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CLIMATE-SMART PRODUCTION OF CHICKPEA: INTEGRATING DROUGHT-RESPONSIVE GENOMICS, RHIZOBIAL INOCULATION, SOIL FERTILITY, AND PRECISION WATER MANAGEMENT

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Abstract

Chickpea (Cicer arietinum L.) is a vital cool-season pulse crop sustaining nutritional security and ecological stability across semi-arid regions, yet terminal drought stress during reproductive and grain-filling phases causes annual yield reductions of 50–70%. This review synthesizes the physiological, molecular, and agronomic mechanisms underpinning climate-smart chickpea production through the integration of four core domains: drought-responsive genomics, rhizobial inoculation, integrated soil fertility management (ISFM), and precision water management. Genomic advances have identified the 'QTL-hotspot' on Linkage Group 04 (CaLG04), refined from 29 cM to 14 cM, harboring 49 diagnostic SNP markers and explaining up to 58.2% phenotypic variance for drought-adaptive traits. The validated candidate gene CaTIFY4b (superior haplotype CaTIFY4b-H2) confers enhanced seed weight and transpiration efficiency, while marker-assisted backcrossing has delivered commercial cultivars such as Pusa Chickpea 10216, exhibiting a 16% yield advantage under rainfed conditions. Symbiotic nitrogen fixation via Mesorhizobium spp. contributes 60–103 kg N ha $^{-1}$, but is highly sensitive to moisture deficit. Co-inoculation with phosphate-solubilizing bacteria and ACC-deaminase-producing PGPR enhances nodulation by over 270% and grain yield by 242% under nutrient-deficient dryland conditions. Biochar amendments (5–20 t ha $^{-1}$) increase available water capacity by 12–30% and reduce nitrate leaching by 26–32%, while strategic deficit irrigation and subsurface drip irrigation improve water use efficiency by 28–68%. Policy interventions, quality-controlled inoculant supply chains, and site-specific nutrient diagnostics are essential for scaling adoption among smallholder farmers.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a paramount cool-season pulse crop that provides crucial nutritional security and ecological sustainability across global agricultural systems. As a nutrient-dense grain legume, chickpea seeds contain approximately 20% to 30% crude protein, 40% complex carbohydrates, essential amino acids, and vital micronutrients while remaining largely free from anti-nutritional factors (Chaturvedi et al., 2026). Cultivated on over 17.8 million hectares globally predominantly across the semi-arid environments of South Asia and Sub-Saharan Africa chickpea serves as a dietary staple for millions and plays a pivotal role in low-input farming systems. However, global climate change has severely escalated the frequency, duration, and intensity of abiotic stresses, posing a profound threat to pulse productivity and agricultural stability (Khatun et al., 2021).

Among these abiotic challenges, water deficit represents the single most devastating constraint to chickpea production. Because the vast majority of global chickpea cultivation relies on stored post-rainy season residual soil moisture, the crop is routinely subjected to severe terminal drought stress during its reproductive and grain-filling phases (Sengupta et al., 2026). Terminal drought induces premature senescence, restricts pod set, impairs photosynthate translocation, and inhibits symbiotic nitrogen fixation, culminating in annual grain yield reductions ranging between 50% and 70%. The global challenge of feeding an estimated population of 9.7 billion by 2050 necessitates an immediate transformation in pulse production paradigms, moving away from single-factor interventions toward integrated climate-smart frameworks (Jayaramaiah et al., 2026).

A climate-smart chickpea production system demands the cross-disciplinary integration of four core domains: advanced drought-responsive genomics, tailored rhizobial inoculation, integrated soil fertility management (ISFM), and precision water management. Historical approaches that treated plant breeding, microbiology, soil science, and irrigation in isolation frequently failed under extreme weather events due to unmitigated physiological bottlenecks (Gelaw et al., 2026). For instance, high-yielding genetic cultivars often underperform in nutrient-depleted soils if biological nitrogen fixation is suppressed by moisture stress. Conversely, precision irrigation alone cannot unlock full yield potential without crop varieties genetically equipped for high transpiration efficiency and optimal canopy architecture (Kumar et al., 2019). This review provides a comprehensive synthesis of the physiological, molecular, and agronomic mechanisms underpinning climate-smart chickpea production, illustrating how genomics, bioinoculants, balanced soil nutrition, and targeted irrigation interact synergistically to build climate resilience and stabilize global pulse yields (Yashavanthakumar et al., 2025).

2. Drought-Responsive Genomics and Molecular Breeding in Chickpea

2.1 The Genomic Architecture of Drought Tolerance and the 'QTL-Hotspot'

Chickpea possesses a diploid genome ($2n = 2x = 16$) with an estimated size of approximately 738 Mb. Dissecting the complex quantitative inheritance of drought tolerance has been significantly accelerated by whole-genome sequencing, dense genetic maps, and marker-assisted selection (MAS) strategies. Extensive genetic mapping across multi-parent and recombinant inbred line (RIL) populations such as ICCRIL03 (ICC 4958 × ICC 1882) and ICCRIL04 (ICC 283 × ICC 8261) revealed that drought tolerance in chickpea is governed by key genomic regions harboring clusters of main-effect quantitative trait loci (M-QTLs) (Asati et al., 2022). The most critical genetic discovery in chickpea drought adaptation is the identification of a genomic region designated as the 'QTL-hotspot', located on Linkage Group 04 (CaLG04, pseudomolecule Ca4). Initially identified as a genetic segment spanning approximately 29 cM (physically corresponding to 7.74 Mb), this single region contains up to 48% of all robust M-QTLs for 12 key drought-adaptive traits (Singh et al., 2023). The 'QTL-hotspot' controls phenotypic variation (PVE) up to 58.2%, modulating fundamental morphological and physiological

features including root biomass, root length density, canopy temperature, early plant vigour, time to flowering, 100-seed weight, and transpiration efficiency under water-limited conditions. Early genetic characterization anchored this region using seven foundational Simple Sequence Repeat (SSR) markers: ICCM0249, NCPGR127, TAA170, NCPGR21, TR11, GA24, and STMS11 (Altaf et al., 2025).

Table 1: Key Genomic Features, Quantitative Trait Parameters, and Physiological Mechanisms of the Chickpea 'QTL-Hotspot'

Genomic Feature / Trait Parameter	Description & Quantitative Value
Genomic Location	Linkage Group 04 (CaLG04 / Pseudomolecule Ca4)
Original vs. Refined Map Distance	Refined from ~29 cM (~7.74 Mb) down to 14 cM
Phenotypic Variance Explained (*PVE*)	Up to 58.20% for multiple drought component traits
Key Anchor SSR Markers	ICCM0249, NCPGR127, TAA170, NCPGR21, TR11, GA24, STMS11
Subregion Partitioning	QTL-hotspot_a (15 genes) and QTL-hotspot_b (11 genes)
Validated Candidate Gene	*CaTIFY4b* (Superior Haplotype: *CaTIFY4b-H2*)
Primary Physiological Mechanisms	Increased seed weight, accelerated flowering, enhanced early vigour, elevated transpiration efficiency (***TE***), deep rooting

2.2 Fine-Mapping, Candidate Genes, and Haplotype Stacking

To enhance the selection efficiency of the 'QTL-hotspot' and eliminate undesirable genetic linkage drag, advanced fine-mapping approaches utilizing Genotyping-by-Sequencing (GBS) and high-density single nucleotide polymorphism (SNP) bin maps were applied. High-density genotyping refined the 29 cM region to a 14 cM interval containing 49 diagnostic SNP markers (Li et al., 2018). Subsequent genomic dissection leveraging recombination bins and gene enrichment analysis partitioned the 'QTL-hotspot' into two distinct subregions: QTL-hotspot_a (encompassing 15 candidate genes) and QTL-hotspot_b (encompassing 11 candidate genes), with 12 core functional genes consistently validated across analytical approaches (Xue et al., 2022).

The physiological cascade driven by these loci begins with deep root expansion and early vegetative vigour, which together allow plants to access subsoil water reserves during early moisture deficits. Sustained root water extraction maintains cellular turgor and canopy hydration, reducing canopy temperature and boosting transpiration efficiency (Wu et al., 2018). This physiological cushioning protects reproductive tissues from heat and desiccation, mitigating flower abortion and terminal yield collapse under drought. Functional validation through quantitative real-time PCR (qRT-PCR) and whole-genome re-sequencing identified key candidate genes regulating cellular stress responses and organ development within this locus (Yao et al., 2026). Notably, the gene *CaTIFY4b* was confirmed as a major driver of seed development under drought stress, where its specific allelic variation (*CaTIFY4b-H2* haplotype) confers superior 100-seed weight under terminal water deficit, providing a precise diagnostic marker (KASP assay) for targeted molecular breeding (Mohanavel et al., 2025).

Beyond bi-parental mapping, multi-parent populations specifically Multi-parent Advanced Generation Intercross (MAGIC) lines comprising over 1,135 RILs derived from eight diverse founders have expanded the genomic resolution of complex drought traits (Bhattarai et al., 2021). Due to rapid linkage disequilibrium (***LD***) decay (decaying within ~1 Mb), MAGIC populations enable precise haplotype mapping. This allows breeders to execute "haplotype stacking" simultaneously pyramiding optimal haploblocks on chromosome 4 for increased plant height

alongside early-flowering haploblocks to avoid late-season drought (Tong et al., 2024).

2.3 Marker-Assisted Backcrossing and Breeding Success Stories

The practical translation of genomic discoveries into commercial cultivars has been demonstrated through Marker-Assisted Backcrossing (MABC). By introgressing the 'QTL-hotspot' from the drought-tolerant donor accession ICC 4958 into high-yielding but drought-sensitive elite cultivars, breeders have successfully generated introgression lines (ILs) that maintain high yield under water stress (Babu et al., 2004).

In India, MABC programs targeted widely grown elite cultivars including Pusa 372, Pusa 362, and DCP 92-3. Using polymorphic foreground SSR markers alongside extensive background selection (recovering >90% of the recurrent parent genome), multiple superior introgression lines were developed. The most notable release, BGM 10216 (derived from the Pusa 372 background), demonstrated a 16% grain yield advantage over its recurrent parent under rainfed field evaluations (Ribaut & Hoisington, 1998). Consequently, it was officially released for commercial cultivation as 'Pusa Chickpea 10216'. Additional prominent introgression lines include BG 3097 and BG 4005 (in the Pusa 362 background) as well as IPC(L4-14), IPC(L4-16), and IPC(L19-1) (in the DCP 92-3 background), all exhibiting enhanced canopy vigour, larger seed size, and superior yield stability across drought-prone rainfed environments (Muranty et al., 2014).

3. Rhizobial Inoculation and Biological Nitrogen Fixation Under Water Deficit

3.1 Mesorhizobium Specificity and Symbiotic Efficiency

As a legume, chickpea satisfies a significant portion of its nitrogen requirements through Biological Nitrogen Fixation (BNF) established via symbiotic association with specialized soil bacteria. Unlike promiscuous legumes, chickpea exhibits tight symbiotic specificity, forming effective nitrogen-fixing root nodules almost exclusively with rhizobial species belonging to the genus *Mesorhizobium* primarily *Mesorhizobium ciceri*, *Mesorhizobium mediterraneum*, and regional species such as *Mesorhizobium muleiense* (Camacho et al.,2025).

The biochemical pathway of this symbiosis starts when atmospheric nitrogen gas (N_2) enters root nodules inhabited by differentiated *Mesorhizobium* bacteroids. Within these bacteroids, the oxygen-sensitive enzyme nitrogenase reduces inert N_2 into bioavailable ammonium (NH_4^+), utilizing host-derived photosynthates to drive ATP generation. The exported ammonium is assimilated into amino acids and organic nitrogen compounds, directly nourishing host tissues to support protein synthesis, canopy growth, and grain filling during water deficit (Romdhane et al., 2009). Under optimal conditions, an effective *Mesorhizobium*-chickpea symbiosis fixes between 60 and 103 kg N ha^{-1} (and up to 140 kg N ha^{-1} under ideal field management), acquiring 60% to 85% of the plant's total nitrogen demand directly from the atmosphere. This biological N input spares synthetic nitrogen fertilizer, reduces cultivation costs, enriches soil organic N pools, and minimizes greenhouse gas emissions associated with industrial fertilizer production (Naveed et al., 2017).

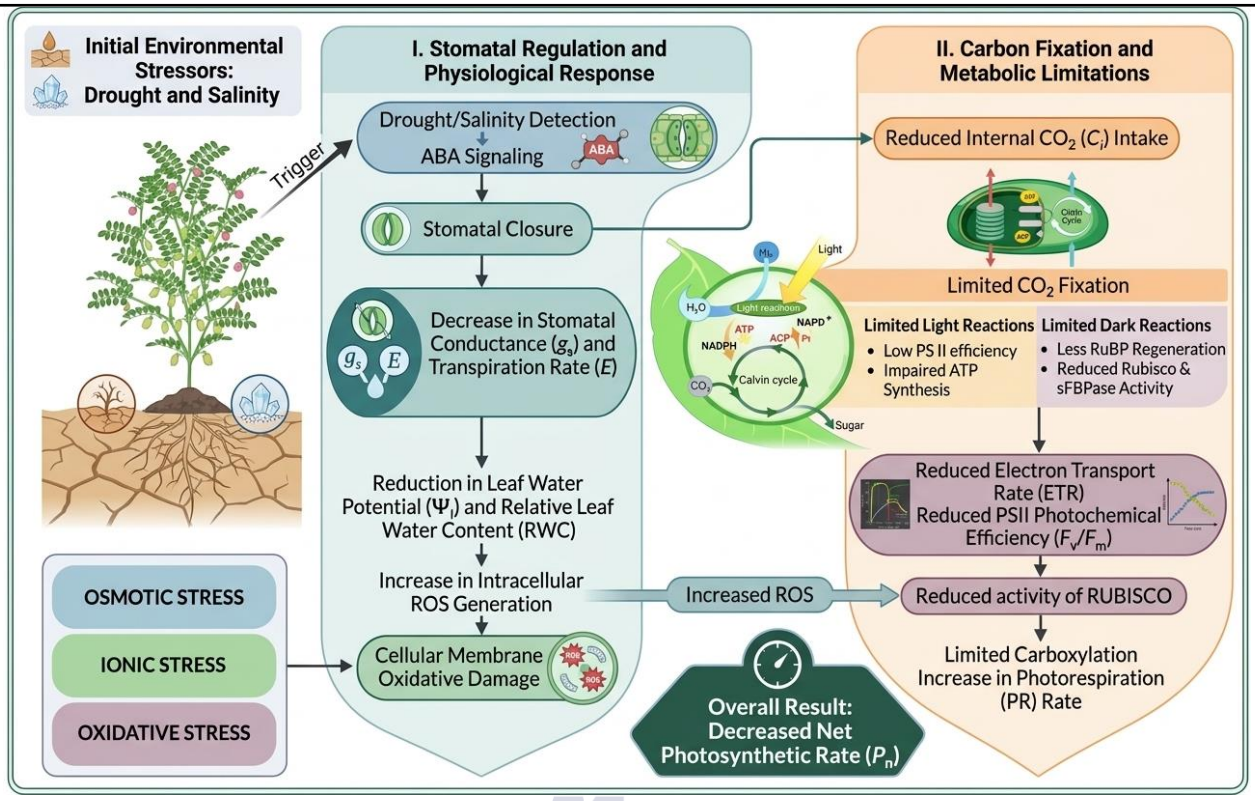


Figure 1: Physiological and Metabolic Cascades Impaired by Drought and Salinity Stress in Chickpea.

3.2 Drought-Induced Physiological Constraints on Nodulation

Biological nitrogen fixation is highly sensitive to abiotic stresses, with water deficit causing rapid inhibition of nodule function. Moisture stress impacts symbiosis through a series of physiological disruptions across spatial and temporal scales (Serraj, 2003).

At the initial phase of infection and nodule initiation, soil drying impairs rhizobial survival in the rhizosphere, prevents root hair curling, and halts infection thread elongation. As water stress progresses to structural stages, moisture deficit induces structural collapse of the inner nodule cortex, markedly increasing resistance to oxygen diffusion (Arrese-Igor et al., 2011). This deprives bacterial bacteroids of the oxygen necessary for oxidative phosphorylation while simultaneously risking irreversible oxidative damage to the oxygen-sensitive nitrogenase enzyme complex. Concurrently, host carbon allocation shifts as the plant restricts sucrose transport to root nodules in order to conserve carbon for shoot tissue survival. Detailed studies evaluating bacteroid physiology under drought reveal acute trade-offs between host shoot growth rates and the allocation of carbon toward rhizobial storage compounds, such as polyhydroxybutyrate (PHB) (Chammakhi et al., 2022).

Despite these severe environmental constraints, substantial genotypic variability exists within chickpea germplasm. Drought-tolerant genotypes including IG70399, IG8256, IG71832, IG70270, and IG70272 maintain significantly higher nodule biomass, nodule fresh weight, and nodule dry weight under severe moisture stress. Quantitative evaluations demonstrate that nodule parameters under drought exhibit a significant positive correlation ($r = 0.36 - 0.38$) with final grain yield, confirming that genetic selection for robust nodulation traits directly enhances overall crop resilience (Lumactud et al., 2023).

3.3 Microbial Synergies: Co-Inoculation with Plant Growth-Promoting Rhizobacteria

To mitigate the negative impacts of drought on biological nitrogen fixation, modern bio-formulations utilize microbial consortia that combine elite *Mesorhizobium* strains with Plant Growth-Promoting Rhizobacteria (PGPR), particularly Phosphate-Solubilizing Bacteria (PSB) such as *Bacillus* spp., *Enterobacter aerogenes*, *Pseudomonas* spp., and *Serratia* spp. (Santoyo et al.,2021).

Table 2: Comparative Performance and Symbiotic Impact of Bioinoculant Regimens Under Water Deficit and Nutrient Stress

Bioinoculant Regimen	Primary Mode of Action	Impact on Nodulation & Growth	Impact on Seed Yield
Single Inoculation (*Mesorhizobium ciceri* / *M. muleiense*)	Symbiotic N_2 fixation; infection via Nod factor signaling	Increases root length, shoot biomass, and chlorophyll content	Increases yield by 6.3% to 15% depending on water regime
Co-Inoculation (*Mesorhizobium* + *Bacillus* / *Pseudomonas*)	Dual N_2 fixation and phytohormone/ACC deaminase modulation	Enhances nodule number, root surface area, and drought tolerance	Substantial yield improvement over single rhizobial strains
Consortium Inoculation (*Mesorhizobium* sp. MA72 + *Enterobacter aerogenes* P1S6)	N_2 fixation combined with high-capacity P-solubilization	>270% increase in nodulation; 192% increase in shoot dry weight	242% increase in grain yield under P-deficient dryland conditions

The biochemical synergy between *Mesorhizobium* and PSB addresses a major physiological bottleneck: biological nitrogen fixation is an energetically expensive process requiring at least 16 molecules of ATP for every molecule of N_2 reduced into NH_3. Because phosphorus availability is severely restricted in dry or alkaline soils, PSB solubilize inorganic phosphates via organic acid secretion, supplying the essential P needed to drive nodule ATP synthesis (Anli et al., 2020). Furthermore, many PGPR produce 1-aminocyclopropane-1-carboxylate (ACC) deaminase, an enzyme that cleaves ACC (the immediate precursor of ethylene in plants). By lowering stress-induced ethylene concentrations in root tissues, ACC-deaminase producing PGPR prevent premature nodule senescence and root growth inhibition under water stress (Pereira et al., 2020).

4. Integrated Nutrient Management and Soil Health Restoration

4.1 Macro- and Micronutrient Dynamics in Symbiotic Systems

Integrated Nutrient Management (INM) and Integrated Soil Fertility Management (ISFM) advocate for the balanced, judicious application of mineral fertilizers, organic amendments, and biological inputs tailored to site-specific crop demands. In chickpea production, nutrient management must cater specifically to the physiological demands of symbiotic nitrogen fixation (Liang et al., 2025).

While chickpea requires minimal nitrogen fertilizer due to BNF, a small "starter dose" of mineral nitrogen (typically 20 kg N ha^{-1}) is critical during seedling establishment before functional nodules develop. Excess mineral N application must be avoided, as high residual soil nitrate depresses nodule initiation and induces early nodule degradation. Phosphorus (P_2O_5 at $40-60$ kg ha^{-1}) and sulfur (S at 20 kg ha^{-1}) are essential for root elongation, energy transfer, and methionine synthesis (Fontaine et al., 2024).

Micronutrient management is equally crucial. Molybdenum (Mo) and Iron (Fe) function as structural cofactors for the nitrogenase enzyme complex (the Fe-protein and MoFe-protein components). Zinc ($ZnSO_4$ at 25 kg ha^{-1}) plays

an important role in preserving cell membrane integrity and scavenging reactive oxygen species (ROS) under drought stress (khan et al., 2024). Applying balanced starter nutrients activates root development, expanding the root surface area to promote early rhizobial infection and nodulation. Elevated nodulation boosts nitrogenase enzyme production, supported by Mo and Fe cofactors. This enzymatic activitymaintains nitrogen fixation, while zinc-mediated ROS scavenging protects photosynthetic machinery from oxidative stress under drought, ultimately increasing Nutrient Use Efficiency (NUE) (Srivastava et al., 2025).

4.2 Soil Conditioners and Biochar Applications

Incorporating carbonaceous soil amendments particularly biochar into INM frameworks offers significant advantages for drought resilience and long-term soil health. Biochar is a highly stable, carbon-rich material produced via the pyrolysis of biomass under oxygen-limited conditions. High-quality biochars characterized by hydrogen-to-carbon (H/C) ratios < 0.7 and oxygen-to-carbon (O/C) ratios < 0.4 exhibit exceptional chemical recalcitrance, persisting in soils for decades to centuries (Pandian et al., 2024).

Biochar functions primarily as a physical and chemical soil conditioner rather than a direct fertilizer. Its highly porous micro-structure and high surface area significantly increase soil water retention, cation exchange capacity (CEC), and nutrient adsorption. Meta-analyses show that biochar amendments increase available water (AW) capacity by approximately 30% in coarse-textured soils, 21% in medium soils, and 12% in fine soils (Kavitha et al., 2018). Furthermore, biochar captures ammonium (NH_4^+) and nitrate (NO_3^-) within its pore networks, reducing nitrate leaching by 26% to 32% and mitigating soil nitrous oxide (N_2O) emissions by 19% to 54%. Field application rates between 5 and 20 t ha^{-1} consistently improve soil structure, stimulate beneficial microbial colonization, and enhance nutrient use efficiency. However, excessive application rates (> 50 t ha^{-1}) must be avoided, as they can induce transient nitrogen immobilization or elevate soil salinity, which negatively affects crop growth (Gabhane et al., 2020).

4.3 Integrated Soil Fertility Management (ISFM) Frameworks

Combining chemical fertilizers, biochar, organic manures (such as Farmyard Manure or vermicompost), and bioinoculants forms a robust ISFM framework. Research demonstrates that substituting 50% of the recommended dose of synthetic nitrogen (RDN) with organic manures and bioinoculants maintains or exceeds the grain yields achieved under 100% synthetic chemical fertilization. This substitution enhances soil microbial biomass, stimulates soil enzymatic activity (e.g., dehydrogenase and phosphatase), and reduces overall production costs while improving soil organic carbon (SOC) sequestration (Vanlauwe et al., 2015).

Table 3: Agronomic Functions, Environmental Impacts, and Quantitative Yield Responses of ISFM Components

INM / Soil Amendment Component	Agronomic & Soil Physical Function	Quantified Environmental / Yield Benefit
Starter Mineral Fertilizer (20 kg N + 40 kg P_2O_5 ha^{-1})	Meets early seedling demand before nodulation without suppressing BNF	Establishes early canopy vigour; prevents seedling nitrogen starvation
Organic Manure Substitution (50% RDN via FYM/Compost)	Supplies secondary/micronutrients; improves soil organic carbon and bulk density	Achieves yields comparable to 100% NPK; improves nitrogen use efficiency

Biochar Amendment ($5 - 20$ t ha^{-1})	Increases macroporosity, plant-available water (AW), and CEC	Increases AW capacity by 12–30%; reduces NO_3^- leaching by 26–32%
Micronutrient Supplementation ($ZnSO_4 + Mo$)	Provides cofactors for nitrogenase; enhances antioxidant enzyme systems	Mitigates ROS damage during drought; maximizes nitrogen fixation efficiency

5. Precision Water Management and Crop Hydraulics

5.1 Irrigation Scheduling and Deficit Water Strategies

Chickpea is highly sensitive to the timing and severity of moisture deficit. While the crop exhibits moderate inherent drought tolerance during early vegetative growth, moisture stress coinciding with flowering and pod development causes severe economic losses. Field trials evaluating water deficit across distinct growth stages reveal that water stress initiated at flower initiation causes a 19.3% yield loss relative to well-irrigated controls, whereas stress occurring during pod fill accounts for an 8.06% reduction (Bwambale et al., 2022).

To maximize water productivity in dryland environments, strategic deficit irrigation must target these critical phenological stages. Providing a single supplemental irrigation (approximately $40 - 50$ mm) at the late vegetative/early flowering stage or pod initiation prevents flower abortion, sustains leaf area index (LAI), and extends the duration of active photosynthate movement to developing seeds (Yaqoob et al., 2026).

5.2 Advanced Micro-Irrigation Technologies

Traditional surface irrigation methods such as border strip or check-basin flooding suffer from high conveyance losses, deep percolation, and uneven distribution, often exacerbating soil compaction and waterlogging, which suppress root respiration and nodulation. Precision micro-irrigation technologies, including surface drip irrigation and subsurface drip irrigation (SDI), offer significantly improved water delivery (Patel et al., 2023)

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Table 4: Technical Comparison of Irrigation Regimens and Micro-Irrigation Technologies in Chickpea Production

Irrigation Strategy / Method	Water Delivery Efficiency	Impact on Water Use Efficiency (WUE)	Agronomic Impact on Chickpea Yield
Conventional Surface Flood	Low ($40 - 50\%$ efficiency); high evaporation & runoff losses	Baseline standard (Low)	Yield variability; susceptible to waterlogging and terminal drought
Strategic Deficit Irrigation	Targeted single/double supplemental application at critical stages	Moderate increase in overall system WUE	Mitigates up to 19.3% yield collapse caused by moisture stress at flowering
Surface Drip Irrigation	High ($85 - 90\%$ efficiency); precise root zone targeting	$28 - 58\%$ boost over broad bed; $45 - 68\%$ boost over surface flood	Significant increase in yield and seed mass; sustained nodule moisture
Subsurface Drip Irrigation (SDI)	Very High ($> 95\%$ efficiency); eliminates soil surface evaporation	Maximum WUE among micro-irrigation systems	14% yield increase over LEPA systems; optimal rhizosphere buffering

Drip irrigation systems deliver water and soluble nutrients directly to the plant root zone at precise volumes and controlled frequencies. Comparative agronomic studies show that drip irrigation increases Water Use Efficiency (WUE) by 28% to 58% compared to broad bed furrow systems, and by 45% to 68% over

conventional flood irrigation. Furthermore, SDI systems which place drip emitters 15–20 cm below the soil surface directly within the active rhizosphere reduce soil surface evaporation, yielding a 14% increase in crop output over Low Energy Precision Application (LEPA) center-pivot configurations.

6. Holistic Systems Integration, Adoption Barriers, and Future Directions

6.1 Multi-Omics and Precision Agriculture Synthesis

Achieving climate-smart chickpea production requires combining genomic, microbial, soil management, and irrigation innovations into an integrated, multi-disciplinary system. The individual pillars described in this review do not operate in isolation; rather, they interact synergistically across biological and physical domains (Praharaj et al., 2016).

At the intersection of genomics and soil management, molecular backcrossing of the 'QTL-hotspot' equips cultivars like Pusa Chickpea 10216 with deeper root systems and higher intrinsic transpiration efficiency (*TE*). When grown in biochar-amended soils, these deep roots explore subsoil layers where biochar has enhanced plant-available water retention, creating a resilient water cushion during dry spells (Kumar et al., 2021).

Similarly, combining microbiology and soil fertility solves metabolic limitations, as solubilization of bound soil phosphorus by PGPR co-inoculants (*Mesorhizobium* + *Enterobacter aerogenes*) supplies the ATP needed to power nitrogenase activity. This keeps biological nitrogen fixation functional even under mild moisture deficits (Narayan, 2019).

Finally, aligning precision water management with rhizosphere biology ensures that drip irrigation maintains consistent moisture within the upper 0–30 cm root zone. This prevents nodule desiccation and preserves the metabolic activity of introduced rhizobial and bacterial bioinoculants, maximizing nutrient uptake and yield stability (Rao et al., 2021).

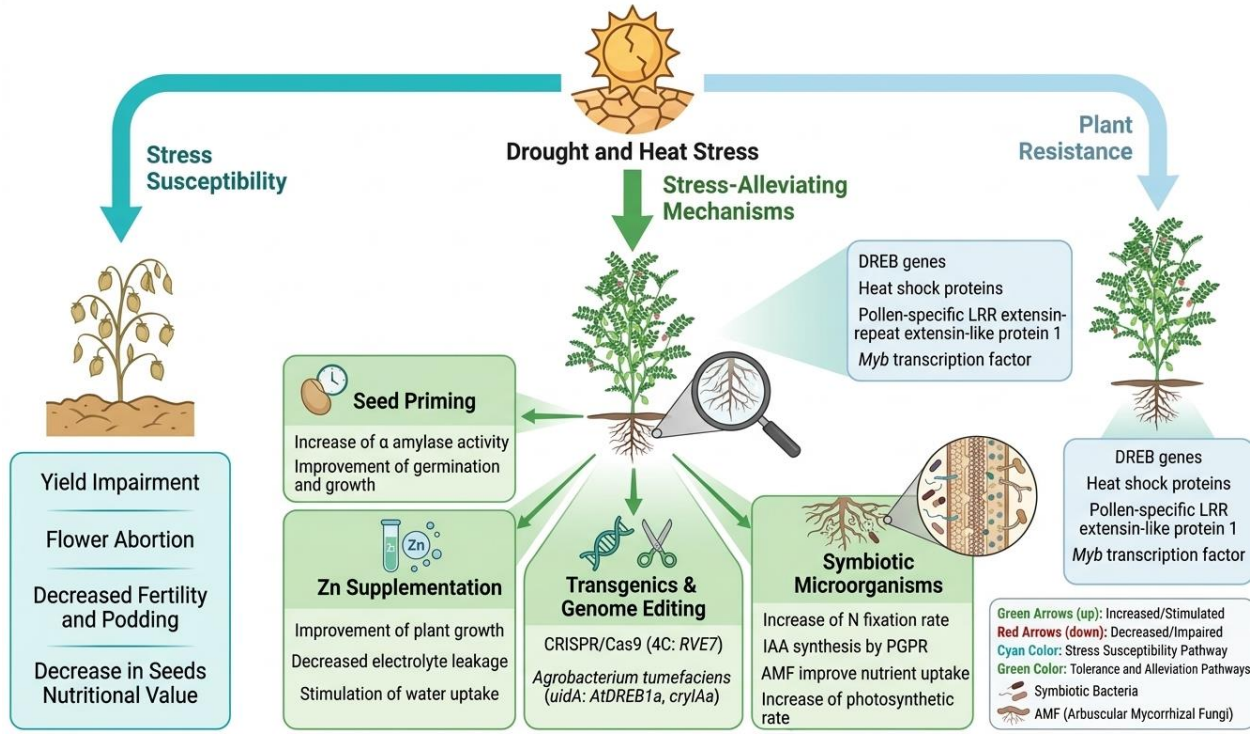


Figure 2: Integrated Agronomic and Biotechnological Strategies to Enhance Stress Resistance and Mitigate Yield Losses Under Drought and Heat Stress.

6.2 Policy, Adoption Barriers, and Multi-Location Implementation

Despite the clear agronomic benefits of an integrated climate-smart system, several practical barriers hinder widespread adoption among smallholder farmers in dryland regions. Addressing these challenges requires targeted technical and policy solutions (Lilischkis, 2003).

A major biological constraint is inoculant quality and supply chain instability, as rhizobial inoculants frequently suffer from short shelf-lives, loss of viability under high ambient temperatures, and poor competitive ability against native, less-efficient soil microbes. Overcoming this requires quality-controlled bio-fertilizer production networks alongside temperature-stable liquid or polymer-encapsulated carrier formulations (Karltorp & Vico, 2025).

Economic challenges also restrict tech adoption, particularly the capital intensity of micro-irrigation infrastructure, which presents a high financial barrier for resource-poor smallholders. Policy interventions such as targeted government subsidies, community-managed micro-irrigation schemes, and custom-hiring service centers are critical to facilitate scale-up (Oyeogbe, 2026).

At the distribution level, seed delivery systems for MABC varieties often experience bottlenecks, slowing the commercial dissemination of elite introgressed cultivars like Pusa Chickpea 10216. Stronger public-private seed partnerships are needed to ensure certified seed reaches farming communities rapidly (Farah et al., 2025).

Finally, agronomic management is often limited by a lack of site-specific nutrient diagnostics, as universal fertilizer recommendations ignore localized soil variability. Deploying scalable site-specific nutrient management (SSNM) tools, digital soil testing kits, and grid-based soil health cards can guide tailored INM recommendations at the field scale (Ekren et al., 2021).

Conclusion

Climate-smart chickpea production cannot be achieved through single-factor interventions; rather, it demands the synergistic integration of genomic, microbial, soil fertility, and water management innovations. This review demonstrates that the 'QTL-hotspot' on CaLG04, particularly the *CaTIFY4b-H2* haplotype, provides a robust genetic foundation for developing drought-adapted cultivars with deep rooting, early vigour, and high transpiration efficiency. Marker-assisted backcrossing has successfully translated these discoveries into elite introgression lines and commercial cultivars such as Pusa Chickpea 10216, delivering measurable yield advantages under rainfed conditions. However, genetic potential alone is insufficient without functional biological nitrogen fixation, which remains highly vulnerable to moisture deficit. Elite *Mesorhizobium* strains, particularly when co-inoculated with phosphate-solubilizing bacteria and ACC-deaminase-producing PGPR, substantially enhance nodulation, nutrient uptake, and yield stability under drought. Integrated soil fertility management combining starter mineral fertilizers, organic manure substitution, biochar amendments, and micronutrient supplementation addresses the metabolic constraints of symbiotic nitrogen fixation while improving soil water retention and carbon sequestration. Precision micro-irrigation technologies, especially subsurface drip irrigation, maximize water use efficiency and maintain rhizosphere moisture, preserving the metabolic activity of introduced bioinoculants. The principal barriers to adoption include inoculant quality instability, capital intensity of micro-irrigation infrastructure, seed delivery bottlenecks, and the absence of site-specific nutrient diagnostics. Overcoming these requires quality-controlled bio-fertilizer production networks, targeted subsidies, community-managed irrigation schemes, public-private seed partnerships, and scalable digital soil testing tools. Future research should prioritize multi-omics integration, haplotype stacking through MAGIC populations, temperature-stable inoculant formulations, and long-term multi-location field validation to ensure that climate-smart chickpea systems deliver resilient, equitable, and sustainable pulse production for smallholder farmers in dryland regions worldwide.

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