

PHENOTYPIC EVALUATION OF COTTON GENOTYPES FOR DROUGHT TOLERANCE AT SEEDLING STAGE

Muhammad Tanees Chaudhary^{*1}, Muhammad Ihsan Ullah², Shoaib Liaqat³, Nouman Bilal⁴,
Zaid Waqas⁵, Hafiz Usama Manzoor⁶, Saima Jameel⁷, Kamran Javed⁸, Suleman Gohar⁹,
Mashal Rehman¹⁰, Asma Parveen¹¹, Muhammad Zahid Aslam¹²

^{*1,8}Cotton Research Station, Vehari-61100, Pakistan

^{2, 3}Cotton Research Institute, Multan-60000, Pakistan

⁴Department of Plant Breeding and Genetics, Ghazi University, Dera Ghazi Khan-32200, Pakistan

⁶Quarantine and Cotton Biotechnology Laboratory, Institute of Plant Breeding and Biotechnology, MNS University of Agriculture, Multan- Multan-60000, Pakistan

⁶Department of Plant Breeding and Genetics, Islamia University, Bahawalpur-63100, Pakistan

⁷Department of Biotechnology, Fatima Jinnah women university, Rawalpindi-46000, Pakistan

⁹Cotton Research Station, Sahiwal-57000, Pakistan

¹⁰Agricultural Research Station, Bahawalpur-63100, Pakistan

¹¹Cotton Research Station, Faisalabad-38000, Pakistan

¹²Cotton Research Station, Bahawalpur-63100, Pakistan

^{*1}tanees_ch227@yahoo.com, ³shoaibliaqat87@gmail.com

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Corresponding Author: *
Muhammad Tanees
Chaudhary

Abstract

Drought stress is a major constraint to sustainable cotton production, making the identification of genotype with desirable growth and root characteristics under limited water availability an important breeding objective. The present study evaluated 60 cotton genotypes under two water regimes i.e. normal and drought conditions using morphological, biomass, leaf, and root-related traits. The experiment was conducted for 40 days at the Cotton Research Station, Vehari, Punjab, Pakistan, using a completely randomized design with two replications. Analysis of variance revealed significant differences among genotypes for all evaluated traits, while genotype × treatment interaction was significant for all traits, indicating considerable variation in genotype response to water availability. Drought stress reduced plant height and number of leaves, whereas root length, root weight, root–shoot ratio, total biomass and several other traits showed comparatively stable or improved performance. Correlation analysis demonstrated strong positive associations of root weight with root–shoot ratio ($r = 0.90$, $P < 0.001$) and total biomass with stem weight ($r = 0.76$, $P < 0.001$) under drought conditions, highlighting the importance of biomass partitioning and root development in drought response. Principal component biplot analysis explained 36% of the total variation through the first two components and separated the genotypes into four major clusters. Based on

favorable multivariate positioning, NH-161, Malmal, A-555 and BH-180 were identified as promising genotypes, particularly in association with root weight, root–shoot ratio and other desirable growth characteristics under the drought stress conditions. Overall, the results demonstrated substantial genetic diversity among the tested cotton genotypes and indicated that combined assessment of morphological, biomass and root traits through correlation and biplot analysis can assist in identifying promising material for drought-tolerance breeding.

INTRODUCTION:

Cotton (*Gossypium* spp.) is one of the world's most important fiber and cash crops and has a central role in the agricultural and industrial economy of Pakistan. The crop provides raw material for the textile and ginning industries and contributes to employment, rural livelihoods, exports and foreign exchange earnings. According to the Pakistan Economic Survey 2025–26, agriculture contributed 23.44% to Pakistan's GDP, while cotton production was estimated at 7.05 million bales, contributing approximately 0.4% to GDP and 1.8% to agricultural value addition. However, cotton production declined slightly from 7.08 million bales in 2024–25 to 7.05 million bales in 2025–26, highlighting the continuing challenges faced by the crop sector. Climate variability, increasing temperature and irregular water availability are among the major factors threatening sustainable cotton production in Pakistan and other cotton-growing regions.

Drought is one of the most important abiotic stresses limiting cotton growth and productivity. Increasing frequency of drought episodes associated with climate change can adversely affect plant water relations, photosynthesis, biomass accumulation and reproductive development. Water deficit may reduce leaf expansion, root and shoot growth, and photosynthetic activity, ultimately affecting yield and fiber production (Zafar et al., 2023). Recent reviews have further emphasized that changing precipitation patterns and extreme climatic events are increasing the vulnerability of cotton production and that the development of drought-resilient cultivars is an important component of

climate adaptation strategies (Iram et al., 2024; Ijaz et al., 2024).

Cotton genotypes exhibit considerable genetic variation in their response to water deficit, providing an opportunity for selection and genetic improvement. Drought tolerance is a complex characteristic involving multiple morphological, physiological, biochemical and molecular mechanisms. Differences among genotypes in root development, biomass allocation, canopy development and water-use characteristics can influence their ability to maintain growth under limited water availability. Recent studies have demonstrated significant genotype-dependent variation in cotton responses to different levels of drought and have identified morphological and physiological traits useful for drought-resilience screening (Shani et al., 2025). Similarly, multi-year and multi-site evaluation of cotton germplasm has confirmed significant variation in drought resistance among genotypes and emphasized the importance of plant growth traits in drought screening (Zhang et al., 2025).

Morphological and biomass traits are particularly useful for evaluating early responses to drought. Plant height, number of leaves and number of nodes provide information about vegetative growth and plant architecture, whereas leaf weight, stem weight and root weight reflect biomass accumulation and partitioning. Root attributes are particularly important because the root system determines the capacity of plants to explore soil and acquire available water. Thus, root length, root volume and root-shoot ratio may provide useful indicators of differences in drought adaptation. Likewise, leaf area and shoot

length influence canopy development and photosynthetic capacity and may decline substantially under water-limited conditions. Recent research has shown that drought stress can produce significant changes in root and shoot growth and that genotypes differ in their capacity to maintain these traits under stress (Shani et al., 2025; Khan et al., 2026).

Evaluation under contrasting moisture regimes is essential because genotype performance under normal conditions does not necessarily predict performance under drought. Previous studies in Pakistan have demonstrated differences in genotype adaptability and stability between normal and water-deficit environments, with biplot-based approaches successfully identifying genotypes possessing desirable adaptation under drought conditions. More recent research has also shown that drought-resistant genotypes can be effectively differentiated using multivariate approaches and stress-related traits (Shani et al., 2025; Zhang et al., 2025). Furthermore, molecular studies have identified markers and genomic regions associated with drought-related traits, demonstrating the potential for integrating phenotypic screening with modern breeding approaches (Liu et al., 2025).

Correlation analysis is a useful tool for determining the strength and direction of relationships among morphological, biomass and root traits. Identifying strongly associated characters can assist breeders in selecting indirect indicators of drought adaptation and understanding how different plant components contribute to stress response. However, because drought tolerance involves several interrelated traits, evaluation based on correlations alone may not adequately distinguish genotypes possessing desirable combinations of characteristics.

Therefore, biplot analysis provides a valuable multivariate approach for simultaneously examining relationships among traits and genotypes. Principal component and biplot analyses have been successfully used in cotton to visualize trait associations, identify superior genotypes and discriminate drought-tolerant

material under contrasting environments. Such approaches are particularly useful when numerous traits are measured simultaneously because they allow genotype performance to be interpreted from an integrated rather than a single-trait perspective.

The present study was therefore conducted to evaluate cotton genotypes under normal and drought conditions using morphological, biomass and root-related traits, including plant height, number of leaves, number of nodes, leaf weight, stem weight, root weight, root-shoot ratio, leaf area, root length, shoot length, root volume and shoot volume. The objectives were to determine the extent of variation among genotypes under contrasting moisture conditions, investigate associations among the evaluated traits through correlation analysis, and identify promising genotypes and important traits through biplot analysis. The findings are expected to provide useful information for the selection of drought-resilient cotton genotypes and support breeding programs aimed at developing climate-resilient cultivars for sustainable cotton production in Pakistan.

Materials and Methodology

Experimental Site and Plant Material

The present study was conducted at the Cotton Research Station, Vehari, Punjab, Pakistan, to evaluate the response of cotton genotypes to contrasting water regimes. Sixty cotton genotypes were evaluated for morphological, biomass, and root-related traits under normal and drought stress conditions (Table 1). The experiment was conducted as a 40-day pot experiment under controlled experimental conditions. The traits evaluated included plant height (PH), number of leaves (NL), number of nodes (NN), leaf weight (LW), stem weight (SW), root weight (RW), root-shoot ratio (RSR), leaf area (LA), root length (RL), shoot length (SL), root volume (RV), and shoot volume (SV). The terminology and trait abbreviations correspond to the experimental ANOVA table provided for the study.

Table No. 1 List of cotton genotypes used in this study

Sr. No	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes
1	FH-142	21	A-011	41	IUB-2013
2	IUB-222	22	BH-178	42	Tarzan-1
3	MNH-886	23	Sitara-12M	43	Tarzan-2
4	FH-172	24	NH-161	44	MG-6
5	AA-904	25	BH-180	45	Sitara-008
6	VH-303	26	SB-149	46	A-555
7	AA-905	27	Sitara-11M	47	Saiban-201
8	CIM-602	28	Sitara-10M	48	Ali Akbar-703
9	FH-118	29	RH-627	49	Ali Akbar-802
10	IR-NIBGE-4	30	KZ-389	50	NS-141
11	IR-NIBGE-5	31	CIM-598	51	FH-113
12	MM-58	32	CIM-600	52	FH-114
13	VH-282	33	Cyto-177	53	IR-NIBGE-3
14	CIM-599	34	Cyto-178	54	CRIS-342
15	NIAB BT-1	35	Cyto-179	55	Sindh-1
16	SILKEE	36	IR-3701	56	NIA-Ufaq-08
17	MNH-456	37	IR-1524	57	Malmal
18	BGC-09	38	IR-NIAB-824	58	FH-1148
19	A-555	39	MNH-988	59	FH-333
20	SUN-1	40	VH-259	60	MNH-SG

Experimental Design and Treatments

The experiment was arranged according to a Completely Randomized Design (CRD) with two replications. Two water regimes were imposed: normal irrigation (control) and drought stress. Each genotype was represented under both treatments in each replication. Thus, the experimental structure consisted of 60 genotypes × 2 water treatments × 2 replications, resulting in

240 experimental observations. For the normal treatment, plants were maintained under adequate soil moisture throughout the experimental period. For drought treatment, water availability was restricted after establishment of the plants and maintained as the stress condition throughout the experimental period. The purpose of imposing the contrasting water regimes was to assess genotypic variation

and identify cotton genotypes capable of maintaining desirable growth and root characteristics under limited water availability.

Soil Collection and Preparation

The soil used for the pot experiment was collected from the surface agricultural soil layer of the experimental area at the Cotton Research Station, Vehari. Before filling the pots, the soil was thoroughly mixed to obtain a relatively homogeneous growing medium and visible plant residues, stones, and other debris were removed. The soil was then air-dried and passed through a suitable sieve to obtain a uniform texture.

The soil was characterized as a loam to sandy-loam agricultural soil, representative of the cotton-growing soils of the Vehari region. The soil was considered suitable for cotton growth because of its good drainage and adequate physical conditions for root development. Soil was placed uniformly into pots of equal size and approximately equal soil quantity was maintained in every experimental unit to minimize variation among pots.

Sowing and Crop Management

Healthy and uniform seeds of each genotype were used for sowing. Pots were properly labelled according to genotype, treatment, and replication. Seeds were sown at a uniform depth, and after emergence, seedlings were maintained under uniform growing conditions. Where necessary, thinning was performed to maintain a uniform number of plants per pot.

All experimental units received similar management with respect to sowing depth, pot size, soil quantity, nutrient management, and environmental conditions. Fertilization was applied uniformly according to the recommended requirements for cotton. Weed control and other routine cultural practices were carried out manually to avoid competition and ensure that differences among genotypes were primarily associated with genetic variation and response to water availability.

Imposition of drought stress

After establishment of seedlings, the drought treatment was imposed by restricting irrigation relative to the normal/control treatment. The normal treatment received adequate water to maintain satisfactory plant growth, whereas irrigation was withheld or substantially reduced at 40% field capacity in the drought treatment to create water-deficit conditions. The stress treatment was maintained until the completion of the 40-day experimental period.

At the end of the experiment, plants from each experimental unit were harvested carefully. Shoots and roots were separated, and roots were gently washed to remove adhering soil without causing substantial damage. Measurements were then recorded for the predefined morphological, biomass, leaf-area, and root traits.

Data recording and trait measurement

Data were recorded separately for each genotype, treatment, and replication. Plant height was measured from the soil surface to the uppermost growing point. Number of leaves and number of nodes were counted for individual plants. Leaf and stem biomass were measured after separating the respective plant components. Root biomass was determined after harvesting and processing the root system.

Root-shoot ratio was calculated from the dry or fresh biomass values of roots and shoots according to the measurement protocol used in the experiment. Leaf area was recorded using the available leaf-area measurement procedure. Root length and shoot length were measured using standard measurement scales, while root volume and shoot volume were determined using the adopted volumetric measurement procedure. The final dataset therefore comprised 13 measured variables, including the 12 evaluated traits and the treatment/genotype structure reflected in the statistical analysis. The supplied ANOVA table specifically lists PH, NL, NN, LW, SW, RW, RSR, LA, RL, SL, RV and SV as the evaluated traits.

Statistical analysis

The data were subjected to statistical analysis to determine the effects of genotypes, water treatments, and genotype $\times$ treatment interaction. Analysis of variance was performed according to the experimental structure, with genotype, treatment, and their interaction considered as major sources of variation. The analysis showed significant variation for most traits and also included genotype $\times$ treatment interaction, indicating differential responses of genotypes to the two water regimes.

In addition to ANOVA, Pearson correlation analysis was performed to determine the degree and direction of association among the evaluated traits under normal and drought condition. Correlation coefficients were used to identify positive and negative relationships among morphological, biomass, leaf, and root traits. Traits showing strong positive associations may be useful as indirect selection criteria, whereas negative associations may indicate potential trade-offs among traits.

Biplot analysis

Biplot analysis was performed to visualize the multivariate relationships among cotton genotypes and the evaluated traits under normal and drought conditions. Principal component-based biplots were used to simultaneously display genotypes and trait vectors, allowing the identification of genotypes with desirable combinations of characteristics and traits contributing most strongly to overall variation.

The biplot was also used to assess relationships among traits based on the angle and direction of trait vectors. Genotypes positioned in favorable directions relative to important trait vectors were considered potentially superior for the corresponding characteristics. Separate or treatment-specific biplots were used where appropriate to compare genotype performance under normal and drought conditions.

Selection of promising genotypes

Genotypes were comparatively evaluated on the basis of their performance across the measured traits and their response to drought. Particular attention was given to genotypes that maintained relatively favorable plant growth, biomass accumulation, root development, and root-shoot balance under drought stress. Correlation and biplot results were considered jointly to identify genotypes and traits that could be useful in subsequent cotton breeding and drought-tolerance selection programs.

Statistical model

The statistical analysis was based on the factorial structure involving genotype and water treatment. The general model considered the effects of genotype, treatment, their interaction, replication, and experimental error. The resulting mean sum of squares were used to determine the magnitude of variation attributable to each source. In the supplied analysis, genotype $\times$ treatment interaction was significant for all listed traits, supporting the evaluation of genotype performance under each water regime separately. All statistical analyses were conducted using GenStat software, and correlation coefficients and biplot results were interpreted at the relevant statistical significance level. The statistical findings were subsequently used to characterize genetic variability and drought response among the 60 cotton genotypes.

RESULTS

Analysis of variance

The analysis of variance revealed substantial genetic variation among the 60 cotton genotypes and clear differences between normal and drought conditions for most seedling traits (Table 2). The treatment effect was highly significant ($P < 0.01$) for plant height, number of leaves, number of nodes, stem weight, root weight, total biomass, root-shoot ratio, leaf area, root length and shoot volume, while leaf weight and shoot length were significant at $P < 0.05$. Genotypes also differed significantly for all evaluated traits. The

significant genotype $\times$ treatment interaction for all traits indicated that genotypes responded differently to drought relative to normal growing conditions.

Among the interaction effects, relatively large mean squares were observed for leaf area (239.06), root length (91.82), shoot volume (54.60), shoot

length (45.52), number of leaves (26.063), plant height (12.68) and number of nodes (5.85), demonstrating considerable differential response of genotypes to the two moisture regimes. The relatively small error mean squares for most traits further supported the reliability of the observed differences.

Table 2. Mean sum of squares (MSS) for all evaluated seedling traits.

Source of variation	D F	PH	NL	NN	LW	SW	R W	TB	RS R	LA	RL	SL	RV	SV
Replication	1	224.53	3.75	3.75	2.12	8.10	1.224	15.60	0.01	182.77	47.86	125.54	6.60	31.74
Treatment	1	1377.6**	992.26**	3.86**	0.40*	3.32**	2.38**	16.08**	0.06**	372.75**	0.03**	178.05**	11.98*	50.63**
Genotypes	59	20.28**	26.88**	5.61**	0.81**	1.89**	0.57*	3.13**	0.07*	185.88**	33.31**	74.97**	2.83*	30.12**
Genotype $\times$ Treatment	59	12.68**	26.063**	5.85**	0.61**	1.58**	0.76**	2.87**	0.09**	239.06**	45.52**	91.82**	4.03**	54.60**
Error	119	0.16	0.22	1.96	0.01	0.06	0.01	0.01	1.92	0.22	0.05	0.11	0.07	0.03
Total	239	—	—	—	—	—	—	—	—	—	—	—	—	—

Where; PH = plant height; NL = number of leaves; NN = number of nodes; LW = leaf weight; SW = stem weight; RW = root weight; TB = total biomass; RSR = root-shoot ratio; LA = leaf area; RL = root length; SL = shoot length; RV = root volume; SV = shoot volume. * $P < 0.05$; ** $P < 0.01$.

Distribution and mean performance of genotypes

The distribution of the 60 genotypes showed considerable variation between the two moisture

regimes. Under normal conditions, the overall means were 50.18 cm for plant height, 18.55 leaves plant⁻¹, 7.35 nodes plant⁻¹, 40.70 cm² leaf area, 22.98 cm root length, 35.79 cm shoot length and 6.36 cm³ root volume. Mean leaf, stem and root weights were 3.41, 6.55 and 2.42 g, respectively, while total biomass, root-shoot ratio and shoot volume averaged 12.39 g, 0.25 and 17.00 g.

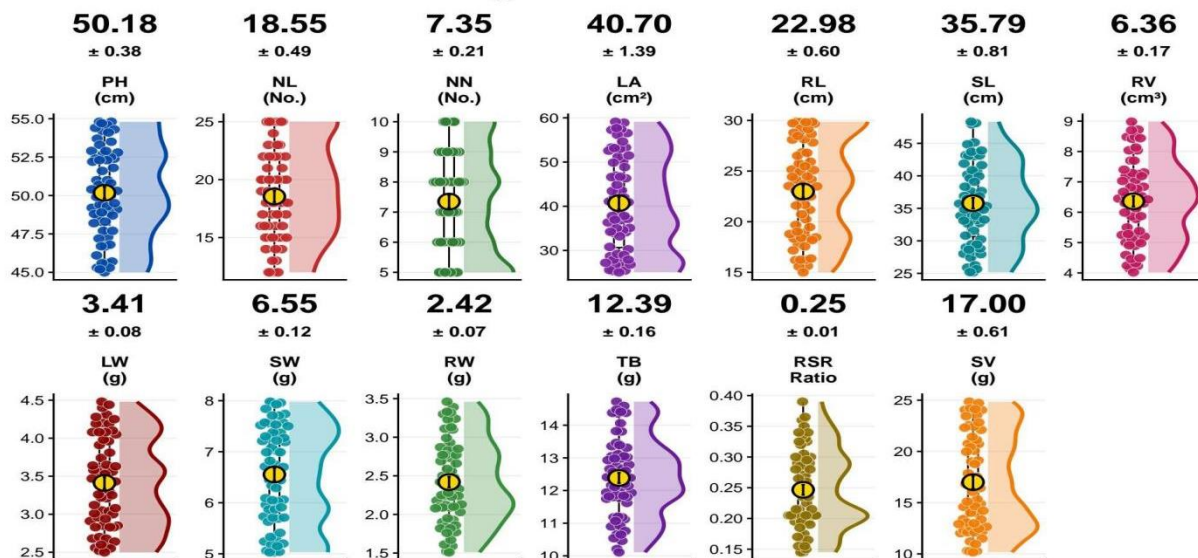


Figure 1. Distribution of seedling traits under normal conditions.

Under drought, mean plant height declined to 45.38 cm and number of leaves to 14.48 plant⁻¹, whereas number of nodes remained relatively stable at 7.10 plant⁻¹. Leaf area was 43.19 cm², root length was 23.01 cm and shoot length was 37.51 cm. Mean leaf, stem and root weights were

3.49, 6.79 and 2.62 g, respectively. Total biomass increased from 12.39 g under normal conditions to 12.90 g under drought, while root-shoot ratio increased slightly from 0.25 to 0.26. Shoot volume increased from 17.00 to 17.92 g.

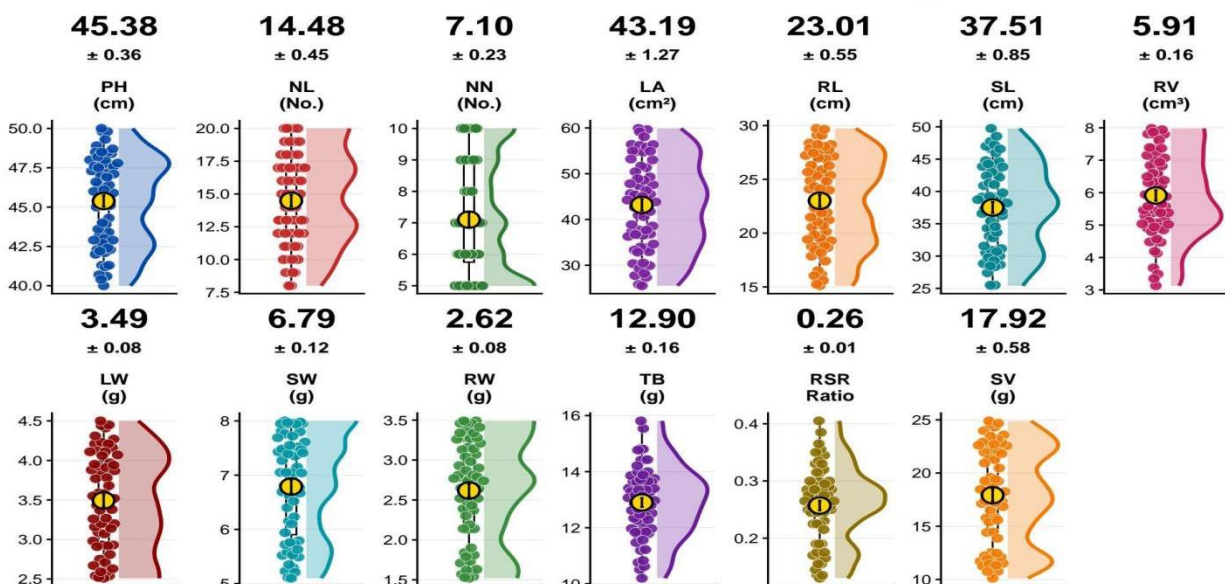


Figure 2. Distribution of seedling traits under drought conditions.

Table 3. Mean $\pm$ SE of the evaluated seedling traits under normal and drought conditions.

Trait	Normal condition	Drought condition
PH (cm)	50.18 $\pm$ 0.38	45.38 $\pm$ 0.36
NL (No.)	18.55 $\pm$ 0.49	14.48 $\pm$ 0.45
NN (No.)	7.35 $\pm$ 0.21	7.10 $\pm$ 0.23
LA (cm ²)	40.70 $\pm$ 1.39	43.19 $\pm$ 1.27
RL (cm)	22.98 $\pm$ 0.60	23.01 $\pm$ 0.55
SL (cm)	35.79 $\pm$ 0.81	37.51 $\pm$ 0.85
RV (cm ³)	6.36 $\pm$ 0.17	5.91 $\pm$ 0.16
LW (g)	3.41 $\pm$ 0.08	3.49 $\pm$ 0.08
SW (g)	6.55 $\pm$ 0.12	6.79 $\pm$ 0.12
RW (g)	2.42 $\pm$ 0.07	2.62 $\pm$ 0.08
TB (g)	12.39 $\pm$ 0.16	12.90 $\pm$ 0.16
RSR	0.25 $\pm$ 0.01	0.26 $\pm$ 0.01
SV (g)	17.00 $\pm$ 0.61	17.92 $\pm$ 0.58

Correlation analysis

Pearson correlation analysis revealed different association patterns under normal and drought conditions. Under drought, the strongest positive association was observed between root weight and root-shoot ratio ($r = 0.90$, $P < 0.001$), followed by stem weight and total biomass ($r = 0.76$, $P < 0.001$), root weight and total biomass (r

$= 0.52$, $P < 0.01$), and leaf weight and total biomass ($r = 0.37$, $P < 0.01$). Significant negative relationships included root-shoot ratio with leaf weight ($r = -0.30$, $P < 0.05$) and number of leaves ($r = -0.37$, $P < 0.01$), while number of leaves was negatively associated with root weight ($r = -0.29$, $P < 0.05$).

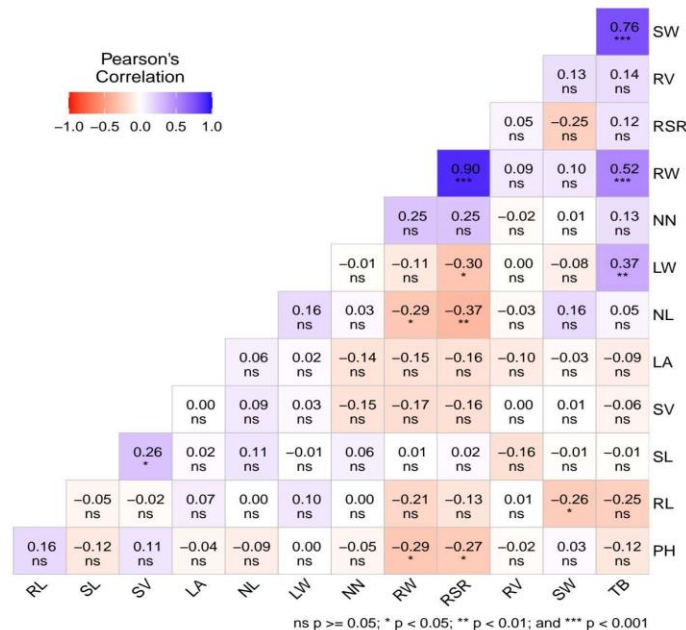


Figure 3. Pearson correlation coefficients among seedling traits under drought conditions.

Under normal conditions, root weight and root-shoot ratio again showed a very strong positive relationship ($r = 0.89$, $P < 0.001$). Stem weight was strongly and positively correlated with shoot volume ($r = 0.77$, $P < 0.001$), but negatively correlated with root-shoot ratio ($r = -0.46$,

$P < 0.001$). Significant positive associations were observed between leaf area and shoot length ($r = 0.31$, $P < 0.05$), number of leaves and shoot volume ($r = 0.27$, $P < 0.05$), and total biomass and shoot volume ($r = 0.33$, $P < 0.05$).

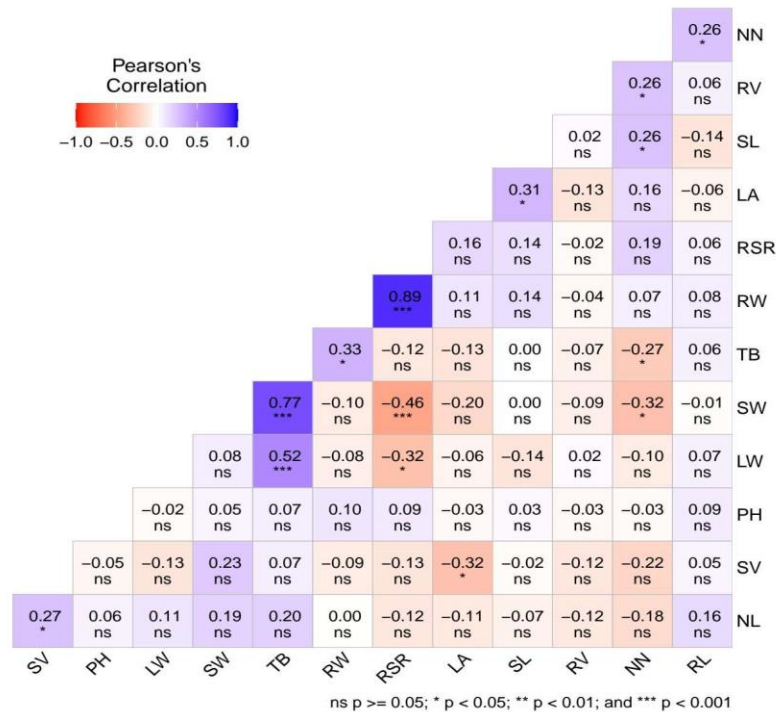


Figure 4. Pearson correlation coefficients among seedling traits under normal conditions.

PCA biplot and cluster analysis

Principal component analysis separated the genotypes into four major clusters and provided a clear visual representation of trait relationships under the two treatments. The first two principal

components explained 36% of the total variation, with PC1 accounting for 19% and PC2 for 17%. The genotypes were distributed across the four quadrants, indicating substantial multivariate diversity among the evaluated cotton genotypes.

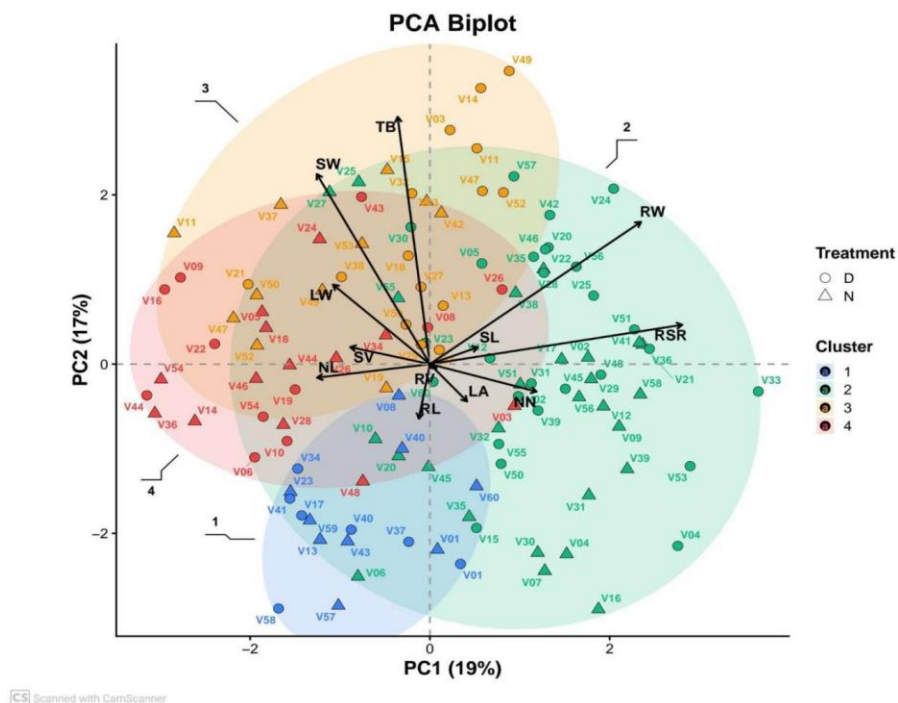


Figure 5. PCA biplot showing distribution of cotton genotypes, treatments and clusters based on seedling traits.

The biplot showed that root weight (RW), root-shoot ratio (RSR), shoot length (SL) and related growth traits contributed strongly toward the positive side of PC1, whereas stem weight (SW), total biomass (TB) and leaf weight (LW) were positioned toward the upper portion of the ordination and contributed to PC2. Genotypes located in the direction of a particular trait vector were relatively associated with higher expression of that trait. The four clusters showed distinct spatial separation, although some overlap was evident. Normal and drought observations were represented by different symbols, demonstrating differential positioning of genotypes under the two moisture regimes. The PCA therefore confirmed substantial multivariate diversity among the cotton genotypes and complemented the results of ANOVA, mean distribution and correlation analysis.

Discussion

Drought is one of the major environmental constraints affecting cotton growth and productivity, and the identification of genotypes capable of maintaining growth under limited water availability is therefore an important objective of cotton breeding. In the present study, significant differences were observed among genotypes, treatments and genotype $\times$ treatment interactions for almost all evaluated seedling traits. The significant genotype $\times$ treatment interaction indicates that the tested genotypes did not respond uniformly to drought, confirming the presence of exploitable genetic variation for drought adaptation. Similar genetic variability in cotton drought response has been reported using morphological, physiological and biochemical traits, emphasizing the importance of screening diverse germplasm under contrasting moisture regimes (Arif et al., 2023; Rasheed et al., 2023).

The reduction in plant height and number of leaves under drought observed in the present

study indicates that water limitation restricted vegetative growth. Plant growth under drought is commonly reduced because limited water availability affects cell expansion, photosynthesis and stomatal regulation. However, the response of individual traits was not uniform. In the present experiment, drought reduced plant height from 50.18 to 45.38 cm and number of leaves from 18.55 to 14.48 plant⁻¹, whereas total biomass increased slightly from 12.39 to 12.90 g. This suggests that the genotypes may have altered biomass allocation under water limitation rather than simply reducing total biomass production. Previous studies have demonstrated considerable differences among cotton genotypes in shoot and root growth under drought, with tolerant materials maintaining comparatively better growth than sensitive genotypes (Hu et al., 2022; Arif et al., 2023).

Root-related traits appeared particularly important in the present study. Root length remained almost unchanged between normal and drought conditions (22.98 and 23.01 cm), while root weight increased from 2.42 to 2.62 g and root-shoot ratio increased from 0.25 to 0.26. Maintenance of root growth under drought may provide an advantage by enabling plants to explore a greater soil volume for available water. Recent cotton research has specifically emphasized root system architecture as an important component of drought tolerance. Guo et al. (2024) reported substantial genetic variation for root system architecture and demonstrated that root traits and canopy characteristics were important components of drought tolerance evaluation. Their PCA and cluster analyses also showed that multivariate assessment incorporating root traits can effectively distinguish cotton cultivars according to drought response.

The correlation analysis further supported the importance of biomass partitioning in drought response. Under drought, root weight exhibited a very strong positive correlation with root-shoot ratio ($r = 0.90$, $P < 0.001$), while root weight was also positively associated with total biomass ($r =$

0.52, $P < 0.01$). Stem weight showed a strong positive association with total biomass ($r = 0.76$, $P < 0.001$). These relationships suggest that differences in root and stem biomass were closely associated with overall plant biomass under water-limited conditions. Conversely, the negative association of root-shoot ratio with number of leaves and leaf weight indicates a possible shift in assimilate allocation between root development and above-ground growth. Such relationships are biologically relevant because drought-tolerant plants may maintain root development while restricting excessive shoot expansion, thereby improving water acquisition relative to transpirational demand. Recent cotton studies similarly indicate that root length, root volume and root number can be useful indicators for distinguishing drought-tolerant and drought-sensitive genotypes at the seedling stage (Hu et al., 2022).

Under normal conditions, the strong positive relationship between root weight and root-shoot ratio ($r = 0.89$, $P < 0.001$) and between stem weight and shoot volume ($r = 0.77$, $P < 0.001$) reflected coordinated vegetative growth in the absence of water limitation. The negative association between stem weight and root-shoot ratio ($r = -0.46$, $P < 0.001$) further indicates that greater allocation toward shoot biomass was associated with a relatively smaller proportion of biomass allocated to roots. The change in correlation structure between normal and drought conditions demonstrates that environmental stress can modify relationships among morphological traits. Thus, selection based on a single trait may not adequately represent drought adaptation, and simultaneous consideration of several root and shoot traits is more appropriate.

The PCA biplot provided additional evidence of substantial multivariate diversity among the evaluated genotypes. The first two principal components explained 36% of the total variation, with PC1 and PC2 accounting for 19 and 17%, respectively. The separation of genotypes into four clusters indicates that the genotypes differed

considerably in their combinations of root, shoot and biomass traits. The association of RW, RSR and other growth traits with the principal components suggests that these variables contributed importantly to genotype discrimination. Similar applications of PCA and cluster analysis have successfully summarized complex drought-response datasets in cotton. Guo et al. (2024) used PCA and systematic cluster analysis to classify 80 cotton cultivars according to drought tolerance and emphasized that multiple root and above-ground traits provide a more comprehensive assessment than individual traits alone.

The present findings therefore demonstrate that drought tolerance in cotton is a complex, multicomponent characteristic involving coordinated changes in plant growth, biomass accumulation and root development. The significant genotype $\times$ treatment interaction, contrasting correlation patterns and separation of genotypes in the PCA biplot collectively demonstrate the presence of useful genetic diversity among the tested material. Similar conclusions have been reported in recent cotton breeding research, where phenotypic diversity under contrasting environments has been identified as an important resource for developing climate-resilient cultivars (Mangi et al., 2024). Future selection should consequently emphasize genotypes that maintain desirable shoot growth while sustaining root development and biomass under drought. Combining phenotypic screening with molecular approaches such as GWAS, QTL mapping and genomic selection may further accelerate the development of drought-resilient cotton cultivars (Rasheed et al., 2023; Zhang et al., 2024).

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Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

All authors declare no competing interests.

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