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ADAPTIVE POTENTIAL AND BREEDING STRATEGIES OF GUAR (*CYAMOPSIS TETRAGONOLOBA*) FOR EXPANDING ITS CULTIVATION WITH CLIMATE CHANGE

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SUMMARY

Guar (*Cyamopsis tetragonoloba* L.) is an important legume and industrial crop valued for its adaptation to arid and semi-arid environments and for its seeds rich in galactomannan (guar gum). These polysaccharides are materials widely used in the food, pharmaceutical, textile, and petroleum industries. With increased climate change pressure, including drought and high temperature, a concentrated interest in guar as a climate-resilient crop has risen. The following review summarized current knowledge on the adaptive potential of guar, with emphasis on drought tolerance mechanisms, physiological responses, and breeding strategies. Physiological adaptations and processes, such as stomatal regulation, osmotic adjustment, antioxidant activity, and maintenance of photosynthetic efficiency, contribute to drought tolerance. Guar genotypes with significant genetic variability provide opportunities for crop improvement through breeding. The genomic resources, molecular markers, and transcriptomic analysis offer promising tools for identifying genes associated with stress tolerance. Integration of physiological approaches with molecular breeding can further accelerate the development of improved guar cultivars. Such strategies could facilitate the expansion of guar cultivation in the new agroecological regions and support climate-resilient cropping systems.

Keywords: Guar (*C. tetragonoloba*), drought tolerance, genetic diversity, molecular markers, plant physiology, stress response, breeding strategies, genomics

Key findings: The review highlighted the adaptive potential, drought tolerance mechanisms, and breeding prospects of guar (*C. tetragonoloba* L.). Integrating physiological and genomic approaches can further support the development of drought-tolerant cultivars for arid regions.

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INTRODUCTION

Guar (*Cyamopsis tetragonoloba* L.) is an annual leguminous crop widely recognized for its adaptability to arid environmental conditions and considerable economic value. The guar seeds are rich in galactomannan, commonly known as guar gum, a natural polysaccharide characterized by robust thickening and stabilizing properties. In guar gum, the galactomannan accounts for 75%–85% of its composition and is responsible for its highest viscosity. Moreover, smaller proportions of moisture (8%–14%), protein (5%–6%), fiber (2%–3%), and ash (0.5%–1%) were also available in the seed endosperm, influencing the physicochemical properties of gum. Owing to these properties, guar gum has become widely used in several industrial sectors, including food processing, pharmaceuticals, cosmetics, paper, and textile industries. However, the largest demand comes from the petroleum industry, where guar gum functions as a stabilizing and thickening agent in drilling fluids during oil extraction (Amrita and Jain, 2003).

The guar gum, with enormous industrial demand, has led to a significant expansion of guar cultivation in previous decades. Traditionally, the said crop has gained growth primarily in arid and semi-arid regions of South Asia, particularly in India and Pakistan, which cover the majority of the global production. However, in other regions, the interest in guar cultivation has also increased, such as in the United States, Australia, and some parts of Europe, due to its adaptability to marginal environments and its economic potential. In addition to its industrial importance, guar contributes to sustainable agricultural systems. As a leguminous crop, it forms symbiotic associations with nitrogen-fixing rhizobia and arbuscular mycorrhizal fungi, which enhance soil fertility and support environmentally friendly cropping systems (Chaudhary *et al.*, 1973; Arora and Pahuja, 2008).

With the current climate change, the significance of guar cultivation has further enhanced, where viable environmental factors, such as drought, high temperature, and

irregular rainfall patterns, pose serious challenges to crop productivity. Guar is generally a crop considered moderately tolerant to drought and heat, proving it promising for cultivation in water-limited environments. Guar genotypes with substantial genetic variability provide valuable opportunities for crop improvement and the development of stress-tolerant cultivars (Gabra *et al.*, 1990; Yuldashov *et al.*, 2023). However, despite its growing importance, knowledge of the physiological and molecular mechanisms underlying stress tolerance in guar remains limited compared with major crop species.

Therefore, understanding the adaptive potential of guar and identifying effective breeding strategies are essential for expanding its cultivation under changing climatic conditions. In this context, the presented review summarized the current knowledge on the adaptive traits of guar, its physiological and genetic responses to environmental stress factors, and the modern breeding approaches for improving guar productivity under climate change scenarios (Thombare *et al.*, 2016).

Guar with adaptation and morphological traits

Guar (*C. tetragonoloba* L.) has received a relatively underutilized crop classification capable of growing under a wide range of soil conditions, including sandy and well-drained clay soils. Guar is predominantly a self-pollinated plant, while natural cross-pollination occurs at a very low frequency. Morphologically, guar exhibited considerable variations in plant height, ranging from 50 cm to 1.5 m, depending on the genotypes' genetic makeup, environments, and their interactions (Figure 1). The stem is typically robust and becomes partially woody as the plant approaches maturity. Guar with a well-developed root system is one of its key adaptive traits. The primary taproot penetrates deeply into the soil profile, allowing plants to access the moisture from deeper soil layers. This root characteristic enables guar to tolerate short periods of drought and contributes to its suitability for cultivation under arid and semi-arid environments (Dzyubenko *et al.*, 2023).

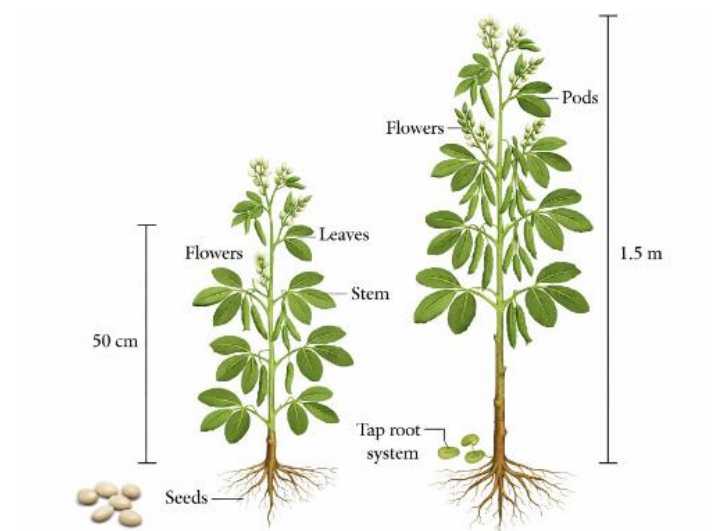


Figure 1. Morphological structure of the guar (*C. tetragonoloba* L.) plant showing the stem, leaves, flowers, pods, seeds, and taproot system (original figure prepared by the authors).

Guar cultivation's primary center is the Indian subcontinent, particularly the northwestern regions of India and neighboring areas of Pakistan. In these regions, growing guar is commonly under rainfed conditions in extremely dry environments, such as the Thar Deserts of India and Pakistan. Low annual precipitation and seasonal rainfall patterns during the monsoon period create challenging growing conditions; however, guar revealed considerable adaptability to these environmental settings. In contrast, cultivars planted for vegetable and food purposes often occur under irrigated conditions to ensure stable yield and quality (El-Sawah *et al.*, 2021).

Guar reproductive structures possess several distinctive features. Pods are usually in a cluster arrangement along the stem, which explains the common name 'cluster bean.' Individual pods may vary in length and typically contain numerous seeds. The seed structure comprises three main components, viz., the embryo, seed coat, and endosperm, with the endosperm serving as the primary storage tissue (Sultan *et al.*, 2013).

The guar endosperm is particularly important because it contains galactomannan, the polysaccharide responsible for its industrial value. Galactomannan forms the foundation of

guar gum production, which is highly favorable for thickening, stabilizing, and acting as a water-binding agent in various industrial applications. These biological characteristics significantly contribute to the economic importance of guar and highlight its potential for wider cultivation under diverse environmental conditions (Ali *et al.*, 2015).

Guar as a drought-tolerant crop

Guar (*C. tetragonoloba*) is a widely recognized drought-tolerant crop, found suitable for cultivation in arid and semi-arid regions. Although detailed information on its physiological and agronomic responses to water deficit conditions is still insufficient compared with many other legume species. However, available past studies revealed that guar can maintain considerable productivity under less water availability (Ravelombola *et al.*, 2021). Field studies conducted in Mediterranean environments have enunciated that agronomic practices, particularly the sowing time, play a vital role in determining water sufficiency during critical growth stages. Therefore, appropriate crop management can significantly improve the plant performance and enhance water-use efficiency under drought stress conditions (Ali *et al.*, 2015).

Research on irrigation management has further shown that guar responds to varying water regimes. Reduced irrigation generally leads to decreases in plant height, leaf area development, pods per plant, and seed yield in guar. However, several guar cultivars exhibited relatively stable productivity even under limited irrigation, revealing the genetic variation in drought tolerance and water-use efficiency (Gresta *et al.*, 2016). Although in guar, the optimal seed yields emerged under adequate moisture conditions, it is also capable of maintaining moderate productivity under reduced water availability.

Drought stress primarily affects the development of reproductive organs in guar. Among yield components, the pods per plant have considerably shown the most sensitive trait under water deficit conditions, while seeds per pod and seed weight revealed generally gaining less effect (MacMillan *et al.*, 2021). Water limitation also influences the vegetative growth traits, including plant height, leaf number, leaf area, and biomass accumulation, emphasizing the importance of a sufficient water supply for normal plant growth and development (Meftahizadeh *et al.*, 2019). Guar responses to drought also vary, depending on the growth and developmental stage. Several studies have identified that the reproductive phase, particularly flowering and early pod formation, as the most critical period for water availability. Drought stress occurring during these stages can significantly reduce pod development and seed yield in guar (Gresta *et al.*, 2019).

Substantial genetic variability of the different guar genotypes is another vital factor contributing to drought adaptation. Multiple guar cultivars' evaluation under arid conditions revealed significant variations in physiological traits, such as biomass production, photosynthetic activity, and plant growth characteristics. Although drought stress generally reduces the growth and productivity, the degree of these effects varies among genotypes, allowing the identification of more drought-tolerant cultivars (Ali *et al.*, 2015). Genotypic variation for drought tolerance has also had reports in studies conducted across different geographical regions. Differences in

plant vigor, biomass accumulation, and growth performance under water-limited conditions highlighted the importance of selecting suitable genotypes for cultivation in drought-prone environments (Heinemann and Hildebrandt, 2021).

Overall, the concerned research disclosed that guar possesses several physiological and agronomic traits contributing to its adaptation to water-limited environments. However, significant genetic variability among the cultivars remains, requiring further studies to better understand the physiological and genetic mechanisms underlying drought tolerance. Such knowledge will support the development of improved guar cultivars capable of maintaining stable productivity under enhanced water scarcity with diverse environmental conditions.

Guar drought tolerance with physiological and metabolic mechanisms

Plants generally adopt three major strategies to cope with drought stress: drought escape, drought avoidance, and drought tolerance. In guar, drought avoidance mechanisms play a crucial role, particularly through stomatal closure that reduces transpiration and water loss. This process has the main regulation of the phytohormone abscisic acid (ABA). In addition, reactive oxygen species (ROS) and calcium ions function as signaling molecules involved in drought-response pathways and regulation of stomatal movement. These signaling processes help maintain cellular water balance and regulate gas exchange under drought stress conditions. Drought stress can also stimulate the development of deeper root systems, enabling plants to access water from deeper soil layers in arid environments (Norboyeva *et al.*, 2026).

Under prolonged water deficit conditions, plants activate metabolic adjustments that subsequently enhance the stress tolerance. These physiological processes include the accumulation of osmoprotective compounds, activation of antioxidant defense systems, and modifications in primary metabolism. Osmolytes, such as soluble sugars and amino acids, contribute to osmotic

adjustment and protect cellular structures from dehydration damage, while antioxidant enzymes detoxify ROS generated during stress conditions (Pareek *et al.*, 2022).

Photosynthesis is one of the most drought-sensitive physiological processes. Water deficit conditions often reduce the photosynthetic efficiency due to stomatal closure, decreased CO₂ uptake, and damage to chloroplast structures. As a result, the use of plant parameters, such as leaf water status, chlorophyll content, and gas exchange, commonly serves to evaluate plant responses to drought stress conditions (Tanwar *et al.*, 2017). In guar, drought stress reduces stomatal conductance, relative leaf water content, and chlorophyll concentration.

However, tolerant genotypes often exhibit protective adjustments, including increased accumulation of carotenoids and anthocyanins, which help protect the photosynthetic apparatus from photodamage (Thakur and Randhawa, 2018). Comparative studies of tolerant and sensitive guar cultivars revealed that drought-tolerant genotypes maintain greater stability of photosynthetic processes under drought-stress conditions. For example, cultivars such as RGC-1002 demonstrated the enhanced capacity to dissipate excess light energy and sustain photosynthetic activity during drought stress conditions (Grigoreva *et al.*, 2021).

Carbohydrate metabolism also plays a pivotal role in drought adaptation. Under water deficit conditions, plants redistribute carbohydrate reserves to support essential metabolic functions and stress responses. Drought-tolerant guar genotypes with more efficient regulation of pathways indicate an association with photosystem II activity, the Calvin cycle, and ROS detoxification. These drought-tolerant genotypes also accumulate the higher concentrations of soluble sugars, such as glucose and fructose, which function as osmoprotective compounds that stabilize cellular structures. In addition, fructans derived from sucrose metabolism contribute to osmotic regulation and maintenance of cell turgor during dehydration stress conditions (Ramanjaneyulu *et al.*, 2018; Grigoreva *et al.*, 2021).

Recent transcriptomic studies further enunciated that in guar the drought tolerance has a connection with variations in gene expression related to carbohydrate metabolism and sugar transport. Reports stated increased expression of genes involved in starch and sucrose metabolism has appeared in drought-tolerant genotypes. Members of the SWEET family of sugar transporters also showed enhanced expression under drought-stress conditions, suggesting their primary role in regulating sugar allocation and osmotic balance in plant tissues (MacMillan *et al.*, 2021).

Overall, in guar, the drought tolerance results from coordinated regulation of stomatal activity, antioxidant defense systems, photosynthetic processes, and carbohydrate metabolism. These mechanisms enable the plants to maintain metabolic stability and growth under water-limited conditions, providing valuable targets for breeding drought-resilient guar cultivars.

Breeding drought-tolerant guar with genomic resources and molecular tools

In guar (*C. tetragonoloba*), the genomic information is still less compared with other legume crops. The comprehensive genomic studies began only in the last decade to develop the genotypes with the advancement of modern sequencing technologies. Early studies revealed that the guar genome has an estimated size of approximately 581 Mb using the flow cytometry analysis. Past research has also described the chloroplast genome, which is about 152 kb in length. Comparative analysis with other legume species helped clarify the evolutionary relationship and molecular organization of guar (Pareek *et al.*, 2022).

Recent studies have attempted to assemble the nuclear genome using next-generation sequencing technologies. One of the first draft genome assemblies succeeded in its generation from the cultivar Vavilovsky 130 by combining Illumina short-read sequencing and Oxford Nanopore long-read technologies. Although this study provided an important genomic framework, the assembly covered only about half of the estimated genome size,

indicating that further work is essential to develop a high-quality reference genome. Based on the genomic data, the phylogenetic analysis showed guar to be in close association with other legume genera, such as *Vigna*, *Glycine*, *Abrus*, and *Lupinus* (Thakur and Randhawa, 2018). Despite incomplete genomic resources, several molecular markers have reached development and successful application in guar research. Commonly used markers include random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), simple sequence repeats (SSR), single nucleotide polymorphism (SNP), and sequence-characterized amplified region (SCAR). These markers have gained wide usage for evaluating genetic diversity, identifying genotype-specific traits, and supporting breeding programs (Thakur and Randhawa, 2018).

Different marker systems have also been effective to investigate agronomic traits in guar. For example, AFLP markers have signified associations with important yield-related traits, such as plant growth patterns, pods per plant, and seed productivity. The SSR markers have been a widely applied method to evaluate genetic diversity within guar germplasm and to identify genetically diverse parental material for breeding programs. In addition, SNP markers have been desirable as useful tools for identifying genomic regions associated with yield components, particularly the number of pods per plant (Pareek *et al.*, 2022).

However, compared with other legumes whose genomes have had full sequences, in guar the genomic resources remain limited. The lack of molecular markers restricts the application of advanced breeding strategies, such as marker-assisted selection and genomic selection. Therefore, expanding genomic resources and developing additional molecular markers remain important priorities for guar improvement in the future (Ravelombola *et al.*, 2021).

Despite these limitations, significant variations among guar genotypes in their responses to environmental stress conditions

revealed considerable genetic potential for crop improvement. Drought-tolerant cultivars represent valuable genetic resources that can benefit breeding programs aimed at improving stress tolerance. In this context, genomic and transcriptomic approaches have become increasingly critical for identifying candidate genes and markers associated with drought resistance in crop plants (Erjigitov *et al.*, 2025; Bakhadirov *et al.*, 2024).

Recent transcriptome-based studies have further expanded genomic resources for guar. Large-scale sequencing of messenger RNA from different cultivars has identified thousands of potential molecular markers. Transcriptome analysis of the cultivars RGC-1066 and M-83 expressed more than 5000 microsatellite markers and numerous SNP markers associated with genes involved in stress responses. These findings exhibited the potential of transcriptomic data for discovering molecular markers related to drought tolerance and other adaptive traits (Pareek *et al.*, 2022).

Meta-analyses of microsatellite markers have also identified several candidate genes associated with stress adaptation and productivity in guar. These markers provide beneficial tools for genetic mapping and marker-assisted selection. However, the advanced genomic studies, such as quantitative trait loci (QTL) mapping and genome-wide association studies (GWAS), have not yet gained wide utilization in guar. As a result, the genetic architecture of valuable traits, such as drought tolerance, remains insufficiently explored (Tanwar *et al.*, 2017).

Overall, in guar, the genomic research is still at an early stage compared with various other crops. Nevertheless, recent progress in sequencing technologies, molecular marker development, and transcriptome analysis offers promising opportunities for accelerating guar breeding programs. Expanding genomic datasets and integrating modern genomic approaches will be essential for developing improved guar cultivars with enhanced drought tolerance and better adaptation to changing climatic conditions.

CONCLUSIONS

Studies revealed that guar (*C. tetragonoloba* L.) possesses several physiological and biochemical mechanisms contributing to drought tolerance, including stomatal regulation, antioxidant defense, osmotic adjustment, and maintenance of photosynthetic activity under water deficit conditions. Among the guar cultivars, significant genotypic variability provides valuable opportunities for selecting drought-tolerant genotypes for breeding programs. Recent advances in genomics and transcriptomics have also improved understanding of the molecular mechanisms underlying drought adaptation. Molecular markers, such as SSR, SNP, RAPD, and AFLP, offer useful tools for enhancing breeding efficiency. However, further research is necessary to expand genomic resources and identify the key genes associated with drought tolerance to support the development of improved guar cultivars for water-limited environments.

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