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COTTON GERMPLASM CHARACTERIZATION FOR DROUGHT TOLERANCE BASED ON MORPHO-PHYSIOLOGICAL AND FIBER QUALITY PARAMETERS

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SUMMARY

Drought tolerance is a quantitative trait that is exceedingly challenging to breed, especially for allotetraploids like cotton. The scenario of limited water resources necessitates developing drought-tolerant cultivars that conserve significant irrigation water throughout the summer. Therefore, the presented study used a design to statistically analyze the morphological, physiological, and fiber quality parameters linked with drought tolerance, which is a comprehensive method for choosing better genotypes from the available cotton germplasm. Measuring these parameters ensued for plants grown under field conditions. The germplasm comprised 150 cotton genotypes studied at two water regimes, i.e., regular and water-stressed conditions for two consecutive seasons of 2015–2016 and 2016–2017. Data recording ran for different morpho-physiological and fiber quality parameters. Significant differences occurred for all the treatments, genotypes, and Genotype × Environment interaction for all the morphological, physiological, and fiber quality parameters under study. Additive Main effects and Multiplicative Interaction (AMMI) analysis and AMMI biplot analysis helped analyze the results, which revealed that the cotton genotypes FH-900, FH-901, FH-312, AS-1, AS-2, AS-3, RH-510, RH-627, AR-2, AR-9, BH-118, BH-175, SLH-74, CIM-1100, CIM-598, and MM-58 were drought tolerant and ranked highest concerning stress condition. Moreover, correlation studies distinguished the relationship between relevant traits concerning drought tolerance.

Keywords: AMMI analysis, cotton, drought tolerance, morpho-physiological traits, field evaluation

Key findings: The drought-tolerant cotton genotypes, FH-900, FH-901, FH-312, AS-1, AS-2, AS-3, RH-510, RH-627, AR-2, AR-9, BH-118, BH-175, SLH-74, CIM-1100, CIM-598, and MM-58, stood out in this study to benefit a cotton breeding program for drought tolerance.

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INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is a leading fiber crop worldwide that faces periodic drought episodes. Its optimum production for good lint yield requires 2,158 to 3,906 m^3 of water for a full-growing season; this requirement varies with locally adopted production technology and meteorological patterns (McWilliams, 2003). Cotton production depends upon many factors broadly categorized into variety, environment, and management practices. Furthermore, crop exposure to multiple abiotic stresses, such as, limited water and high temperature, is often simultaneously. Even though cotton genotypes adapt well to drought and heat, extended exposure to both often leads to losses (Dabbert and Gore, 2014; Sajid *et al*., 2022). Water stress is the fundamental biotic stress that reduces plant growth and yield (Osakabe *et al*., 2014; Makhmadjanov *et al*., 2023). There are two main reasons for plants to experience drought stress; a lesser water supply to the roots and higher transpiration rates. These conditions prevail mainly in arid and semiarid climatic conditions (Rahdari and Hoseini, 2012; Muminov *et al*., 2023).

The screening studies under controlled conditions and container cultivation, i.e., pot experiments, have many disadvantages, and their results are also difficult to extrapolate to field conditions (Passioura, 2006). Different morphological traits, like stem, leaf, root, and physiological parameters, can be potential selection criteria for developing cotton drought-tolerant genotypes (Loka *et al*., 2011). Consideration is necessary for comprehensive plant adaptive mechanisms and physiological and genetic understating of crop plants under drought stress (Muhammad *et al*., 2011). Several multiple mechanisms exist by which plants respond to water stress that may enhance crops' drought tolerance (Deikman *et al*., 2012; Juenger, 2013).

The relative water content (RWC) indicates the balance in the leaf tissue between transpiration rate and water availability (Lugojan and Ciulca, 2011). Drought stress significantly reduced leaf RWC for all the genotypes under study (Parida *et al*., 2007; Abdel-Kader *et al*., 2015). For sustainability in water deficit conditions, the plants express various mechanisms, like deep roots, an increase of water-resistive diffusion, pumping of salts into the vacuole and out of the cells, and the formation of smaller, more succulent leaves to avoid excessive transpiration (Aroca *et al*., 2012). With such a short season of growth to produce a high-yielding and high-quality crop, certain phases, such as development and growth, cell division, elongation and differentiation, increase in volume, and intensification of weight, are all essentially irreversible, and changes from drought severely impact productivity (Taiz, 2010).

Drought affects photosynthesis, reduces the CO_2 assimilation rate, and disrupts the pigments and primary photosynthetic reactions (Ashraf and Harris, 2013). Decreased stomatal conductance with leaf water potential affects the net photosynthetic rate, reducing growth and development and decreasing the yield (Nikinmaa *et al*., 2013). Water stress conditions are responsible for biochemical and structural impairment of the reactions that require light and carboxylation processes of photosynthesis (Ghotbi-Ravandi *et al*., 2014). Drought stresses badly affected the fiber quality parameters in cotton (Du *et al*., 2015). The study on two cotton genotypes suggested that the four water regimes differently affected the fiber quality parameters of fiber length, strength, and fineness. Drought impacted all the parameters, from morphological and physiological to the cotton quality produced. Therefore, a comprehensive field study ran for two years on all the parameters (morpho-physiological and fiber grade) related to drought tolerance to identify the drought-tolerant cotton genotypes from the available cotton germplasm to benefit future breeding programs.

MATERIALS AND METHODS

Plant material

A germplasm population of 150 cotton genotypes was grown twice during the cotton

growing season in 2015 and 2016 at the Cotton Research Station (CRS), Ayub Agricultural Research Institute, Faisalabad (AARI), Pakistan, field area. Collected seeds came from the Cotton Research Station, AARI, Faisalabad, and Cotton Research Institute, Multan, Pakistan.

Experimental location and design

The experiment used a randomized complete block design (RCBD) with three replications in each environment. Tests ran on four independent conditions for cotton genotypes with no blocking. Plant-to-plant and row-to-row distances were 30 cm and 75 cm, respectively. A 100-cm distance between the stressed and non-stressed plots prevailed, while a 90-cm distance was between replications. Recorded observations were for 10 grown plants for each entry and data from eight plants. During the first year, a 24-acre inch of irrigation water flowed to the regular plot, while half or 12-acre inches to the stress plot. During the second year, the same procedure occurred to manage the irrigation applied to the experimental material. Delivering recommended agronomic practices and pesticide control ensued for a healthy crop stand.

Data collection

Data from three randomly selected plants of each genotype in each replication comprised plant morphological, physiological, fiber quality, and yield parameters. Plant height used a meter rod centimeters from the first node to an apical bud of the cotton plant. Collecting seed cotton from each replication from all mature bolls got placed in paper bags. Three pickings happened to ensure complete harvesting. Picking transpired at noon, with sunshine to evaporate any dew. Weighing with electronic balance was in grams. Five randomly selected plants from each replication of each variety gained recording for the number of nodes by visual observation, starting from the present node above the cotyledonous leaves. Calculating data of indirect fruiting (monopodial) branches continued at maturity.

Data recording of direct fruiting (sympodial) branches followed at maturity. Noted data of the mature bolls picked included each replication from all the genotypes. Calculating the average from each replicate resulted in data analysis. The average boll weight per plant was taken by dividing plant yield by the number of mature bolls picked from the plant. The quality parameters, fiber length (mm), fiber strength (g/tex), fiber fineness (µg), and fiber maturity ratio used the fibro graph HVI-900 from the fiber technology lab at the Cotton Research Station, AARI, Faisalabad, for the measurements. Taking canopy leaf samples from the middle of the plant, attained polythene bags cover. In the laboratory, measuring first fresh weight (FW), the specimens were kept for hydration in water for taking turgid leaf weight (TW). Leaves were kept in a dry oven at 70 °C overnight for the dry weight (DW). Taking the RWC used the following formula:

$$RWC\ (\%) = (FW - DW)/(TW - DW) \times 100$$

A pressure chamber (Model 600, Pressure Chamber Instrument, PMS International Company) measured the water potential by following the procedure elaborated by Scholander *et al*. (1964). Sampling ran from 6:00 to 9:00 a.m. to avoid evaporation losses. Measurements taken from fully expanded young leaves were usually 16–18 days old, with the leaves placed in the pressure chamber immediately to prevent error. Measurements occurred for both the regular and stressed plots separately.

After measuring water potential, freezing the cotton leaves continued in a freezer (-20 °C) to fix and measure osmotic potential. Once fully frozen, the leaves underwent thawing in the Eppendorf tubes, then collecting the cell sap by pressing the leaves with a glass rod. Calibration of the osmometer started first, then osmotic potential measurement followed by pouring a drop of sap on the cryoscopic osmometer (Osmomat 030-D, Cryoscopic osmometer printer, Genatec). An infrared thermometer (Model 510B; Everest Interscience Inc., Tucson, AZ, USA) measured the canopy temperature (CT).

Statistical analysis

Analysis of variance proceeded for significant differences among cotton genotypes, treatments, and genotypes by treatment interactions (Steel *et al*., 1997). AMMI biplot analyses (Gauch and Richard, 1988) checked the response of different environments using the agricolae package in R-software, treating the variables as random. Two years of the cotton-cropping season and two water regimes, i.e., regular and water stress, and 150 cotton genotypes (points) attained plotting against the treatment combinations. The first and second AMMI components were plotted along the X-axis and Y-axis of the graph, respectively. A simple correlation between different traits of interest also engaged the method described by Pearson (1920).

RESULTS

Data recording under field conditions consisted of morphological, physiological, biochemical, and quality parameters for the cotton-cropping season 2015 and 2016 under two water regimes, i.e., regular irrigation and water stress conditions. Significant differences arose for all the treatments, genotypes, and genotype × environment (treatment) interaction for all morpho-physiological and fiber quality parameters under study (Table 1). AMMI analysis performed for the traits exhibited significant differences for genotypes in environment interaction. Furthermore, AMMI biplot analysis ran for the interactive evaluation of genotypes under different environments (normal irrigation and water-stress conditions). The coded cotton genotypes used for AMMI biplot analysis and cluster dendrograms appear in Table 2. Based on the AMMI biplot analysis, ranking the cotton genotypes for each environment explained the top performers.

Table 1. Mean squares of 150 cotton genotypes for morphophysiological and fiber quality parameters under normal irrigation and water stress conditions for the cropping season, 2015 and 2016.

SOV	Env	Rep(Env)	Gen	Gen × Env	Residuals
DF	3	8	149	447	1192
PH	100312**	89	4465**	48**	3
Node	1371.42**	6.41	43.22	5.01**	0.53
Monp	0.6859**	12.505	13.1709	0.6494**	0.1454
Sym	1794.9**	12.7	93.2	7.4**	1.2
BW	140.666**	0.016	6.543	0.168**	0.002
BLS	24316.1**	14	848.4	55.1**	1.5
PW	104208**	94	1303	51**	6
Physiological parameters					
WP	31.1784**	0.1374	2.216**	0.0245**	0.0001
OP	27.8866**	0.0021	0.1052**	0.0161**	0
SC	28566.1**	1739.1	14265.1**	130.8**	0.5
CT	301.512**	0.35	116.174**	0.054**	0
RWC	85355**	41	14441**	20**	0
Fiber Quality parameters					
SL	663.08**	1.11	10.83**	1.73**	0
SS	42.996**	3.404	90.404**	24.717**	0.013
SU	0.84027**	0.01986	0.00155**	0.00032**	0.0001
Fine	14.1995**	0.04	1.3279**	0.0033**	0.0001

SOV = Source of variation, DF = Degree of freedom, Gen = Genotypes, Rep= Replications, Env = Environments, PH = Plant height, Node = No. of nodes, Monp = No. of monopodial branches, Sym = No. of sympodial branches, BW = Boll weight, BLS = No. of bolls, PW = Plant weight, WP = Water potential, OP =Osmotic Potential, SC = Stomatal conductance, CT = Canopy temperature, RWC = Relative water content, SL = Staple length, SS = Staple strength, SU = Staple uniformity, Fine = Fiber fineness, ** Highly significant.

Table 2. Coding of genotypes for AMMI Biplot Analysis.

Code No.	Genotype	Code No.	Genotype	Code No.	Genotype	Code No.	Genotype
1.	AGC-777	41.	CH-019	81.	A-162	121.	COKER-310
2.	S-11/3	42.	CH-009	82.	BJAHL	122.	IR-NIAB-824
3.	SLH-74	43.	CH-003	83.	BLANCO-3363	123.	DP-148
4.	FH-312	44.	AR-25	84.	ALBACALA(70)19	124.	DP-165
5.	ABRI/5	45.	AR-22	85.	CIM-616	125.	IUB-2009
6.	IR-NIBGE-6	46.	AR-23	86.	CYTO-177	126.	SB-149
7.	FH-142	47.	AR-21	87.	CBS-1	127.	IR-NIBGE-3
8.	MNH-456	48.	108-F	88.	FH-118	128.	DP-15-26
9.	RH-627	49.	124-F	89.	VH-305	129.	FH-113
10.	SILKEE	50.	199-F	90.	IUB-13	130.	TARZEN-1
11.	BH-180	51.	208-HYBI	91.	CIM-599	131.	E-302
12.	PB-899	52.	268-F	92.	MNH-886	132.	EXOTIC
13.	FH-942	53.	281GL(443)	93.	BOSS-111	133.	F-281GL-44
14.	FH-4243	54.	407-26	94.	BROWN-BHW	134.	FE-4252
15.	FH-330	55.	448/4727C	95.	BS-1	135.	FH-1000
16.	RH-510	56.	4-F	96.	C2(37)1473	136.	FH-113
17.	AS-2	57.	AET-5	97.	C-24	137.	FH-1185
18.	AS-1	58.	ACALA-P3	98.	CAPTAIN-2833	138.	FH-2000
19.	CIM-600	59.	ACALA-7203-4	99.	CEDIX	139.	FH-2006
20.	CIM-598	60.	YU-MM2	100.	CIM-200	140.	FH-2925
21.	CEMB-55	61.	ACALA-157C	101.	CIM-240	141.	FH-900
22.	AS-3	62.	ACA-285	102.	CIM-243	142.	C-HIR-1628
23.	AGC-999	63.	AC-307	103.	CIM-443	143.	KZ-181
24.	MM-58	64.	61-F/89	104.	CIM-446	144.	FH-53
25.	FH-142S	65.	AMS-139	105.	CIM-473	145.	FH-901
26.	NS-161	66.	AMS-170	106.	CIM-482	146.	DPL-SL
27.	CIM-1100	67.	ASA\965)-650	107.	CIM-496	147.	KZ-191
28.	AR-9	68.	AU-59	108.	CIM-499	148.	SITARA-009
29.	AR-2	69.	AUBURH	109.	CIM-70	149.	N-131
30.	AR-3	70.	AUR-56	110.	CIM-83	150.	N-141
31.	AR-1	71.	B-403	111.	COKER		
32.	VH-300	72.	B-557	112.	SLH-2010-11		
33.	AR-14	73.	B-622	113.	CBS-2		
34.	AR-13	74.	BAR F/8	114.	DELCOTT-227		
35.	AR-17	75.	BH-580	115.	AONE		
36.	FH-324	76.	BH-118	116.	BH-175		
37.	FH-341	77.	BH-128	117.	SITARA-008		
38.	FH-314	78.	BARNT-205-4	118.	CRIS-468		
39.	FH-168	79.	BH-100	119.	CRIS-134		
40.	IUB-222	80.	BH-36	120.	CP-15		

Morphological traits

Plant height

AMMI biplot analysis for plant height under four environmental conditions, i.e., non-stress, NS2015 (standard irrigation during 2015), S2015 (water stress during 2015), NS2016 (normal irrigation during 2016), and S2016 (water stress during 2016) occurred for principal components and the first two and their interaction sufficiently explained the variation. Plotting the genotype against the environment resolved the interaction of environment x genotype. The projection for BH-162, CH-019, BH-128, and Silkee genotypes fell on the NS2015 vector, which proved a strong positive interaction at NS2015. RH-510, IR-NIBGE-6, AS-2, CBS-1, AGC-777, and FH-312 ranked highest during 2015 under water-deficit conditions for plant height. Similarly, genotypes, ABRI/S, FH-320, CEMB-

55, and Cyto-177, ranked highest in NS2016, while FH-142, CIM-598, BH-36, and BH-580 gave better results concerning plant height. (Figure 1.a). NS2015 and NS2016 interacted with genotypes more relative to S2015 and S2016, as the angle between NS2015 and NS2016 vectors is narrow compared with S2015 and S2016, which are comparatively broader.

Nodes to first fruiting branch

Cultivars FH-900, MNH-886, IUB-2009, AGC-77, N-141, and VH-305, ranked highest in S2015 concerning the number of nodes to the first fruiting branch. CIM-200, B-403, B-557, CH-003, and AS-2, ranked highest during S2016. Similarly, FH-113, CIM-446, CP-15, FH-2006, and KZ-191, 108-F, FH-901, and AUR-56 ranked highest in NS2016 and NS2015, respectively (Figure 1.b).

Number of monopodial branches

The genotypes near the origin of the graph, i.e., FH-314, AR-17, and RH-510, proved stable. The S2016 was the most interactive environment, followed by NS2016, S2015, and NS2015, depending on the spoke length. The genotypes, including FH-142, FH-341, and AR-14 at S2015; FH-312, AGC-999, MM-58, and AR-1 at NS-2015; and CIM-1100, BH-128, 199F, and Cyto-177 at NS2016 environments, gave strong positive interaction, whereas, cotton genotypes AS-1, FH-4243, and RH-627 at S2016 had a strong negative interaction (Figure 1.c).

Sympodial branches per plant

All the four environments interacted differently with the genotypes FH-113, AS-3, SB-149, and CIM-1100 in S2015; FH-901, 199-F, AET-5, and Cooker in NS2015; AGC-999, MM-58, IUB-222 CH-003, and FH-941 in NS2016, indicating positive interactions with the ecosystems. On the other hand, the genotypes, Boss-111, CAPTAIN-2823, BH-118, and CIM-600 in S2016 had strong negative interaction (Figure 1.d).

Bolls per plant

The genotypes BH-175, Sitara-008, FH-142, and AR-2 ranked higher in the water stress environment during 2015, while BH-118, B-622, IUB-13, VH-305, and FH-142 ranked higher in the water stress environment concerning the number of bolls per plant. Genotypes Cyto-177, FH-4243, BLANCO-3363, and BH-128 ranked higher in NS2015, while AS-3, SLH-76, Silkee, and FH-330 ranked higher in NS2016 (Figure 1.e).

Bolls weight

Genotypes FH-312, SLH-74, FH-142, and MM-58 ranked highest in the water stress environment during 2015, and Coker310 and DELCOTT-227 were better in the water stress environment concerning boll weight. Similarly, genotypes CIM-482, VH-305, CBS-2, BH-118, and BH-128 ranked highest in NS2015, while AGC-999, MNH-456, CIM-598, and CEMB-55 were better in NS2016 concerning the number of bolls per plant (Figure 1.f).

Plant weight

Genotypes at the graph origin, i.e., FH-142, CIM-600, AS-3, and A-162 proved stable. The S2016 was the most interactive environment, followed by S2015, NS2015, and NS2016. The genotypes, including CIM-1100, B-622, MM-58, and FH-142S, ranked highest in S2015, and VIM-443, CIM-446, FH-113, and RH-510 ranked highest in S2016 for the plant yield. Conversely, the genotypes, FH-312, 268-F, N-141, and FH-330 ranked highest in NS2015, though Sitara-009, AC-307, BS-1, and IUB-222 ranked highest in NS2016 (Figure 1.g).

Physiological parameters

Water potential (-MPa)

All four treatments interacted with genotypes contrastingly for water potential. ACALA-15, 108-F, and FH-341 ranked higher in the stress condition of 2016, while CIM-598, AS-1, AGC-777, and AS-2 ranked higher in the stress

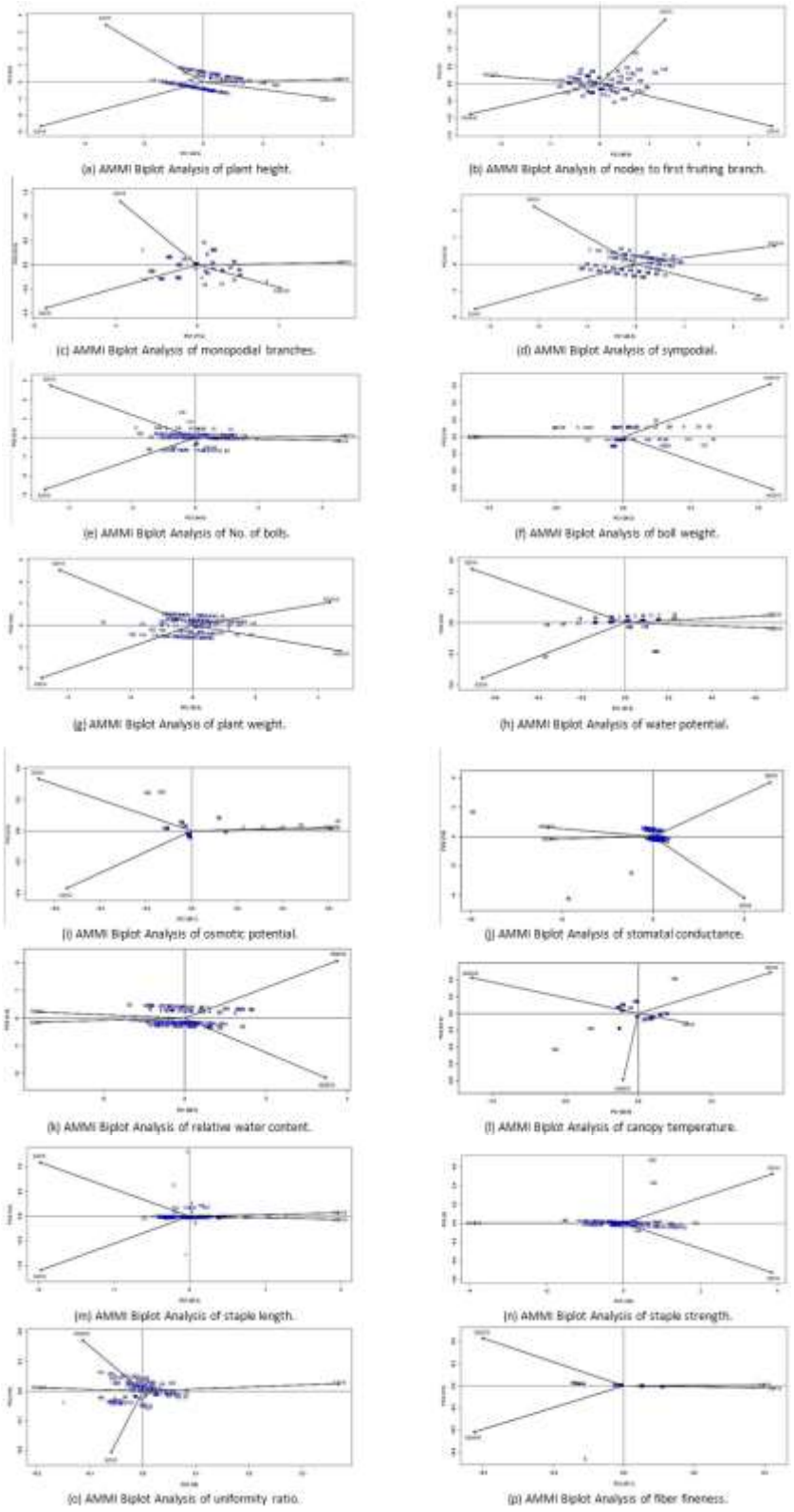

Figure 1. AMMI analysis for various morphological, yield, physiological, and fiber quality traits in *Gossypium hirsutum* L.

condition of 2015. Conversely, KZ-191, DP-15-26, Tarzen-1, and FH-900 ranked higher in NS2015, but FH-142, SLH-74 BH-180, and FH-312 ranked higher in NS2016 (Figure 1.h.).

Osmotic potential (-MPa)

Figure 1.i exhibited 99% interaction between PC1 and PC2 for the osmotic potential for AMMI biplot analysis under S2015, NS2015, S2016, and NS2016. S2016 was the most interactive environment, followed by S2015, NS2015, and NS2016, based on spoke length. Most cotton genotypes lay near the origin, suggesting they are stable in different environments concerning their leaf osmotic potential.

Relative water contents (%)

Genotypes CRIS-134, IR-NIAB-824, and FH-113 ranked highest in the water stress environment in 2015, while CH-009 and RH-510 were better in the water stress environment concerning RWC in 2016. Similarly, genotypes MNH-886, BH-118, and ACALA-P3 ranked highest in NS2015, and FH-314, VH-300, and VH-305 performed well in NS2016 (Figure 1.j).

Canopy temperature (°C)

For canopy temperature, IUB-2009 ranked highest in water stress environment during 2015, but SITARA-009 was better in water stress environment concerning CT. Likewise, genotypes N-131, AMD, and N-141 ranked highest in NS2015, while 268-F and AS-1 exhibited better in NS2016 (Figure 1.k).

Stomatal conductance (mmol m−2 s−1)

Most of the cotton genotypes were near the origin, suggesting they are stable in different environments concerning stomatal conductance (Figure 1.l).

Quality parameters

Staple length (mm)

Analysis of staple strength under four treatments, i.e., normal irrigation during 2015, water stress during 2015, normal irrigation during 2016, and water stress during 2016, resulted in PC1 and PC2 exhibiting interaction (100%). Stress and non-stress vectors appeared in opposite directions. The spoke length of the S2016 vector was the longest, which showed maximum interaction for that environment, followed by S2015, NS2016, and NS2015. Cotton genotypes DPL-SL, N-141, FH-900, and FH-901 ranked higher in S2015, yet AMS-170, 268F, Sitara-009, and AR-25 emerged best in S2016 concerning staple strength. Conversely, AGC-999, BH-36, AR-14, and CIM-1100 top the rank in NS2015, while FH-4243, IUB-13, CBS-1, and FH-142 in NS2016 (Figure 1.m).

Staple strength (g/tex)

The non-stress vectors in the same directions mentioned the impact of irrigation on fiber strength; conversely, the opposite directions of stress vectors described the negative influence of limited irrigation on fiber strength. DPL-SL, N-141, FH-900, and FH-901 ranked higher in S2015, while AMS-170, 268F, Sitara-009, and AR-25 performed best in S2016 concerning staple strength, a vital parameter of cotton quality. In contrast, AGC-999, BH-36, AR-14, and CIM-1100 ranked higher in NS2015, with FH-4243, IUB-13, CBS-1, and FH-142 topping the rank in NS2016 (Figure 1.n).

Uniformity ratio (%)

EXOTIC, Sitara-11, NS-141, and KZ-181 came out best in S2015, while DP-148, BH-175, BOSS-111, and AR-9 ranked higher in S2016 concerning cotton quality parameter.

Conversely, AMS-139, VH-305, AR-14, and CIM-616 did well in NS2015, and DELCOTT-227, IR-NIBGE-3, IUB-2009, and CRIS-465 in NS2016 (Figure 1.o).

Fiber fineness (µg)

The opposite directions of the non-stress (NS2015 and NS2016) and stress (S2015 and S2016) vectors clearly illustrated that the number of irrigations highly influences the fiber fineness quality. Moreover, the identical directions of the stress vectors (S2015 and S2016) showed that the weather factors (relative humidity, rainfall, and temperature) did not affect the fiber fineness. All the genotypes exhibited relatively stable behavior plotted close to the origin, with this trait relatively unaffected due to different treatments (Figure 1.p).

Correlation of morphophysiological and quality traits

Correlation studies measured characters within each treatment. The first correlation study was for the 2015 cotton cropping season under normal water conditions (Table 3). The results revealed that plant height exhibited a positive and significant connection with the number of sympodial branches per plant, number of bolls, plant weight, staple length, and RWC; however, a negative and significant one occurred between plant height and canopy temperature. A relevant and positive link showed between sympodial branches and the number of bolls, plant weight, staple length, and RWC; however, a negative and significant correlation emerged between sympodial branches and canopy temperature. The number of bolls per plant indicated positive and significantly associated with plant weight, staple length, and RWC, and negatively and considerably related with canopy temperature. A positive and substantial correlation between plant weight with the staple length and RWC appeared, and a notable negative relationship with canopy temperature. Quality parameter staple length was positively and significantly associated with RWC, whereas it correlated negatively and extensively with canopy temperature. A negative and meaningful relationship emerged between RWC and canopy temperature.

Correlation studies under water stress conditions in 2015 revealed a positive and significant correlation between plant height and the number of sympodial branches and bolls per plant, plant weight, staple length, staple strength, and relative water content (Table 4). Plant height showed a negative and notably correlated with canopy temperature. Monopodial branches linked positively and substantially with the number of bolls per plant. The number of sympodial branches also emerged as definite and relevantly correlated with the number of bolls per plant, plant weight, staple length, staple strength, and relative water content. The number of sympodial branches per plant exhibited negative and meaningful correlation with canopy temperature. The number of bolls per plant provided positive and weighty relationships with plant weight, staple length, staple strength, and relative water content. The number of bolls per plant displayed a negative association with canopy temperature. Plant weight had a positive and noteworthy connection with staple length, staple strength, and relative water content, but negatively correlating with canopy temperature. Staple strength indicated a positive and considerable link with relative water content, yet, significantly and negatively correlated with canopy temperature. Relative water content had a significant negative correlation with canopy temperature.

Interaction studies during 2016 under normal conditions revealed a positive and significant correlation among plant height and number of sympodial branches and bolls per plant, plant weight, staple length, and relative water content, whereas a significant negative correlation with canopy temperature (Table 5). A relevant and encouraging correlation also occurred between the number of sympodial branches and bolls per plant, plant weight, staple length, and relative water content; however, notable and negative correlation with canopy temperature. The number of bolls per plant has a suggestive positive correlation with plant weight, staple length, and relative water

Table 3. Correlation coefficients of different parameters of 150 cotton genotypes under normal irrigation during 2015.

	PH	Node	Monp	Sym	BW	BLS	PW	SL	SS	SU	Fine	WP	OP	SC	CT
Node	0.070														
Monp	0.085	0.008													
Sym	0.970**	0.081	0.076												
BW	0.084	0.113	-0.029	0.051											
BLS	0.981**	0.076	0.070	0.970**	0.097										
PW	0.979**	0.074	0.066	0.0953**	0.112	0.987**									
SL	0.876**	0.025	0.057	0.825**	0.179	0.860**	0.879**								
SS	0.145	0.024	0.001	0.170	0.091	0.151	0.118	0.175							
SU	0.035	0.063	-0.116	0.011	-0.068	0.026	0.055	-0.001	-0.043						
Fine	-0.087	-0.102	0.229	-0.108	0.096	-0.103	-0.101	-0.047	0.026	-0.057					
WP	0.071	0.056	0.197	0.068	-0.029	0.086	0.090	0.126	-0.088	0.035	0.004				
OP	-0.118	-0.069	-0.108	-0.087	-0.105	-0.110	-0.120	-0.156	0.001	0.012	-0.090	-0.137			
SC	0.044	0.084	-0.072	0.059	-0.017	0.051	0.055	0.071	0.058	0.078	-0.104	0.052	-0.112		
CT	-0.978**	-0.059	-0.083	-0.955**	-0.066	-0.968**	-0.967**	-0.846**	-0.128	-0.057	0.105	-0.076	0.133	-0.070	
RWC	0.980**	0.074	0.077	0.946**	0.093	0.966**	0.963**	0.861**	0.122	0.031	-0.079	0.061	-0.140	0.067	-0.967**

PH= Plant height, Node= Nodes to first fruiting branch, Mon= Monopodial branches, Sym= No. of sympodial branches, BLS= No. of bolls per plant, BW= Boll weight, SL= Staple length, SS= Staple strength, SU= Staple uniformity, Fine= Fiber fineness, WP= Water potential, OP= Osmotic potential, SC= Stomatal conductance, CT= Canopy temperature, RWC=Relative Water Contents, ** Highly significant.

Table 4. Correlation coefficients of different parameters of 150 cotton genotypes under water stress conditions during 2015.

	PH	Node	Monp	Sym	BW	BLS	PW	SL	SS	SU	Fine	WP	OP	SC	CT
Node	0.100														
Monp	0.051	0.089													
Sym	0.940**	0.102	0.138												
BW	0.066	0.047	0.006	0.020											
BLS	0.972 **	0.091	0.065	0.927**	0.091										
PW	0.972**	0.075	0.023	0.908**	0.121	0.977**									
SL	0.848**	-0.027	0.021	0.771**	0.141	0.851**	0.858**								
SS	0.144	0.016	0.011	0.138	0.077	0.161	0.149	0.136							
SU	0.041	0.071	-0.180	-0.049	-0.074	-0.031	0.054	-0.073	-0.019						
Fine	-0.099	-0.076	0.203	-0.129	0.070	-0.090	-0.109	-0.048	0.024	-0.075					
WP	0.051	-0.039	0.122	0.105	-0.075	0.098	0.052	0.157	-0.092	-0.141	-0.002				
OP	-0.106	0.003	-0.115	-0.134	-0.071	-0.124	-0.073	-0.177	0.001	0.172	-0.075	-0.128			
SC	0.036	0.058	-0.042	0.033	-0.054	0.064	0.040	0.055	0.052	0.015	-0.115	0.032	-0.102		
CT	-0.976**	-0.099	-0.060	-0.920**	-0.051	-0.958**	-0.956**	-0.825**	-0.133	-0.049	0.103	-0.066	0.124	-0.065	
RWC	0.978**	0.107	0.037	0.915	0.050	0.949**	0.950**	0.813**	0.107	0.058	-0.098	0.028	-0.121	0.053	-0.965**

PH= Plant height, Node= Nodes to first fruiting branch, Mon= Monopodial branches, Sym= No, of sympodial branches, BLS= No. of bolls per plant, BW= Boll weight, SL= Staple length, SS= Staple strength, SU= Staple uniformity, Fine= Fiber fineness, WP = Water potential, OP= Osmotic potential, SC= Stomatal conductance, CT= Canopy temperature, RWC= Relative water content, ** Highly significant.

Table 5. Correlation coefficients of different parameters of 150 cotton genotypes under normal water conditions during 2016.

	PH	Node	Monp	Sym	BW	BLS	PW	SL	SS	SU	Fine	WP	OP	SC	CT
Node	0.132														
Monp	0.198	-0.078													
Sym	0.760**	0.146	0.278												
BW	0.167	0.226	0.038	0.151											
BLS	0.806**	0.164	0.294**	0.937**	0.187										
PW	0.813**	0.179	0.275	0.930**	0.226	0.977**									
SL	0.737**	0.180	0.183	0.506**	0.143	0.565**	0.551**								
SS	0.967**	0.118	0.155	0.716**	0.189	0.758**	0.784**	0.707**							
SU	0.015	0.020	-0.121	- 0.049	-0.050	-0.057	-0.055	-0.004	0.024						
Fine	-0.052	-0.124	0.156	-0.029	0.083	-0.007	-0.038	-0.043	-0.069	-0.047					
WP	0.041	0.056	0.108	0.081	0.055	0.084	0.103	0.088	0.063	0.082	-0.043				
OP	-0.143	-0.129	0.050	-0.102	-0.189	-0.112	-0.132	0.010	-0.130	-0.016	-0.043	-0.156			
SC	-0.007	0.164	-0.002	0.019	0.033	0.024	0.043	-0.024	-0.016	0.010	-0.098	0.092	-0.128		
CT	-0.926**	-0.131	-0.145	-0.750**	-0.157	-0.784**	-0.794**	-0.615**	-0.909**	-0.058	0.086	-0.072	0.170	-0.033	
RWC	0.994**	0.145	0.200	0.756**	0.170	0.804 **	0.808**	0.741**	0.960**	0.022	-0.048	0.043	-0.131	-0.009	-0.923**

PH= Plant height, Node= Nodes to first fruiting branch, Mon= Monopodial branches, Sym= No. of sympodial branches, BLS= No. of bolls per plant, BW= Boll weight, SL= Staple length, SS= Staple strength, SU= Staple uniformity, Fine= Fiber fineness, WP= Water potential, OP= Osmotic potential, SC= Stomatal conductance, CT= Canopy temperature, RWC= Relative water content, ** Highly significant.

Table 6. Correlation coefficients of different parameters of 150 cotton genotypes under water stress conditions during 2016.

	PH	Node	Monp	Sym	BW	BLS	PW	SL	SS	SU	Fine	WP	OP	SC	CT
Node	0.176														
Monp	0.200	-0.014													
Sym	0.704**	0.175	0.174												
BW	0.189	0.188	0.031	0.272											
BLS	0.813**	0.189	0.216	0.839**	0.242										
PW	0.819**	0.192	0.269	0.805**	0.211	0.904**									
SL	0.756**	0.230	0.168	0.509**	0.137	0.570**	0.541**								
SS	0.947**	0.127	0.113	0.635**	0.191	0.752**	0.769**	0.703**							
SU	-0.001	0.053	-0.246	0.011	-0.129	0.032	0.019	-0.048	0.052						
Fine	-0.036	-0.089	0.142	0.061	0.080	-0.043	0.003	-0.043	-0.069	0.052					
WP	0.072	0.036	0.070	0.044	0.049	0.080	0.108	0.095	0.051	-0.115	-0.043				
OP	-0.084	-0.056	0.169	-0.077	-0.129	-0.072	-0.073	0.061	-0.104	-0.172	-0.072	-0.026			
SC	0.025	0.111	-0.032	0.091	0.033	0.038	0.034	-0.026	-0.015	-0.024	-0.099	0.071	-0.112		
CT	-0.900**	-0.155	-0.091	-0.636**	-0.160	-0.763**	-0.782**	-0.613**	-0.909**	-0.038	0.089	-0.075	0.144	-0.033	
RWC	0.979**	0.165	0.149	0.657**	0.168	0.787**	0.799**	0.734**	0.959**	0.038	-0.050	0.030	-0.095	-0.012	-0.924**

PH= Plant height, Node= Nodes to first fruiting branch, Mon= Monopodial branches, Sym= No. of sympodial branches, BLS= No. of bolls per plant, BW= Boll weight, SL= Staple length, SS= Staple strength, SU= Staple uniformity, Fine= Fiber fineness, WP= Water potential, OP= Osmotic potential, SC= Stomatal conductance, CT= Canopy temperature, RWC= Relative water content, ** Highly significant.

content and a negative substantial association with canopy temperature. Plant weight has a positive significant correlation with staple length, relative water content and a negative weighty correlation with canopy temperature. Quality parameter staple length has an undesirable relevant connection with canopy temperature and a confirmed valuable correlation with relative water content. A negative and significant correlation between relative water content and canopy temperature transpired under normal irrigation conditions during 2016.

Similarity studies under water stress conditions during 2016 revealed a positive and significant correlation among plant height and the number of sympodial branches and bolls per plant, plant weight, staple length strength, and relative water content, but a relevant negative association with canopy temperature (Table 6). The number of sympodial branches also indicated positive and significantly connected with the number of bolls per plant, plant weight, staple length, strength, and relative water content; however, having a significant negative correlation with canopy temperature. The number of bolls per plant showed a positive and significant correlation with plant weight, staple length, strength, and relative water content. The number of bolls per plant had an undesirable link with canopy temperature. Plant weight correlated positively and significantly with staple length and strength, and relative water content; conversely, it negatively correlated with canopy temperature. Staple strength resulted in a positive and substantial connection with relative water content and has a significant negative correlation with canopy temperature. Relative water content provided a negative association with canopy temperature.

DISCUSSION

Water stress (drought) is the most influential that affects crop production adversely by disturbing the normal physiological and molecular processes in the crop plants. In the climate-changing scenario, freshwater availability becomes limited day by day. About 10% of the total cultivated land is free of stress. However, 25% of the world's agricultural land faces water stress, especially in warm and dry crop production areas. Increasing population pressure depletes the cultivated land and demands a continuous increase in crop production to provide food and clothing. Cotton production has water deficit conditions negatively influencing it.

The research concerning the potential to encounter stresses or margins forced by environmental conditions is limited. However, it is worth understanding how to minimize the effect of stress efficiently by considering different ideas and clarifying the impact of increasing the yield potential of cotton under drought stress. Among various ideas to deal with the adverse influence of drought conditions on crop plants, assessing available genetic diversity concerning drought tolerance is vital. For this, a better idea is to understand different morphological, physiological, and molecular parameters affecting crop yield for screening/evaluating the available germplasm against water stress conditions is necessary. It can provide valuable information on the resources to exploit genetic variability. Previous scientists like Iqbal *et al*. (2011) used morphological and physiological parameters for screening drought-sensitive and tolerant cotton genotypes (Shakoor *et al*. 2010).

The effects of drought stress on plants rely on its duration, plant growth stage, severity, and cultivar. Loka *et al*. (2011) studied drought stress influences on cotton growth and development, yield, and physiology. Indeterminate growth habits and perennial nature resulted in the different flowering and fruiting phases in cotton plant. This uncertainty conflicts further with various stages of crop development, most sensitive to water stress conditions (Loka *et al*., 2011). The initial flowering stage in cotton is the most sensitive to drought conditions. Still, others like Orgaz *et al*. (1992) determined the effect of drought proved more pronounced when the cotton crop is at flowering peak. Another study (Radin *et al*., 1992) reported that the boll development stage is most sensitive to drought conditions. Plant breeders need partitioning variation due to G and G × E interaction for

selecting superior genotypes in the evaluation trials (Yan *et al*., 2000). Among the various statistical method, GGE biplot and AMMI biplot analysis are the most promising (Yan and Tinker, 2006).

Biplot analysis is one of the popular data visualization tools in crop breeding experiments and other fields of study (Yan *et al*., 2000). AMMI analysis can help match superior genotypes to environmental conditions with relatively higher mean performance (Gauch *et al*., 2008). Higher genotypic projections on the CAE ordinate axis indicate more interaction with the environment and more unstable genotypes (Yang *et al*., 2009). The closest to an ideal genotype is one having a mean average yield that ranks consistently high in all environmental conditions. Graphically, the supreme genotype must have the lengthiest vector in PC1, while PC2 is without projections, with an arrow representing it in the center (Yan and Rajcan, 2002). The ideal environment is characteristically having a higher PC1 score (greater power to discriminate genotypes from main genotype effects) and minimum (zero) PC2 score (Yang *et al*., 2009).

This method is very effective for G × E interaction (genotype × environment) and selecting promising genotypes under different environmental conditions (Aina *et al*., 2007). Biplot analysis gives valuable information about the degree of divergence among the accessions, environment with ideal performance, and genotypic stability (Miranda *et al*., 2009). Generally, water stress intensively restricts growth and development by affecting the plant height, nodes, leaf area index, cotton quality, and root and canopy development (Loka *et al*., 2011). The morphological parameter assessed for the field evaluation study under different water levels revealed AMS-139, DPL-SL, BS-1, CIM-83, SLH-2010-11, FH-330, VH-300, AR-13, and RH-510 were tolerant genotypes due to being stable in the AMMI biplot analysis.

The reduction of plant yield in cotton is due to a less number of bolls per plant, followed by lesser flowers and increased shedding in the stress condition compared with regular irrigation or ample rainfall (Pettigrew, 2004). Cotton genotypes CIM-598, AS-1 AS-2, FH-341,108-F, MNH-886, RH-627, and RH-510 gained label as tolerant genotypes due to lower negative values for water and osmotic potential, and for water potential the genotypes, AR-22, FH-142, MNH-886, FH-341, and FH-118 were characterized as drought-tolerant genotypes. The leaf water potential for the water stress treatment was significantly lower than that of the normal irrigated treatment (Papastylianou and Argyrokastritis, 2014).

Stomatal conductance is a basic mechanism to regulate and optimize CO_2 assimilation and evaporative water loss. Under water stress condition, stomatal closure accomplished water conservation, controlled by an active/passive (ABA-mediated/hydraulic-mediated) mechanism. (Tombesi *et al*., 2015). A negative effect on osmotic balance is noticeable when water stress occurred in cotton. In decreasing the osmotic potential concerning water stress condition, the plant accumulates different organic and inorganic compounds (Fang and Xiong, 2015). In the drought-tolerant genotypes, a higher negative value of water potential and osmotic potential than in the drought-sensitive genotypes appeared (Sayar *et al*., 2008).

Higher relative water contents and lower canopy temperature emerged in drought-tolerant cultivars than those sensitive to water stress conditions. Traits measurement of economic importance in plants for correlations ensured they respond similarly to selection or to reveal if different mechanisms controlled these (Azhar *et al*., 2004). Correlation studies reflected a positive significant correlation of plant height with seed cotton yield and the number of bolls per plant. A similar positive correlation resulted between sympodial branches and bolls per plant. Analogous positive correlation results also came from several studies (Pettigrew, 2004; Annapurve *et al*., 2007; Whitaker *et al*., 2008; Ritchie *et al*., 2009; Salahuddin *et al*., 2010; Khokhar *et al*., 2017).

CONCLUSIONS

Environmental conditions strongly influence cotton production, leading to considerable variations in yield. Identifying genotypes for improving certain traits for abiotic stresses, particularly drought, using AMMI analysis is the key to using morphological, physiological, and quality parameters. The drought-tolerant cotton genotypes identified in this study can benefit future plant breeding programs. The identified genotypes can also serve in bi-parental population generation for identifying molecular markers linked with essential drought-related morpho-physiological and quality parameters.

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