

ORIGINAL ARTICLE OPEN ACCESS

Integrating Physiological and Biochemical Traits to Identify Drought-Resilient Guar Genotypes Through MGIDI Analysis

Warqaa Muhammed ShariffAl-Sheikh¹ | Evan Abdulhassan Mohammed Ali² | Hussam F. Najerb Alawadi² | Heidar Meftahizade³

¹Faculty of Basic Science Branch, Faculty of Dentistry, University of Al-Qadisiyah, Diwaniyah, Al-Qadisiyah, Iraq | ²College of Agriculture, University of Al-Qadisiyah, Diwaniyah, Al-Qadisiyah, Iraq | ³Department of Horticultural Sciences, Faculty of Agriculture & Natural Resources, Ardakan University, Ardakan, Iran

Correspondence: Heidar Meftahizade (hmeftahizade@ardakan.ac.ir)

Received: 16 February 2026 | **Revised:** 31 March 2026 | **Accepted:** 16 April 2026

Keywords: antioxidant capacity | flavonoid drought stress | genetic diversity | nutritional value | seed gum

ABSTRACT

Guar (*Cyamopsis tetragonoloba* L.) is a drought-tolerant crop and an important source of gum and bioactive compounds. The present study was conducted to investigate the response of 15 different guar genotypes under three soil moisture levels (100%, 70%, and 45% FC). The results indicated that drought stress caused significant reductions in physiological traits such as relative water content (RWC), seed gum (SG), viscosity, and dry matter digestibility (DMD). For instance, mean RWC decreased from 85.96% under non-stress conditions to 79.58% at 70% FC and 64.23% at 45% FC, whereas genotypes showed considerable variation in their responses (at 70% FC, the lowest reduction was observed in S6673 with −2.0%, and the highest reduction in RGC-1066 with −13.6%). SG decreased from 28.17 at 100% FC to 25.63 and 21.11 at 70% and 45% FC, respectively, and DMD declined from 46.96 to 43.63 and 37.1. Viscosity also decreased from an average of 2645 under non-stress conditions to 1906 and 1603 at 70% and 45% FC, respectively. In contrast, bioactive compounds and antioxidant indices increased under drought stress. Reductions in protein and carotenoids were also observed; protein content decreased from 28.07 to 24.2 and 16.29, and carotenoids declined from 2.12 to 1.58 and 1.25. Based on the MGIDI, genotype RGC-986 showed the highest similarity to the ideal genotype and was identified as the superior genotype with high performance in physiological and biochemical traits. Genotypes RGC-1031, Saravan, and S6566 also exhibited acceptable performance under drought stress, whereas genotypes such as S-5885 and BR-99 showed the lowest adaptability. These results demonstrated that despite reductions in some quantitative and nutritional traits, drought stress enhanced phenolic compounds, tannins, flavonoids, and antioxidant capacity, and these findings can be utilized in breeding programs and targeted cultivation of guar in water-limited regions.

1 | Introduction

Guar (*Cyamopsis tetragonoloba* L.) is a short-duration, drought-tolerant leguminous forage species belonging to the family Fabaceae, and it is widely recognized as a major natural source of guar gum with extensive industrial, food, and pharmaceutical applications (Avola et al. 2020; Khurizadeh

et al. 2024). This crop is well adapted to arid and semiarid regions worldwide and exhibits satisfactory performance under conditions of low rainfall and high temperatures, a characteristic that renders guar a strategic crop under warm and water-limited environments (Ravelombola et al. 2021; Kumari et al. 2024). The galactomannan compounds present in guar seeds constitute the primary source of guar gum, which is

This is an open access article under the terms of the [Creative Commons Attribution](https://creativecommons.org/licenses/by/4.0/) License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2026 The Author(s). *Legume Science* published by Wiley Periodicals LLC.

extensively utilized as a thickening, stabilizing, and emulsifying agent in the food industry, as well as in non-food sectors including oil and gas extraction (hydraulic fracturing), textiles, pharmaceuticals, paper manufacturing, and cosmetics (Gresta et al. 2014). Guar's ability to fix atmospheric nitrogen through symbiotic associations with *Rhizobium* bacteria, along with its positive effects on soil fertility, makes it a suitable option for crop rotation systems and a low-input agricultural crop (Mudgil et al. 2014; Ravelombola et al. 2021). In addition to its industrial importance, guar is consumed as a fresh vegetable and used as livestock fodder in certain regions, highlighting its multifunctional role in diverse agricultural systems (Mudgil et al. 2014).

Recent studies have demonstrated that guar can be successfully cultivated and achieve acceptable performance under the semi-arid climatic conditions (Ghorbani et al. 2019; Mahdipour-Afra et al. 2021; Hoseinollahi et al. 2025). Given the increasing global demand for natural products and the diverse industrial and food applications of guar, coupled with its potential for sustainable production in water-limited environments, this crop has emerged as an important target for scientific research, genetic improvement, and the development of climate-resilient agricultural systems (Ravelombola et al. 2021; Hoseinollahi et al. 2025). Therefore, investigating and improving guar genotypes and elucidating their physiological and biochemical responses to abiotic stresses such as drought can contribute to enhanced yield, production stability, and added economic value, which constitutes the core focus of the present study (Avola et al. 2020). In addition to its industrial importance as a major source of guar gum with a high galactomannan content (~28%–32% of the seed), guar possesses considerable nutritional value and is recognized as an important source of protein, dietary fiber, and bioactive compounds used in human diets and animal feed (Khurizadeh et al. 2024; Rani et al. 2025). Guar seeds contain substantial levels of protein, reported to range from approximately 24% to 45%, and provide a valuable source of essential amino acids; moreover, their dietary fiber content contributes to improved digestive health (Mohamed et al. 2011; Rani et al. 2025). The presence of phenolic and flavonoid compounds in guar, such as quercetin and gallic acid, confers notable antioxidant capacity and highlights their potential role as health-promoting bioactive constituents (Hamdani and Wani 2017).

Recent climate change has intensified drought events, severely impacting plant growth, reproduction, and physiological efficiency (Alshameri et al. 2019; Mahdipour-Afra et al. 2021; Habibi et al. 2024; Hoseinollahi et al. 2025). Drought stress (DS) reduces relative water content (RWC), disrupts photosynthesis, and impairs enzymatic and chloroplast functions, whereas elevated temperatures exacerbate water deficits (Avola et al. 2020; Pandey et al. 2022; Khurizadeh et al. 2024). In crops like guar, DS decreases protein, fiber, and carotenoid contents due to limited photosynthesis and altered resource allocation yet simultaneously enhances phenolic and flavonoid compounds as part of antioxidant defense mechanisms (Kusvuran and Kusvuran 2019; Ghotbi et al. 2022; Sarwar et al. 2024). These complex biochemical responses can negatively affect nutritional quality (protein and carotenoids) while improving bioactive properties (phenolics), highlighting the importance of understanding plant responses for developing drought-tolerant

genotypes with stable nutritional value and supporting sustainable agriculture (Ravelombola et al. 2021).

Evaluating genetic diversity and screening superior genotypes for enhanced nutritional value and stress tolerance, particularly drought, are essential strategies in plant breeding for sustainable crop development (Avola et al. 2020; Habibi et al. 2025). Genetic diversity provides the basis for identifying beneficial genes to improve drought resilience and supports the selection of genotypes with optimal performance and nutritional traits, including higher protein, fiber, and phenolic content under water-limited conditions (Ghotbi et al. 2022; Vahdati et al. 2023). Assessing diversity enables the distinction of drought-tolerant and sensitive groups, reduces yield risk under adverse conditions, and facilitates the integration of well-adapted genotypes into breeding programs (Zubair et al. 2017; Malani et al. 2024; Sarwar et al. 2024). Focusing on nutritional traits during screening can lead to cultivars with improved protein quality and antioxidant content, maintaining both yield and food quality under drought (Ravelombola et al. 2021; Kumari et al. 2024; Hoseinollahi et al. 2025). Overall, combining genetic diversity assessment with targeted trait evaluation ensures the development of drought-tolerant, nutritionally superior crops while conserving valuable germplasm for future breeding efforts (Malani et al. 2024).

Understanding the physiological and biochemical responses of guar genotypes to DS is therefore essential for the identification of drought-tolerant cultivars capable of maintaining productivity and quality under water-limited conditions. Genetic diversity within guar germplasm provides valuable opportunities for selecting superior genotypes with improved drought tolerance and desirable nutritional characteristics. Screening diverse genotypes using physiological and biochemical indicators can help identify genetic resources with enhanced adaptability and resilience, thereby supporting breeding programs aimed at developing climate-resilient cultivars suitable for arid and semiarid regions.

Therefore, the present study aimed to evaluate the responses of 15 guar genotypes under three irrigation regimes (100%, 70%, and 40% field capacity) in order to investigate the effects of DS on key physiological, biochemical, and nutritional traits, including RWC, seed gum (SG) content, viscosity, dry matter digestibility (DMD), protein, carotenoids, and antioxidant-related compounds. The study also aimed to identify superior genotypes capable of maintaining gum quality, physiological stability, and nutritional value under drought conditions, thereby providing useful information for guar breeding programs and sustainable cultivation in water-limited environments.

2 | Materials and Methods

2.1 | Field Site Description, Plant Materials, and Research Design

The study was conducted at Ardakan University, Yazd Province, Iran. A total of 15 guar (*C. tetragonoloba* L.) genotypes originating from three geographical regions: India, Pakistan, and Iran were evaluated. Iranian local genotypes were collected and taxonomically verified by the Medicinal Plant Research Institute

of Ardakan University, whereas non-native genotypes were obtained from the Rajasthan Agricultural Research Center (India) and Bahawalpur (Pakistan) (Table 1). Prior to planting, the experimental field was plowed, disked, and leveled in June to prepare a uniform seedbed. Guar seeds were sown at a depth of 2 cm, with inter-row and intra-row spacing of 50 and 30 cm, respectively, resulting in a plant density of approximately 8 plants m⁻². Each experimental unit measured 2 × 4 m, and treatments were arranged in a randomized complete block design (RCBD) with three replications. Number of plants per plot was 60 plants, and for physiological and biochemical analysis, 10 representative plants were randomly selected from the central rows of each plot to avoid border effect.

Water stress was applied during experiment (4 months) using three gradient levels. Soil moisture content in each plot was daily measured by means of a time-domain reflectometry sensor from a 20 cm soil layer. The depth of water (d_{iw}) required to bring moisture content of soil back to the FC was assessed according to the following equation (Cuenca 1989):

$$d_{iw} = (PFC - P_i) \times D \times B_d \tag{1}$$

PFC and P_i are water content at FC and at the time before irrigation (in terms of weight percentage), respectively, B_d is bulk specific gravity in g cm⁻³, and D is effective root depth in cm. The total volume of irrigation water in the scale of plot area was

TABLE 1 | The specification of guar (*Cyamopsis tetragonoloba* L.) genotypes.

ID	Genotypes	Origin
1	RGC-986	Rajasthan, India
2	S6673	Bahawalpur, Pakistan
3	BR-99	Bahawalpur, Pakistan
4	S6566	Bahawalpur, Pakistan
5	S-6560	Rajasthan, India
6	S-5885	Bahawalpur, Pakistan
7	S-6581	Bahawalpur, Pakistan
8	Grembite	Sistan va Baluchistan, Iran
9	S6260	Bahawalpur, Pakistan
10	Saravan	Sistan va Baluchistan, Iran
11	S6553	Bahawalpur, Pakistan
12	S6486	Bahawalpur, Pakistan
13	RGC-1031	Bahawalpur, Pakistan
14	RGC-1066	Rajasthan, India
15	Pishen	Sistan va Baluchistan, Iran

TABLE 2 | The soil physical and chemical characteristics of the experimental field before planting.

Texture	Clay (%)	Silt (%)	Sand (%)	K (mg/kg)	P (mg/kg)	N (%)	OC (%)	pH	EC (dS/m)
Clay-silt	40	32	28	264	8.4	0.17	1.07	7.8	3.12

determined after calculation of d_{iw}. Irrigation at each stage was performed when soil's moisture content was not more than FCs.

The experiment was conducted on clay silt textured soil, and the main physicochemical characteristics of the soil are summarized in Table 2. Prior to sowing, a basal fertilization was applied at rates of 40 kg ha⁻¹ nitrogen and 50 kg ha⁻¹ phosphorus (P₂O₅). Irrigation was supplied using a drip (trickle) irrigation system to ensure precise water application. Weed management was carried out manually throughout the growing season using hand hoeing.

2.2 | RWC

The RWC of fully expanded young leaves was measured according to the formula: RWC (%) = [(FM – DM)/(TM – DM)] × 100. Here, FM represents the fresh weight of the leaves at the time of sampling, TM is the turgid weight obtained after immersing the leaves in distilled water at 4°C for 24 h in complete darkness, and DM corresponds to the dry weight measured following oven-drying at 75°C for 72 h.

2.3 | Guar Gum Extraction

Guar gum was isolated from the seeds using established protocols with slight modifications. Initially, the seeds were immersed in distilled water and allowed to hydrate for a period of 7 h to facilitate softening of the seed coat. Following hydration, the seeds were manually processed to separate the structural components, namely, the seed coat (hull), endosperm, and embryo. The extraction of gum from the isolated endosperm was subsequently carried out according to the procedure reported by Ganatra et al. (2013), which was specifically designed for efficient recovery of guar gum polysaccharides.

2.4 | Chemical Composition Analysis

The proximate composition of guar seeds was evaluated through standardized analytical methods. Protein concentration (calculated as %N × 6.25) was determined following the guidelines of the American Association of Cereal Chemists (American Association of Cereal Chemists (AACC) Approved Methods Committee 2000). Lipid and crude fiber contents were measured using automated systems, specifically the Soxtec 2045 (Foss) for lipids and Fibertech 2023 (Foss) for crude fiber, according to the manufacturer's protocols.

2.5 | Viscosity Assessment

The rheological properties of guar gum were evaluated following Sabahelkheir Murwan et al. (2012). Purified gum powder was fully hydrated in water, centrifuged to remove insoluble residues,

and precipitated with ethanol. The resulting fibrous gum was oven-dried at 40°C for 6 h. Aqueous solutions at 0.1%, 0.25%, and 0.5% w/w were prepared and magnetically stirred overnight. Viscosity measurements were conducted using a Brookfield DV3 Ultra viscometer as described by Casas et al. (2000).

2.6 | DMD

The digestibility of dry matter was evaluated using a two-step in vitro procedure as outlined by Tilley and Terry (1963). Initially, the samples were oven-dried at 105°C until a constant weight was achieved, then ground, and sieved through a 1-mm mesh. A 0.5 g aliquot of the prepared sample was incubated anaerobically with a buffer solution and fresh rumen fluid at 39°C for 48 h to simulate microbial fermentation in the rumen. Following this, the gastric digestion phase was conducted by adding a pepsin-containing hydrochloric acid solution and incubating the mixture for an additional 48 h under the same temperature conditions. After the completion of both incubation stages, the remaining residues were dried and weighed. The DMD was then calculated according to the standard formula.

$$\text{DMD (\%)} = \frac{[\text{initial dry weight} - \text{residual dry weight}]}{[\text{initial dry weight}] \times 100}$$

2.7 | Determination of Tannin Content

For tannin analysis, 0.2 g of the powdered seed material was precisely weighed and extracted using a 70% (v/v) acetone-water solution in a 3:1 ratio. The mixture was then centrifuged at 2000 rpm for 5 min to remove solids, and the residue was subjected to a second extraction with the same acetone solution. The combined extracts were subsequently separated into two phases by adding a sodium chloride solution. The aqueous fraction was further extracted with 70% acetone, followed by solvent removal through evaporation. To complete the extraction, 2 mL of distilled water was added to the remaining solution, and the process was repeated three times. Any residual solvent was eliminated using a rotary evaporator under reduced pressure. The final extract's absorbance was determined at 765 nm with a spectrophotometer according to the protocol described by Price et al. (1979).

2.8 | Total Phenolic Content (TPC)

The total phenolic content (TPC) of guar flour was quantified using the Folin-Ciocalteu colorimetric assay, as per the procedure outlined by Singleton et al. (1999). This method relies on the reduction of the Folin-Ciocalteu reagent by phenolic hydroxyl groups, producing a blue chromophore. Absorbance was measured at 765 nm using a spectrophotometer (Thermo Spectronic 200, India) to calculate the phenolic concentration on a percentage basis.

2.9 | Flavonoid Content

The quantification of flavonoids was conducted using the aluminum chloride colorimetric assay following the procedure

described by Chang et al. (2002). For this analysis, 0.2 g of dried sample powder was extracted with 10 mL of 80% methanol. The extract was then centrifuged at 3000 rpm for 10 min, and the supernatant was collected. A 0.5 mL aliquot of the extract was combined with 0.1 mL of 10% aluminum chloride solution, 0.1 mL of 1 M potassium acetate, and 3.4 mL of distilled water and then incubated for 30 min at room temperature in darkness. Absorbance was recorded at 415 nm using a spectrophotometer. The flavonoid concentration was calculated against a quercetin standard curve and expressed as a percentage of dry weight.

2.10 | Carotenoids

Total carotenoids were measured using a modified version of the method described by Lichtenthaler (1987). Initially, 0.2 g of dried sample powder was extracted with 10 mL of 80% acetone and stirred in the dark for 15 min. After centrifugation at 3000 rpm for 10 min, the clear supernatant was collected. Absorbance readings were taken at 470, 645, and 663 nm using a spectrophotometer, and total carotenoid content was calculated based on the standard Lichtenthaler equations. Results were reported as milligrams of carotenoids per gram of fresh sample weight.

2.11 | Total Antioxidant Capacity (TAC)

The total antioxidant activity (TAC) was assessed through the DPPH (1,1-diphenyl-2-picrylhydrazyl) radical scavenging assay according to Koleva et al. (2002). Different concentrations of guar seed extract were prepared, and 0.025 g/L of DPPH solution was added to each. The mixtures were kept at room temperature in the dark for 30 min. A blank sample was included for reference. Absorbance was measured at 517 nm using a spectrophotometer. Quercetin was used as the reference standard. The percentage inhibition of free radicals (%I) for each extract was calculated using the standard formula.

$$\text{TAC (\%)} = (A \text{ control} - A \text{ sample}) / A \text{ control} \times 100$$

2.12 | Statistical Analysis

Mean comparisons were performed using Duncan's multiple range test at a 5% significance level. All statistical analyses were carried out using R software. Phenotypic plasticity (PP) between the stress and control treatments were calculated using the equation: $\text{PP (\%)} = [(\text{stress value} - \text{control value}) / \text{stress value}] \times 100$. Multivariate analyses, including hierarchical cluster analysis (HCA) and heat map visualization, were performed using the factextra and pheatmap packages in R. Pearson correlation coefficients were calculated to evaluate relationships between traits using the ggplot2 package for visual display. Associations between physiological variables were assessed using linear regression analyses also provided by the ggplot2 package in R. Principal component analysis (PCA) was performed to extract key traits and explain variance. In addition, the multi-trait genotype-ideotype distance index (MGIDI) was used to systematically evaluate and rank genotypes based on multiple traits. An ideotype genotype was

defined based on the desired values for each trait and the distance of each. The genotype was calculated from this ideotype to produce the MGIDI. The genotypes with the smallest distance showed the closest match to the ideotype. The results were used to rank the genotypes, identify the superior genotypes, and visualize using MGIDI graphs (Olivoto and Nardino 2021).

3 | Results

3.1 | Relative Leaf Water Content

Descriptive statistics of the RWC across the 15 guar genotypes are presented in Table 3. The relative changes in RWC of different guar genotypes under 70% FC and 45% FC irrigation regimes, compared with the 100% FC, further demonstrated that the magnitude of RWC reduction increased with drought severity in all genotypes. At 70% FC, the percentage changes in RWC among genotypes ranged from -2.0% to -13.6% . At this level, genotype S6673 exhibited the lowest reduction in RWC (-2.0%), whereas the greatest reduction was observed in genotype RGC-1066 (-13.6%) (Figure 1A and Figure 6A). At 45% FC, the decline in RWC was substantially greater in all genotypes, with percentage changes ranging from -22.2% to -29.7% . The highest reduction in RWC at this stress level was recorded in genotype BR-99 (-29.7%), whereas genotype S-6560 showed the lowest reduction (-22.2%) (Figure 1A and Figure 6B).

3.2 | SG Content

Table 3 summarizes the descriptive statistical parameters of the SG content in the 15 different guar genotypes. The relative changes in SG among guar genotypes under 70% FC and 45% FC,

compared with the control condition, indicated that the magnitude of SG reduction increased consistently with drought severity across all genotypes. At 70% FC, the percentage reduction in SG among genotypes ranged from -1.4% to -14.1% . At this level, genotype S6553 exhibited the lowest reduction in SG (-1.4%), whereas genotype BR-99 showed the greatest reduction (-14.1%) (Figure 1B and Figure 6A). At 45% FC, SG reduction was more severe in all genotypes, with percentage changes ranging from -16.3% to -31.4% . The highest reduction in SG at this stress level was observed in genotype S-6560 (-31.4%), whereas genotype S6553 exhibited the lowest reduction (-16.3%) (Figure 1B and Figure 6B).

3.3 | Viscosity

The descriptive statistics associated with the viscosity traits in 15 guar genotypes are reported in Table 3. The results of changes in viscosity among different guar genotypes under the two irrigation regimes of 70% FC and 45% FC compared with the control condition demonstrated that the reduction in this trait was considerable across all genotypes and intensified with increasing DS severity. At the 70% FC level, percentage changes in viscosity among genotypes ranged from -11.6% to -40.0% . At this level, genotype S-5885 exhibited the lowest reduction in viscosity (-11.6%), whereas genotype S6673 showed the highest reduction (-40.0%). Additionally, genotypes Pishen, BR-99, and RGC-1031 recorded substantial reductions of -39.6% , -35.4% , and -33.5% , respectively (Figure 1C and Figure 6A). At the 45% FC level, viscosity reduction was more severe in all genotypes, with percentage changes ranging from -30.2% to -49.3% . The greatest reduction at this level was observed in genotype Pishen (-49.3%), whereas the lowest reduction was recorded for genotype Saravan (-30.2%) (Figure 1C and Figure 6B).

TABLE 3 | The descriptive statistics of the studied variables in 15 genotypes of guar (*Cyamopsis tetragonoloba*) under 100% FC, 70% FC, and 45% FC.

	100% FC				70% FC				45% FC			
	Min	Max	Mean	CV	Min	Max	Mean	CV	Min	Max	Mean	CV
RWC	81.5	89.6	85.96	2.7	71.2	86.5	79.58	4.88	57.8	69.5	64.23	3.93
SG	24.5	33.4	28.17	7.55	22.4	29.4	25.63	6.62	18.5	24.5	21.11	7.09
Flavonoids	0.21	0.29	0.25	7.78	0.24	0.36	0.309	10.02	0.29	0.44	0.3487	9.24
TAC	41.5	48.2	44.9	3.57	44.1	54.3	48.35	5.73	43.5	55.6	51.03	5.25
TPC	0.57	2.1	1.04	32.05	0.98	2.5	1.55	22.34	1.8	3.5	2.367	16.19
Viscosity	2200	3500	2645	13.57	1325	2600	1906	20.57	1150	2200	1603	16.8
TO	1.8	3.5	2.59	17.16	2.1	3.3	2.48	13.14	1.5	2.9	2.213	11.58
Fiber	10.2	13.2	11.71	5.513	9.58	12.1	10.4	4.32	8.5	10.2	9.377	3.69
Tannin	1.9	2.98	2.43	8.77	2.45	3.3	2.81	7.39	2.8	3.6	3.27	6.24
Protein	24	35	28.07	9.19	20	28	24.2	7.19	12	22	16.29	11.46
DMD	42.38	52.4	46.96	5.9	40.1	48.5	43.63	4.11	31.2	45.4	37.94	13.88
Carotenoids	1.3	2.8	2.12	15.66	1.1	2.2	1.58	17.54	0.8	1.6	1.253	13.88

3.4 | DMD

The descriptive statistics associated with the DMD in 15 guar genotypes are reported in Table 3. The results related to changes in DMD among different guar genotypes under the two irrigation regimes of 70% FC and 45% FC relative to the control condition indicated that the magnitude of DMD reduction increased in all genotypes with increasing DS intensity. At the 70% FC level, percentage changes in DMD ranged from -1.3% to -12.4% . At this level, genotype Pishen exhibited the lowest reduction in DMD (-1.3%), whereas the highest reduction was observed in genotype S-6581 (-12.4%) (Figure 2A and Figure 6A). At the 45% FC level, DMD reduction was more

severe across all genotypes, with a substantially wider range of variation, such that percentage changes ranged from -14.8% to -47.6% . The greatest reduction in DMD at this level was recorded for genotype S-5885 (-47.6%), whereas the lowest reduction was observed in genotype S6673 (-14.8%) (Figure 2A and Figure 6B).

3.5 | Fiber Content

Descriptive statistics of the fiber traits across the 15 guar genotypes are presented in Table 3. The findings related to changes in fiber content among different guar genotypes under the two

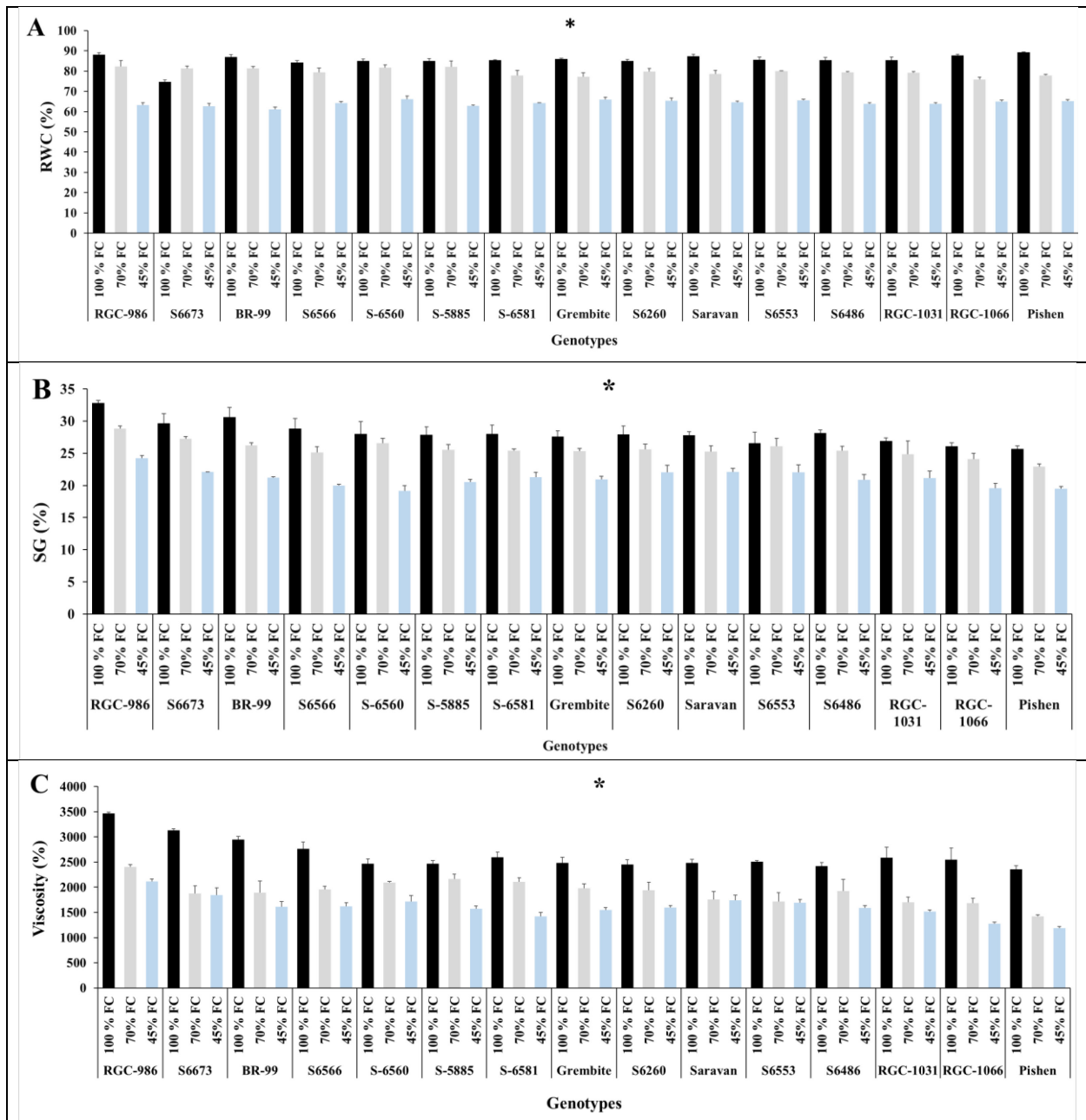


FIGURE 1 | Impact of three irrigation regimes (100% FC, 70% FC, and 45% FC) on 15 guar genotypes for (A) relative leaf water content (RWC), (B) seed gum (SG), and (C) viscosity. Bars represent the mean $\pm$ standard deviation of each genotype under the respective irrigation treatment. Asterisks indicate the significance level of treatment effects: * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, and ns denotes nonsignificant differences.

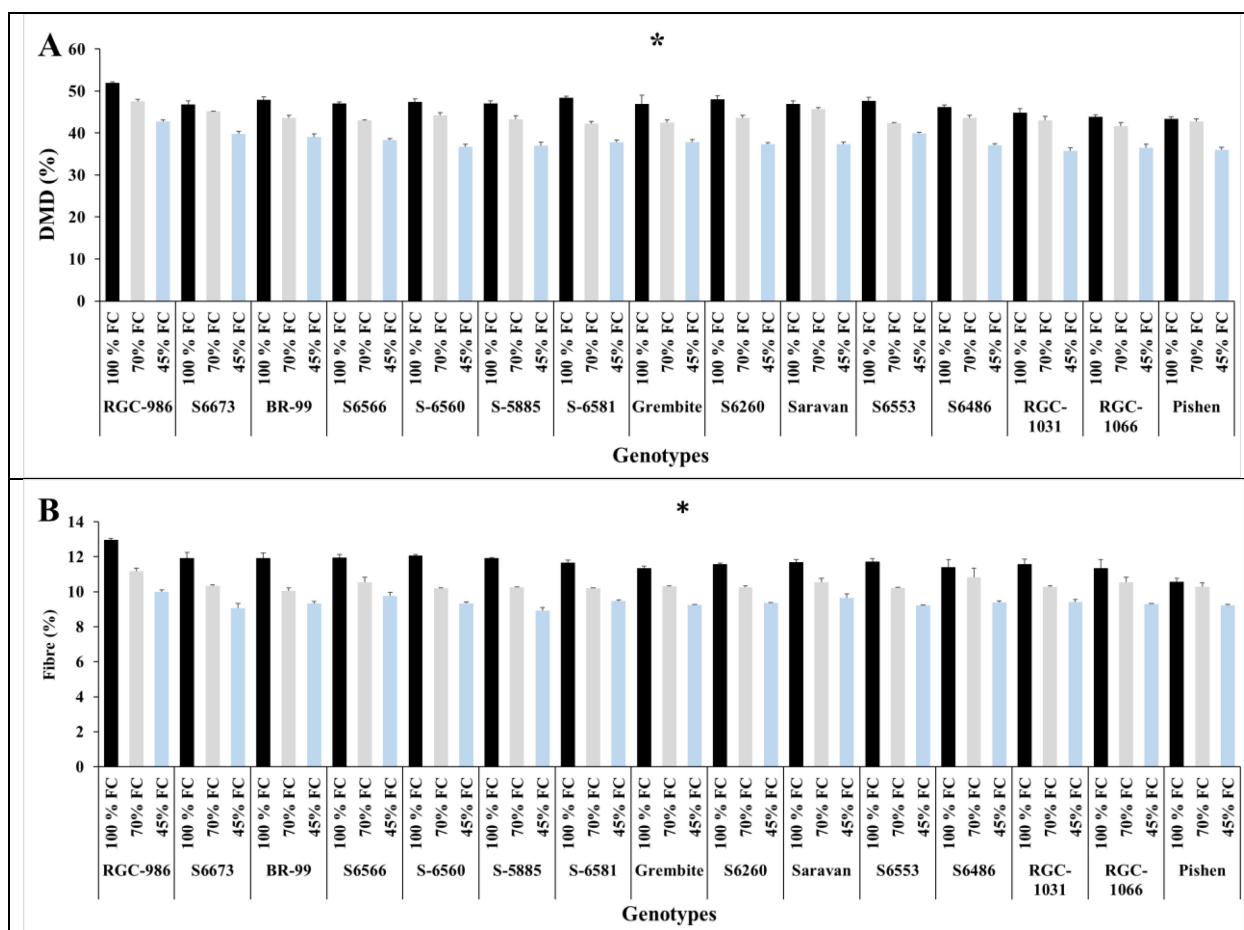


FIGURE 2 | Impact of three irrigation regimes (100% FC, 70% FC, and 45% FC) on 15 guar genotypes for (A) dry matter digestibility (DMD) and (B) fiber. Bars represent the mean $\pm$ standard deviation of each genotype under the respective irrigation treatment. Asterisks indicate the significance level of treatment effects: * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, and ns denotes nonsignificant differences.

irrigation regimes of 70% FC and 45% FC relative to the control condition indicated that the magnitude of fiber reduction increased in all genotypes with increasing DS intensity. At the 70% FC level, percentage changes in fiber content ranged from -2.7% to -15.7% . At this level, the lowest reduction in fiber content was observed in genotype Pishen (-2.7%), whereas the highest reduction was recorded for genotype BR-99 (-15.7%) (Figure 2B and Figure 6A). At the 45% FC level, fiber reduction was more severe across all genotypes, with percentage changes ranging from -12.7% to -25.2% . The greatest reduction in fiber content at this level was observed in genotype S-5885 (-25.2%), whereas the lowest reduction was recorded for genotype Pishen (-12.7%) (Figure 2B and Figure 6B).

3.6 | Total Oil (TO)

The results of the interaction effects of three different soil moisture levels on total oil (TO) content in 15 guar genotypes showed that this trait did not show significant differences in response to DS severity. However, significant differences were observed for the main effects of genotype and DS (Figure 3A,B). Under 100% FC, TO values ranged from 1.8 to 3.5 with an overall mean of 2.59. With soil moisture reduced

to 70% FC, TO values showed a slight decrease, with minimum and maximum values being 2.1 and 3.3, respectively, and the average TO decreased to 2.48. Under 45% FC, a more pronounced decrease in TO was observed, with values ranging from 1.5 to 2.9 and an overall mean of 2.213 (Table 3 and Figure 3A). Also, the results of the main effect of genotypes showed that the first genotype showed the highest oil content (Figure 3B).

3.7 | Tannin Content

Table 3 summarizes the descriptive statistical parameters of the tannin traits in the 15 different guar genotypes. The results related to changes in tannin content among different guar genotypes under the two irrigation regimes of 70% FC and 45% FC relative to the control condition indicated that tannin levels increased in all genotypes with increasing DS severity. At the 70% FC level, percentage changes in tannin content among genotypes ranged from 0.8% to 39.1%. At this level, the lowest increase in tannin content was observed in genotype BR-99 (0.8%), whereas the highest increase was recorded in genotype Pishen (39.1%) (Figure 4A and Figure 6A). At the 45% FC level, tannin accumulation intensified across

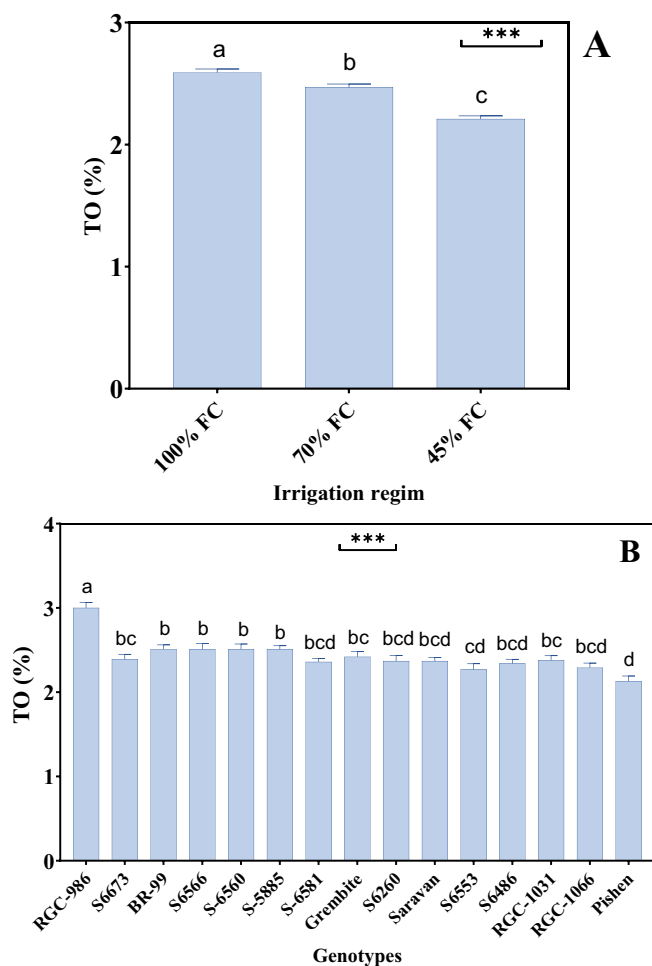


FIGURE 3 | Effect of the individual three irrigation regimes level (100% FC, 70% FC, and 45% FC) (A) and the main effect of genotype (B) on total gum content in 15 guar genotypes. Bars represent the mean $\pm$ standard deviation for each genotype under the respective irrigation regimes levels. Asterisks indicate the significance of the effects: * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, and ns denotes nonsignificant differences.

all genotypes, and the range of percentage changes expanded from 22.3% to 53.4%. The highest tannin increase at this level was observed in genotype Pishen (53.4%), whereas the lowest increase was recorded in genotype S6260 (22.3%) (Figure 4A and Figure 6B).

3.8 | Protein Content

Descriptive statistics of the protein content across the 15 guar genotypes are presented in Table 3. The findings related to changes in protein content among different guar genotypes under the two irrigation regimes of 70% FC and 45% FC relative to the control condition indicated that protein reduction was considerable in all genotypes as DS intensified. At the 70% FC level, percentage changes in protein content among genotypes ranged from -5.3% to -20.6% . At this level, the lowest reduction in protein content was observed in genotype Pishen (-5.3%), whereas the highest reduction was recorded in genotype S6566

(-20.6%) (Figure 4B and Figure 6A). At the 45% FC level, protein reduction intensified across all genotypes, and percentage changes ranged from -34.3% to -49.2% . The greatest protein reduction at this level was observed in genotype S6566 (-49.2%), whereas the lowest reduction was recorded in genotype Saravan (-34.3%) (Figure 4B and Figure 6B).

3.9 | Carotenoid Content

The descriptive statistics associated with the carotenoid content in 15 guar genotypes are reported in Table 3. The results related to changes in carotenoid content among different guar genotypes under the two irrigation regimes of 70% FC and 45% FC relative to the control condition indicated that carotenoid reduction intensified in all genotypes as DS severity increased. At the 70% FC level, percentage changes in carotenoid content among genotypes ranged from -1.9% to -35.2% . At this level, the lowest reduction in carotenoid content was observed in genotype Pishen (-1.9%), whereas the highest reductions were recorded in genotypes S-5885 and S-6581 (-35.2%) (Figure 4C and Figure 6A). At the 45% FC level, carotenoid reduction became more severe across all genotypes, and the range of percentage changes expanded from -18.4% to -49.3% . The highest reduction at this level was observed in genotype S6486 (-49.3%), whereas the lowest reduction was recorded in genotype Pishen (-18.4%) (Figure 4C and Figure 6B).

3.10 | TPC

Table 3 summarizes the descriptive statistical parameters of the TPC in the 15 different guar genotypes. The findings related to changes in TPC among different guar genotypes under the two irrigation regimes of 70% FC and 45% FC relative to the control condition indicated that TPC increased in all genotypes with increasing DS severity. At the 70% FC level, percentage changes in TPC among genotypes ranged from 7.3% to 238.1%. At this level, the lowest increase in TPC was observed in genotype Pishen (7.3%), whereas the highest increase was recorded in genotype RGC-986 (238.1%). Genotypes S-6581, S6553, and Grembite also exhibited high increases, ranging from 184.1% to 220.4% (Figure 5A and Figure 6A). At the 45% FC level, TPC continued to increase across all genotypes, and the range of percentage changes expanded from 70.7% to 238.1%. The highest TPC increase at this level was observed in genotype RGC-986 (238.1%), whereas the lowest increase was recorded in genotype Pishen (70.7%) (Figure 5A and Figure 6B).

3.11 | Flavonoid Content

The descriptive statistics associated with the flavonoid content in 15 guar genotypes are reported in Table 3. The findings related to changes in flavonoid content among different guar genotypes under the two irrigation regimes of 70% FC and 45% FC relative to the control condition indicated that flavonoid content increased in all genotypes as DS intensified. At the 70% FC level, percentage changes in flavonoid content among genotypes

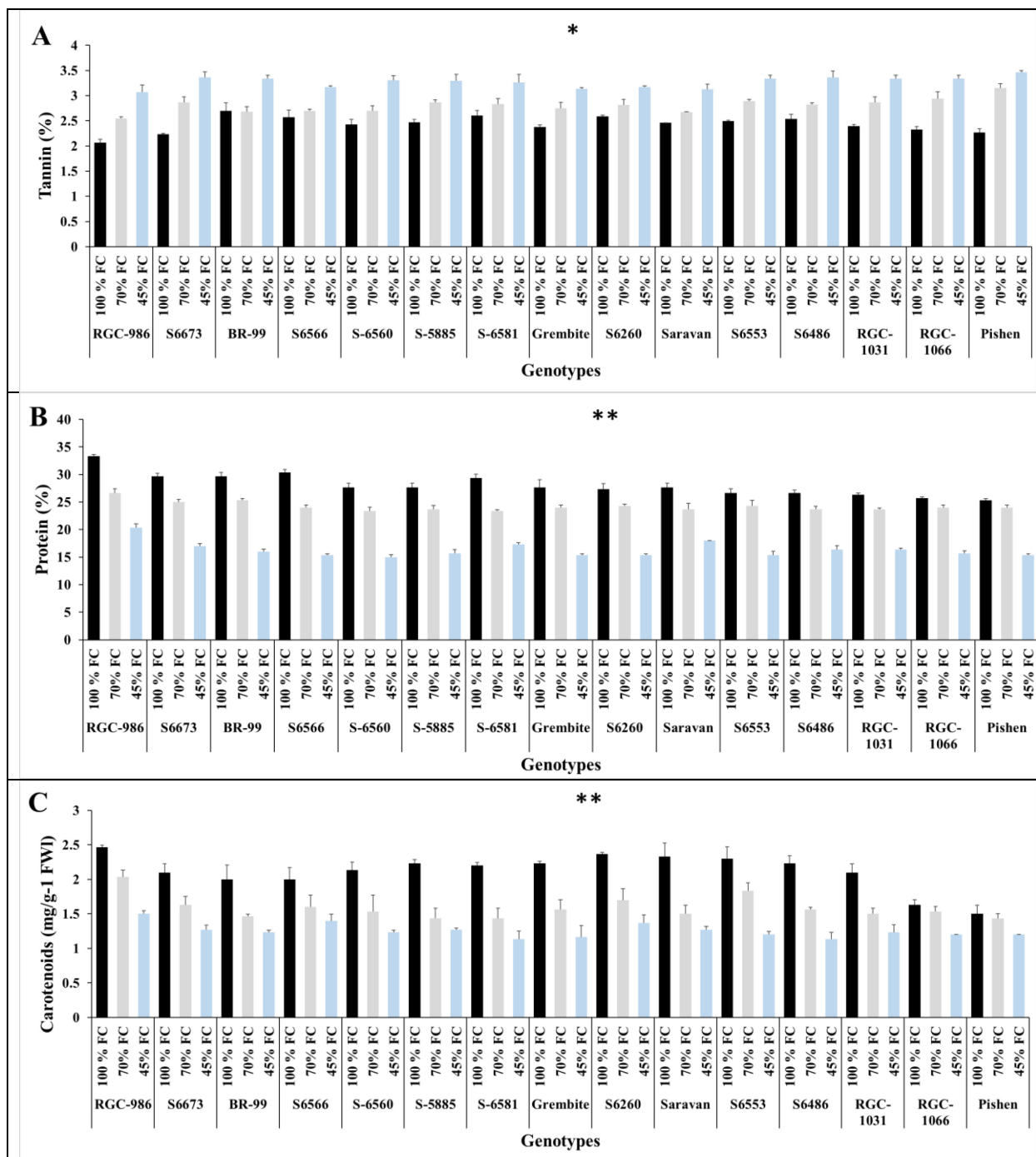


FIGURE 4 | Impact of three irrigation regimes (100% FC, 70% FC, and 45% FC) on 15 guar genotypes for (A) tannin, (B) protein, and (C) carotenoids. Bars represent the mean $\pm$ standard deviation of each genotype under the respective irrigation treatment. Asterisks indicate the significance level of treatment effects: * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, and ns denotes nonsignificant differences.

ranged from 12.1% to 77.7%. At this level, the lowest increase in flavonoid content was observed in genotype S-5885 (12.1%), whereas the highest increase was recorded in genotype RGC-986 (77.7%) (Figure 5B and Figure 6A). At the 45% FC level, flavonoid accumulation continued across all genotypes, and the range of percentage changes expanded from 28.4% to 77.7%. The highest flavonoid increase at this level was observed in genotype RGC-986 (77.7%), whereas the lowest increase was recorded in genotype Saravan (28.4%) (Figure 5B and Figure 6B).

3.12 | TAC

Table 3 summarizes the descriptive statistical parameters of the TAC in the 15 different guar genotypes. The findings related to changes in TAC among different guar genotypes under the two irrigation regimes of 70% FC and 45% FC relative to the control condition indicated that TAC values changed across all genotypes with increasing DS severity. At the 70% FC level, changes in TAC among genotypes ranged

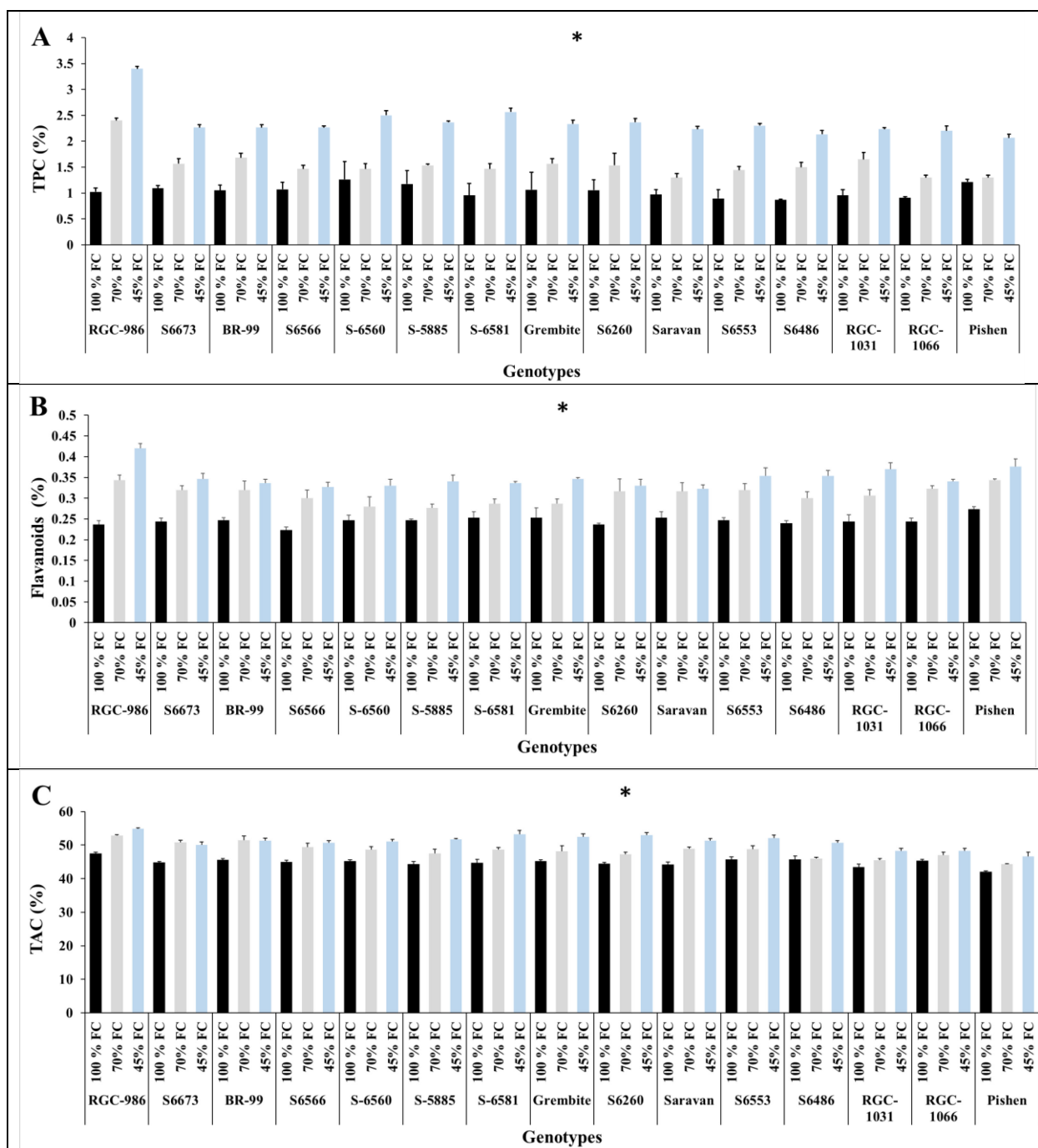


FIGURE 5 | Impact of three irrigation regimes (100% FC, 70% FC, and 45% FC) on 15 guar genotypes for (A) total phenolic content (TPC), (B) flavonoids, and (C) total antioxidant capacity (TAC). Bars represent the mean $\pm$ standard deviation of each genotype under the respective irrigation treatment. Asterisks indicate the significance level of treatment effects: * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, and ns denotes nonsignificant differences.

from 0.7% to 19.4%. At this level, the lowest increase in TAC was observed in genotype S6486 (0.7%), whereas the highest increase was recorded in genotype S-6581 (19.4%) (Figure 5C and Figure 6A). At the 45% FC level, TAC values in all genotypes showed either an increasing or stabilizing trend, and the range of changes expanded from 6.4% to 19.4%. The highest TAC at this level was again observed in genotype S-6581 (19.4%), whereas the lowest increase was recorded in genotype RGC-1066 (6.4%) (Figure 5C and Figure 6B).

3.13 | PCA

PCA conducted on 15 guar genotypes and their morphophysiological and chemical traits under 70% FC revealed that the first two principal components, PC1 and PC2, accounted for 57.7% and 17.0% of the total variance, respectively (Figure 7A). PC1 mainly represents traits related to seed quality and nutritional performance (protein, TPC, SG, carotenoid, and fiber), whereas PC2 primarily reflects variation in secondary metabolites.

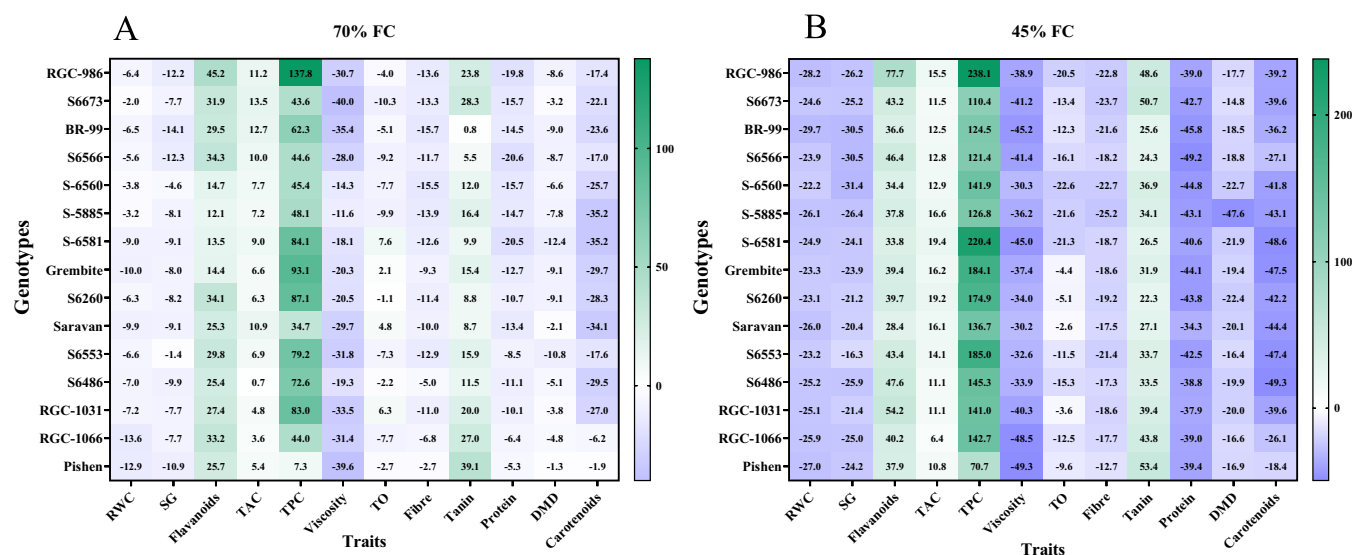


FIGURE 6 | Heatmap plot showing the percentage change in all phenotypic traits between the control and each treatment of genotypes under 70% (A) and 45% (B) FC. For the definitions of the measured traits and treatments, refer to Figures 1–5.

Particularly tannins and flavonoids, which are associated with antioxidant defense mechanisms under DS. Collectively, these two components explained 74.7% of the overall data variability, indicating a strong explanatory power. Along the PC1 axis, the genotypes RGC-986, S6673, and BR-99 were positioned on the positive side, whereas S-6560, S-5885, and S-6581 were located on the negative side of this axis. The remaining genotypes, including Pishen, RGC-1066, S6553, S6260, Saravan, S6486, RGC-1031, S6566, and Grembite, occupied intermediate positions along PC1. Along the PC2 axis, genotype Pishen exhibited the highest positive score, whereas S-6581 and S-5885 showed more negative scores.

For the 45% FC treatment, PCA revealed that the first two principal components (PC1 and PC2) explained 51.9% and 12.0% of the total variance, respectively (Figure 7B). Together, they accounted for more than 63% of the overall variability, reflecting a high explanatory capacity of these two components. Along the PC1 axis, variables related to seed quality and nutritional traits, including protein, TPC, SG, TO, fiber, carotenoids, and TAC, were aligned in a common direction, indicating that PC1 represents the principal axis of quantitative trait differentiation among the samples. In contrast, PC2 tended to separate samples with higher tannin and flavonoid contents, suggesting that these traits exhibit relative independence from the other measured variables. At the genotype level, RGC-986, with strongly positive scores along PC1 and near-zero values on PC2, was clearly separated from the other genotypes, reflecting superior characteristics associated with protein content and phenolic compounds. Conversely, genotypes such as S6566, S6260, and Saravan were located on the negative side of PC1, indicating lower values for these traits. Additionally, genotypes including Pishen, S6673, and BR-99 were positioned on the positive side of PC2, which was associated with higher tannin and flavonoid contents, distinguishing them from the remaining genotypes in this regard.

3.14 | MGIDI Analysis Under 70% and 45% FC

The results of the MGIDI calculated to evaluate the multi-trait performance of guar genotypes under DS at 70% FC revealed substantial differences in the distance of genotypes from the ideal genotype. According to this index, RGC-986, with the lowest MGIDI value (0.87), was identified as the genotype closest to the multi-trait ideotype under mild DS conditions. This was followed by S6673 and BR-99, with MGIDI values of 2.54 and 2.96, respectively, indicating a moderate distance from the ideal genotype (Figure 8A). The results of the MGIDI calculated to evaluate the multi-trait performance of 15 guar genotypes under 45% FC indicated a pronounced increase in the distance of genotypes from the ideal genotype. Under this stress level, RGC-986 exhibited the lowest MGIDI value (1.07), showing the smallest deviation from the multi-trait ideotype and was therefore identified as the superior genotype in terms of desirable trait combination under severe drought conditions. This was followed by RGC-1031, which ranked second with an MGIDI value of 3.15 (Figure 8B).

3.15 | Contribution of Genotypes to MGIDI Factors 70% and 45% FC

The results related to the contribution of guar genotypes to the first (FA1) and second (FA2) factors of the MGIDI under 70% FC revealed a markedly heterogeneous distribution of genotype contributions between the two factors. At this stress level, RGC-986 exhibited the highest contribution to FA1 (69.96%) and a lower contribution to FA2 (30.04%), indicating a strong dependence on the first factor. This was followed by Pishen, which contributed 59.24% to FA1 and 40.76% to FA2. The genotype RGC-1066 showed a more balanced pattern, with 48.90% contribution to FA1 and 51.10% to FA2. In contrast, the genotypes S-6560 and S-5885 exhibited dominant contributions to FA2, with FA2 accounting for 99.63%

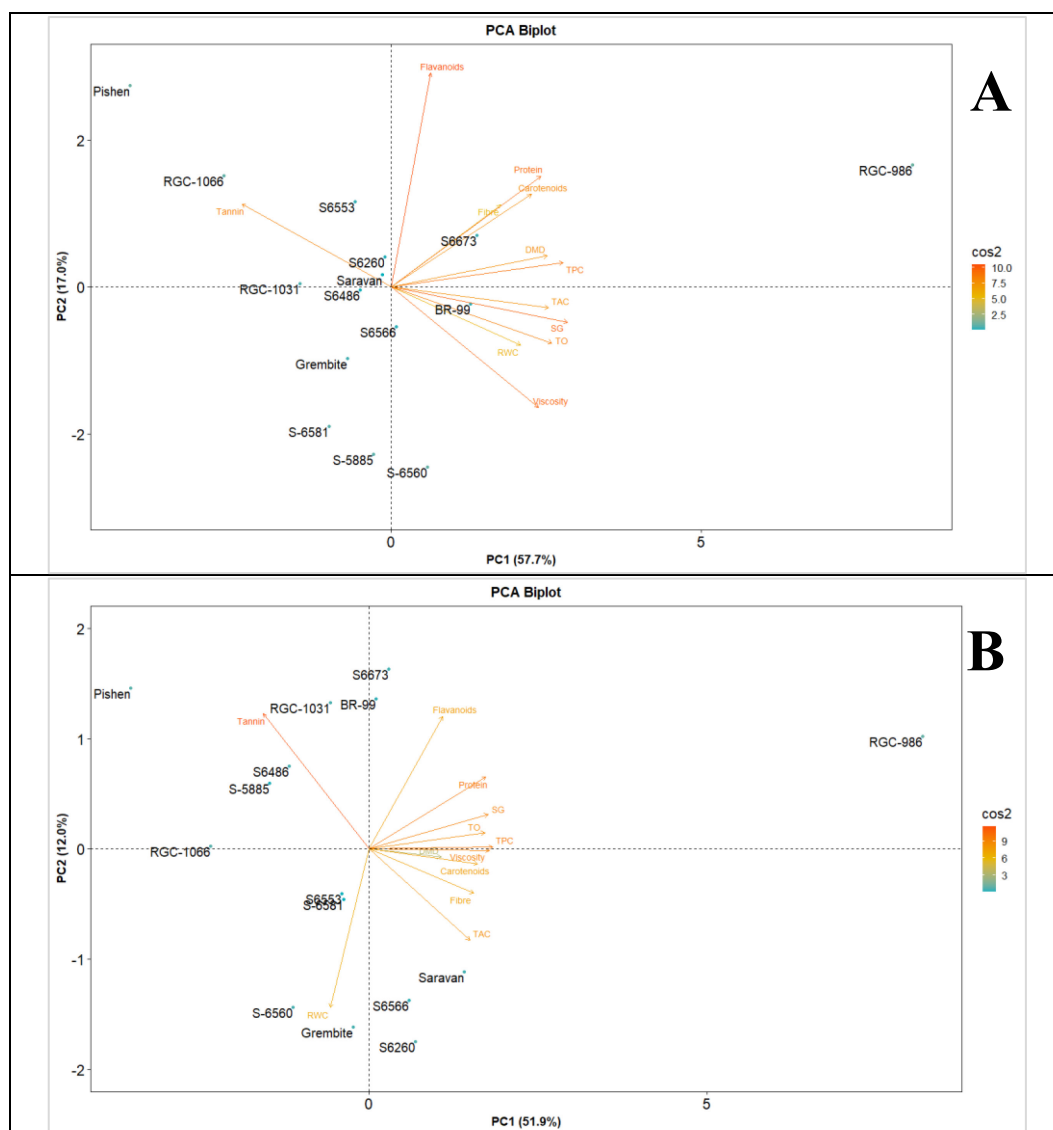


FIGURE 7 | Principal component analysis (PCA) biplot illustrating the biochemical traits of 15 difference genotype of Guar under 70% (A) and 45% (B) FC. The biplot displays the first two principal components (PC1 and PC2), which explain the major proportion of total variance among the measured traits. Circles represent the sample scores, whereas arrows indicate the loading vectors corresponding to each trait.

and 92.80% of their total contributions, respectively, although their FA1 contributions remained below 8%. Similarly, S-6581, BR-99, and Grembite were grouped with genotypes showing predominant dependence on FA2, with FA1 contributions of less than 21%. The remaining genotypes, including RGC-1031, S6260, Saravan, S6486, S6673, and S6566, displayed relatively balanced contribution patterns between the two factors, with FA1 contributions ranging from 21.2% to 32.3% and FA2 contributions between 67.7% and 78.8%. In addition, S6553, with 39.63% contribution to FA1 and 60.37% to FA2, represented an intermediate pattern between balanced genotypes and those predominantly influenced by FA2 (Figure 9A).

The results related to the contribution of guar genotypes to the three MGIDI factors (FA1, FA2, and FA3) under 45% FC revealed a highly heterogeneous and genotype-dependent distribution pattern. Under this stress level, RGC-986 showed the highest contribution to FA1 (66.69%), although its contributions to FA2 and FA3 were 4.95% and 28.36%, respectively.

Similarly, Pishen exhibited a multi-factor contribution pattern, with 44.06% contribution to FA1 and 16.32% and 39.62% contributions to FA2 and FA3, respectively. In contrast, the highest contributions to FA3 were observed in S-5885, S-6581, and S6553, for which FA3 accounted for 91.65%, 84.86%, and 84.85% of their total contributions, respectively, whereas contributions to FA1 and FA2 remained minimal (Figure 9B). The genotype BR-99 also showed a strong dependence on FA3, with 81.31% contribution. The genotypes S6486, S6673, and Saravan likewise allocated a major proportion of their contributions to FA3, with FA3 contributions of 75.06%, 77.53%, and 64.07%, respectively. In contrast, S6566 exhibited its highest contribution to FA2 (47.46%), whereas FA3 accounted for 52.04% and FA1 contributed less than 1%. The genotypes Grembite, S-6560, S6260, and RGC-1066 displayed more dispersed contribution patterns across the three factors, with FA3 contributions ranging from 51.97% to 67.46%, FA2 contributions between 24.23% and 32.72%, and relatively lower contributions to FA1. Moreover, RGC-1031, with contributions

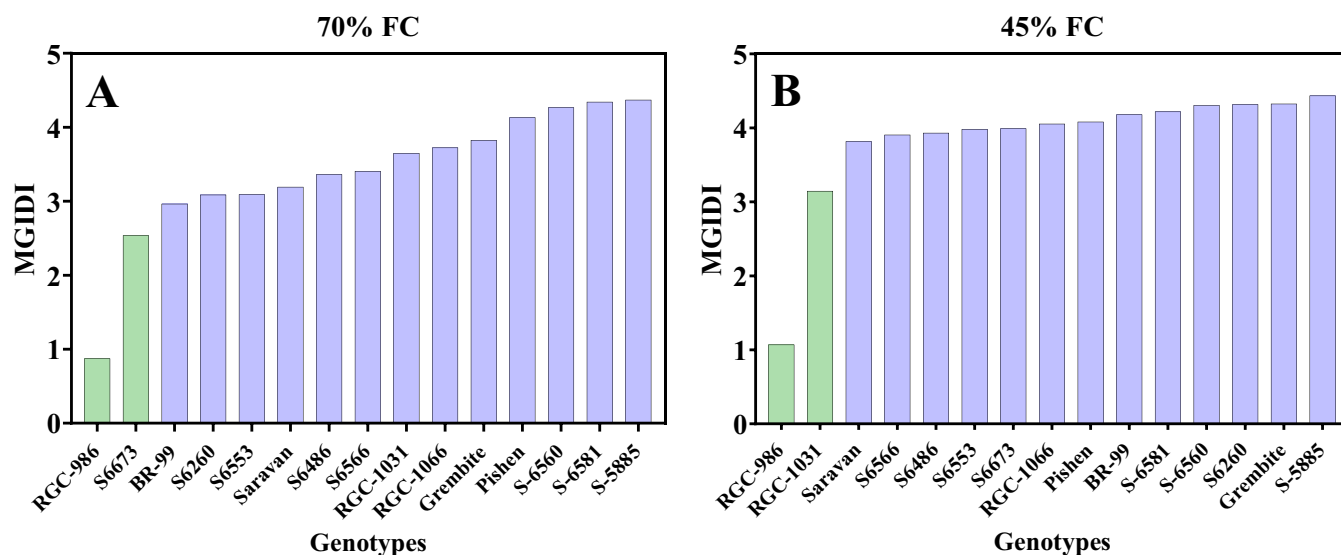


FIGURE 8 | Genotypes ranking of 15 genotypes of guar (*Cyamopsis tetragonoloba* L.) based on the MGIDI under 70% and 45% FC, with selected superior genotypes highlighted in green.

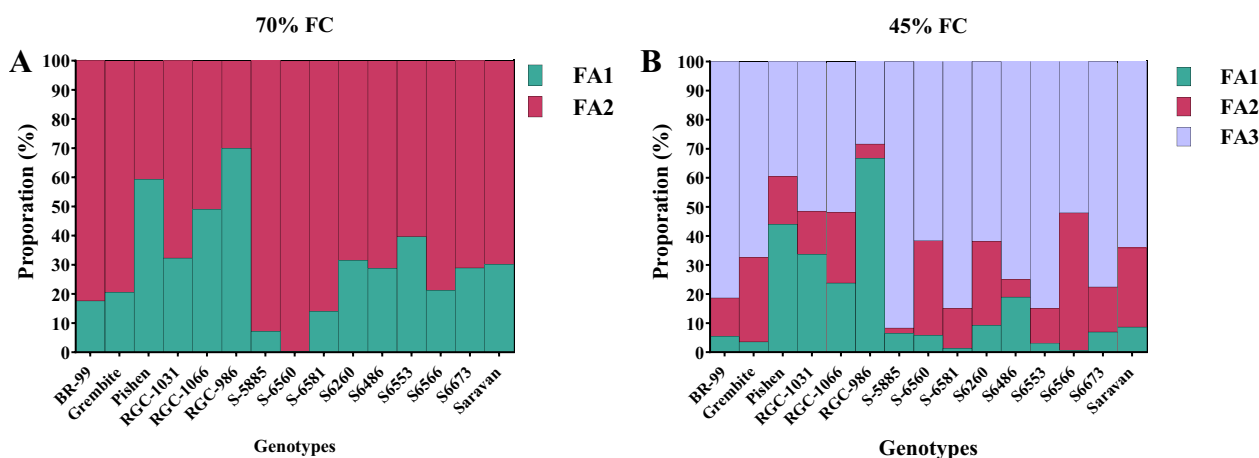


FIGURE 9 | Percentage distribution of strengths and weaknesses of the all genotypes based on the MGIDI method under 70% and 45% FC.

of 33.61% to FA1, 14.96% to FA2, and 51.43% to FA3, showed a relatively balanced distribution between the first and third factors.

3.16 | Results of Factor Analysis of Traits Under 70% and 45% FC

Under 70%, FC, two main factors (FA1 and FA2) were extracted, explaining the underlying structure of variation among the studied traits. The FA1 exhibited strong negative factor loadings for viscosity (−0.94), SG (−0.86), TO (−0.85), TAC (−0.73), RWC (−0.72), TPC (−0.68), and DMD (−0.60), whereas tannin showed a strong positive loading (0.85) on this factor. The FA2 was mainly characterized by high positive loadings for flavonoids (0.90), protein (0.83), carotenoids (0.74), fiber (0.64), DMD (0.58), and TPC (0.58). Communality values indicated that flavonoids (0.94), viscosity (0.88), SG (0.88), protein (0.85), and TPC (0.81) were the traits most strongly explained by the extracted factors, whereas fiber (0.47) exhibited the lowest communality.

Correspondingly, uniqueness values revealed a low proportion of specific variance (error) for flavonoids (0.06) and for viscosity and SG (each 0.12) (Table 4).

Under 45% FC, three main factors (FA1, FA2, and FA3) were extracted, reflecting a more complex structure of trait variation. The first factor (FA1) showed strong negative loadings for TAC (−0.92), viscosity (−0.75), SG (−0.64), DMD (−0.62), TPC (−0.58), and TO (−0.54), whereas tannin displayed a dominant positive loading (0.83) on this factor. The second factor (FA2) was primarily defined by a very high positive loading for RWC (0.85), accompanied by moderate negative loadings for SG (−0.48), DMD (−0.46), protein (−0.44), and flavonoids (−0.40). The third factor (FA3) accounted for the highest positive loadings for flavonoids (0.81), fiber (0.72), TPC (0.63), protein (0.61), TO (0.59), and carotenoids (0.65). Communality estimates at this stress level demonstrated that tannin (0.90), TAC (0.86), flavonoids (0.83), SG (0.80), and viscosity (0.79) were well explained by the extracted factors, whereas TO (0.66) exhibited the lowest communality. Uniqueness values further indicated a low level

TABLE 5 | Predicted genetic gain for traits influencing MGIDI index of the studied variables in 15 genotypes of guar (*Cyamopsis tetragonoloba*) at 70% FC and 45% FC.

Traits	Factor	70% FC								
		Xo	Xs	SD	SDperc	h2	SG	SGperc	Sense	Goal
RWC	FA1	79.58	80.93	1.35	1.69	0.59	0.80	1.00	Increase	100
DMD	FA1	43.63	45.74	2.12	4.85	0.78	1.64	3.77	Increase	100
Vis	FA1	1906.31	2076.36	170.05	8.92	0.73	123.39	6.47	Increase	100
SG	FA1	25.63	27.72	2.09	8.14	0.87	1.81	7.06	Increase	100
TPC	FA1	1.54	1.89	0.34	22.37	0.81	0.28	18.09	Increase	100
Tannin	FA1	2.81	2.75	−0.05	−1.95	0.56	−0.03	−1.09	Increase	0
TAC	FA1	48.35	51.17	2.81	5.82	0.81	2.28	4.71	Increase	100
TO	FA1	2.47	2.70	0.23	9.40	0.89	0.21	8.32	Increase	100
Carotenoids	FA2	1.58	1.71	0.13	7.96	0.51	0.06	4.03	Increase	100
Pro	FA2	24.18	25.33	1.16	4.78	0.70	0.81	3.33	Increase	100
Flavonoids	FA2	0.31	0.32	0.01	4.58	0.63	0.01	2.90	Increase	100
Fiber	FA2	10.40	10.60	0.20	1.91	0.56	0.11	1.06	Increase	100

Traits	Factor	45% FC								
		Xo	Xs	SD	SDperc	h2	SG	SGperc	Sense	Goal
DMD	FA1	37.94	39.18	1.24	3.28	0.95	1.18	3.11	Increase	100
Vis	FA1	1602.89	1786.47	183.58	11.45	0.86	157.65	9.84	Increase	100
SG	FA1	21.11	22.53	1.42	6.74	0.90	1.29	6.09	Increase	100
Tannin	FA1	3.27	3.23	−0.04	−1.07	0.50	−0.02	−0.54	Increase	0
TAC	FA1	51.03	51.46	0.43	0.85	0.81	0.35	0.69	Increase	100
RWC	FA2	64.34	64.08	−0.26	−0.40	0.31	−0.08	−0.13	Increase	0
Carotenoids	FA3	1.25	1.26	0.01	0.52	0.06	0.00	0.03	Increase	100
TPC	FA3	2.37	2.80	0.43	18.15	0.95	0.41	17.33	Increase	100
Pro	FA3	16.24	18.04	1.79	11.04	0.86	1.54	9.48	Increase	100
Flavonoids	FA3	0.35	0.39	0.04	10.62	0.80	0.03	8.54	Increase	100
Fiber	FA3	9.38	9.60	0.22	2.35	0.66	0.15	1.55	Increase	100
TO	FA3	2.21	2.39	0.18	8.17	0.82	0.15	6.72	Increase	100

and TPC were grouped within one subcluster, whereas fiber, DMD, flavonoids, SG, and protein were grouped within another subcluster. Furthermore, the highest positive correlations were observed between TPC, flavonoids, and protein with genotype RGC-986, highlighting its superior biochemical performance under severe DS. In contrast, the strongest negative correlation was detected between DMD and genotype S-5885 (Figure 10B).

3.19 | Correlation Analysis of Traits Under 70% and 45% of FC

In the present study, correlation analysis among the investigated traits was conducted in 15 guar (*C. tetragonoloba* L.) genotypes under two DS levels, namely, 70% and 45% of FC. The correlation

results under the 70% FC revealed strong positive associations between SG and carotenoids (0.66***), DMD (0.63***), protein (0.73***), fiber (0.65***), and viscosity (0.72***). In addition, viscosity showed significant positive correlations with carotenoids (0.66***), protein (0.66***), and fiber (0.64***), while exhibiting a strong negative correlation with tannin content (−0.60***). Moreover, fiber content exhibited strong positive correlations with carotenoids (0.67***), DMD (0.70***), and protein (0.73***) (Figure 10C).

Under 45% FC, The RWC showed strong positive correlations with carotenoids (0.79***), DMD (0.68***), protein (0.84***), fiber (0.84***), viscosity (0.77***), and SG (0.80***). In contrast, RWC exhibited strong negative correlations with TPC (−0.83***), TAC (−0.87***), and flavonoids (−0.84***). Similarly, SG displayed

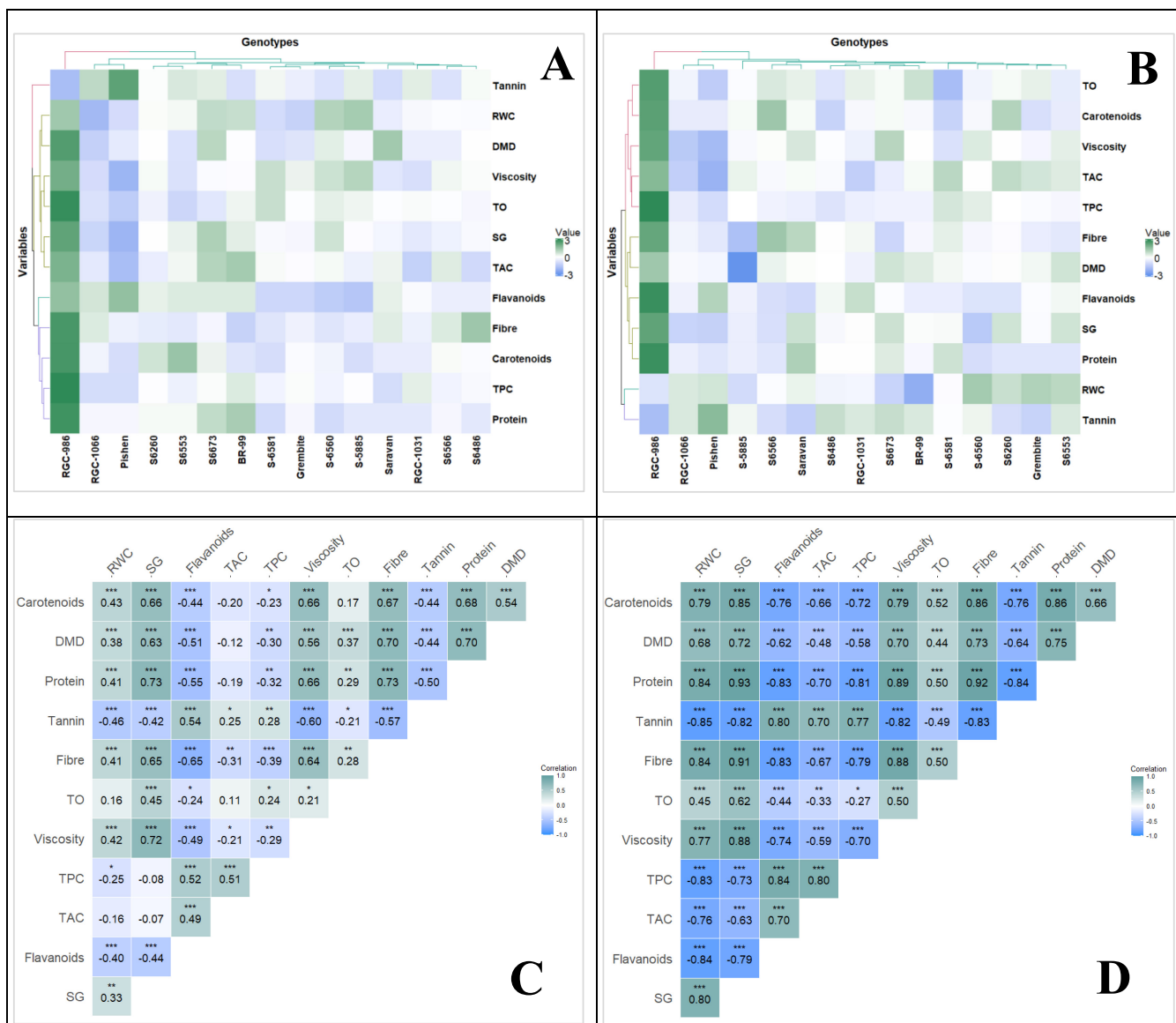


FIGURE 10 | Cluster analysis based on the heatmap of at 70% FC (A) and 45% FC (B) and Pearson correlation coefficients of the studied variables at 70% FC (C) and 45% FC (D) in 15 difference genotypes. The color scale, ranging from green to blue, represents correlations from highly positive to highly negative. The numbers in the figure indicate the Pearson correlation coefficients between the traits. Square stars denote the significance of the correlation coefficients (* $p \leq 0.05$, ** $p \leq 0.01$, and *** $p \leq 0.001$).

strong positive correlations with DMD (0.72***), protein (0.93***), fiber (0.91***), and viscosity (0.88***), while showing strong negative associations with tannin (−0.82***), TPC (−0.73***), TAC (−0.63***), and flavonoids (−0.79***). (Figure 10D). Also, RWC showed a significant positive relationship with SG (0.683***), protein content (0.776**), and carotenoids (0.546***), while exhibiting a strong negative association with TPC (−0.592***). (Figure 11A–D). In addition, a strong positive relationship was observed between flavonoids and TPC (0.517***), as well as between TPC and TAC (0.517***). (Figure 11E,F).

4 | Discussion

DS is a major agricultural constraint that markedly affects plant water status and physiological performance in guar. Leaf

RWC is a sensitive and widely used indicator of plant responses to water deficit, and its reduction reflects decreased leaf water-holding capacity under limited moisture conditions. Numerous studies have consistently reported significant declines in RWC in guar subjected to DS (Avola et al. 2020; Upreti et al. 2021; Khurizadeh et al. 2024). Drought-tolerant genotypes are generally able to maintain higher RWC levels, whereas drought-sensitive genotypes show more pronounced reductions, highlighting RWC as a reliable marker of physiological adaptation to water deficit (Shrestha et al. 2022; Khurizadeh et al. 2024). Genetic variation in drought response has been documented, with tolerant genotypes maintaining relatively higher RWC, particularly during early stress stages, compared with sensitive ones. Overall, the reduction in RWC remains a robust and reliable indicator for assessing drought tolerance and sensitivity among guar genotypes.

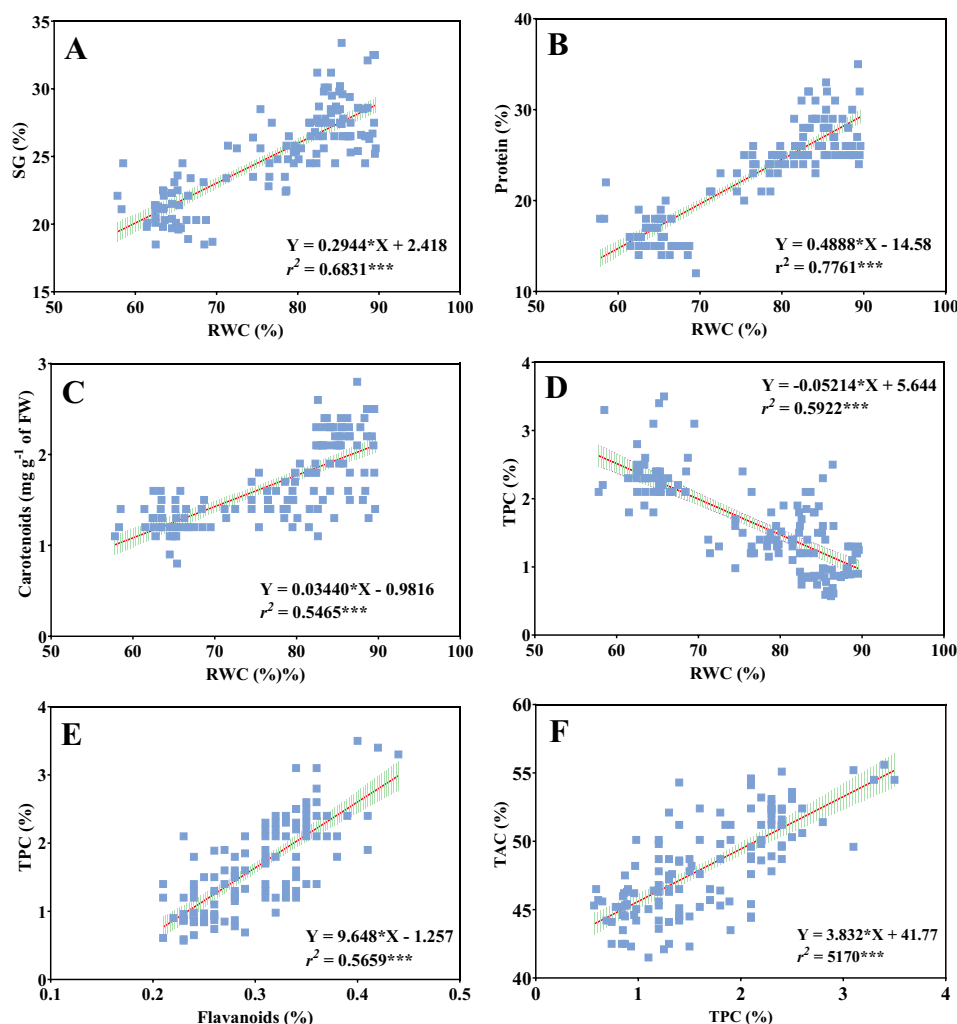


FIGURE 11 | Relationships between (A) relative water content (RWC) with (A) seed gum (SG), (B) protein, (C) carotenoids, (D) total phenol compounds (TPC), (E) flavonoids, and (F) total antioxidant capacity (TAC), with TPC and F TPC with TAC after interaction of 15 genotypes of guar under three irrigation (100%, 70%, and 45% FC). The coefficients of determination (R^2) of the relationships are given ($p < 0.01$).

The results of the present study also demonstrated that gum content (SG) in the leaves of the 15 guar genotypes declined markedly with increasing DS intensity. This physiological response is in close agreement with changes reported in previous studies on guar under DS, as water limitation disrupts metabolic processes and alters the distribution of soluble components within leaves, with variable effects among guar genotypes (Khurizadeh et al. 2024). Under 70% FC, the observed reduction in SG indicated a decreased ability of the genotypes to maintain leaf soluble content compared with the control treatment, reflecting a dynamic plant response to reduced water availability—a pattern also reported as a common response in guar under drought conditions (Upreti et al. 2021; Gresta et al. 2017). With further intensification of DS to severe levels (40% field capacity), SG declined more sharply across genotypes, indicating an expansion of the adverse effects of water deficit on the plant's capacity to retain soluble compounds in leaf tissues. This finding is consistent with previous reports on biochemical and physiological alterations in guar subjected to DS (Pandey et al. 2022; Khurizadeh et al. 2024). Earlier studies have also highlighted enhanced activity of osmotic adjustment pathways and shifts in carbohydrate metabolism as key adaptive mechanisms in guar

under DS, processes that may be closely associated with changes in SG, as this parameter reflects the status of soluble compounds within leaf tissues (Ghotbi et al. 2022; Sarwar et al. 2024).

The findings of this study demonstrated that a reduction in soil moisture resulted in a significant decline in guar gum viscosity, and the pattern of variation among genotypes revealed clear differences in DS responses. Specifically, drought-tolerant genotypes exhibited smaller reductions in viscosity compared with drought-sensitive ones. Under 70% FC, the magnitude of viscosity reduction among genotypes ranged from 11.6% to 40.0%. With increasing drought severity to 45% FC, viscosity reductions intensified across all genotypes, with values ranging from −30.2% to −49.3%. At this stress level, genotype Pishen exhibited the greatest reduction in viscosity (−49.3%), whereas Saravan showed a comparatively smaller decline (−30.2%), reflecting differential physiological responses among guar genotypes. These results indicate that guar genotypes respond differentially to DS in terms of leaf physiology, carbohydrate metabolism, and other key functional traits, and that such variation provides a valuable basis for the selection and improvement of drought-tolerant guar genotypes in breeding programs.

Water deficit reduces the activity of enzymes involved in metabolic processes and negatively affects the nutritional quality of plant tissues (Sodaeizadeh et al. 2024). Under 70% DMD values varied widely among genotypes, with some exhibiting only slight reductions and others showing more pronounced declines, confirming the presence of genetic variability and differing adaptive capacities among guar genotypes, an observation also reported in studies examining genetic diversity and drought responses in guar (Narayan et al. 2023). At this stress level, genotype Pishen exhibited the smallest reduction in DMD, whereas S-6581 showed the greatest decline, illustrating the broad range of genotypic responses to water deficit. Previous research has similarly confirmed contrasting physiological responses between drought-tolerant and drought-sensitive guar genotypes (Vishnyakova et al. 2023). With further intensification of DS to 45% FC, the range of DMD variation increased markedly, with genotype S-5885 showing the greatest reduction and S6673 exhibiting the smallest decline. This pattern suggests that guar genotypes differ substantially in their capacity to maintain dry matter quality under water-limited conditions, consistent with molecular and physiological studies indicating that drought responses in guar are strongly influenced by genetic background and metabolic adaptability.

The evaluation of soil moisture regimes revealed that TO content in guar was significantly affected by DS intensity, with clear genotype-dependent responses. Under optimal irrigation (100% FC), TO levels reflected the inherent oil synthesis capacity of the genotypes, consistent with previous reports indicating that guar can maintain compositional traits under adequate water supply (Ali et al. 2020). At moderate stress (70% FC), TO decreased in some genotypes while increasing in others, highlighting distinct genotypic strategies for coping with water limitation, as previously observed in guar (Khurizadeh et al. 2024). Notably, S6673 showed the largest reduction, whereas S-6581, RGC-1031, and Saravan exhibited increased TO, indicating differential metabolic adaptation (Azizi et al. 2022). It seems that these findings confirm that drought severity alters lipid accumulation in guar through genotype-specific modifications of lipid metabolism and energy balance (Ali et al. 2020).

Under optimal irrigation (100% FC), fiber levels reflected the inherent capacity of genotypes to maintain cell wall structure, which is critical for the nutritional and industrial quality of guar (Pileh et al. 2025). At moderate stress (70% FC), fiber content decreased overall, but clear genotypic variation was observed, with some genotypes maintaining higher fiber levels than others, indicating differential drought responses (Vishnyakova et al. 2023). Under severe stress (45% FC), fiber reduction became more pronounced in all genotypes, with S-5885 and Pishen showing the greatest and smallest decreases, respectively. These results highlight substantial genotypic differences in the ability of guar to maintain structural integrity under increasing drought severity, reflecting coordinated metabolic and structural responses to water limitation. Numerous studies have demonstrated that DS leads to increased accumulation of TPC and flavonoids; these compounds mitigate ROS activity, inhibit lipid peroxidation, and contribute to the stabilization of membranes and proteins, playing a key role in stress tolerance (Khurizadeh et al. 2024; Pileh et al. 2025). In the present study, a significant increase in TPC and flavonoid content was observed across all guar genotypes as

drought intensity increased from 100% FC to 70% FC and subsequently to 45% FC. In particular, the enhancement of TPC under moderate and severe drought conditions reflects the active stimulation of the phenylpropanoid pathway in response to reduced water availability, leading to increased production of nonenzymatic antioxidants (Puzanskiy et al. 2025).

This progressive increase with drought severity is mediated by the activation of phenolic and flavonoid biosynthetic pathways, a response that has also been widely reported in previous studies (Khurizadeh et al. 2024). Beyond their antioxidant function, phenolic and flavonoid compounds contribute to drought tolerance by regulating stress-related signaling pathways and modulating the expression of genes associated with stress responses. For instance, studies in other plant species have shown that key genes involved in flavonoid biosynthesis are upregulated under DS, promoting enhanced phenolic accumulation and improved drought tolerance (ElSayed et al. 2019; Soltani-Gerdefaramarzi et al. 2024).

At the level of the antioxidant defense system, an increase in TAC was observed under both moderate and severe DS, indicating an overall enhancement of the plant's ability to neutralize ROS. This increase in TAC is largely attributed to the accumulation of phenolic compounds and flavonoids as nonenzymatic antioxidants, which contribute to mitigating oxidative damage at the cellular level. Similar trends have been reported in numerous previous studies, confirming the critical role of TAC in maintaining physiological performance and reducing lipid peroxidation under DS (Sarker and Oba 2018; Mohagheghian et al. 2025). Moreover, the present study revealed a very strong positive correlation between phenolic compounds and TAC, in agreement with earlier reports documenting a close association between phenolic accumulation and antioxidant potential (Hamdani and Wani 2017; Habibi et al. 2024; Soltani-Gerdefaramarzi et al. 2024).

DS enhances ROS production, which can lead to protein oxidation, membrane damage, and reduced metabolic activity. In many plant species, water deficit is associated with a decline in total protein content in leaf tissues, as DS suppresses protein synthesis while accelerating protein degradation through oxidative pathways and increased energy demand for cellular defense. This phenomenon is consistent with the observations in the present guar genotypes, which showed a substantial reduction in protein content with increasing drought severity (up to approximately 42% at 45% FC), reflecting diminished physiological and metabolic activity under stress conditions (Tahmouzi et al. 2023; Habibi et al. 2023). In contrast to proteins, flavonoids, TPC and tannins, as major components of the nonenzymatic antioxidant defense system, exhibited significant increases under DS. These compounds play a crucial role in scavenging ROS and indicate that plants reinforce their secondary defense line against oxidative stress through enhanced accumulation under water deficit conditions (Shrestha et al. 2022; Farajpour 2025). The pronounced increase in tannins and flavonoids, particularly under severe drought across different guar genotypes, demonstrates the activation of the phenylpropanoid pathway for antioxidant production. This adaptive response is more pronounced in drought-tolerant genotypes, as enhanced accumulation of these compounds contributes to improved cellular protection. Numerous studies have similarly reported

that phenolic and flavonoid traits are strongly associated with ROS scavenging capacity and tend to accumulate to a greater extent in stress-tolerant genotypes (Alshameri et al. 2020; Pileh et al. 2025). Conversely, carotenoids that play a vital role in protecting the photosynthetic apparatus and photoprotective systems generally decline with increasing DS. This reduction may result from chlorophyll degradation, increased lipoxygenase activity, and structural damage to chloroplasts under water deficit conditions (Ghotbi et al. 2022). Although carotenoids normally protect chloroplast membranes against oxidative damage, their decline under severe drought reflects damage to photosynthetic structures and an imbalance between carotenoid biosynthesis and degradation (Mohamed et al. 2011; Rani et al. 2025). At the genotypic level, drought-tolerant guar genotypes not only experience smaller reductions in protein content but also demonstrate a greater capacity to accumulate tannins and phenolic compounds and to activate antioxidant pathways, thereby limiting the progression of ROS-induced damage (Avola et al. 2020; Mahdipour-Afra et al. 2021). These genotypes may possess more efficient hormonal regulatory systems, enhanced biosynthetic pathways, and tighter regulation of stress-related gene expression, enabling improved maintenance of photosynthetic performance, antioxidant production, and cellular integrity (Yan et al. 2016). In contrast, drought-sensitive genotypes exhibit more pronounced protein loss, lower tannin accumulation, and a limited ability to preserve carotenoid content, reflecting a weaker defensive capacity against oxidative stress (Zubair et al. 2017; Khurizadeh et al. 2024; Sarwar et al. 2024).

5 | Conclusion

The results of this study demonstrated that guar genotypes exhibit diverse responses to DS, and the severity of soil moisture reduction has a significant effect on the physiological, nutritional, and biochemical traits of the plants. Genotypes that exhibited superior performance in physiological and nutritional traits, such as RGC-986, RGC-1031, and Saravan, showed high potential for cultivation in water-limited regions. These genotypes, while tolerating DS, were able to maintain nutritional quality and enhance the accumulation of bioactive compounds, making them valuable genetic resources for guar breeding programs. Overall, the findings of this study emphasize the importance of identifying and selecting drought-tolerant genotypes with high nutritional quality and demonstrate that integrating quantitative and qualitative trait analyses with multi-trait indices provides a comprehensive and effective approach for the development of guar cultivation under water-limited environmental conditions. This approach can contribute to improved yield, enhanced production sustainability, and increased economic and nutritional value of guar in arid regions and may serve as a transferable model for other drought-tolerant crops.

Author Contributions

Warqaa Muhammed ShariffAl-Sheikh: data curation, software, formal analysis. **Evan Abdulhassan Mohammed Ali:** investigation, software, supervision, resources, data curation, writing – original draft. **Hussam F. Najerb Alawadi:** investigation, visualization, formal analysis, data curation. **Heidar Meftahizade:** writing – review and editing, conceptualization, project administration, supervision, methodology.

Funding

The authors have nothing to report.

Ethics Statement

The authors have nothing to report.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

Data are provided within the manuscript.

References

- Ali, Z., M. Ashraf, M. Y. Ashraf, S. Anwar, and K. Ahmad. 2020. "Physiological Response of Different Accessions of *Sesbania sesban* and *Cyamopsis tetragonoloba* Under Water Deficit Conditions." *Pakistan Journal of Botany* 52, no. 2: 395–404.
- Alshameri, A., F. Al-Qurainy, A. R. Gaafar, et al. 2020. "Identification of Differentially Expressed Drought-Responsive Genes in Guar [*Cyamopsis tetragonoloba* (L.) Taub]." *International Journal of Genomics* 2020, no. 1: 4147615.
- Alshameri, A., F. Al-Qurainy, S. Khan, et al. 2019. "Morpho-Physiological Responses of Guar [*Cyamopsis tetragonoloba* (L.) Taub.] to Multiple Stresses of Drought, Heat and Salinity." *Pakistan Journal of Botany* 51, no. 3: 817–822.
- American Association of Cereal Chemists (AACC) Approved Methods Committee. 2000. *Approved Methods of the American Association of Cereal Chemists*. Vol. 1. American Association of Cereal Chemists.
- Avola, G., E. Riggi, C. Trostle, O. Sortino, and F. Gresta. 2020. "Deficit Irrigation on Guar Genotypes (*Cyamopsis tetragonoloba* (L.) Taub.): Effects on Seed Yield and Water Use Efficiency." *Agronomy* 10, no. 6: 789.
- Azizi, G., S. G. Moosavi, M. Seghatoleslami, and R. Baradaran. 2022. "Investigating the Effect of Plant Density and Nutrient Application on Yield and Physiological Characteristics of Guar (*Cyamopsis tetragonoloba*)." *Gesunde Pflanzen* 74, no. 4: 791–800.
- Casas, J. A., A. F. Mohedano, and F. García-Ochoa. 2000. "Viscosity of Guar Gum and Xanthan/Guar Gum Mixture Solutions." *Journal of the Science of Food and Agriculture* 80, no. 12: 1722–1727.
- Chang, C. C., M. H. Yang, H. M. Wen, and J. C. Chern. 2002. "Estimation of Total Flavonoid Content in Propolis by Two Complementary Colorimetric Methods." *Journal of Food and Drug Analysis* 10, no. 3: 178–182.
- Cuenca, R. H. 1989. *Irrigation System Design – An Engineering Approach*. Prentice Hall Inc.
- ElSayed, A. I., M. A. El-Hamahmy, M. S. Rafudeen, A. H. Mohamed, and A. A. Omar. 2019. "The Impact of Drought Stress on Antioxidant Responses and Accumulation of Flavonolignans in Milk Thistle (*Silybum marianum* (L.) Gaertn)." *Plants* 8, no. 12: 611.
- Farajpour, M. 2025. "Fate of Pistachio Production in Iran Holds Lessons for the World." *Nature* 639, no. 8054: 306.
- Ganatra, S. H., A. M. Ramteke, S. P. Durge, and S. U. Patil. 2013. "Phytochemicals Investigation and TLC Profiling of *Cyamopsis tetragonoloba* L. Seeds (Fabaceae)-Pea Family." *International Journal of Pharmaceutical Sciences and Research* 4: 1551–1555.
- Ghorbani, M., S. H. R. Ramazani, H. R. Fallahi, and S. M. Mousavi Koohi. 2019. "Effect of Drought Stress and Bio-Fertilizer on Yield and Yield Components of Guar *Cyamopsis tetragonoloba* (L.) Taub." *Journal of Medicinal Plants and By-Products* 8, no. 1: 13–19.

- Ghotbi, V., A. Mahrokh, A. M. Tehrani, and H. Asadi. 2022. "Evaluation of Forage Yield and Quality of Cowpea, Guar, and Mung Bean Under Drought Stress Conditions." *Chemistry Proceedings* 10, no. 1: 62.
- Gresta, F., G. Ceravolo, V. L. Presti, A. D'Agata, R. Rao, and B. Chiofalo. 2017. "Seed Yield, Galactomannan Content and Quality Traits of Different Guar (*Cyamopsis tetragonoloba* L.) Genotypes." *Industrial Crops and Products* 107: 122–129.
- Gresta, F., A. I. De Luca, A. Strano, et al. 2014. "Economic and Environmental Sustainability Analysis of Guar (*Cyamopsis tetragonoloba* L.) Farming Process in a Mediterranean Area: Two Case Studies." *Italian Journal of Agronomy* 9, no. 1: 565.
- Habibi, A., S. Sarikhani, M. M. Arab, et al. 2024. "Drought and Heat Stress Interactions: Unveiling the Molecular and Physiological Responses of Persian Walnut." *Plant Physiology and Biochemistry* 217: 109237.
- Habibi, A., S. Sarikhani, M. M. Arab, et al. 2025. "Combined Drought and Heat Stress Intensifies Antioxidant Responses and Gene Expression in Persian Walnut (*Juglans regia* L.)." *Bmc Plant Biology* 26: 1–18.
- Habibi, A., N. Yazdani, M. Koushesh Saba, et al. 2023. "Natural Preservation and Improving Lipid Oxidation Inhibition of Fresh Walnut." *Horticulture, Environment, and Biotechnology* 64, no. 1: 133–142.
- Hamdani, A. M., and I. A. Wani. 2017. "Guar and Locust Bean Gum: Composition, Total Phenolic Content, Antioxidant and Antinutritional Characterisation." *Bioactive Carbohydrates and Dietary Fibre* 11: 53–59.
- Hoseinollahi, M., S. Soltani-Gerdefaramarzi, and A. Azizian. 2025. "Effect of Biochar on the Chemical Properties of Soil Under Cultivation of Two Cultivar of Guar (*Cyamopsis tetragonoloba* L.) Under Drought Stress." *Applied Soil Research* 12, no. 4: 46–60.
- Khurizadeh, S., R. Naderi, H. Meftahizadeh, S. Hazrati, and S. Nicola. 2024. "Foliar Application of Methyl Jasmonate and Chitosan Improve Growth, Yield, and Quality of Guar (*Cyamopsis tetragonoloba* L.) Under Water-Deficit Stress." *Plants* 13, no. 21: 3099.
- Koleva, I. I., T. A. Van Beek, J. P. Linssen, A. D. Groot, and L. N. Evstatieva. 2002. "Screening of Plant Extracts for Antioxidant Activity: A Comparative Study on Three Testing Methods." *Phytochemical Analysis* 13, no. 1: 8–17.
- Kumari, M., R. Gangwar, and R. Prasad. 2024. "Delineating the Response of Antioxidant Enzymes Comparatively in Four Guar Genotypes Under Drought Stress." *Journal of Plant Biochemistry and Biotechnology* 33, no. 3: 384–399.
- Kusvuran, A., and S. Kusvuran. 2019. "Using of Microbial Fertilizer as Biostimulant Alleviates Damage From Drought Stress in Guar (*Cyamopsis tetragonoloba* (L.) Taub.) Seedlings." *International Letters of Natural Sciences* 76: 147–157.
- Lichtenthaler, H. K. 1987. "Chlorophylls and Carotenoids: Pigments of Photosynthetic Biomembranes." In *Methods in Enzymology*, vol. 148, 350–382. Academic Press.
- Mahdipour-Afra, M., M. AghaAlikhani, S. Abbasi, and A. Mokhtassi-Bidgoli. 2021. "Growth, Yield and Quality of Two Guar (*Cyamopsis tetragonoloba* L.) Ecotypes Affected by Sowing Date and Planting Density in a Semi-Arid Area." *PLoS ONE* 16, no. 9: e0257692.
- Malani, S., W. Ravelombola, A. Manley, and H. Pham. 2024. "Genetic Diversity and Population Structure Analysis in Guar." *Plants* 13, no. 22: 3183.
- Mohagheghian, B., G. Saeidi, and A. Arzani. 2025. "Phenolic Compounds, Antioxidant Enzymes, and Oxidative Stress in Barley (*Hordeum vulgare* L.) Genotypes Under Field Drought-Stress Conditions." *BMC Plant Biology* 25, no. 1: 709.
- Mohamed, I. K., M. A. Osama, M. Samiha, and E. M. Zahrat. 2011. "Biochemical Studies on *Plantago major* L. and *Cyamopsis tetragonoloba* L." *International Journal of Biodiversity and Conservation* 3, no. 3: 83–91.
- Mudgil, D., S. Barak, and B. S. Khatkar. 2014. "Guar Gum: Processing, Properties and Food Applications—A Review." *Journal of Food Science and Technology* 51, no. 3: 409–418.
- Narayan, S., R. K. Sharma, V. Kumar, I. Sanyal, and P. A. Shirke. 2023. "Alterations in Plant Anatomy and Higher Lignin Synthesis Provides Drought Tolerance in Cluster Bean [*Cyamopsis tetragonoloba* (L.) Taub.]." *Plant Physiology and Biochemistry* 201: 107905.
- Olivoto, T., and M. Nardino. 2021. "MGIDI: Toward an Effective Multivariate Selection in Biological Experiments." *Bioinformatics* 37, no. 10: 1383–1389.
- Pandey, K., R. S. Kumar, P. Prasad, V. Pande, P. K. Trivedi, and P. A. Shirke. 2022. "Coordinated Regulation of Photosynthesis and Sugar Metabolism in Guar Increases Tolerance to Drought." *Environmental and Experimental Botany* 194: 104701.
- Pileh, F., A. Ebadi, Z. Zamani, M. Babalar, M. F. L. Climent, and A. Habibi. 2025. "Improving Salt Stress Tolerance in Grapevine Rootstocks and Cultivars Through Foliar Application of Ascorbic Acid." *Scientific Reports* 15, no. 1: 41860.
- Price, M. L., L. G. Butler, J. C. Rogler, and W. R. Featherston. 1979. "Overcoming the Nutritionally Harmful Effects of Tannin in Sorghum Grain by Treatment With Inexpensive Chemicals." *Journal of Agricultural and Food Chemistry* 27, no. 2: 441–445.
- Puzanskiy, R. K., D. A. Romanyuk, E. A. Zorin, M. A. Vishnyakova, and V. A. Zhukov. 2025. "Metabolomic Analysis of Drought Response in Guar (*Cyamopsis tetragonoloba* (L.) Taub.) Seeds." *Agronomy* 15, no. 12: 2778.
- Rani, R., D. Kaushik, G. E. Babagil, et al. 2025. "Exploring the Deciphering Properties of *Cyamopsis tetragonoloba*: Its Food Application, Feasibility, and Future Aspects." *International Journal of Food Science and Technology* 60, no. 1: vvae098.
- Ravelombola, W., A. Manley, C. Adams, et al. 2021. "Genetic and Genomic Resources in Guar: A Review." *Euphytica* 217, no. 11: 199.
- Sababelkheir Murwan, K., H. Abdalla Abdelwahab, and H. Nouri Sulafa. 2012. "Quality Assessment of Guar Gum (Endosperm) of Guar (*Cyamopsis tetragonoloba*)." *ISCA Journal of Biological Sciences* 1, no. 1: 67–70.
- Sarker, U., and S. Oba. 2018. "Drought Stress Enhances Nutritional and Bioactive Compounds, Phenolic Acids and Antioxidant Capacity of Amaranthus Leafy Vegetable." *BMC Plant Biology* 18, no. 1: 258.
- Sarwar, M. K. S., M. Usman, F. Asif, R. Kalsoom, S. Tabbusam, and M. Zeeshan. 2024. "Effect of Drought Stress and Response in Cotton." *Trends in Plant Science* 4: 61–73.
- Shrestha, R., C. B. Adams, and N. Rajan. 2022. "Does the Drought Tolerance of Guar [*Cyamopsis tetragonoloba* (L.) Taub.] Extend Belowground to Root Nodules?" *Journal of Agronomy and Crop Science* 208, no. 5: 599–608.
- Singleton, V. L., R. Orthofer, and R. M. Lamuela-Raventós. 1999. "Analysis of Total Phenols and Other Oxidation Substrates and Antioxidants by Means of Folin-Ciocalteu Reagent." *Methods in Enzymology* 299: 152–178. [https://doi.org/10.1016/s0076-6879\(99\)99017-1](https://doi.org/10.1016/s0076-6879(99)99017-1).
- Sodaeizadeh, H., A. A. Karimian, S. H. Jafari, and A. M. Arani. 2024. "A Preliminary Study on Heavy Metal Monitoring in Soil and Guar (*Cyamopsis tetragonoloba*) Biomass Amended With Sewage Sludge." *Environmental Monitoring and Assessment* 196, no. 2: 201.
- Soltani-Gerdefaramarzi, S., M. Hoseinollahi, H. Meftahizadeh, F. Bovand, and M. Hatami. 2024. "Differential Responses of Two Local and Commercial Guar Cultivars for Nutrient Uptake and Yield Components Under Drought and Biochar Application." *Scientific Reports* 14, no. 1: 23665.

- Tahmouzi, S., H. Meftahizadeh, S. Eyshi, et al. 2023. "Application of Guar (*Cyamopsis tetragonoloba* L.) Gum in Food Technologies: A Review of Properties and Mechanisms of Action." *Food Science & Nutrition* 11, no. 9: 4869–4897.
- Tilley, J. M. A., and D. R. Terry. 1963. "A Two-Stage Technique for the In Vitro Digestion of Forage Crops." *Grass and Forage Science* 18, no. 2: 104–111.
- Upreti, P., S. Narayan, F. Khan, L. M. Tewari, and P. A. Shirke. 2021. "Physiological Attributes Associated With Leaf Spectral Alterations in Guar [*Cyamopsis tetragonoloba* (L.) Taub.] Under Drought." *3 Biotech* 11, no. 3: 125.
- Vahdati, K., A. Sheikhi, M. M. Arab, S. Sarikhani, A. Habibi, and H. Ataee. 2023. "Cultivars and Genetic Improvement." In *Temperate Nuts*, 79–111. Springer Nature Singapore.
- Vishnyakova, M. A., N. Frolova, and A. Frolov. 2023. "Drought Stress Response in Guar (*Cyamopsis tetragonoloba* (L.) Taub): Physiological and Molecular Genetic Aspects." *Plants* 12, no. 23: 3955.
- Yan, W., Y. Zhong, and Z. Shangguan. 2016. "A Meta-Analysis of Leaf Gas Exchange and Water Status Responses to Drought." *Scientific Reports* 6, no. 1: 20917.
- Zubair, M., L. H. Akhtar, R. Minhas, et al. 2017. "Performance of Guar Genotypes Under Irrigated and Drought Stress Conditions as Evaluated Through PCA and Cluster Analysis." *International Journal of Biology and Biotechnology* 14, no. 4: 623–628.