracting

CITE THIS ARTICLE

Yehia W M B, El-Hashash E F, Al-Qahtani S M, Al-Harbi N A. Assessment of genotype by year interaction for yield components and physiological traits in cotton under drought stress using multivariate analysis and genetic parameters. Plant Science Today (Early Access). https://doi.org/10.14719/pst.1909

Abstract

The objective of this study was to identify genotype high yielding and drought-tolerant, by understanding the interaction GY pattern for yield, yield components and physiological traits in 24 cotton genotypes over 5 years under drought stress conditions using AMMI analysis, genetic parameters and multivariate analysis. All assessed traits were significantly impacted by genotypes and GY interaction using the AMMI model, with the exception of chlorophyll b by GY interaction. Meanwhile, seed cotton yield/plant, number of open bolls/plant, lint percentage, lint cotton yield/plant and number of fruiting branches/plant were significantly affected by the year's factor. High BSH coupled with high GAM% was observed for all studied traits, indicating the heritability due to additive type of gene action and, the importance of these genotypes and the possibility of effective selection for drought-tolerant genotype development. A statistically significant correlation was discovered between cotton yield and most investigated traits under drought stress conditions. Direct selection can be done through these traits based on genetic parameters and Pearson's correlations analyses, which will be effective for drought tolerance and enhancing cotton yield. The results of our study's Pearson's correlation analysis, PCA and cluster analysis could be relevant and appropriate for studying drought tolerance mechanisms and cotton yield improvement. According to PCA and cluster analysis, the genotypes G20 and G19 followed by G5, G4 and G21 genotypes showed the best performance in response to drought stress regarding the yield, yield components and physiological-related traits. The previous genotypes could be used in future cotton breeding efforts in Egypt to promote drought tolerance, improve cotton productivity and sustainable production during drought stress conditions.

Keywords

AMMI model, cluster analysis, correlation, cotton genotypes, drought stress, genetic components, PCA, years

Introduction

Cotton is the most important natural textile fiber crop in the world and one of the major important cash crops in Egypt. It is a flowering plant belonging to the family Malvaceae and the genus *Gossypium* (G). The G. genus is comprised of ~50 species. The most important cultivated species of the genus are *G. hirsutum*, *G. barbadense* (allotertraploid 2n = 52), *G. herbaceum* and *G. arboreum* (diploid 2n = 26) (1). In Egypt, cotton is commonly known as "white gold", due to its important role in industrial development (fiber and oil) and employment

generation. The Egyptian cotton varieties are belonging to *G. barbadense* L., and originated from crossing between older varieties or lines, except only one variety (Dandara) produce by direct selection from the field of Ashmouni (2, 3). All the Egyptian varieties had the same name (Giza) then followed by a serial number (3). Egypt's cotton area, yield and production were 0.10 million ha, 1.00 metric ton ha^{-1} and 0.10 million metric tons respectively, according to a February 2022 report, USDA. When compared to the previous year, Egypt's cotton production changed by 53.85% in the 2021/2022 cropping season (4).

Due to drought stress, major crop harvests globally have been observed to be reduced by 50% on average (5), and a 35% reduction in cotton production in 2021 (6). Plants have developed several physiological, morphological, biochemical and molecular defences against drought stress (7). Proline is increased in leaves of cotton varieties on exposure to drought stress (6, 8), but no significant change in chlorophyll content was observed under limited water supply (6). Plants under drought stress experience stunted growth as a result of the severe and quick fall in chlorophyll a, b and total contents which ultimately reduce photosynthate production (9). Low levels of photosynthate and decreased photosynthesis caused by drought stress lead to square and boll sheds and low lint yields (10).

Exploring the possibilities of drought-tolerant crops is the time required for all terrestrial crop species especially in the climate change scenario (11). Drought tolerance is defined by Hall (12) as a genotype's relative yield compared to other genotypes under the same drought stress. Drought resistance is a complex phenomenon and multi-gene-controlled that manifests both drought tolerance such as tissue tolerance, photosystem maintenance and so on and drought avoidance such as deep root, leaf rolling and so on (13). Drought resistance is hampered by poor heritability and a lack of effective selection strategies (14). As a result, cotton genotype selection in Egypt should be acclimatized to drought stress circumstances.

The phenotypic expression of an individual is determined by both genotype and environmental effects (15) and the phenotypes can be observed, measured, classified, or counted. The association between the environment and the phenotypic expression of a genotype is commonly known as the genotype x environment interaction (GEI). Environmental factors (non-genetic factors) such as locations, growing seasons, years, drought conditions, rainfall, the amount of precipitation received in each season, temperature etc. may have positive or negative impacts on genotypes (16). The main target of plant breeding programmes is to increase stability and stabilize crop yield across environments (locations and/or years). Genotype x environment interaction (GEI) is of major importance to the plant breeder in developing improved varieties. It was reported that when varieties are compared over a series of environments, the relative rankings usually differ (17). Also, it was noted that GEI is a major problem when comparing the performance of genotypes across environments (18). It was mentioned that the ranking of genotypes depends on the particular environmental conditions where they are grown, where the basic cause of differences between genotypes in their yield stability is the wide occurrence of GEI (19). So, the study of the GEI may assist in the understanding of the stability concept. Because of their greater flexibility and stability, cotton genotypes with the least genotype by environment interaction are regarded as ideal for breeding.

There are several statistical methods for analyzing and interpreting data from multi-environment trials (20), such as multivariate methods. The additive main effect and multiplicative interaction (AMMI) model established (21) is the most well-known of the multivariate methods. The AMMI model characterizes genotype and environment main effects using analysis of variance as an additive model and their interactions using principal components analysis as a multiplicative model (IPCA). Cotton breeders all over the world have been using AMMI analysis of variance to investigate GE interaction in multi-environment trials (22-26).

The development of high-yielding genotypes necessitates a thorough understanding of the genetic variability in the crop's germplasm, as well as the relationships between yield components, input requirements and agriculture practices (27). Furthermore, understanding the source of genetic variability for cotton yield, yield components and physiological attributes is critical for improving yield and quality by developing superior genotypes in cotton. Heritability is important for selection since it reflects the amount to which a trait can be passed down through generations and the quality of phenotypic data in multilocation experiments (28). Another key selection criterion that supports breeders in a selection scheme is genetic advance as % of the mean (29). The phenotypic coefficient of variation (PCV) and the genotypic coefficient of variation (GCV) can both be used to detect the degree of variability in a germplasm group. Heritability combined with high genetic advance would be more effective in forecasting the subsequent effect in the selection of the optimal genotypes for yield and yield contributing variables (30). It is feasible to select the optimum genotype for obtaining the required traits in the descendants by combining heritability information with PCV and GCV values (31). According to one report (30), differences in genotypic values might rise or decrease from one environment to the next, causing genotypes to rank differently in among environments.

To visualize the outcomes of cotton breeding trials, principal component analysis (PCA) is required, where Many researchers have used the PCA to assess the relationship and diversity between several cotton germplasms, in addition to knowing the relationships between yield, its components, and other traits (32-39).

The objective of this study was to investigate the magnitude of genotype by year interaction using the

AMMI model and genetic parameters, as well as determining the relationships using Pearson's correlation coefficient and PCA for yield components and physiological traits in 24 cotton genotypes under drought stress, thus identifying cotton genotype drought-tolerant during drought stress conditions in Egypt .

Materials and Methods

Genetic material and field procedure

A total of 24 cotton genotypes belonging to *Gossypium barbadense* L. were used in this study (Table 1). Healthy seeds of cotton genotypes were obtained from Cotton Research Institute, Agriculture Research Center, Giza, Egypt. Field experiments were conducted at Sakha Agriculture Research Station, Kafr El- Sheikh Governorate, Egypt over a period of 5 years from 2016 to 2020 under drought stress conditions. Cotton genotypes were evaluated in Randomized Complete Block Design (RCBD) with three replicates. Each experimental plot has 5 rows and the genotypes were planted using standard agronomic practices and proper plant geometry with a row length of 4 m. Under each plot, the row x row and plant x plant distances were 70 and 30 cm respectively. The drought treatment received only 5 irrigations with one at the time of sowing and the other 4 irrigations with an interval of 30 days during the growing season through the 5 growing seasons. In each experiment, a basin irrigation system with PE pipes and a volumetric counter was used. Normally, the cotton crop received eight irrigations during the growing season as per the recommended rules. The drought stress experiments were not provided with any supplemental irrigation after drainage even if the stress was very severe. All agronomic practices were carried out and the crop was sown in a single day under uniform field conditions to minimize environmental variations to the maximum possible extent. The average of temperature (°C), total rainfall (mm), relative humidity (%) and wind speed (10M) from April to October during five growing seasons were provided by the Climate Change Information Center and Renewable Energy, Agriculture Research Center, Cairo, Egypt (Fig. 1).

Table 1. List of 24 cotton genotypes used for drought tolerance assessment.

No.	Genotypes	Pedigree	Origin
G1	Giza 89	Giza 89 x 6022	Egypt
G2	Z101	Unknown	Unknown
G3	Giza 85	Giza 67 x CB58	Egypt
G4	Giza 75	Unknown	Egypt
G5	Giza 94	10229 x Giza 86	Egypt
G6	A106	Unknown	Unknown
G7	A101	Unknown	Unknown
G8	Z102	Unknown	Unknown
G9	Giza 89 x Giza 86	Unknown	Egypt
G10	Giza 45	Giza 28 x Giza 7	Egypt
G11	A108	Unknown	Unknown
G12	Giza 93	Giza 77 x S106	Egypt
G13	D101	Unknown	Unknown
G14	Giza 70	Giza 59A x Giza 51B	Egypt
G15	A105	Unknown	Unknown
G16	G102	Unknown	Unknown
G17	R101	Unknown	Unknown
G18	G101	Unknown	Unknown
G19	Giza 96	(Giza 84 x (Giza 70 x Giza 51B)) x S62	Egypt
G20	Giza 86	Giza 75 x Giza 81	Egypt
G21	Giza 95	(Giza 83 x (Giza 75 x 5844)) x Giza 80	Egypt
G22	S106	Unknown	Unknown
G23	S107	Unknown	Unknown
G24	S109	Unknown	Unknown

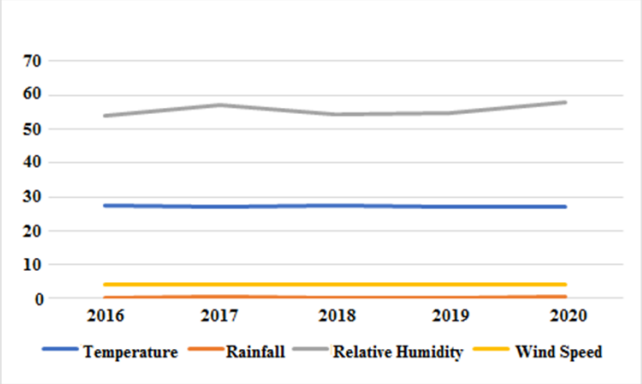

Fig. 1. Weather data at each season in the region.

Data recording

Data were recorded on 10 guarded plants for morphological traits including seed cotton yield/plant (SCY/P) in gram, number of open bolls/plant (No. B/P), seed index (SI) in g, lint percentage (L %), lint cotton yield/plant (LCY/P) in g, number of fruiting branches/plant (No.F.B/P) and plant height (PH). Meanwhile, fifty bolls were collected in order to calculate the average boll weight (BW) in gms. Also, physiological traits including contents of chlorophyll a (*Chl. a*), chlorophyll b (*Chl. b*), total chlorophyll (T. *Chl.*), total carotenoids and proline were measured.

Photosynthetic pigments estimation:

To determine the *Chl. a*, *Chl. b* and carotenoid content from the plants of each cultivar (40), 200 mg leaf blade samples were extracted with 100% acetone and were homogenized with the B-Brawn type homogenizer at 1000 rpm for one min. The homogenate was filtered by 2-layer cheese cloths and was centrifuged using the NüveFüj 647 model centrifuge at 1500 rpm for ten min. The supernatant was separated and the absorbance of acetone extracts was measured at 663, 645 and 470 nm using an Analytik Jena Specord 200 model spectrophotometer. The *Chl. a*, *Chl. b* and total content of carotenoids were calculated as the following equation (40):

$$Chl.\ a\ (mg/g^{-1}\ FW) = [(12.7 \times A_{663}) - (2.69 \times A_{645})] \times V/(1000 \times W)$$

$$Chl.\ b\ (mg/g^{-1}\ FW) = [(22.9 \times A_{645}) - (4.68 \times A_{663})] \times V/(1000 \times W)$$

$$\text{Carotenoids } (mg/g^{-1}\ FW) = [(1000\ A_{470}) - (2.27\ Chl.\ a) - (81.4\ Chl.\ b)\ /226] \times V/(1000 \times W)$$

Where, A_{663}, A_{645} and A_{670} are the corresponding wavelengths of the light density value respectively, V is the volume of extracting liquid and W is the weight of fresh leaf sample in gms.

Proline estimation:

The proline content of leaves in all cotton genotypes was estimated at 16 DAA following the standard method (41). The leaves from each replication of each genotype were collected and immediately kept in the ice bag and brought to the Laboratory. Using mortar and pestle, 0.5 g fresh sample was grinded and thoroughly homogenized in 3% sulpho salicylic acid (10 mL) until digestion of plant material. The filtration of homogenate was performed using filter paper (Whatman No. 2). Proline standards (0, 2, 4, 6, 8, 10, 12, 14,16, 18 and 20 µg/mL) were prepared with distilled water. Ninhydrin reagent was prepared and utilized for proline estimation within two hours of preparation. Then, in a Pyrex test tube, filtrate (2 mL) and standard proline solution were reacted with ninhydrin reagent (2 mL) and glacial acetic acid (2 mL). These were subsequently boiled in a water bath covered with aluminum foil to hamper evaporation for 1 h at 100 °C. Subsequently, cooling of mixture in ice bath was performed and toluene (4 mL) was added to each tube with the help of a dispenser. The shaking of each tube for 15-20 s with the help of an electrical shaker was performed to allow the layers to separate. The spectrophotometer (SPECTRO UV-VIS RS Spectrophotometer, Labo Med, Inc.) at 520 nm, having pure toluene as a blank, was used to absorb the layer. From a standard curve, proline content was estimated on a fresh weight basis by following the below equation:

Proline (µmoles/g of fresh plant materials) = {(µg proline/mL x mL toluene)/115.5 µg/µmoles}/(g sample/5).

Statistical approaches

The normality of data distribution was verified using the Komolgorov- Smirnov test. The analysis of variance by AMMI model was performed to determine the main and interactions effects of genotypes and 5 years under drought stress conditions on yield, yield components and physiological traits. The CV% estimates were categorized as very high (CV≥21%), high (15%≤CV≤21%), moderate (10%<CV≤15%) and low (CV<10%) (42). The variances components due to the main and interactions effects of two studied experimental factors were estimated with analysis of variance (ANOVA) (43). Broad sense heritability (BSH) estimates were calculated using the standard formula (44). The extent of genetic advance to be expected by selecting ten percent of the superior progeny was calculated (45). Genotypic (GCV%), phenotypic (PCV%) and error (ECV%) coefficients of variation were calculated (46). The heritability and genetic advance estimates were categorized (45, 47) [0-30% = low; 31-60% = moderate; above 60% = high) and (0-10% = low, 10-20% = moderate and above 20% = high] respectively. The AMMI model, Plot Pearson's correlation coefficient, cluster analysis and PCA were done using computer software programs PBSTAT, PAST version 4.03 and OriginPro 2018 version b9.5.0.193.

Results

1. AMMI analysis of variance

The results of the combined ANOVA with AMMI analysis of the main and interactions effects of genotypes (G) and years (Y) under drought stress conditions on cotton quantitative traits are shown in Table 2. In the AMMI analysis, the mean squares due to genotypes ($P < 0.01$) and interaction GY ($P < 0.05$ and $P < 0.01$) were significant for all investigated traits under drought stress conditions, except chlorophyll b by interaction GY. While the years mean squares were significant for seed cotton yield/plant, number of open bolls/plant, lint percentage, lint cotton yield/plant ($P < 0.01$) and number of fruiting branches/plant ($P < 0.05$). Genotypes accounted for a considerable part of the overall variation in cotton yield and all examined traits, followed by years, with the interaction GY accounting for the smallest portion. After removing sums of squares due to error and replication, the sums of squares% remaining among years, genotypes and interaction GY ranged from 80% of seed index to 90% of carotenoids. The highest contribution to the sum of squares (%) of the total variance was due to genotypes for all studied traits, followed by years for seed and lint cotton yields/plant traits and followed by interaction GY for remaining studied traits. The variance due to genotypes accounted for more than 70% of the total variance for all studied traits except seed cotton yield/plant (45%), number of open bolls/plant (54%), seed index (46%), lint percentage (55%) and lint cotton yield/plant (44%). The interaction GY partitioned into four principal components (PCs). The PC1 was significant for all studied traits ($P < 0.05$ and $P < 0.01$). Also, PC2 exhibited significance for all studied traits ($P < 0.05$ and $P < 0.01$) except number of fruiting branches/plant, chlorophyll a, chlorophyll b and total chlorophyll. While, the PC3 had only significant for seed index ($P < 0.05$) and lint percentage ($P < 0.01$). The contribution of PC1 of the GE interaction SS ranged from 53% of plant height to 80% of number of open bolls/plant, while the contribution of PC1 varied from 31% to 11% for the same traits, respectively. The PC1 and PC2 together represent from 81% to 91% of the total interaction GY variation for number of fruiting branches/plant and number of open bolls/plant traits, respectively. The traits of seed cotton yield/plant, number of open bolls/plant and lint cotton yield/plant had moderate coefficients of variation (CV%), with values of 12.56%, 13.77% and 12.98% respectively. In contrast to the other measured traits, the values of CV% were low (CV<10%) under experimental conditions evaluated (Table 2).

2. Main effects of years and genotypes on cotton trait

The mean performance of yield, yield components and physiological traits acquired for 24 cotton genotypes and 5 years under drought stress conditions are shown in Table 3. The 2017 year was significantly increased boll weight, seed cotton yield/plant, number

of open bolls/plant, seed index, lint % and lint cotton yield/plant compared with other years, this increase could be due to increased rainfall in the 2017 year (Fig. 1). The effects of years were not significant on other studied traits. For cotton yield and other measured traits, the mean performance of 24 cotton genotypes across five cropping years under drought stress conditions revealed significant genetic variability. The results indicated positive effects of interaction GY on cotton yield and other studied traits drought stress conditions.

Under drought stress conditions, some genotypes had greater values compared with the grand mean for all investigated traits. G7 had the highest boll weigh and seed index, while it had the lowest contents of chlorophyll *a* and total chlorophyll. G19 and G20 genotypes showed the maximum seed cotton yield/plant, number of open bolls/plant and lint cotton yield/plant, in contrast to G12 genotype, in which the minimum values of the same traits were recorded. G8 and G9 genotypes produced the maximum values for lint % and number of fruiting branches/plant traits.

Table 2. Combined ANOVA with AMMI analysis for studied traits of cotton genotypes evaluated across 5 years under drought stress conditions.

S.O.V	d.f	BW	SCY/P	No.B/P	SI	L%	LCY/P	No.F.B/P	PH	*Chl. a*	*Chl. b*	*T. Chl*	Carot.	Prol.
		Mean squares												
Years (Y)	4	0.26	12888.55**	1452.41**	0.56	17.04**	1867.88**	3.89*	34.19	0.01	0.01	0.01	0.02	0.34
Replication/Y	10	0.13**	220.87*	72.02**	0.48**	0.15	29.09*	0.68	21.69	0.01	0.02	0.04	0.02	0.13
Genotype (G)	23	1.23**	4155.08**	917.13**	2.03**	12.30**	556.95**	41.34**	2125.71**	1.03**	1.84**	3.28**	0.92**	8.25**
GxY	92	0.05**	385.04**	74.65**	0.34**	1.06**	52.73**	1.06**	60.78**	0.04**	0.02	0.08*	0.02**	0.24**
PC1	26	0.12**	1049.73**	210.55**	0.83**	2.02**	143.98**	2.41**	114.93**	0.11**	0.05*	0.23**	0.04**	0.59**
PC2	24	0.03**	192.08*	31.62*	0.22**	1.01**	26.48*	0.69	72.45**	0.02	0.01	0.04	0.02**	0.17*
PC3	22	0.02	96.00	22.67	0.13*	0.66**	13.53	0.47	29.55	0.01	0.01	0.02	0.01	0.11
PC4	20	0.01	70.45	6.82	0.07	0.33	8.75	0.38	10.73	0.01	0.003	0.02	0.00	0.03
Residuals	230	0.01	117.66	20.00	0.07	0.26	15.43	0.65	30.74	0.03	0.02	0.07	0.01	0.11
S.O.V	d.f	Sum of squares												
Years (Y)	4	1.05	51554.21	5809.64	2.23	68.16	7471.53	15.56	136.78	0.03	0.05	0.05	0.09	1.35
Replication/Y	10	1.30	2208.74	720.23	4.83	1.49	290.93	6.78	216.89	0.14	0.17	0.40	0.16	1.32
Genotype (G)	23	28.32	95566.93	21094.07	46.65	282.91	12809.75	950.93	48891.35	23.78	42.42	75.39	21.26	189.84
GxY	92	4.37	35423.96	6868.12	31.32	97.89	4851.51	97.21	5591.58	3.82	1.59	7.77	1.84	22.45
PC1	26	3.01	27292.94	5474.20	21.65	52.61	3743.50	62.69	2988.13	2.75	1.19	6.04	1.02	15.21
PC2	24	0.78	4610.00	758.87	5.39	24.28	635.43	16.46	1738.70	0.57	0.22	0.85	0.58	4.18
PC3	22	0.41	2111.92	498.66	2.81	14.46	297.62	10.36	650.15	0.27	0.12	0.54	0.17	2.45
PC4	20	0.17	1409.09	136.39	1.47	6.54	174.96	7.69	214.60	0.22	0.07	0.33	0.07	0.60
Residuals	230	3.27	27061.88	4600.54	15.74	60.23	3547.99	148.57	7069.60	6.17	5.74	15.52	2.29	24.25
		Contribution to the SS (%) of total variance explained												
% due to Y		2.74	24.34	14.86	2.21	13.35	25.79	1.28	0.22	0.09	0.10	0.05	0.35	0.56
% due to G		73.92	45.12	53.96	46.29	55.40	44.21	78.01	78.98	70.06	84.89	76.05	82.92	79.36
% due to G x Y		11.41	16.72	17.57	31.08	19.17	16.75	7.97	9.03	11.26	3.18	7.84	7.18	9.39
		PCs variance percent of the total variance of variables												
PC1		68.80	77.00	79.70	69.10	53.70	77.2	64.50	53.40	72.10	75.00	77.70	55.50	67.80
PC2		17.90	13.00	11.00	17.20	24.80	13.1	16.90	31.10	15.10	13.50	11.00	31.60	18.60
PC3		9.50	6.00	7.30	9.00	14.80	6.1	10.70	11.60	7.00	7.30	7.00	9.10	10.90
PC4		3.80	4.00	2.00	4.70	6.70	3.6	7.90	3.80	5.90	4.20	4.30	3.70	2.70
CV%		3.72	12.65	13.77	3.14	1.45	12.98	5.43	3.89	7.22	7.90	6.31	7.14	4.78

Statistically significant differences at *p ≤ 0.05 and **p ≤ 0.01; ns: indicate the non-significant difference. BW: boll weight; SCY/P: seed cotton yield/plant; No. B/P: number of open bolls/plant; SI: seed index; L %: lint percentage; LCY/P: lint cotton yield/plant; No.F.B/P: Number of fruiting branches/plant; PH: plant height; *Chl. a*: chlorophyll *a*; *Chl. b*: chlorophyll *b*; *T. Chl*: total chlorophyll; Carot: carotenoids; Prol: proline.

Table 3. Mean values of studied traits of 5 years and 24 cotton genotypes grown under drought stress conditions

Factors	BW	SCY/P	No.B/P	SI	L%	LCY/P	No.FB/P	PH	*Chl. a*	*Chl. b*	*T. Chl*	Carot.	Prol.
Years													
2016	2.70	85.84	32.61	8.45	35.18	30.30	14.69	142.39	2.42	1.77	4.19	1.42	6.84
2017	2.79	102.78	37.71	8.58	35.78	36.81	14.51	143.31	2.39	1.79	4.18	1.41	7.03
2018	2.68	94.86	36.04	8.43	35.40	33.62	15.02	142.17	2.41	1.81	4.21	1.39	6.95
2019	2.66	72.51	27.77	8.36	34.45	24.99	14.96	143.04	2.40	1.78	4.18	1.38	6.93
2020	2.63	72.80	28.19	8.36	35.08	25.60	15.04	141.58	2.40	1.79	4.19	1.39	6.94
Genotypes													
G1	2.73	89.47	33.24	8.38	36.11	32.33	16.48	149.93	2.25	2.06	4.31	1.20	6.18
G2	2.90	81.90	28.33	7.54	36.04	29.56	16.37	124.44	2.16	2.19	4.35	1.18	7.21
G3	2.87	68.38	23.74	8.24	34.33	23.57	16.84	123.62	2.26	1.92	4.18	1.37	6.20
G4	2.84	105.01	36.83	7.99	35.39	36.98	15.01	129.39	2.31	2.25	4.56	1.60	7.87
G5	2.38	108.11	45.51	7.78	34.59	37.44	16.43	140.44	2.54	2.37	4.91	1.18	6.41
G6	2.84	93.00	32.92	8.07	35.72	33.23	14.43	142.84	2.60	2.34	4.94	1.55	7.58
G7	3.27	75.85	23.14	9.08	34.75	26.49	16.19	136.60	1.50	1.77	3.27	1.50	6.64
G8	3.01	85.46	28.46	8.84	36.68	31.37	14.01	148.13	2.26	1.70	3.96	1.34	7.12
G9	2.82	82.76	29.41	8.56	34.21	28.33	17.78	142.44	2.31	1.76	4.07	1.37	7.27
G10	2.53	72.45	28.59	8.68	33.55	24.39	16.73	156.87	2.67	1.49	4.16	1.30	7.14
G11	2.82	73.40	26.32	8.26	34.18	25.15	14.06	164.58	2.32	1.44	3.77	1.32	6.40
G12	2.82	57.87	20.45	8.39	34.17	19.83	15.28	164.05	2.51	1.49	4.00	1.15	6.50
G13	3.20	66.90	20.98	8.88	35.97	24.07	15.71	146.55	2.30	1.45	3.74	1.18	6.44
G14	2.90	81.09	28.14	8.46	35.94	29.18	12.66	130.24	2.54	1.64	4.17	1.28	6.39
G15	2.33	93.67	40.20	8.79	36.52	34.25	15.00	152.57	2.18	1.56	3.73	1.37	5.78
G16	2.74	83.82	31.10	8.60	34.68	29.13	14.55	155.36	2.42	1.36	3.78	1.38	6.34
G17	2.41	92.78	38.58	8.61	35.78	33.30	14.41	133.90	2.73	1.95	4.68	1.66	7.70
G18	2.31	83.99	36.46	8.85	36.26	30.74	13.64	141.30	2.42	1.37	3.79	1.17	6.79
G19	2.48	120.58	48.81	8.03	34.97	42.21	13.63	157.28	2.68	1.99	4.67	1.84	8.17
G20	2.78	126.38	45.71	8.37	35.62	45.18	13.65	128.58	2.69	2.21	4.90	1.88	8.37
G21	2.22	92.64	41.78	8.32	34.70	32.20	14.34	135.68	2.67	2.25	4.92	2.03	8.44
G22	2.30	71.15	30.82	8.46	35.49	25.24	12.00	137.49	2.29	1.57	3.86	1.13	6.68
G23	2.40	69.32	28.88	8.68	33.63	23.36	10.85	131.74	2.43	1.24	3.66	1.31	6.45
G24	2.66	82.14	30.81	8.56	35.00	28.75	16.14	145.92	2.64	1.55	4.19	1.22	6.53
G. Mean	2.69	85.76	32.47	8.43	35.18	30.26	14.84	142.50	2.40	1.79	4.19	1.40	6.94

BW: boll weight; SCY/P: seed cotton yield/plant; No. B/P: number of open bolls/plant; SI: seed index; L %: lint percentage; LCY/P: lint cotton yield/plant; No.F.B/P: number of fruiting branches/plant; PH: plant height; *Chl. a*: chlorophyll *a*; *Chl. b*: chlorophyll *b*; *T. Chl*: total chlorophyll; Carot: carotenoids; Prol: proline

The highest values for plant height, chlorophyll *a*, chlorophyll *b* and total chlorophyll were obtained by genotypes G11, G17, G5 and G6 respectively. The G21 genotype registered the highest contents of carotenoids and proline and the lowest boll weight. In contrast, the lowest values for lint percentage by G10 genotype, for plant height by G3 genotype and for number of fruiting branches/plant and chlorophyll *b* by G23 genotype were observed.

3. Cluster analysis

In Fig. 2, the cluster analysis classified the 24 cotton genotypes based on all studied traits across drought stress conditions into 2 major groups (A and B). Groups A and B were categorized into 3 and 2 clusters, which accounted for 58% and 42% of the total genotypes respectively. The number of genotypes in each cluster varied, with fewer genotypes in the first cluster (G19 and G20), 4 genotypes in the fourth cluster (G11, G10, G13 and G12), and 6 genotypes in each remaining cluster (equal). The second cluster is comprised of genotypes G5, G4, G21, G17, G15 and G6. The third cluster consisted of genotypes G8, G1, G16, G18, G24 and G9.

While G14, G2, G23, G22, G7 and G3 genotypes belonged into the fifth cluster. The tree diagram revealed the lowest distance between genotypes inside each cluster, whereas the genotypes between clusters in the 2 groups had the highest distance. The first cluster had high-cotton yielding genotypes with moderate to high yield components and physiological traits, followed by the second, third, fourth and fifth groupings, in that order. Generally, G19 and G20 genotypes under drought stress conditions were found to be the most drought-tolerant, followed by G5, G4, G21 and G17, according to the mean performance and cluster analysis.

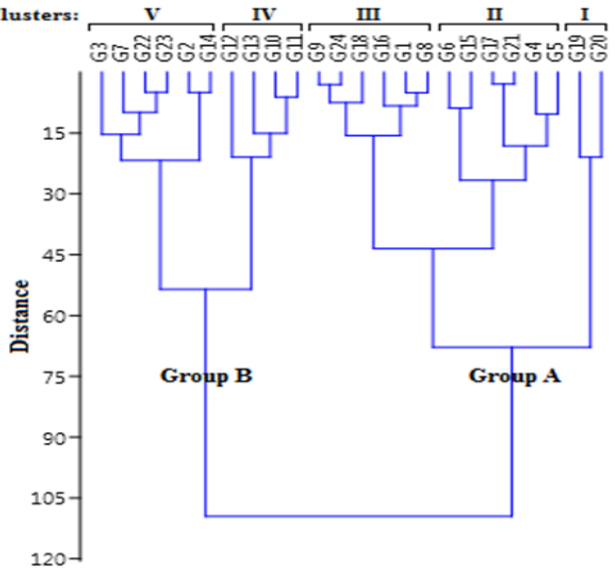

Fig. 2. Tree diagram of 24 cotton genotypes based on all studied traits using ward's method with Euclidean distance.

4. Variance components and genetic parameters

The variance components and genetic components for the analyzed traits were estimated using mean squares in combined ANOVA and are presented in Table 4. This analysis assumes a random genetic effects model under drought stress conditions. The highest genotypic variances were observed for all studied traits, followed by genotypes x years variances for seed index and lint percentage traits as well as it followed by error variances for other studied traits. Seed cotton yield/plant had the highest phenotypic variance, followed by plant height and number of open bolls/plant traits and concentrations of carotenoids and chlorophyll *a* had the lowest. The ratio of the genotypic variance of phenotypic variance (σ_g^2/σ_{ph}^2) had equal to one for boll weight, chlorophyll *a*, chlorophyll *b* and carotenoids, but for other studied traits, it was less than one. The ratio of error variance of phenotypic variance (σ_e^2/σ_{ph}^2) was less than one for all investigated traits. The greatest σ_g^2/σ_e^2 ratios were found for boll weight (8.00), followed by chlorophyll *b* and carotenoids concentrations (6.00). On the other hand, the seed index had the lowest σ_g^2/σ_e^2 ratio (1.57).

The highest broad-sense heritability (BSH>60%) values were registered for all investigated traits, ranging from 83.22% for seed index to 99.06% for chlorophyll *b*. All evaluated traits with high BSH had the highest genetic advance (GA) and genetic advance as a percent of the mean (GAM%), showing the predominance of additive gene action. The phenotypic coefficients of variation (PCV%) were larger than genotypic coefficients of variation (GCV%) for all traits tested, except for boll weight, chlorophyll *a*, chlorophyll *b* and carotenoids, which had equal. Seed index, lint % and plant height traits were found to have low PCV% and GCV% values, with values less than 10%. For number of open bolls/plant, very high PCV% and GCV% values were observed, with values of more than 21%. High PCV% and GCV% values were noticed in seed cotton yield/plant, lint cotton yield/plant, chlorophyll *b* and carotenoids (>15%). Other traits had a moderate % of PCV and GCV (10%<CV≤15%). In this study, the DPG is the difference between PCV% and GCV%, which is interesting to observe. In the case of DPG, all of the traits examined showed very little difference or were not observed at all. Seed cotton yield/plant, number of open bolls/plant and lint cotton yield/plant had moderate ECV% values (10%<CV≤15%), but other studied traits in this study had low ECV% (<10%). It's worth mentioning that the analyzed traits relative coefficients of variation (RCV= GCV%/ECV%) were the most volatile. Where the RCV of all traits evaluated was more than one (>1).

5. Pearson's correlation coefficient

Based on the main effects of 24 cotton genotypes and 5 cropping years under drought stress conditions, Pearson's correlations analysis was performed to study the relationship among yield, yield components and physiological traits (Fig. 3). The data demonstrated that under drought stress conditions, 33 correlation coefficients were significantly different ($p < 0.05$ and $p < 0.01$). There were 26 positive correlations and 7 negative correlations among these. Seed cotton yield/plant, number of open bolls/plant, lint cotton yield/plant, chlorophyll *b*, total chlorophyll, carotenoids and proline were all found to be positively and significantly related ($p < 0.05$ and $p < 0.01$). The boll weight and lint % positively and significantly correlated with number of fruiting branches/plant and lint cotton yield/plant ($p<0.05$) respectively. The content of chlorophyll *a* had a significant positive correlation with the number of open bolls per plant, proline ($p<0.05$) and total chlorophyll ($p<0.01$), but had a positive correlation with seed and lint cotton yields/plant and plant height traits.

Table 4. Variance components and genetic parameters estimates for yield, its components and physiological traits of cotton genotypes assessed in 5 years under drought stress conditions.

Parameters	BW	SCY/P	No.B/P	SI	L%	LCY/P	No.FB/P	PH	*Chl. a*	*Chl. b*	*T. Chl*	Carot.	Prol.
Variance components													
σ_g^2	0.08	251.34	56.17	0.11	0.75	33.61	2.69	137.66	0.07	0.12	0.21	0.06	0.53
σ_{gy}^2	0.01	89.13	18.22	0.09	0.27	12.44	0.14	10.01	0.00	0.00	0.01	0.00	0.05
σ_e^2	0.01	117.66	20.00	0.07	0.26	15.43	0.65	30.74	0.03	0.02	0.07	0.01	0.11
σ_{ph}^2	0.08	277.01	61.14	0.14	0.82	37.13	2.76	141.71	0.07	0.12	0.22	0.06	0.55
$\sigma_g^2 / \sigma_{ph}^2$	1.00	0.91	0.92	0.79	0.91	0.91	0.97	0.97	1.00	1.00	0.95	1.00	0.96
$\sigma_e^2 / \sigma_{ph}^2$	0.13	0.42	0.33	0.50	0.32	0.42	0.24	0.22	0.43	0.17	0.32	0.17	0.20
σ_g^2 / σ_e^2	8.00	2.14	2.81	1.57	2.88	2.18	4.14	4.48	2.33	6.00	3.00	6.00	4.82
Genetic parameters													
BSH	96.14	90.73	91.86	83.22	91.35	90.53	97.44	97.14	95.98	99.06	97.42	97.84	97.04
GA	56.02	3110.76	1479.64	64.14	170.41	1136.38	333.47	2382.13	52.31	70.69	94.13	49.37	148.25
GAM%	2082.40	3627.28	4556.95	760.91	484.38	3755.37	2247.11	1671.67	2179.64	3949.15	2246.53	3526.40	2136.19
GCV%	10.51	18.49	23.08	3.93	2.46	19.16	11.05	8.23	11.02	19.35	10.94	17.50	10.49
PCV%	10.51	19.41	24.08	4.44	2.57	20.14	11.19	8.35	11.02	19.35	11.19	17.50	10.69
DPG	0.00	0.92	1.00	0.50	0.11	0.98	0.14	0.12	0.00	0.00	0.26	0.00	0.20
ECV%	3.72	12.65	13.77	3.14	1.45	12.98	5.43	3.89	7.22	7.90	6.31	7.14	4.78
RCV	2.83	1.46	1.68	1.25	1.70	1.48	2.03	2.12	1.53	2.45	1.73	2.45	2.20

: genotypic variance; : genotype x environment interaction variance; : error variance; : phenotypic variance on entry-mean basis; BSH: broad-sense heritability on entry-mean basis (%); GA: genetic advance; GAM%: genetic advance as percent of mean; GCV%, PCV% and ECV%: genotypic, phenotypic and error coefficients of variation, respectively; DPG: difference between PCV% and GCV%; RCV: relative coefficient of variation. BW: boll weight; SCY/P: seed cotton yield/plant; No. B/P: number of open bolls/plant; SI: seed index; L %: lint percentage; LCY/P: lint cotton yield/plant; No.F.B/P: Number of fruiting branches/plant; PH: plant height; Chl. *a*: chlorophyll *a*; *Chl. b*: chlorophyll *b*; *T. Chl*: total chlorophyll; Carot: carotenoids; Prol: proline.

Regarding the negative correlation under stress drought conditions, the boll weight negatively and significantly correlated with the number of open bolls/plant ($p<0.01$) and chlorophyll *a* ($p<0.05$). Seed index also had a negative and significant association with seed cotton yield/plant, lint cotton yield/plant ($p<0.05$), chlorophyll *b* and total chlorophyll ($p<0.01$). While plant height has a negative and significant relationship with chlorophyll *b* ($p<0.05$).

6. Principal component analysis (PCA)

Statistical analysis PCA was used in this study to discover drought tolerance in 24 cotton genotypes and to quantify the associations between the analyzed characteristics over a 5-year period under drought stress conditions. Five PCs were selected from the 13 PCs based on eigenvalue values across the mean performance for studied variables respectively (Table 5). The eigenvalues of the first 5 PCs recovered were more than one and they explained 86.98% of the total variance of studied variables across genotypes and 5 years. On the other hand, the eigenvalues of the other PCs were less than one (Eigenvalue 1). Under drought stress conditions, the PC1, PC2, PC3, PC4 and PC5 contributed 44.70%, 14.68%, 11.36%, 8.37% and 7.87% of the overall variability in the data respectively. PC1 contributes the most

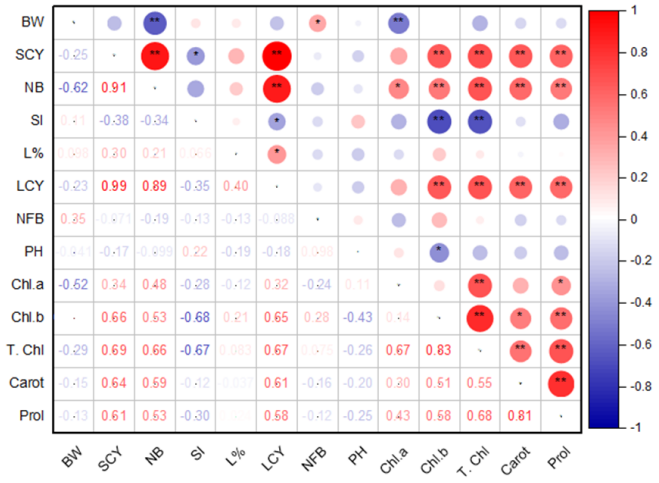

Fig. 3. Correlation matrix plot among yield, yield components and physiological traits of 24 cotton genotypes under drought stress conditions. BW: boll weight; SCY: seed cotton yield/plant; NB: number of open bolls/plant; SI: seed index; L %: lint percentage; LCY: lint cotton yield/plant; NFB: Number of fruiting branches/plant; PH: plant height; Chl. *a*: chlorophyll *a*; Chl. *b*: chlorophyll *b*; *T. Chl*: total chlorophyll; Carot: carotenoids; Prol: proline. Plot showing positive correlation (red) and negative correlation (blue) among traits. * and ** indicate statistically significant differences at p ≤ 0.05 and p ≤ 0.01 respectively.

data variability, followed by PC2. As a result, PC1 and PC2 can be used to examine the association between measured traits and to identify drought-tolerant genotypes during years impacts under drought stress conditions.

Based on the data in Table 5, the PC1 was described by all studied traits with positive factor loadings, except boll weight, seed index, number of fruiting branches/plant and plant height. Except for the number of open bolls/plant, seed index, plant height, chlorophyll *a* and carotenoids, all examined traits had positive factor loadings in PC2. The PC3, PC4 and PC5 had positive loadings with cotton yield and most studied traits, but the highest values were observed on PC3 and PC4 in lint % and on PC5 in plant height.

To assess the association between studied variables by the main influences of genotypes and years under drought stress conditions, the PC1 and PC2 were utilized to draw a biplot (Fig. 4). A sharp angle between most studied traits was discovered under the contribution of genotypes and years, showing a positive correlation between these traits, however, they vary in their degree and consistency in quantity. PCA analysis corroborated the conclusions of Pearson's correlation coefficient. In biplot (Fig. 4), the PC1 and PC2 allowed to group 24 cotton genotypes and studied traits according to their phenotypic similarities into 2 groups. The PC1 (first group) showed clustering of chlorophyll *b*, total chlorophyll, lint cotton yield/plant, seed cotton yield/plant and proline with G4, G5, G6 and G20 genotypes (first quarter), and carotenoids, number of open bolls/plant and chlorophyll *a* with G17, G19 and G21 (fourth quarter). These traits are substantially positively correlated with these genotypes, indicating their outstanding performance in terms of yield and physiological traits under drought stress conditions. The second group was related to PC2 and included the other traits tested in the second and third quarters with the other genotypes. The PCA scree plot of the major impacts of 28 cotton genotypes on cotton yield and other measured variables during drought stress years revealed that the PC1 and PC2 eigenvalues correspond to the entire percentage of variance in the dataset (Fig. 5). The PCA analysis results confirmed the results of cluster analysis (Fig. 2). Generally, PC1 has a high production potential and has the most stable genotypes, therefore it can be used to select drought-tolerant genotypes, in contrast PC2.

Discussion

Drought is a major limitation to cotton and other crops production both globally and in Egypt. The objective of

Table 5. Results of principal component analysis (PCs) in the first 5 PCs for the studied traits during the main effects of genotypes and years under drought stress conditions

Traits	Principal Components				
	PC1	PC2	PC3	PC4	PC5
Boll weight	-0.15	0.52	0.09	-0.23	0.24
Seed cotton yield/plant	0.38	0.02	0.19	0.12	0.21
No. of open bolls/plant	0.37	-0.21	0.13	0.20	0.09
Seed index	-0.23	-0.23	0.40	-0.27	0.32
Lint %	0.08	0.16	0.61	0.37	-0.10
Lint cotton yield/plant	0.37	0.03	0.26	0.16	0.19
No. of fruiting branches/plant	-0.04	0.45	-0.33	0.23	0.43
Plant height	-0.12	-0.30	-0.17	0.29	0.68
Chlorophyll *a*	0.22	-0.39	-0.32	0.06	-0.07
Chlorophyll *b*	0.33	0.39	-0.11	0.05	-0.07
Total chlorophyll	0.37	0.07	-0.26	0.07	-0.09
Carotenoids	0.30	-0.04	0.07	-0.54	0.25
Proline	0.32	0.01	-0.04	-0.47	0.10
Eigenvalues	5.81	1.91	1.48	1.09	1.02
Variance %	44.70	14.68	11.36	8.37	7.87
Cumulative%	44.70	59.38	70.74	79.11	86.98

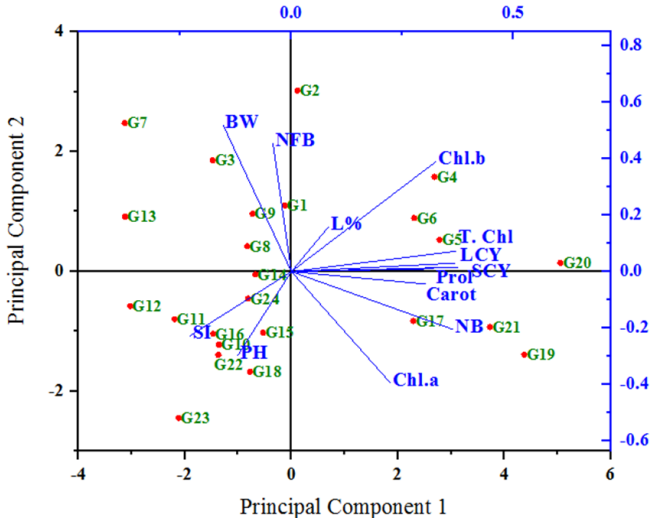

Fig. 4. Biplot diagram based on PC1 and PC2 shows similarities and dissimilarities relationships among the measured traits across 28 genotypes drought stress years' conditions. BW: boll weight; SCY: seed cotton yield/plant; NB: number of open bolls/plant; SI: seed index; L %: lint percentage; LCY: lint cotton yield/plant; NFB: Number of fruiting branches/plant; PH: plant height; *Chl. a*: chlorophyll *a*; *Chl. b*: chlorophyll b; *T. Chl*: total chlorophyll; Carot: carotenoids; Prol: proline

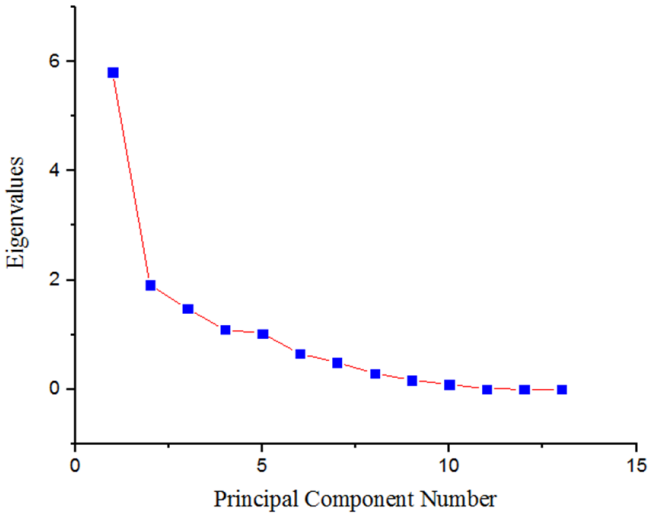

Fig. 5. Scree plot of PCA between respective eigenvalues % and components number

this study was to understand the interaction GY pattern for yield, yield components and physiological traits in 24 cotton genotypes growing 5-year period under drought stress conditions using AMMI analysis, genetic parameters and multivariate analysis. Thus identifying genotype high yielding and drought-tolerant during drought stress conditions in Egypt. According to the AMMI analysis of variance, the years factor had a significant impact on seed cotton yield/plant, number of open bolls/plant, lint %, lint cotton yield/plant and number of fruiting branches/plant. This indicates that the testing years were different and involved in the variation of the genotypic performance for these traits, so identifying best genotypes for adapted to the 5-year period under drought stress conditions. These differences could also be explained by the fact that these genotypes were tested in environments with varying precipitation, temperature and relative humidity (Fig. 1). Under drought stress conditions, ANOVA across years revealed significant variation among 24 cotton genotypes and interaction GY for all traits studied. This shows not only the amount of variation there was between years, but also the sufficient and desirable genetic variety there was among these genotypes under drought conditions, which might be used to boost cotton yields in Egypt's drought-prone regions. There are reports on the significant effects of genotypes, environments and their interactions on cotton quantitative traits using AMMI analysis of variance (22-26).

When sums of squares attributable to error and replication were removed, the genotypic effect contributed the most to overall variance, ranging from 44% to 58% in cotton yield and all investigated traits as compared to years and interaction GY effects. This suggests that there were significant variances in genotypes response over years, resulting in variations in cotton yield and the majority of traits studied, that can help in the selection of ideal genotypes under drought conditions. Genotypes and GE interaction variances helped in the selection of the better genotypes for studied traits, and reducing the impact of environmental main effects is critical in such conditions (48). The PC1 exhibited a greater contribution than the other PCs, ranging from 53% to 80% of the total interaction GY, demonstrating that the AMMI model effectively partitioned the variability in all studied traits. Because of the significant effect of GE interaction on the characteristics, various genotypes reacted and responded differently to environmental variation, necessitating the identification and selection of superior genotypes in environments (49).

Based on CV% values, the years factor affects seed cotton yield/plant, number of open bolls/plant, and lint cotton yield/plant compared to the other traits. Under drought stress conditions, the size of CV% suggested that the genotypes possessed exploitable genetic variability during the selection of cotton yield and other traits. Furthermore, the low CV% demonstrated the accuracy of the cotton experiment under drought stress conditions, similar to an earlier report (50). The lowest CV% was observed in physiological and some yield component traits, indicating that these parameters are drought resilient and can be considered one of the most essential drought tolerance features. In cotton, the CV% values for studied traits were low than10% (51, 52) and were more than 10% (53).

Under drought stress conditions, cotton yield and most examined traits of genotypes performed better in 2017 than in other years. According to this study, the average relative humidity and rainfall were at their greatest levels this year. Plants can respond to drought stress in three ways: physiologically, by reducing growth rates, molecularly, by increasing expression of ABA biosynthesis genes and biochemically, by accumulating stress metabolites such as proline and so on (54). The usefulness and effectiveness of yield components and physiological traits in grouping cotton genotypes under drought stress were discovered using mean performances and cluster analysis. It also revealed a considerable level of variability among the genotypes studied. As a

result, these genotypes were divided into five clusters. The first cluster comprised high-cotton yielding genotypes with moderate to high yield components and physiological traits, followed by the second, third, fourth and fifth clusters in that order. In the first cluster, G19 and G20 genotypes have high yield and physiological traits and were determined to be the most drought-tolerant, followed by G5, G4, G21 and G17 genotypes. Cotton genotype with high relative water content and photosynthesis performed better under drought conditions (55). While the G14, G2, G23, G22, G7 and G3 genotypes exhibit poor yield and physiological traits related with drought sensitivity (fifth cluster). These genotypes' excellent performance and drought tolerance could be explained by their good genetic background or increased contents of chlorophyll, carotenoids and proline. When compared to drought-sensitive genotypes, drought-tolerant genotypes can evolve a set of mechanisms that are more successful in protecting their structure and membrane functions (56). Our results are in accordance with earlier findings on cotton under drought stress, higher chlorophyll, carotenoids and proline contents were reported in drought-tolerant genotypes of cotton (38, 57-59). Drought-tolerant genotypes grow faster in drought stress, due to increased relative water content (60). Where chlorophyll-rich plants may store more assimilates, helping them to develop and generate more strong shoots and leaves (61) and therefore help to maintain crop yield under drought stress conditions (62). The carotenoids help in the heat dissipation of excess excitation energy in the photosynthetic machinery, preventing the generation of superoxide in plants receiving excessive light energy as photosynthesis declines under drought stress conditions (63). Proline is an osmolyte that also helps in the stabilization of subcellular structures (such as membranes and proteins), the scavenging of free radicals and the buffering of cellular redox potential under drought stress conditions (64).

Drought tolerance breeding is difficult because it is a complex quantitative trait with multipart phenotypes, it is controlled by many genes and it exhibits significant GEI. The genetic variability of crops necessitates the study of traits that contribute to drought tolerance and the exploration of their genetic variation (65), thus genetic variability is essential for selection (66). The heritable part of the overall observed variability can be studied using variance components, BSH, GA, GAM%, GCV% and PCV% parameters (67). The current study discovered a high genetic variance in drought tolerance for all traits tested, resulting in high BSH estimations. The high genotypic variance and BSH estimates for all investigated traits indicate that genotypes are primarily responsible for the formation/manifestation of these traits, with environments and GY interaction playing a minor role. The σ_g^2/σ_{ph}^2 ratio was higher than the σ_e^2/σ_{ph}^2 ratio due to the high genotypic variance found across all traits. According to the genetic study, the genotypic variance was higher than environmental variance, leading to a high σ_g^2/σ_e^2 ratio for all traits studied. Similar results for variance components of cotton genotypes were also reported (37, 50, 68-71).

The highest degree of heritability indicates the importance of cotton genotypes and traits simultaneously for genotype development under drought stress conditions (37). The predominance of additive gene action in the expression of all studied traits and genotype ability to drought tolerance was shown by high BSH combined with high GA and GAM%, indicating that these traits were under genetic control and their importance in providing a large amount of genetic gain as an important source for the selection of drought stress tolerance, leading to evaluation and chances of effective selection of superior genotype under drought stress conditions. As a result, breeding programmes without progeny tests can be employed to improve these traits (37, 72). It was found a similar degree of heritability and genetic advance under drought stress conditions (50, 71, 73). The combination of high heritability and genetic advance provides a clear picture of the traits in the selection process (71), implying that traits selection will be useful (50) and thus improvement in these traits is likely to be achieved through mass and progeny selection processes (74).

High to moderate values of GCV% and PCV% corresponded to high BSH estimates for cotton yield and most studied traits, indicating that these traits should be selected to develop desirable and adaptable genotypes under drought stress. Low or zero DPG values imply that the evaluated traits have little or no environmental impact under drought stress conditions, that their variation is genotypic in nature, and that genes with non-additive genetic effects are involved in the expression of these traits to drought tolerance. Thus, the genotypes can be improved and selected for these traits to drought tolerance. Interestingly, it was mentioned similar results of PCV% and GCV% (39, 50, 73, 75). Because the variability in observed traits was primarily due to genetic factors, the low differences between GCV% and PCV% suggested that these traits might be employed as selection criteria for further crop improvement (76). The genotypic variance was higher than the environmental variance due to the genotypes under drought stress circumstances, as indicated by high RCV (>1) for all examined characteristics, which may suggest that drought stress tolerance is heritable. The high genetic parameters of cotton yield and most studied traits indicated these genotypes under drought stress conditions may be a valuable source of genetic diversity for drought tolerance, so there is the presence of great opportunity to select and use genotypes drought-tolerant in cotton improvement programs. It indicates that if these traits are subjected to any selection procedures for exploiting fixable genetic variance, a widely adopted genotype can be developed under drought stress conditions (11).

Positive correlations between the 2 traits indicate that selection for the increasing value of one trait will lead to an increase in the value of the other (51). The positive and significant correlation was registered

among seed cotton yield/plant, number of open bolls/plant, lint cotton yield/plant, chlorophyll *b*, total chlorophyll, carotenoids and proline. Seed cotton yields/plant showed a positive association with lint percentage and chlorophyll *a*. These findings suggested that these traits had an impact on cotton yield under drought stress and were important to consider during the selection process, as these cotton yield can be improved and increased by increasing these traits. The positive correlation for yield, yield components and physiological traits have been reported in several studies (38, 39, 50, 71, 77, 78). The correlations of these traits indicated that their drought tolerance abilities are controlled by genes in linkage disequilibrium and/or with pleiotropic effects (15).

For the purpose of maintaining and exploiting genetic variety, the entire variance of the analyzed variables is divided into PCs. The first 5 PCs extracted had eigenvalues higher than one and contributed 86.98% of the total variability for combined data of genotypes and 5 years during drought stress conditions. The PC1 and PC2 accounted for more than 59% of the total variance of all analyzed variables, so can be the basis in the weighting of distribution and selection of genotypes and studied traits under drought stress conditions. The results of eigenvalues were consistent with earlier studies (37-39) who reported that PC1 and PC2 contributed the highest variance proportion under drought conditions with a value of 64%, 55% and 61% of the total variability respectively. Cotton genotypes and studied traits were divided into 2 categories on the PC1 and PC2 based on their phenotypic similarities. The traits chlorophyll *b,* total chlorophyll, lint cotton yield/plant, seed cotton yield/plant and proline with G4, G5, G6 and G20 genotypes, as well as carotenoids, number of open bolls/plant and chlorophyll *a* with G17, G19 and G21 genotypes, all contributed significantly to PC1 under drought stress conditions. These traits have a strong positive correlation with these genotypes, showing that they perform very well in terms of yield and physiological traits under drought stress. While PC2 was related to diversity among other genotypes due to other investigated traits with their positive contribution. Interestingly, PC1 appears to represent genotypes with high yield and physiological traits associated with drought tolerance, both of which are important for increasing cotton yield under drought stress. Whereas PC2 appears to represent genotypes with low yield and physiological traits associated with drought sensitivity. In cotton, drought-tolerant genotypes distribution and location are close to studied parameters vectors, indicating how these genotypes respond to studied variables (37). The results of PCA analysis confirmed correlation coefficient results among studied traits and cluster analysis results for cotton genotypes under drought stress conditions. The same trend of results in cotton has been reported earlier (51).

Conclusion

During drought stress conditions, the AMMI analysis of variance revealed significant variability due to the effects of genotypes, years and GY interaction on cotton yield, most yield components and physiological parameters. This suggests that the genetic variations between these genotypes were large enough to successfully select against drought stress. The high genetic parameters of cotton yield and most measured traits suggested that these genotypes under drought stress could be a rich source of genetic diversity for drought tolerance and provide a significant opportunity to select and exploit drought-tolerant genotypes. Cotton yield and most studied traits displayed positive and significant correlation, indicating these traits can be used as direct selection criteria to improve cotton yield under drought stress conditions. PCA and cluster analysis could be used as suitable methods for studying the drought tolerance mechanisms in cotton and were useful in identifying the G20, G19, G5, G4 and G21 genotypes have a huge potential for high yielding and drought tolerant, as the yield components and physiological traits had a significant heritability, which can be utilized as a source for drought tolerance in future breeding programs to develop a useful genotype to encounter the climate change scenario in Egypt.

Acknowledgements

This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

Authors contributions

This work was carried out in collaboration with all authors. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest : Authors do not have any conflict of interests to declare.

Ethical issues : None.

References

1. Rehman A, Farooq M. Morphology, Physiology and Ecology of Cotton Chapter 2. Cotton Production, 1st Ed. Edited Khawar Jabran and Bhagirath Singh Chauhan. John Wiley & Sons Ltd. 2020.
2. Al Didi MA. History of Egyptian cotton varieties. Egypt Cotton Gazette. 1972;58: 36-56.
3. Abdelbary AM, Hamoud HM, Yehiya WM, Abdelmoghny AM, Rabi EM, Ali SE et al. "Giza 97" A new Egyptian long staple cotton variety. Egyptian J of Agric Res. 2021;99(3):284-95. DOI: 10.21608/EJAR.2021.89116.1125
4. USDA. World Agricultural Production United States Department of Agriculture Foreign Agricultural Service, Office of Global Analysis, Circular Series, WAP 2-22, February 2022: 1-39. https://apps.fas.usda.gov/psdonline/circulars/production.pdf

5. Lamaoui M., Jemo M, Datla R, Bekkaoui F. Heat and drought stresses in crops and approaches for their mitigation. Front in Chem. 2018;6:26. https://doi.org/10.3389/fchem.2018.00026
6. Rehman T, Tabassum B, Yousaf S, Sarwar G and Qaisar U. Consequences of drought stress encountered during seedling stage on physiology and yield of cultivated cotton. Front Plant Sci. 2022;13:906444. doi: 10.3389/fpls.2022.906444
7. Mahmood T, Khalid S, Abdullah M, Ahmed Z, Shah MKN, Ghafoor A, Du X. Insights into drought stress signaling in plants and the molecular genetic basis of cotton drought tolerance. Cells. 2019;9:105-35. doi: 10.3390/cells9010105
8. Jie Z, Wei H, Li Y-X, He J-Q, Zhu H-H, Zhou Z-G. Screening of drought resistance indices and evaluation of drought resistance in cotton (*Gossypium hirsutum* L.). J Integ Agric. 2020;19:495-508. doi: 10.1016/S2095-3119(19)62696-1
9. Manivannan P, Jaleel CA, Sankar B, Kishorekumar A, Somasundaram R, Lakshmanan GMA, Panneerselvam R. Growth, biochemical modifications and proline metabolism in *Helianthus annuus* L. as induced by drought stress. Colloids Surf B Biointerfaces. 2007;59: 141-49. doi: 10.1016/j.colsurfb.2007.05.002
10. Meshram JH, Singh SB, Raghavendra KP, Waghmare VN. Chapter 6 - Drought stress tolerance in cotton: progress and perspectives, Editors: Arun K. Shanker, Chitra Shanker, Anjali Anand, M. Maheswari, Climate Change and Crop Stresspp. 2022;135-69. https://doi.org/10.1016/B978-0-12-816091-6.00005-5
11. El-Hashash EF, Agwa MA. Genetic parameters and stress tolerance index for quantitative traits in barley under different drought stress severities. Asian J of Res in Crop Sci. 2018;1(1): 1-16. https://doi.org/10.9734/AJRCS/2018/38702
12. Hall AE. Is dehydration tolerance relevant to genotypic differences in leaf senescence and crop adaptation to dry environments? In: Close T.J. and Bray E.A. (Editors). Plant Responses to Cellular Dehydration during Environmental Stress. 1993; p.1-10.
13. Solis J, Gutierrez A, Mangu V, Sanchez E, Bedre R, Linscombe S. Baisakh N. Genetic mapping of quantitative trait loci for grain yield under drought in rice under controlled greenhouse conditions. Front in Chem. 2018;5: 1-12. https://doi.org/10.3389/fchem.2017.00129
14. Blum A. Plant Breeding for Stress Environments. Florida: CRC Press. p. 212.
15. Falconer DS, TFC Mackay. 1996. Introduction to Quantitative Genetics, 4th edition Longman, New York. 1988;132-33p.
16. El-Hashash EF, EL-Agoury RYA, El-Absy KM, Sakr SMI. Genetic parameters, multivariate analysis and tolerance indices of rice genotypes under normal and drought stress environments. Asian J of Res in Crop Sci. 2018;1(3): 1-18. https://doi.org/10.9734/AJRCS/2018/41549
17. Eberhart SA, Russel WA. Stability parameters for comparing varieties. Crop Sci. 1966;6(1): 36-40. https://doi.org/10.2135/cropsci1966.0011183X000600010011x
18. Kang MS. Genotype-by-environment interaction and plant breeding. Louisana State University Agricultural Center, Baton Rouge, LA, USA. 1990; pp 392.
19. El-Hashash EF, Tarek SM, Rehab AA, Tharwat MA. Comparison of non-parametric stability statistics for selecting stable and adapted soybean genotypes under different environments. Asian J of Res in Crop Sci. 2019;4(4): 1-16. https://doi.org/10.9734/ajrcs/2019/v4i430080
20. Becker HC, Leon. J. Stability analysis in plant breeding. Plant Breeding. 1988;101(1): 1-23. https://doi.org/10.1111/j.1439-0523.1988.tb00261.x
21. Zobel RW, Wright MG,. Gauch HG. Statistical analysis of yield trial. Agron J. 1988;80(3): 388-93. https://doi.org/10.2134/agronj1988.00021962008000030002x
22. Campbell BT, Jones MA. Assessment of genotype × environment interactions for yield and fiber quality in cotton performance trials. Euph. 2005;144: 69-78. https://doi.org/10.1007/s10681-005-4336-7
23. Xu N, Fok M, Zhang G, Li J, Zhou Z. The application of GGE biplot analysis for evaluat ng test locations and mega-environment investigation of cotton regional trials. J of Integr Agric. 2014;13(9): 1921-33. https://doi.org/10.1016/S2095-3119(13)60656-5
24. Maleia MP, Jamal EC, Savanguane JW, João J, Teca JO. Stability and adaptability of cotton (*Gossypium Hirsutum* L.) genotypes under multi environmental conditions in mozambique. J of Agron and Agric Sci. 2019;2: 017. DOI:10.24966/AAS-8292/100017
25. Teodoro PE, Azevedo CF, Farias FJC, Alves RS, Peixoto LA, Ribeiro LP, Carvalho LP, Bhering. LL. Adaptability of cotton (*Gossypium hirsutum*) genotypes analysed using a Bayesian AMMI model. Crop and Past Sci. 2019;70(7): 615-21. https://doi.org/10.1071/CP18318
26. Lingaiah N, Sudharshanam A, Rao VT, Prashant Y, Kumar MV, Reddy PI, Prasad BR, Reddy PRR, Rao PJM. AMMI Biplot Analysis in Cotton (*Gossypium hirsutum* L.) Genotypes for genotype x environment interaction at four agro-ecologies in Telangana State. Curr J of Appl Sci and Tech. 2020;39(15): 98-103. https://doi.org/10.9734/cjast/2020/v39i1530722
27. Dutta P, Dutta PN, Borua PK. Morphological traits as selection indices in rice: A statistical view. Univ J of Agric Res. 2013;1(3): 85-96. DOI: 10.13189/ujar.2013.010308
28. Sabesan T, Suresh R, Saravanan K. Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamilnadu. Electron J Plant Breed. 2009;1:56-59.
29. Shukla S, Bhargava A, Chatterjee A, Singh S. Estimates of genetic parameters to determine variability for foliage yield and its different quantitative and qualitative traits in vegetable amaranth (*A. tricolor*). J Gene Breed. 2004;58: 169-76.
30. El-Hashash EF, EL-Agoury RYA. Comparison of grain yield-based drought tolerance indices under normal and stress conditions of rice in Egypt. Scholars J of Agric and Vet Sci. 2019;6(1):41-54. DOI: 10.21276/sjavs.2019.6.1.6
31. Burton GW, Devane EM. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron J. 1953;45:478-81.https://doi.org/10.2134/agronj1953.00021962004500100005x
32. Rathinavel K. Principal component analysis with quantitative traits in extant cotton varieties (*Gossypium hirsutum* L.) and parental lines for diversity. Currr Agric Res J. 2018;6(1). http://dx.doi.org/10.12944/CARJ.6.1.07
33. Shah SAI, Khan SJ, Ullah K, Sayal OU. Genetic diversity in cotton germplasm using multivariate analysis. Sarhad J of Agric. 2018;34(1): 130-35. http://dx.doi.org/10.17582/journal.sja/2018/34.1.130.135
34. Abdel-Monaem, MA, Abido WAE, Hadházy A, Ghoneima MH, EL-Mansy YM, EL-Shazly MW. Genetic divergence among Egyptian cotton genotypes under water deficit conditions. Acta Eco Sin. 2020. https://doi.org/10.1016/j.chnaes.2020.11.007
35. Sarwar G, Nazir A, Rizwan M, Shahzadi E, Mahmood A. Genetic diversity among cotton genotypes for earliness, yield and fiber quality traits using correlation, principal component and cluster analyses. Sarhad J of Agric. 2021;37(1): 307-14. http://dx.doi.org/10.17582/journal.sja/2021/37.1.307.314
36. Raza I, Hu D, Ahmad A, Li H, He S, Nazir MF et al. Correlation analysis of stem hardness traits with fiber and yield-related traits in core collections of *Gossypium hirsutum*. J of Cotton Res. 2021;4:8. https://doi.org/10.1186/s42397-021-00082-8
37. Mahmood T, Wang X, Ahmar S, Abdullah M, Iqbal MS, Rana RM et al. Genetic potential and inheritance pattern of phenological growth and drought tolerance in cotton (*Gossypium hirsutum* L.). Front Plant Sci. 2021;12:705392. https://doi.org/10.3389/fpls.2021.705392
38. Zahid Z, Khan MKR, Hameed A, Akhtar M, Ditta A, Hassan HM, Farid G. Dissection of drought tolerance in upland cotton through morpho-physiological and biochemical traits at

seedling stage. Front Plant Sci. 2021;12:627107. doi: 10.3389/fpls.2021.627107
39. Zafar MM, Jia X, Shakeel A, Sarfraz Z, Manan A, Imran A et al. Unraveling heat tolerance in upland cotton (*Gossypium hirsutum* L.) using univariate and multivariate analysis. Front Plant Sci. 2022;12: 727835. https://doi.org/10.3389/fpls.2021.727835
40. Lichtenthaler HK. Chlorophylls and carotenoids: pigments of photosynthetic biomembranes. In: Packer, L.; Douce, R., Editors. Methods in enzymology. London: Academic Press. 1987;148: 350-82. https://doi.org/10.1016/0076-6879(87)48036-1
41. Bates LS, Waldren RP Teare ID. Rapid determination of free proline for water-stress studies. Plant Soil. 1973;39: 205-07. https://doi.org/10.1007/BF00018060
42. Gomes FP. Curso de estatística experimental. 15.ed. Piracicaba: Esalq. 2009; p 477.
43. Searle SR, Casella G, McCulloch CE. Variance components. New Jersey: A John Wiley & Sons Inc. 2006.
44. Fehr WR. Principle of Cultivars Development. Macmillan publishing company. A division of Macmillan Inc. New Yor. 1987; pp.1: 1-465.
45. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and degree of dominance in corn. Agron J. 1949;41(8): 353-59. https://doi.org/10.2134/agronj1949.00021962004100080005x
46. Burton GW. Quantitative Inheritance in Grasses. Proceeding of 6th International Grassland Congress, Vol. 1, Pennsylvania State College. 17-23 August: 1952; 277-83.
47. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soya bean. Agron J. 1955;47: 318-24. https://doi.org/10.2134/agronj1955.00021962004700070009x
48. Gauch HG Jr. 1992. Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Elsevier Science Publishers. 1992.
49. Enyew M, Feyissa T, Geleta M, Tesfaye K, Hammenhag C, Carlsson AS. Genotype by environment interaction, correlation, AMMI, GGE biplot and cluster analysis for grain yield and other agronomic traits in sorghum (*Sorghum bicolor* L. Moench). PLoS ONE. 2021;16(10): e0258211. https://doi.org/10.1371/journal.pone.0258211
50. Manan A, Zafar M, Ren M, Khurshid M, Sahar A, Rehman A, Firdous H, Youlu Y, Razzaq A, Shakeel A. Genetic analysis of biochemical, fiber yield and quality traits of upland cotton under high-temperature. Plant Prod Sci. 2021. https://doi.org/10.1080/1343943X.2021.1972013
51. Yehia WMB, El-Hashash EF. Correlation and multivariate analysis across non-segregation and segregation generations in two cotton crosses. Egyptian J of Agric Res. 2021;99(3): 354-64. DOI: 10.21608/EJAR.2021.81571.1117
52. El-Hashash EF, Yehia WMB. Estimation of heritability, genes number and multivariate analysis using non- segregation and segregation generations in two cotton crosses. Asian J of Bioch Genet and Mol Bio. 2021;9(3): 45-62. https://doi.org/10.9734/ajbgmb/2021/v9i330221
53. Li B, Tian Q, Wang X, Han B, Liu L, Kong X et al. Phenotypic plasticity and genetic variation of cotton yield and its related traits under water-limited conditions. The Crop J. 2020;8(6): 966-76. https://doi.org/10.1016/j.cj.2020.02.003
54. Fang Y, Xiong L. General mechanisms of drought response and their application in drought resistance improvement in plants. Cell and Mol Life Sci. 2015;72: 673-89. https://doi.org/10.1007/s00018-014-1767-0
55. Anwar M, Saleem MA, Dan M, Malik W, Ul-Allah S, Ahmad MQ et al. Morphological, physiological and molecular assessment of cotton for drought tolerance under field conditions. Saudi J of Biolog Sci. 2022;29(1): 444-52. https://doi.org/10.1016/j.sjbs.2021.09.009
56. Grzesiak S, Hordyńska N, Szczyrek P, Grzesiak MA, Noga A, Szechyńska-Hebda M. Variation among wheat (*Triticum easativum* L.) genotypes in response to the drought stress: I – selection approaches. J of Plant Interac. 2019;14(1): 30-44. https://doi.org/10.1080/17429145.2018.1550817
57. Parida AK, Dagaonkar VS, Phalak MS, Umalkar GV, Aurangabadkar LP. Alterations in photosynthetic pigments, protein and osmotic components in cotton genotypes subjected to short-term drought stress followed by recovery. Plant Biotech. Repor. 2007;1: 37-48. https://doi.org/10.1007/s11816-006-0004-1
58. Parida AK, Dagaonkar VS, Phalak MS, Aurangabadkar LP. Differential responses of the enzymes involved in proline biosynthesis and degradation in drought tolerant and sensitive cotton genotypes during drought stress and recovery. Acta Physiolo. Planta. 2008;30(5): 619-27. doi: 10.1007/s11738-008-0157-3
59. Ergashova GS. Determination of chlorophyll content in leaves of *G. hirsutum* L. species in conditions of water shortage. Intern J of Sci and Res. 2020;9(8): 1427-30. DOI: 10.21275/SR20813122004
60. Ahmadizadeh M. Physiological and agro-morphological response to drought stress. Middle East J of Scient Res. 2013;13(8): 998-1009. DOI: 10.5829/idosi.mejsr.2013.13.8.3531
61. Ahmad A, Aslam Z, Javed T, Hussain S, Raza A, Shabbir R et al. Screening of wheat (*Triticum aestivum* L.) genotypes for drought tolerance through agronomic and physiological response. Agron. 2022;12: 287. https://doi.org/10.3390/agronomy12020287
62. Monteoliva MI, Guzzo MC,. Posada GA. Breeding for drought tolerance by monitoring chlorophyll content. Gene Technolo. 2021;10:165.
63. Reddy AR, Chaitanya KV, Vivekanandan M. Drought-induced responses of photosynthesis and antioxidant metabolism in higher plants. J of Plant Physiolo. 2004;161(11): 1189-202. https://doi.org/10.1016/j.jplph.2004.01.013
64. Iqbal S. Physiology of wheat (*Triticum aestivum* L.) accessions and the role of phytohormones under water stress Quaid-I-Azam University. 2009; Available online at: http://173.208.131.244:9060/xmlui/handle/123456789/7315
65. Dhanda SS, Sethi GS, Behl RK. Indices of drought tolerance in wheat genotypes at early stages of plant growth. J Agron Crop Sci. 2004;190(1): 6-12. https://doi.org/10.1111/j.1439-037X.2004.00592.x
66. Sarif HM, Rafii, MY, Ramli A, Oladosu Y, Musa HM, Rahim HM et al. Genetic diversity and variability among pigmented rice germplasm using molecular marker and morphological traits. Biotechnology and Biotechnological Equip. 2020; 34 (1): 747-62. https://doi.org/10.1080/13102818.2020.1804451
67. Garg HS, Kumar, P, Bhattacharya C, Panja S, Kumar R. Genetic parameters estimation for yield and yield related traits in rice (*Oryza sativa* L.) with drought tolerance trait under stress condition. J of Crop and Weed. 2017;13(1):83-88.
68. Yehia WMB, Hamoud, HME, EL-Akhader AAA, Abd EL-Gelil MA. Yield and fiber quality potential for triallel hybrids in cotton .2- Superiority J Agric Sci. Mansoura Univ. 2009;34(6): 6145-62. DOI: 10.21608/JACB.2009.90279
69. Khokhar ES, Shakeel A, Maqbool MA, Anwar MW, Tanveer Z, Irfan MF. Genetic study of cotton (*Gossypium hirsutum* L.) genotypes for different agronomic, yield and quality traits. Pakistan J of Agric Res. 2017;30(4):363-72. http://dx.doi.org/10.17582/journal.pjar/2017/30.4.363.372
70. Sahar A, Zafar MM, Razzaq A, Manan A, Haroon M, Sajid S et al. Genetic variability for yield and fiber related traits in genetically modified cotton. J of Cotton Res. 2021;4:19. https://doi.org/10.1186/s42397-021-00094-4
71. Abro S, Rizwan M, Deho ZA, Abro SA, Sial MA. Identification of heat tolerant cotton lines showing genetic variation in cell membrane thermostability, stomata and trichome size and its effect on yield and fiber quality traits. Front Plant

Sci. 2022;12: 804315. https://doi.org/10.3389/fpls.2021.804315

72. Khodadadi M, Fotokian MH, Miransari M. Genetic diversity of wheat (*Triticum aestivum* L.) genotypes based on cluster and principal component analyses for breeding strategies. Australian J of Crop Sci. 2011;5: 17-24.
73. Magwanga RO, Lu, P, Kirungu JN, Cai X, Zhou Z, Agong SG et al. Identification of QTLs and candidate genes for physiological traits associated with drought tolerance in cotton. J of Cotton Res. 2020;3: 3. https://doi.org/10.1186/s42397-020-0043-0
74. Soomro AW. Estimation of genetic variability parameters in segregating F2 generation of cotton. Fuuast J of Bio. 2020;10(2):83-87.
75. Chaudhari M, Faldu G, Ramani HJAIB. Genetic variability, correlation and path coefficient analysis in cotton (*Gossypium hirsutum* L.). Adva in Bioresea. 2017;8(6): 226-33..DOI: 10.15515/abr.0976-4585.8.6.226233
76. Sabri RS, Rafii MY, Ismail MR, Yusuff O, Chukwu SC, Hasan N. Assessment of agro-morphologic performance, genetic parameters and clustering pattern of newly developed blast resistant rice lines tested in four environments. Agron. 2020;10(8):1098. https://doi.org/10.3390/agronomy10081098
77. Majeed S, Malik TA, Rana IA, Azhar MT. Antioxidant and physiological responses of upland cotton accessions grown under high-temperature regimes. Iranian J of Sci and Tech Transactions A: Sci. 2019;43:2759-68. https://doi.org/10.1007/s40995-019-00781-7
78. Yehia WMB, El-Hashash EF. Combining ability effects and heterosis estimates through line x tester analysis for yield, yield components and fiber traits in Egyptian cotton. Elixir Agric. 2019; 131: 53238-46.

§§§