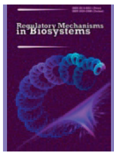

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Evaluation of drought tolerance in naturally colored cotton (*Gossypium hirsutum*) under water deficit conditions

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Drought stress is one of the major environmental factors limiting cotton (*Gossypium hirsutum* L.) productivity, particularly in arid and semi-arid regions. Naturally colored cotton (NCC) has gained attention due to its eco-friendly fiber production; however, its drought tolerance remains insufficiently studied. This study aimed to evaluate the drought tolerance of colored cotton genotypes under water deficit conditions by assessing key agronomic traits and conducting molecular marker screening. Field experiments were conducted under two irrigation regimes: well-watered conditions (4,800–5,000 m^3/ha) and drought stress conditions (2,800–3,000 m^3/ha). The results showed that drought stress significantly reduced boll number, boll weight, fiber yield percentage, and total seed cotton yield across all genotypes. However, genotypes A-800, 011250, and 010108 exhibited higher Drought Tolerance Index (DTI) and Stress Tolerance Index (STI) values, indicating their superior drought resilience. Molecular screening using the NAU1190 DNA marker identified the 220 bp allele in genotypes 011460 and 011250, suggesting its potential association with drought tolerance. The ANOVA analysis revealed significant genotype × water regime interactions, indicating that both genetic and environmental factors influence drought tolerance. These findings provide valuable insights for breeding drought-tolerant colored cotton varieties, contributing to sustainable fiber production in water-limited regions.

Keywords: colored cotton; *Gossypium hirsutum*; drought stress; agronomic traits; molecular markers; drought tolerance index.

Introduction

Cotton (*Gossypium hirsutum* L.) is one of the most economically significant fiber crops, providing raw material for the global textile industry (Shavkiev et al., 2021). While white fiber cotton has traditionally dominated production, increasing environmental concerns and the demand for eco-friendly textile products have led to renewed interest in naturally colored cotton (NCC). Unlike conventional cotton, NCC does not require chemical dyeing, thus reducing water and energy consumption while minimizing environmental pollution (Dickerson et al., 1999; Crews & Hustvedt, 2005). This has encouraged efforts to develop new colored cotton genotypes with improved fiber quality and yield (Dutt et al., 2004).

Naturally colored cotton exhibits a variety of fiber colors, including brown, green, reddish, and tan hues, resulting from genetic pigmentation (Romanov, 1943). Early research on colored cotton breeding dates back to the mid-20th century, with significant contributions from scientists in the United States, China, India, and Uzbekistan (Podolnaya et al., 2015). However, despite its environmental benefits, NCC genotypes generally have lower fiber quality, strength, and yield compared to white cotton, making their large-scale adoption challenging (Carvalho et al., 2014). Additionally, their response to abiotic stresses, particularly drought stress, remains insufficiently studied (Barros et al., 2020).

Drought stress is one of the major limiting factors affecting cotton production, particularly in arid and semi-arid regions, where water scarcity significantly impacts plant growth, fiber development, and yield (Bates et al., 1973). Cotton plants exhibit various physiological and biochemical responses to water deficit conditions, including reduced boll formation, lower fiber yield, and alterations in fiber quality parameters (Backe, 1994). Studies indicate that colored cotton genotypes may possess unique drought adaptation mechanisms, but these have not been extensively characterized (Fox, 1987).

In addition to agronomic and physiological traits, the use of molecular markers associated with drought tolerance genes provides an efficient approach for identifying stress-resistant genotypes (Azeem et al., 2010). Studies have shown that quantitative trait loci (QTL) and specific DNA markers are associated with drought tolerance in cotton, offering potential applications in marker-assisted selection (MAS) to breed drought-tolerant varieties (Chen et al., 2007). However, limited research has focused on combining agronomic and molecular approaches to evaluate drought tolerance in colored cotton (Cohen et al., 2017).

This study aims to assess the drought tolerance of naturally colored cotton genotypes under water deficit conditions by evaluating key agronomic traits, including boll number per plant, boll weight, fiber yield percentage per plant, and seed weight. Additionally, PCR-based screening of drought-tolerance-associated DNA markers was conducted to identify genetic variations contributing to drought resilience. The findings of this research will provide valuable insights for developing drought-tolerant colored cotton varieties, ensuring their sustainable cultivation in water-limited environments.

Materials and methods

Collection of germplasm. The study was conducted using naturally colored cotton (*Gossypium hirsutum* L.) genotypes from the cotton collections of the Institute of Genetics and Plant Experimental Biology and the Scientific Research Institute of Cotton Breeding, Seed Production, and Agricultural Technologies. The following genotypes, listed in Table 1, were used in this study.

Experimental design and drought treatment. The field experiments were conducted at the experimental farm of the Institute of Genetics and Plant Experimental Biology, located in Zangiota district, Tashkent region.

The field trials were carried out under different irrigation regimes:

1) control treatment (well-watered condition): cotton plants were irrigated four times following a 1:2:1 scheme. The total irrigation water used was 4,800-5,000 m^3/ha;

2) drought stress treatment (simulated drought condition): plants were irrigated only twice following a 1:1:0 scheme, using a total of 2,800–3,000 m^3/ha of irrigation water. The drought stress was applied by reducing irrigation frequency during the flowering and boll formation stages, and stopping irrigation during the maturation stage.

All other agronomic practices were kept the same for both treatments.

Yield, yield components and quality. Cotton bolls from 20 plants at the center of each plot were harvested for yield measurements. The bolls were harvested on October 15, 2024. The harvested seed cotton was collected in nylon mesh bags and stored in a drying room for 20 days before weighing to determine the seed cotton yield. For cotton with a moisture content of less than 12%, weighing was carried out on the ginned cotton to determine the lint cotton yield.

To assess the drought tolerance of the genotypes, the following indices were calculated based on the general productivity parameters of the colored and white cotton genotypes grown under different conditions:

– Drought Tolerance Index (DTI) (Fischer & Maurer, 1978);

– Stress Tolerance Index (STI) (Fernandez, 1992);

– Stress Susceptibility Index (SSI) (Rosielle & Hamblin, 1981);

Molecular-genetic methods. Genomic DNA was extracted from young cotton leaves using the Invitrogen PureLink™ Genomic Plant DNA Purification Kit (Thermo Fisher, USA).

Polymerase chain reaction (PCR) was performed using the Phusion™ Plus PCR Master Mix (Thermo Fisher, USA), which contains DNA polymerase, salts, magnesium, and dNTPs. The primers used for PCR amplification are listed in Table 2.

Table 1
Colored cotton genotypes used in the study

Cotton genotypes and varieties	Species	Fiber color
011460	*G. hirsitum* L.	green fiber
A-2384	*G. hirsitum* L.	brown fiber
A-1025	*G. hirsitum* L.	brown fiber
010108	*G. hirsitum* L.	brown fiber
09965	*G. hirsitum* L.	brown fiber
A-800	*G. hirsitum* L.	brown fiber
011250	*G. hirsitum* L.	brown fiber
010105	*G. hirsitum* L.	brown fiber
02408	*G. hirsitum* L.	brown fiber
04489	*G. hirsitum* L.	brown fiber
010764	*G. hirsitum* L.	green fiber
04494	*G. hirsitum* L.	brown fiber
010765	*G. hirsitum* L.	brown fiber
A-2953	*G. hirsitum* L.	green fiber
07223	*G. hirsitum* L.	brown fiber
011022	*G. hirsitum* L.	brown fiber
08492	*G. hirsitum* L.	brown fiber
011302	*G. hirsitum* L.	green fiber
Sadaf	*G. hirsitum* L.	white fiber
Gulshan	*G. hirsitum* L.	white fiber

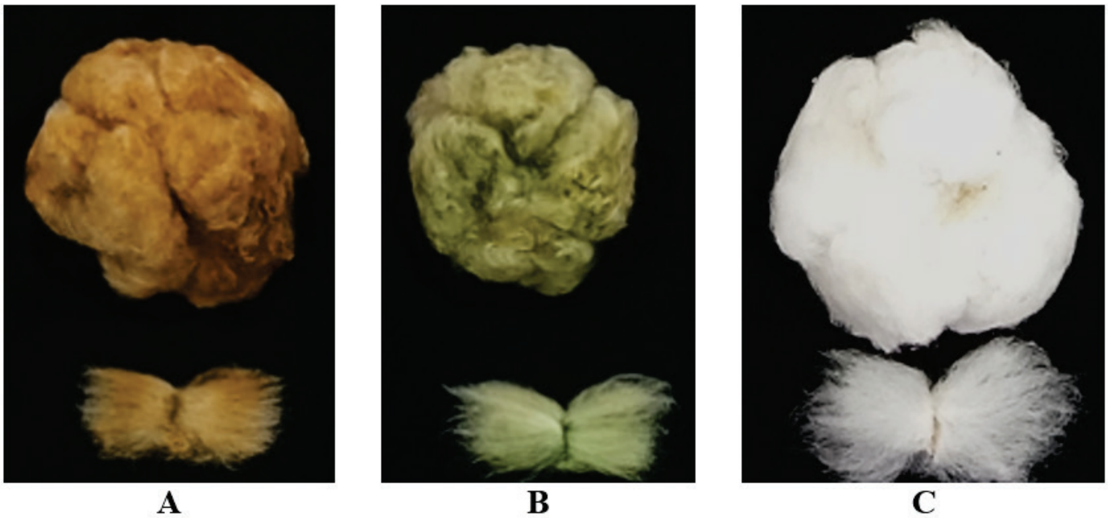

Fig. 1. Fiber color of cotton samples: *A* – brown fiber, *B* – green fiber, *C* – white fiber

Table 2
DNA marker panel used in the study

	Marker name	Forward primer sequence	Reverse primer sequence
1.	NAU2715	TGGCTGAACTTTGCAATTTA	AAGCAAGGGAGGTAATCCTT
2.	NAU2954	CGAAAGATGGTTCCATTAGG	GGGGGTTCAGGAGATTTTAG
3.	NAU3011	CCTTCACCATTTGCTTACCT	CTCCGTTTCTATTCCCAAAA
4.	NAU3414	CAACTTCCCAAGCTCGTATT	GTTCAACTTCTCTCTTCCCTCT
5.	NAU2691	TCACATCTTGCAAGCTCATT	AGTTAAAACCGGGCTGAGAT
6.	NAU1141	CCCCTCTCTCTGTTTCTCAA	AAGGGGTTTGAAGGGTTATC
7.	NAU1190	CCATGTCCGTATCCATGTTA	TAAGGCAAGATAGGGTCAGG
8.	NAU6672	GCAATCAGCTCATCTTGCTT	TGACGAAAATTTGTTGGATG
9.	NAU8406	TGGCCAGTTGTTTTGAGTTA	TTTGTTTTGGGTTGTTGAGA
10.	NAU6790	CGTCTGGATTGAACAGTGATC	CAACTTGATCTAACTATTGCATACG
11.	NAU6866	ACTGAAAAGAGAGAATACGTATGGAG	GTGTTAGGTTTCGAGCTAGCTAC
12.	NAU6871	GATCGGTAATGTTTCGTAACCCTAC	AGAATTAGGTATAGAGGTTGGTGCG
13.	NAU8527	ACCAAACTCCTAAACCCTCA	AGCAATAGAAGCCATTGGAG
14.	NAU2954	AAGGAAATGCTGCCAACTAC	AGACTTGCTCTGGTCTGCTT

Statistical analysis. All statistical analyses were performed using Statgraphics 18 software. Descriptive statistics, including means, standard deviations, and coefficients of variation, were calculated for each measured trait to assess variability among the studied cotton genotypes under different water regimes.

A multi-factor analysis of variance (ANOVA) was conducted to evaluate the effects of genotype, water regime, and their interactions on agronomic traits such as boll number per plant, boll weight, fiber yield percentage per plant, seed weight, and crop yield. The model included the following fixed factors:

– genotype (G) – different colored and white cotton genotypes;

– water regime (W) – well-watered vs. drought stress conditions;

– G × W interaction – to assess the combined effect of genotype and drought stress.

The significance of factors and their interactions was determined using F-tests, and differences between means were compared using

Fisher's Least Significant Difference (LSD) test at $P < 0.05$ significance level.

For drought tolerance assessment, indices such as Drought Tolerance Index (DTI), Stress Tolerance Index (STI), and Stress Susceptibility Index (SSI) were calculated. Pearson's correlation analysis was performed to determine relationships between agronomic traits and drought tolerance indices.

Results

Boll number per plant. In this study, we analyzed the number of bolls per plant, a key component of productivity in colored cotton genotypes. Under well-watered conditions, the highest number of bolls per plant was recorded in brown fiber genotypes 04494, 010765, and 04489, as well as the green fiber genotype A-2953, with values of 19.4, 19.3, 19.0, and 19.1 bolls per plant, respectively.

Conversely, the lowest boll numbers were observed in the brown fiber genotypes 07223, A-1025, and 011022, with values of 15.9, 16.1, and 16.4 bolls per plant, respectively.

Under drought stress conditions, the number of bolls per plant decreased across all genotypes. However, the highest boll numbers were still observed in brown fiber genotypes 04494, 09965, and A-800, with values of 16.0, 15.8, and 15.0 bolls per plant, respectively.

Boll weight. Boll weight is a critical factor influencing cotton productivity. Under optimal irrigation, the highest boll weights were recorded in brown fiber genotype 011022 (5.64 g) and green fiber genotype 011302 (5.52 g). Other genotypes, such as 010108, 04494, 07223, 011460, and 04489, also exhibited relatively high boll weights, ranging from 5.04 to 5.13 g.

The lowest boll weights were found in the brown fiber genotypes A-2384 (4.09 g) and 09965 (4.36 g).

Under drought stress conditions, boll weight was reduced across all genotypes. However, relatively high values were still recorded in green fiber genotype 011302 (4.71 g), light brown fiber genotype 04489 (4.52 g), and brown fiber genotypes 07223 (4.36 g) and 010108 (4.33 g). The lowest boll weights were observed in brown fiber genotypes 010105 (3.29 g), 09965 (3.31 g), and 02408 (3.45 g).

Crop yield per plant. The total seed cotton yield per plant at the end of the growing season was evaluated. Under well-watered conditions, the highest yields were recorded in brown fiber genotypes A-800 (72.5 g) and 010108 (72.2 g), as well as green fiber genotype 011460 (70.5 g). Among the white fiber genotypes, Sadaf and Gulshan had seed cotton yields of 64.4 g and 71.2 g, respectively.

Under drought stress conditions, yield was reduced across all genotypes. However, the highest yields were recorded in brown fiber genotypes 011250 (55.3 g), A-800 (52.5 g), and 09965 (52.1 g), as well as green fiber genotype 011460 (53.2 g). The lowest yields were observed in brown fiber genotypes 08492, 04489, A-1025, 02408, and 010765, as well as green fiber genotype 010764, with values ranging from 32.7 g to 39.4 g per plant.

Fiber yield percentage per plant. Fiber yield is a key economic trait in cotton production. Under optimal irrigation, the highest fiber yield percentages were recorded in brown fiber genotypes A-2384 (36.5%), A-1025 (35.3%), and 010765 (34.6%), as well as in the white fiber genotype Sadaf (37.0%).

The lowest fiber yield percentages were observed in green fiber genotypes A-2953 (17.9%) and 011302 (19.1%), and brown fiber genotype 010105 (18.3%).

100-Seed weight. Seed weight is another important agronomic trait in cotton. Under well-watered conditions, the highest 100-seed weights were recorded in green fiber genotype 011302 (13.3 g) and brown fiber genotype 011022 (13.1 g). The lowest values were observed in brown fiber genotypes A-2384 (9.4 g) and A-1025 (10.3 g).

Under drought stress conditions, seed weight was reduced across all genotypes. However, green fiber genotype 011302 maintained the highest 100-seed weight (12.4 g), followed by light brown fiber genotype 04489 (11.9 g). The lowest values were recorded in brown fiber genotypes A-2384 (8.7 g) and A-1025 (8.1 g).

Table 3
Agronomic traits of the studied cotton genotypes under optimal and drought stress conditions

No.	Genotype	Number of bolls per plant, pcs.		Boll weight, g		Fiber yield percentage, %		100-seed weight, g		Crop yield, g/plant	
		OIC	DSC	OIC	DSC	OIC	DSC	OIC	DSC	OIC	DSC
1	011460	17.2	14.0	5.1	4.2	28.1	26.1	10.9	10.7	70.5	53.2
2	A-2384	17.0	12.4	4.1	3.6	36.5	35.6	9.4	8.1	61.9	43.4
3	A-1025	16.1	12.3	4.6	3.9	35.3	39.1	10.3	8.7	51.5	36.9
4	010108	17.2	12.2	5.1	4.3	28.2	27.5	11.2	10.6	72.2	48.8
5	09965	17.6	15.8	4.4	3.3	27.6	30.8	11.3	9.2	66.9	52.1
6	A-800	18.6	15.0	4.9	4.1	31.4	34.0	11.3	10.9	72.5	52.5
7	011250	18.3	14.4	4.5	4.2	24.3	27.7	12.4	10.9	63.2	55.3
8	010105	18.0	13.9	4.7	3.3	18.3	19.0	12.6	11.8	57.6	41.7
9	02408	18.2	13.7	4.6	3.5	26.7	29.6	12.5	11.4	49.1	38.4
10	04489	19.0	12.2	5.0	4.5	31.4	32.4	12.5	11.9	47.5	36.6
11	010764	18.0	14.5	4.7	3.8	23.5	25.3	12.4	11.5	45.0	33.4
12	04494	19.4	16.0	5.1	3.9	28.4	29.9	11.6	10.7	50.4	43.2
13	010765	19.3	14.6	4.8	4.2	34.6	35.3	10.9	10.3	44.4	39.4
14	A-2953	19.1	13.9	4.6	3.5	17.9	18.4	12.3	9.9	57.9	44.5
15	07223	15.9	11.0	5.1	4.4	21.8	22.2	12.3	11.7	62.0	47.3
16	011022	16.4	11.6	5.6	3.6	28.5	29.5	13.1	11.5	52.5	40.6
17	08492	17.6	10.9	4.5	3.5	31.3	36.5	11.2	9.6	44.0	32.7
18	011302	18.4	12.4	5.5	4.7	19.1	16.1	13.3	12.4	60.7	49.6
19	Sadaf	18.2	12.4	5.5	4.9	37.0	36.7	12.5	11.5	64.4	55.8
20	Gulshan	17.8	14.4	5.7	5.1	35.3	36.3	12.8	12.2	71.2	57.6
	Mean	17.8	13.4	4.9	4.0	28.2	29.4	11.8	10.8	58.2	45.2
	SD	1.0	1.5	0.4	0.5	6.0	6.6	1.0	1.2	9.7	7.7

Notes: OIC – optimal irrigation condition, DSC – drought stress condition, SD – standard deviation, SE – standard error.

Drought tolerance assessment. According to previous studies (Fischer & Maurer, 1978), the drought tolerance index (DTI) is used to determine the productivity reduction under drought conditions compared to well-watered conditions. In our experiments, the highest DTI values were recorded in A-800 (1.07), 011250 (0.96), 010108 (0.98), and 010765 (0.90) genotypes, as well as in Sadaf (0.96) and Gulshan (0.99) varieties, indicating their higher drought tolerance. In contrast, the lowest DTI values were observed in 011022 (0.62), A-2384 (0.60), A-2953 (0.68), 07223 (0.71), 09965 (0.80), 011302 (0.68), and 011460 (0.79) genotypes, suggesting their higher sensitivity to drought stress.

Several researchers (Fernandez, 1992) have emphasized the stress tolerance index (STI) as an effective parameter for selecting drought-tolerant genotypes. In our study, the highest STI values were recorded in A-800 (1.14), 010108 (1.08), and Gulshan (1.07), indicating their strong adaptability to drought conditions. In contrast, 011022 (0.54) and A-2953 (0.65) genotypes exhibited the lowest STI values, suggesting their lower tolerance to drought stress (Fig. 2).

Fischer & Maurer (1978) also proposed the stress susceptibility index (SSI) as a parameter to assess plant sensitivity to drought conditions. Ullah et al. (2010) reported that SSI values greater than or equal to 1 indicate high water demand and low drought tolerance. In our study, the highest SSI values were observed in A-2384 (1.51) and 011302 (1.17) genotypes, indicating their high susceptibility to drought stress. On the other hand, 010765 (0.45), 011250 (0.51), and Sadaf (0.68) genotypes exhibited the lowest SSI values, suggesting their better adaptation to drought conditions (Fig. 2).

Multi-factor analysis of variance (ANOVA). Table 4 presents the mean squares from the variance analysis (ANOVA) for the different agronomic traits studied under both optimal irrigation and drought stress conditions.

Highly significant ($P < 0.01$) differences were observed among genotypes for all traits, including boll number per plant, boll weight, fiber yield percentage, 100-seed weight, and total seed cotton yield.

This indicates genotypic variation plays a crucial role in determining these traits, regardless of the water regime.

The water regime significantly affected all traits ($P < 0.01$), confirming that drought stress led to a reduction in boll number, boll weight, fiber yield percentage, 100-seed weight, and crop yield. The highest impact was recorded for crop yield (1721.3), indicating that drought stress had a strong negative effect on total productivity.

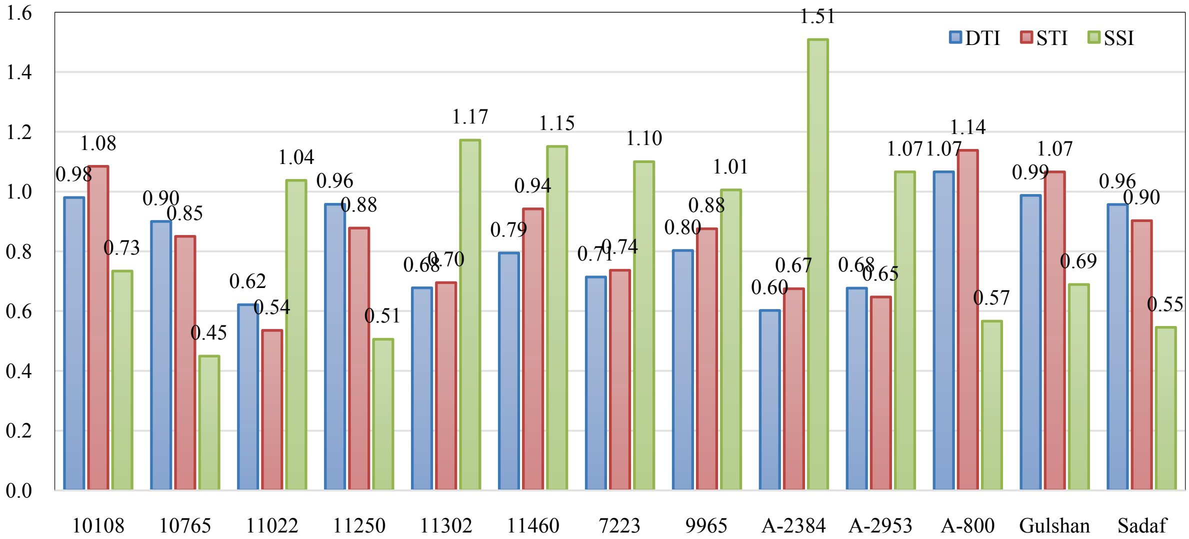

Fig. 2. Drought tolerance indices of different genotypes under drought stress conditions:
DTI – Drought Tolerance Index; STI – Stress Tolerance Index; SSI – Stress Susceptibility Index

Table 4
Mean squares values of variance analysis for different traits

Source of variation	Df	Number of bolls per plant, pcs.	Boll weight, g	Fiber yield percentage, %	100-seed weight, g	Crop yield, g/plant
Genotype (G)	19	2.5**	0.4**	78.5**	221.5**	143.8**
Water regime (W)	1	201.2**	7.7**	12.9*	1147.0**	1721.3**
G × W interaction	19	0.8**	0.1**	2.0**	16.1**	10.1**
Total	39	263.57	16.5	1542.2	5660.9	4646.9

Molecular marker analysis for drought tolerance. Polymerase chain reaction (PCR) analysis was conducted using a panel of DNA markers to identify cotton genotypes carrying marker alleles associated with abiotic stress tolerance.

According to the PCR results obtained using the NAU1190 DNA marker, the 220 bp allele, which is genetically linked to drought tolerance, was found in a heterozygous state in the genomes of the green fiber genotype 011460 and the dark brown fiber genotype 011250. In contrast, in other colored and white fiber genotypes (011250, 010108, 010765, Sadaf, and Gulshan), the corresponding allele of the NAU1190 marker was observed in a homozygous state.

The remaining 12 genotypes (011022, A-2384, A-2953, 011302, 07223, 09965, 010108, A-800, and 011461) did not carry the 220 bp drought tolerance allele in their genomes. To evaluate the effectiveness of DNA markers associated with drought tolerance, we performed a one-way ANOVA analysis, comparing the drought tolerance indices of genotypes carrying the NAU1190 allele versus those without it. The statistical analysis revealed that only the NAU1190 marker showed a significant association with drought tolerance.

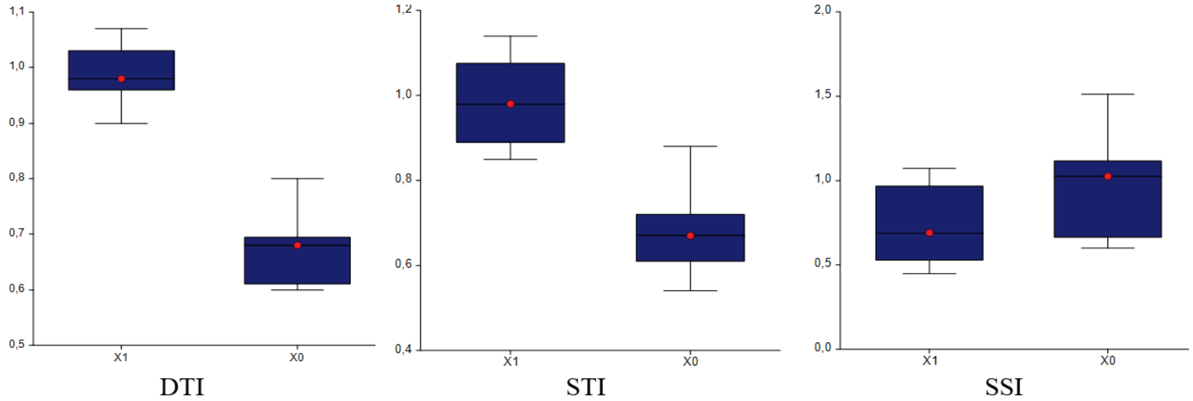

Fig. 3. Assessment of the effect of the NAU1190 DNA marker on drought tolerance (one-way ANOVA analysis):
X1 – genotypes carrying the allele, X0 – genotypes lacking the allele

Discussion

Drought stress significantly impacted the agronomic traits of colored cotton genotypes, leading to a reduction in boll number per plant, boll weight, fiber yield percentage, and overall crop yield. The results indicate that drought tolerance varies among genotypes, with some maintaining relatively high productivity despite water limitations. Similar findings have been reported in previous studies, where drought stress reduced boll formation and fiber yield in cotton genotypes (Pettigrew, 2004; Ullah et al., 2017).

Under well-watered conditions, the highest boll numbers were observed in brown fiber genotypes 04494, 010765, and 04489, and green fiber genotype A-2953. However, under drought stress conditions, the boll number per plant decreased, with the most significant reductions in genotypes 07223, A-1025, and 011022. These findings are consistent with studies by Zhang et al. (2020), who reported that drought stress affects boll retention and reduces overall productivity in cotton.

Similarly, boll weight was reduced under drought conditions, with 011022 and 011302 maintaining relatively higher boll weights, suggesting their potential as drought-tolerant genotypes. Loka et al. (2011) also noted that drought stress limits carbohydrate availability in cotton, affecting boll development and reducing boll weight.

Fiber yield percentage, an essential economic trait, also showed genotypic variation under stress conditions. The highest fiber yields were observed in A-2384, A-1025, and 010765 under well-watered conditions, while A-2953, 011302, and 010105 exhibited the lowest values. Studies by Bozorov et al. (2016) support these findings, suggesting that drought-sensitive genotypes exhibit significant reductions in fiber yield due to impaired photosynthetic activity.

The results indicate that genotypes A-800, 011250, 010108, and 010765, as well as Sadaf and Gulshan varieties, exhibited higher DTI values, suggesting their superior drought resilience. These findings align with those of Fischer & Maurer (1978), who reported that higher DTI values correspond to enhanced drought tolerance in crop plants.

STI values were also highest in A-800, 010108, and Gulshan, confirming their ability to maintain productivity under stress conditions. Fernandez (1992) noted that genotypes with high STI values are suitable for both optimal and stress environments.

On the other hand, A-2384 and 011302 exhibited high SSI values, indicating greater susceptibility to drought stress. Ullah et al. (2010) previously reported that genotypes with SSI values ≥ 1 are more prone to yield losses under drought conditions.

Molecular screening using PCR-based DNA markers identified the NAU1190 marker as significantly associated with drought tolerance. The 220 bp allele was detected in the genomes of 011460 and 011250 in a heterozygous state, while it was absent in several other genotypes. These results suggest that NAU1190 could serve as a useful marker for selecting drought-tolerant cotton genotypes.

Several studies have emphasized the role of molecular markers in identifying drought-resistant genes in cotton (Chen et al., 2007; Abdelraheem et al., 2019). The findings of our study are consistent with those of Cohen et al. (2017), who demonstrated that marker-assisted selection (MAS) could be effectively used to breed drought-tolerant cotton cultivars.

Conclusion

This study assessed the drought tolerance of naturally colored cotton (*Gossypium hirsutum* L.) genotypes by evaluating key agronomic traits and conducting molecular screening using DNA markers. The results demonstrated that drought stress significantly reduced boll number, boll weight, fiber yield percentage, and total seed cotton yield, confirming the substantial impact of water deficit on cotton productivity. However, the extent of yield reduction varied among genotypes, indicating genetic differences in drought response.

Among the studied genotypes, A-800, 011250, and 010108 exhibited the highest drought tolerance index (DTI) and stress tolerance index (STI) values, suggesting their ability to maintain productivity under limited water availability. In contrast, A-2384 and 011302 showed high stress susceptibility index (SSI) values, indicating their greater sensitivity to drought conditions.

Molecular analysis revealed that the NAU1190 DNA marker was significantly associated with drought tolerance, with the 220 bp allele detected in genotypes 011460 and 011250. This suggests that NAU1190 could serve as a potential marker for drought resistance, which can be utilized in marker-assisted selection (MAS) programs to develop drought-tolerant colored cotton varieties.

The significant genotype × water regime interaction observed in the ANOVA analysis underscores the importance of both genetic factors and environmental conditions in determining drought tolerance. These findings highlight the potential of certain colored cotton genotypes for cultivation in drought-prone regions, contributing to the development of more resilient and sustainable cotton breeding programs.

To further enhance drought tolerance in colored cotton, future research should focus on large-scale field trials across diverse environmental conditions and employ advanced genomic techniques such as genome-wide association studies (GWAS) and quantitative trait locus (QTL) mapping to identify additional drought-resistance genes.

Overall, this study provides valuable insights into the genetic diversity of colored cotton under drought stress and supports the integration of molecular and agronomic approaches for the development of drought-resilient cotton varieties, ensuring sustainable fiber production in water-limited regions.

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