Journal of Cereal Research
Volume 17 (3): 221-263
Homepage: http://epubs.icar.org.in/ejournal/index.php/JWR

Review Article

Climate-Smart Strategies for Mitigating Abiotic Stresses in Cereal Crops: A Review

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Article history:
Received: 16 May, 2025
Revised: 18 Aug., 2025
Accepted: 26 Aug., 2025

Citation:
Yashavanthakumar K J, P Pawar, Basavaraj PS, M Oak, CN Mishra, Mamrutha HM, S Biradar, SA Desai, Sudhir Navathe. 2025. Climate-Smart Strategies for Mitigating Abiotic Stresses in Cereal Crops: A Review. *Journal of Cereal Research* ***17 (3):*** *221-263. http://doi.org/10.25174/2582-2675/2025/166751*

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Abstract

Climate variability has intensified the frequency and severity of abiotic stresses, including drought, heat, salinity, waterlogging, nutrient deficiency or toxicity, chilling, ultraviolet radiation, and increased atmospheric CO_2 levels. These stresses hamper plant growth by modifying physiological balance, biochemical processes, and gene expression networks, leading to significant reductions in yield and quality in major crops. Addressing these challenges requires a comprehensive understanding of plant adaptation, tolerance mechanisms, and strategies for mitigating stress. This review synthesises recent advancements in understanding the morpho-physiological, biochemical, and molecular responses of plants to various abiotic stresses and examines how this knowledge can inform climate-smart agricultural practices. Conventional breeding, supported by high-throughput phenotyping and precision selection, is essential for crop improvement. Meanwhile, modern genomics and biotechnology–including marker-assisted selection, genomic selection, transcription factor engineering, and genome editing–facilitate targeted enhancement of stress resilience. Complementary innovations such as speed breeding, nanotechnology, microbiome engineering, and nutrient-efficient agronomy provide additional methods to enhance plant performance in challenging environments. The incorporation of artificial intelligence and machine learning into phenomics and genomic datasets has facilitated the modelling of complex genotype–environment interactions, expedited the identification of resilient genotypes, and enhanced the prediction of crop behaviour in future climates. The integration of genetic, agronomic, and digital methodologies in climate-smart agriculture offers a sustainable framework for mitigating the adverse effects of various abiotic stresses. The combined application of molecular breeding, resource-efficient management, and data-driven technologies is essential for achieving global food and nutritional security, sustaining ecosystem balance, and developing resilient agricultural systems in the context of unpredictable climate change.

Keywords: Abiotic stress; Drought and Heat; Climate change, Climate Smart Agriculture, Resilient Crop Varieties

1. Introduction

The World Meteorological Organisation (WMO) warned about the alarming situation of food security. It is projected that the situation may deteriorate due to global climate change and a massive increase in the world population. Hence, to fulfil the need for food security, the production and productivity of agricultural produce should double by 2050 (Hunter *et al.,* 2017). However, agricultural production is not keeping up with this pace because the amount of land available for cultivation is expected to remain constant or decrease due to the growing demand for non-agricultural purposes. While investment in technological advancement and utilising climate-smart strategies can enhance productivity, ultimately, it will result in greater accessibility and absorption of food. These gaps are most significant among lower-income populations, who suffer the most from the effects of climate change.

Climate change exacerbates the issue, with abiotic stresses posing a significant obstacle to sustaining crop productivity (Das *et al.,* 2019). (WMO) reported that the Earth was the warmest compared to the past 8 years. Meanwhile, the world faces frequent rainfall patterns, including heat and cold waves (Hossain *et al.,* 2021). Dry and semi-dry regions of the world are more prone to abiotic stresses (Alwan *et al.,* 2022), which negatively impact agriculture by degrading soil, susceptibility to pests and diseases, lowering the crop yield and quality in the area, resulting in a threatto global food security (Boscaiu and Fita, 2020; Mondal *et al.,* 2016).

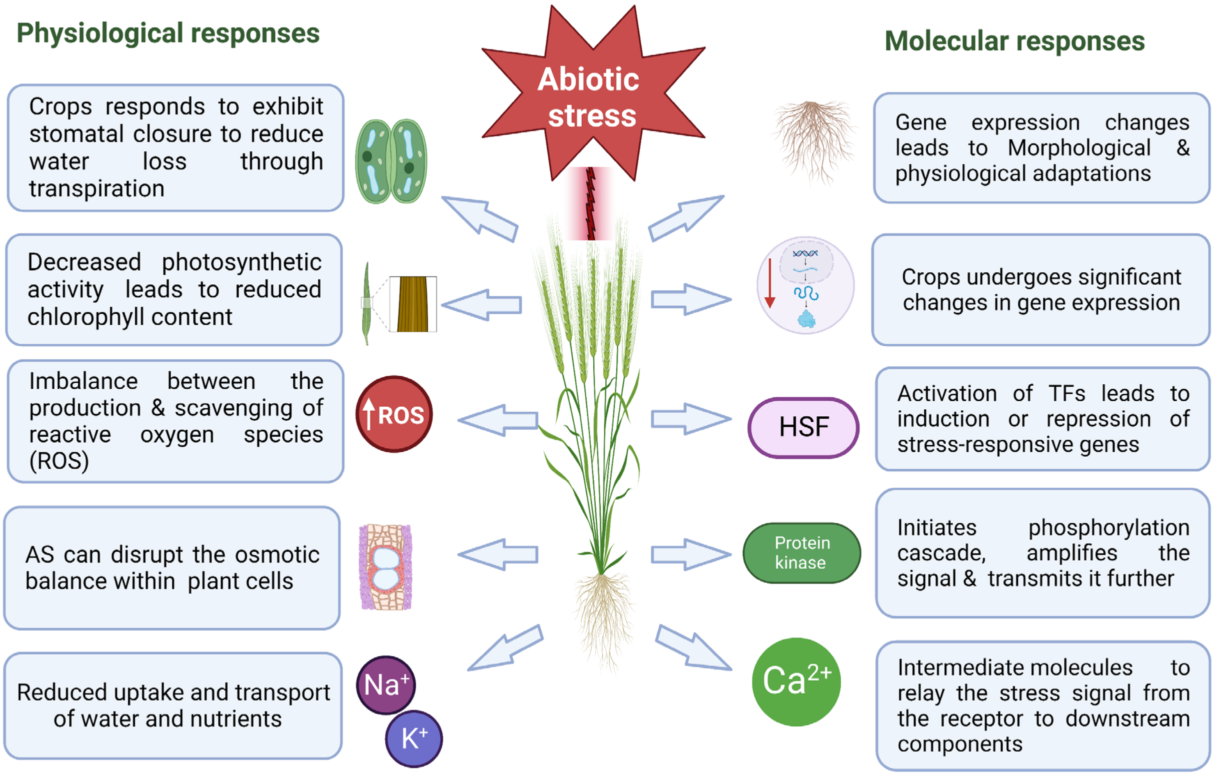
Under stressful conditions, plant changes their morphological, physiological, biochemical, and molecular patterns, which can hinder growth and productivity (Boscaiu and Fita, 2020). However, animals and other large living creatures manage to survive with the variety of highly developed metabolic and physiological systems, including locomotion and shelter. According to an estimation (Acquaah, 2009), nearly 70% of crop yield reduction is directly or indirectly influenced by abiotic stresses.It has been demonstrated that the effect of stress on growth and productivity depends on the type of stress and phenological status of the plant.

These abiotic stresses significantly impact the flowering, pollination, and grain filling of most crops, resulting in a negative effect on ovary development, pollen fertility, and fruit set, as well as reduced end-use quality(Fahad *et al.,* 2015; B. V. G. Prasad and Chakravorty, 2015; Sreenivasulu *et al.,* 2015). On the other hand, conditions like abundant rainfall may positively impact yield but can damage plants due to higher relative humidity, which predisposes them to disease outbreaks(Lekshmy *et al.,* 2015; Singh *et al.,* 2018). Further, crop growth and productivity depend on efficient resource use, especially when exposed to abiotic stresses. These stressors affect the plant's nutrient uptake and utilisation efficiency, leading to nutrient stress (Gong *et al.,* 2020). For example, nitrogen (N) deficiency can increase the susceptibility of wheat to heat stress, whereas zinc (Zn) deficiency can reduce plant growth and yield under stressful environmental conditions. Enhancing nutrient use efficiency (NUE) is necessary for building resilience to abiotic stresses, which is vital for sustaining productivity and food security in a changing climate (Mittler, 2006).

Therefore, understanding the causes of abiotic stresses is essential for effectively managing these stresses. Hence, the primary goal of most global research activities is to develop mitigation and sustainable adaptation strategies to combat the negative impacts of abiotic stresses (Elum *et al.,* 2017). Development and deployment strategies, such as climate-resilient crop varieties, matching agronomic practices, efficient cropping systems, and the use of artificial intelligence and machine learning in agriculture, can have a distinct and observable impact on reducing the negative effects on agriculture (Boraiah *et al.,* 2021; Shahzad *et al.,* 2019). This review highlights the various types of abiotic stresses, their overall impact on morphophysiological, biochemical, and molecular parameters of crop plants, and potential areas of innovative research for climate-smart production. In addition, we focused on Integrated agronomical interventions, novel genomic approaches, and biotechnological tools and techniques, combined with climate-smart breeding tools, for developing sustainable, climate-resilient agricultural products.

2. Plant Response to abiotic stresses and the mechanism of tolerance

Abiotic factors, such as drought, waterlogging, salinity, and extreme temperatures, harm plant's growth and development, resulting in reduced genetic yield potential. Plants have developed various mechanisms of tolerance and adaptation to cope with these stresses. These processes can be generally divided into physiological, biochemical, and molecular responses (Fig. 1).


Physiological responses

Crops responds to exhibit stomatal closure to reduce water loss through transpiration

Decreased photosynthetic activity leads to reduced chlorophyll content

Imbalance between the production & scavenging of reactive oxygen species (ROS)

AS can disrupt the osmotic balance within plant cells

Reduced uptake and transport of water and nutrients

Molecular responses

Gene expression changes leads to Morphological & physiological adaptations

Crops undergoes significant changes in gene expression

Activation of TFs leads to induction or repression of stress-responsive genes

Initiates phosphorylation cascade, amplifies the signal & transmits it further

Intermediate molecules to relay the stress signal from the receptor to downstream components

Fig. 1: The physiological and molecular reactions of plants in response to numerous abiotic stresses. Created with BioRender.com.

2.1. Drought Stress

Drought is among the most severe and widespread abiotic stresses influencing global agriculture and food production. It occurs when plants experience prolonged periods of inadequate water availability, often intensified by high temperature, erratic precipitation, and deteriorating soil quality. Drought impacts nearly all developmental stages in most crop species, disrupting photosynthesis, respiration, nutrient uptake, and reproductive success. The impact is especially significant in key cereals, including rice and wheat, as well as legumes such as chickpeas, where yield losses can exceed 50% under conditions of severe water limitation. Plants exposed to drought initiate a complex set of morphological, physiological, biochemical, and molecular responses that collectively influence their ability to endure or recuperate from stress (Mukarram *et al.,* 2021).

2.1.1. Morpho-physiological responses

The primary plant response to drought is stomatal regulation, which decreases transpirational water loss; however, this also restricts CO_2 assimilation and diminishes photosynthetic efficiency (Rodriguez-Dominguez and Brodribb, 2020). Abscisic acid (ABA) plays a crucial role in this process by promoting guard cell closure and activating the expression of genes responsive to drought (Li *et al.,* 2021). Drought modifies canopy morphology and leaf anatomy by decreasing leaf area, increasing cuticle thickness, and enhancing trichome density to reduce water loss. Drought conditions lead to increased root length density, deeper rooting angles, and the proliferation of lateral roots in deeper soil layers, thereby improving access to sub-soil moisture (Homulle *et al.,* 2021).

Controlled studies in wheat indicate that water deficit during the vegetative and reproductive stages significantly decreases relative water content (RWC), stomatal conductance (gsw), and chlorophyll stability, while hastening leaf senescence. Drought conditions during stem elongation and anthesis, both in greenhouse and field settings, resulted in a reduced phenological duration, indicating a drought-escape response characterised by earlier flowering. The most substantial decrease in yield (approximately 51%) was observed in grain number and weight. Several wild wheat genotypes, including *Triticum monococcum* subsp. *sinskajae, T. boeoticum*, and *T. dicoccoides* exhibited higher relative water content (RWC) and displayed avoidance and tolerance mechanisms, suggesting their potential as donor sources for resilience breeding (Pantha *et al.,* 2024).

2.1.2. Responses at the biochemical and molecular levels:

Plants utilise osmotic adjustment at the biochemical level to sustain turgor during dehydration. Compatible solutes, including proline, glycine betaine, soluble sugars, and polyols, accumulate within cells to stabilise proteins and membranes while maintaining enzymatic activity (Al-Yasi *et al.,* 2020). Drought increases the production of reactive oxygen species (ROS), requiring the activation of antioxidant enzymes such as superoxide dismutase (SOD), catalase (CAT), ascorbate peroxidase (APX), glutathione reductase (GR), and guaiacol peroxidase (GPOX). These enzymes neutralise reactive oxygen species and protect cellular components from oxidative damage.

Experiments conducted in both field and pot settings with wheat and chickpea demonstrate that water deficit markedly raises MDA content, which serves as an indicator of lipid peroxidation, while also increasing levels of proline, sugars, glycine betaine, and antioxidant activity. In the chickpea genotypes ICC 4958 and HC-6, cultivated at 50% and 25% field capacity, there was a decline in morphological attributes, including shoot length (−14%), leaf number (−17%), and yield (−56%). Conversely, root length (+9%), flower number (+25%), and pod number (+34%) exhibited increases, indicating adaptive morphological plasticity. Physiological traits, such as relative water content (RWC), decreased by 13.5%, while cell membrane stability declined by 29.6%; however, electrolyte conductivity increased by 38%. Simultaneously, levels of proline (+55 %), SOD (+49 %), CAT (+50 %), APX (+45 %), and GR (+49 %) increased, alongside a greater accumulation of anthocyanins, flavonoids, and phenolics, indicating an enhanced antioxidative and secondary-metabolite defence system (Keerthi Sree *et al.,* 2023).

Drought at the molecular level triggers the expression of stress-responsive transcription factors, including DREB, AREB/ABF, and NAC, which in turn regulate downstream genes associated with osmotic adjustment, detoxification, and signal transduction (Mei *et al.,* 2022). Microbial associations, specifically arbuscular mycorrhizal fungi (AMF) and plant growth-promoting rhizobacteria (PGPR), enhance drought tolerance through improved nutrient and water uptake efficiency.

2.1.3. Strategies for adaptation

Drought resistance in plants typically involves three interconnected mechanisms: escape, avoidance, and tolerance. Drought escape refers to the completion of the life cycle before the onset of severe water scarcity, a phenomenon frequently observed in short-duration species (Labastida *et al.,* 2023). Drought avoidance depends on sustaining tissue water potential via efficient root systems and minimising transpirational loss (Yang *et al.,* 2020). Drought tolerance enables plants to maintain metabolic functions in conditions of low water availability through biochemical modifications, including the accumulation of osmoprotectants and an improved antioxidative capacity. Numerous species exhibit developmental plasticity by reducing reproductive output in response to stress and optimising yield under favourable moisture conditions (Lippmann *et al.,* 2019).

Morphological, physiological, biochemical, and molecular adaptations collectively determine a plant's capacity to withstand drought. The integration of physiological screening, nanotechnological tools, and advanced genomics into breeding programs represents a comprehensive approach to developing multi-stress-resilient cultivars. Comprehending the mechanisms induced by drought is essential for the development of climate-resilient crops and for promoting sustainable agriculture and global food security amidst rising climatic variability.

2.2. Waterlogging Stress

Waterlogging is the term used to describe a situation where the soil is overly saturated with water, as the pores between soil particles are filled with water to the point where despite improvements in agricultural production technology that have enhanced stress, various mechanisms have developed to tolerate and adapt to this challenging condition. An essential response is aerenchyma formation, which consists of air-filled cavities facilitatingoxygen transport from the plant's above-ground parts to the submerged roots(Teoh *et al.,* 2022). Additionally, waterlogged plants switch to anaerobic respiration, altering their metabolic pathways to generate energy in the absence of oxygen(Gu *et al.,* 2021). Many species exhibit root plasticity, adjusting their root architecture to reach available oxygen in shallower soil layers(Pedersen *et al.,* 2021). Ethylene, a plant hormone, plays a significant role in responding to waterlogging, triggering the formation of adventitious roots (Qi *et al.,* 2019)and the shedding of lower leaves(Gu *et al.,* 2021). Tolerant plants also activate specific genes,*viz*., *GPX*, *GST*, *WRKY*, and ERF, associated with antioxidant production to counteract oxidative stress(Hong *et al.,* 2023). These adaptive strategies, along with other mechanisms such as osmotic adjustment, ion transport regulation, and endophytic microbial associations, collectively help plants survive and grow in waterlogged conditions.

2.3. Salinity Stress

Salinity stress induces osmotic stress, as the increased salt concentrations diminish water accessibility to plant cells, leading to water stress and, in turn, ion toxicity due to the overabundance of sodium and chloride ions, which can disrupt essential plant biochemical processes. In the face of these challenges, salt-tolerant plants have developed several strategies to thrive in saline environments. These strategies encompass ion exclusion, in which specialised transporters permit the selective entry of essential ions, such as potassium, while excluding detrimental ones(Joshi *et al.,* 2022). Another critical mechanism is ion compartmentalisation, whereby excess sodium and chloride ions are sequestered within vacuoles, diminishing their harmful effects on the plant's cellular cytoplasm (Balasubramaniam *et al.,* 2023). To counteract osmotic stress, plants often accumulate compatible solutes, such as proline, glycine betaine, and sugars, which help maintain a water balance(Ahmed *et al.,* 2021). The production of antioxidant enzymes, like superoxide dismutase and catalase, mitigates oxidative damage from generating reactive oxygen species during salt stress (Sagar *et al.,* 2020). Plant hormones, notably abscisic acid (ABA), play a pivotal role in regulating responses to salt stress by managing stomatal closure, thereby reducing water loss and preventing the influx of salt into leaves(Parveen *et al.,* 2021). Activation of ion transporters, such as *SOS1* (*Salt Overly Sensitive 1*) and *NHX* (Na+/H+ Exchanger), holds significant importance in a plant's response to salinity stress and its development of salt tolerance. *SOS1*, located in the plasma membrane, plays a crucial role by actively pumping toxic sodium ions from the cell into the external environment(Rao *et al.,* 2021). *NHX* in the tonoplast surrounding the vacuole contributes to ion compartmentalisation, safely storing excess sodium ions away from the cytoplasm to reduce their toxic effects(Joshi *et al.,* 2021).

2.4. High Temperature Stress

High-temperature stress has become a significant abiotic factor constraining global crop productivity. When ambient temperatures exceed the optimum threshold for a given species, plants experience extensive physiological and biochemical disruptions that impair growth, metabolism, and reproduction. Increased temperature accelerates phenological development, often reducing the duration of critical growth stages, such as flowering and grain filling, resulting in diminished yield potential (Lamichhane *et al.,* 2021). Excessive heat during reproductive phases leads to pollen sterility, diminished pollen tube growth, inadequate fertilisation, and heightened rates of flower or pod abortion, culminating in substantial yield reduction or total crop failure in extreme cases (Salgotra *et al.,* 2023). Plants mitigate these effects through intricate defence mechanisms, which include the synthesis of heat-shock proteins (HSPs), adjustments to antioxidant systems, and the initiation of osmoprotective and hormonal responses that collectively sustain cellular homeostasis (Nayak *et al.,* 2023; Sehar *et al.,* 2023).

2.4.1. Morphological and Physiological Changes

High temperature profoundly influences the structural and functional integrity of plants. Plants subjected to heat stress exhibit decreased height, biomass, and leaf expansion, resulting from the suppression of cell division and elongation. Changes in leaf structure, such as rolling, folding, or curling, reduce the surface area exposed to solar radiation, thereby decreasing the heat load and transpiration. Elevated temperatures expedite developmental transitions, leading to premature senescence, earlier flowering, and shorter grain-filling durations, thereby significantly limiting yield potential. The reproductive organs exhibit significant sensitivity to temperature; increased temperatures inhibit anther dehiscence, reduce pollen viability, and compromise fertilisation, leading to suboptimal seed set (Salgotra *et al.,* 2023).

Thermal stress during the anthesis and grain-filling stages in wheat significantly diminishes kernel weight, photosynthetic efficiency, and chlorophyll content, while simultaneously elevating membrane injury and electrolyte leakage. The screening of northwestern plain zone (NWPZ) wheat genotypes at 37 °C demonstrated significant variation in tolerance levels. Cultivars DBW88 and PBW550 displayed superior tolerance, characterised by higher relative water content, enhanced chlorophyll stability, and reduced membrane damage. In contrast, HD3086 and WB2 were classified as susceptible due to reduced root and shoot biomass, as well as increased oxidative damage (Pandey *et al.,* 2023).

High temperatures in *Pisum sativum* (field pea) resulted in significant reductions in plant growth, seed yield, and photosynthetic pigment concentration, especially in susceptible genotypes (P-1541-16 and IM 9102). Tolerant genotypes (EC 341743 and P-1384-3) exhibited higher chlorophyll and carotenoid contents, reduced cell injury, and enhanced activity of protective enzymes, demonstrating their effective capacity for heat acclimation (Sharma *et al.,* 2023).

Comparable effects are observed in cowpea (Vigna unguiculata L.), where heat stress during the reproductive phase leads to reduced flower and pod formation, smaller seed size, and lower yield. The evaluation of 250 cowpea accessions under late-sown (high-temperature) conditions revealed significant genotypic variability. Notably, several accessions, including EC240920, IC488085, and IC488270, displayed stable performance across environments, attributed to mechanisms such as early maturity, photothermal insensitivity, and the maintenance of cooler canopy temperatures (Biradar *et al.,* 2025).

In barley, the simultaneous occurrence of heat and drought stress during microgametogenesis exacerbated the damage to the photosynthetic apparatus and pigment stability. The tolerant variety Lambada exhibited superior photosynthetic efficiency, chlorophyll content, and leaf ultrastructure integrity compared to the sensitive Spinner genotype, suggesting that maintaining chloroplast structure and continuing carbon assimilation are critical factors in thermo-tolerance (Jampoh *et al.,* 2023). Heat stress significantly modifies various essential physiological processes. The photosynthetic machinery is one of the components most sensitive to temperature variations. A powerful tool that accelerates the breeding cycle, reduces the cost of labour, and compromises the efficiency of photosystem II (PSII). Rubisco activity and the regeneration of ribulose-1,5-bisphosphate (RuBP) decrease, leading to diminished CO fixation and carbon acquisition (Jahan *et al.,* 2021). At the same time, respiration rates rise disproportionately, depleting stored carbohydrates and resulting in a negative carbon balance. Stomatal closure, membrane instability, and rapid water depletion exacerbate stress, resulting in wilting and premature senescence.

2.4.2. Biochemical and Molecular Alterations

Heat stress induces oxidative damage, protein denaturation, and metabolic imbalance at the biochemical and molecular levels. The overproduction of reactive oxygen species (ROS), including superoxide radicals, hydrogen peroxide, and hydroxyl radicals, leads to the oxidation of lipids, nucleic acids, and proteins, based on marker data, thereby obviating the need for enzymatic and non-enzymatic antioxidant defences. The activities of SOD, CAT, APX, peroxidase (POD), and GR generally increase in response to heat stress, thereby limiting ROS accumulation and maintaining redox homeostasis (Sehar *et al.,* 2023). Tolerant field pea and wheat genotypes demonstrate markedly elevated activities of SOD, POD, and CAT compared to sensitive genotypes, indicating that increased antioxidant capacity is a key characteristic of thermo-tolerance (Sharma *et al.,* 2023; Pandey *et al.,* 2023). Elevated temperatures promote the accumulation of osmoprotectants, including proline, glycine betaine, and soluble sugars, which help stabilise proteins, membranes, and enzymes, thereby preserving cellular osmotic balance. Elevated concentrations of these metabolites are associated with enhanced yield stability in heat-tolerant genotypes (Sharma *et al.,* 2023; Biradar *et al.,* 2025).

The synthesis of heat-shock proteins (HSPs) represents a significant molecular defence mechanism against heat stress. Heat shock proteins (HSPs) function as molecular chaperones by preventing the aggregation of denatured proteins, aiding in the refolding of damaged polypeptides, and maintaining enzyme activity during thermal stress (Nayak *et al.,* 2023). Genes that encode small heat shock proteins, as well as the HSP70 and HSP90 families, are rapidly activated in response to heat exposure, providing temporary protection to the proteome.

Elevated temperatures disrupt the balance of phytohormones, leading to increased accumulation of abscisic acid (ABA) and ethylene, while inhibiting the biosynthesis of auxin and gibberellin (Tiwari *et al.,* 2022). This hormonal reprogramming facilitates stomatal closure and senescence, contributing to stress avoidance while limiting growth. Metabolic adjustments involve changes in carbohydrate partitioning, characterised by increased starch degradation, reduced sucrose synthesis, and a redirection of carbon metabolism towards pathways that confer stress protection.

Genomic and transcriptomic investigations in wheat have revealed quantitative trait loci (QTLs) and SSR markers associated with heat-tolerance characteristics, including grain filling duration, flag-leaf area, and kernel weight. Hierarchical clustering utilising SSR profiles categorised genotypes into specific tolerance groups, with Saudi genotypes KSU106, KSU105, KSU115, and 16HTWYT-22 demonstrating significant antioxidant capacity and limited yield reduction in high-temperature conditions (Sallam *et al.,* 2024).

These integrated physiological, biochemical, and molecular adaptations allow plants to acclimate to or endure thermal stress. The integration of phenotyping, biochemical assays, and molecular markers facilitates the accurate identification of heat-tolerant germplasm, thereby expediting the breeding of climate-resilient crops. Understanding these mechanisms provides critical insights for developing crop improvement strategies that ensure sustainable productivity in the context of rising global temperatures.

2.5. Low-Temperature Stress

Plants exhibit a range of responses to low-temperature stress, such as chilling and freezing. The immediate consequences of low-temperature stress on plants encompass direct effects, such as the solidification of membrane lipids and the slowing of enzymatic reactions, which occur within a relatively short timeframe (Liang *et al.,* 2020). In contrast, the secondary injury symptoms, which emerge more gradually, include the leakage of solutes from cells(Aazami *et al.,* 2021), an imbalance between respiration and photosynthesis(Bhattacharya, 2022), resulting in energy perturbations, depletion of adenosine triphosphate (ATP), the buildup of harmful substances, and visible signs of distress like wilting due to water loss (Sharma *et al.,* 2020). Ice crystal formation and growth in extracellular compartments pose a significant challenge for plants during freezing stress, which can damage plants at the whole-plant, tissue, and cellular levels (Ritonga *et al.,* 2020). As ice crystals expand and grow in extracellular spaces, they can disrupt the delicate balance of plant tissues and cells. One critical aspect of their response is maintaining cell membrane stability, which involves adjusting lipid composition to counteract membrane rigidity and reduced permeability. Cold stress typically triggers a rise in the ratio of unsaturated fatty acids within plant membranes. This change in lipid composition is a vital response, ensuring the flexibility and effectiveness of membranes in cold conditions(Wang *et al.,* 2022). Plants activate a series of cold-responsive genes, such as *CBF/DREB1* (C-repeat binding factors/ dehydration-responsive element-binding factors), which include those encoding transcription factors and proteins necessary for cold acclimation (Sanghera *et al.,* 2011). Certain plants also produce cryoprotectants, such as antifreeze proteins, that inhibit ice nucleation and growth, thereby safeguarding cells from freezing damage(Jahed *et al.,* 2023). To protect chloroplasts, which are crucial for photosynthesis, plants reorganise thylakoid membranes and accumulate osmiophilic globules within chloroplasts during cold stress(Wang *et al.,* 2020).

2.6. Elevated CO_2 (eCo_2)

The negative impacts of increased atmospheric carbon dioxide (CO_2) concentrations on crop growth and development are referred to as “elevated eCO_2 stress” in agriculture. The primary reasons for the increased concentration of CO_2 are the constant growth of the global population, the increased emission of greenhouse gases into the atmosphere, mainly CO2, through the burning of fossil fuels, industrial activities, and deforestation(Dong *et al.,* 2018).According to the Intergovernmental Panel on Climate Change’s (IPCC, 2013) assessments, the concentration of eCO_2 in the atmosphere is increasing. It is expected to reach 700 $\mu mol \cdot mol^{-1}$ by the end of the twenty-first century. This eCO_2 may disrupt plants’ physiological and biochemical processes, significantly impacting crop development, growth, and agricultural output. At the leaf level, eCo_2 results in an increased rate of net photosynthesis and a decreased stomatal conductance(Hossain *et al.,* 2021). A study byChaturvedi et al. (2017)revealed a considerable impact of eCo2 on the grain quality of rice, reporting increased chalkiness (69–83%), amylose content (18–37%), a 4% decrease in protein content, and alterations to the mineral component. Similarly, eCo2 increases vegetable yield but may lead to a decrease in nutrient content. According to a study on lettuce, tomatoes, and potatoes, eCo2 increases the levels of soluble sugars, ascorbic acid, phenols, and flavonoids, while lowering the levels of protein, nitrate, Mg, Fe, and Zn (Dong *et al.,* 2018).

2.7. Ultraviolet (UV)Radiation Stress

Sunlight is a crucial element in photosynthesis, energy production, and cellular respiration, all of which are essential for plant growth and development. When plants are exposed to sunlight, they also face the harmful effects of UV radiation, whichcan negatively impact crop productivity,referredto as UV radiation stress. The radiation emitted by the sun is divided into three main types: UVA (320-390 nm), UVB (280-320 nm), and UVC (below 280 nm)(Bishnoi *et al.,* 2017). The stratospheric ozone layer filters most UVC (the most damaging type) and a portion of UVB. At the same time, UVA reaches the Earth's surface in relatively higher amounts as it is less damaging to biological systems than UVB and UVC(Pournavab *et al.,* 2019).Several studies have reported the various morphological and molecular alterations in plants depending on the strength, duration, and type of UV irradiation.The potential targets itcan harm include several cell constituents, such as proteins, membrane lipids, and nucleic acids, resulting in reduced growth and productivity of the crops. Long-term exposure to UV radiation can directly damage the plant DNA, leading to mutations and changes in the integrity of their genomes(Bishnoi *et al.,* 2017; Pournavab *et al.,* 2019). Other consequences include reduced photosynthesis, inhibited by the inhibition of photosystem II (PSII) activity, decreased chlorophyll content, and interference with electron transport. UVB stress negatively impacts the end-use quality of soybeans by reducing oil quality and deterioration of seed mineral nutrients(Choudhary and Agrawal, 2016).According toPournavab et al. (2019),the susceptibility of wheat and soybean seeds to UVB and UVC radiation was low, but it increases with increasing radiation dose.

In contrast to the other species studied, UVB and UVC radiation had the most detrimental effects on sunflowers, causing abiotic stress due to high radiation and heat. To protect sensitive plant tissues from excessive UV exposure, UV radiation causes the production of reactive oxygen species (ROS) and plant pigments, primarily flavonoids and phenolics(Choudhary and Agrawal, 2016). Understanding these physiological responses and their effects on crop growth and development is crucial for developing strategies to mitigate the adverse effects of UV radiation and ensure long-term crop production.

2.8. Nutrient Stress

Nutrient stress is the unavailability, imbalance, deficiency or excess of essential nutrients required for proper plant growth and development. According to requirements, nutrients are mainly categorised into two major groups: macronutrients and micronutrients, which plants absorb from the soil and fertiliser applications. Low soil fertility, pH, improper fertiliser application, competition for limited nutrient resources and imbalance in the relative proportion of nutrients in the soil are the major factors causing nutrient stress.When essential nutrients like potassium (K), phosphorus (P), and nitrogen (N) are insufficient, it severely affects the yield and quality of produce.Phosphorus (P) deficiency alone in agriculture affects more than 70% of crop productivity of globally available arable land(Mareri *et al.,* 2022). Lowcrop nutrient status has typically been assessed by identifying nutrient-specific symptoms, such as stunting, yellowing, and energy deprivation, and estimating the amounts of different nutrients in the plant. In this context, Chea et al. (2021) investigated the effects of phosphorus (P) deficiency and toxicity in potatoes, finding a reduction in plant height in P deficiency conditions and an accumulation of proline in P toxicity conditions.Present breeding programs are mainly associated with evaluating genotypes for high yield potential and their good response to fertilizer under fertile soil. These modern cultivars developed under optimal conditions cannot perform the same under nutrient stress because of a reduction in genetic diversity associated with tolerance to low nutrient conditions.Also, farmers need to invest in additional fertilizers and treatments to mitigate the nutrient stress,increasing the cultivation cost.

Hence, there is a need to develop climate-smart economic strategies that can help assess and minimize the effect of nutrient stress on crop productivity.

2.9. Other Abiotic Stresses:

Wind and heavy metal stress can also affect plant growth, productivity, and quality. Studies have shown that different, sometimes conflicting, signalling pathways control plant stress and defence responses. The plant activates specific signaling cascades and metabolic pathways depending on stress. The combination of specific stresses, their intensity, and plant developmental stage determines plant response. These challenges arise from stress interactions, crop adaptability, resource scarcity, and climate change. Although much is known about plant responses to a single stress factor, crop responses to simultaneous biotic and abiotic stresses are little understood(Farooq *et al.,* 2011, 2014). Abiotic stresses are challenging to manage, even though agricultural production technology has improved crop yield and biotic stress management(Raza *et al.,* 2022). Thus, scientists are developing molecular, physiological, and innovative agriculture management strategies to mitigate abiotic stresses.

3. Cutting Edge Crop Improvement Strategies for Mitigation of Abiotic Stresses

3.1. Conventional breeding

3.1.1. Exploration of genetic resources:

Increasing the availability of genetic resources for crop improvement through the introgre, RNA Interference (RNAi), Microbiome Engineering, and tissue culture-assisted breeding, have also been utilised to enhance tolerance to multiple abiotic stresses simultaneously, providing a broader spectrum of resistance in lise the evolutionary potential of extensive seed collections locked away in cold rooms(Mascher *et al.,* 2019). The rich gene pools in cultivated forms, landraces, wild relatives, and related genera improve any crop. Reports for most crop plants suggest genetic variation in adaptation traits for different stresses in breeding material, landraces, and wild relatives. For instance, landraces from dry regions serve as a source of drought tolerance in oilseed crops(Meena and Sujatha, 2022). Wild species of many crops are a treasured source of novel allelic variation for biotic and abiotic stress tolerance(Basavaraj *et al.,* 2020). Studies of root system architecture genes in wild soybean (*Glycine soja*) have identified critical genetic factors that improve water uptake efficiency, presenting potential targets for enhancing yield and drought resilience in cultivated soybean (Glycine max). Traits identified in wild barley (*Hordeum spontaneum*) have provided valuable alleles linked to selenium accumulation tolerance, sodium exclusion, and enhanced agronomic performance under post-anthesis drought conditions. *Hordeum bulbosum*, another wild barley species, has been employed as a genetic resource to improve abiotic stress tolerance in cultivated barley. In rice (*Oryza sativa* L.), quantitative trait loci (QTLs) associated with enhanced yield and stress tolerance have been identified and introgressed from its wild relatives, *Oryza rufipogon* and *Oryza nivara.* Similarly, wild wheat species including *Aegilops tauschii, Triticum turgidum* ssp. *dicoccoides*, and *Triticum spelta* act as reservoirs for genetic loci that confer drought and heat tolerance. The studies highlight the essential function of wild relatives as sources of adaptive genetic variation, which can be utilized to improve abiotic stress tolerance and yield stability in contemporary crop breeding programs (Brozynska *et al.,* 2015; Bohra *et al.,* 2022).

3.1.2. Breeding for the development of climate-resilient varieties

Through conventional breeding, much progress has been made in developing and deployingclimate-resilient smart varieties in many crop plants (Table 1) (Boraiah *et al.,* 2021). In conventional breeding, phenotypic selection is the primary focus of breeders, and they have made some progress in a positive direction. In addition to morpho-physiological features,selection indices such as the stress susceptibility index and stress tolerance index are also helpful in selecting stress-tolerant genotypes. However, a major bottleneck in plant breeding is the time required to develop an improved crop variety, in addition to the complex nature of abiotic stresses.

Because stress affects crops differently, especially when they are exposed to multiple stresses, breeding crop varieties for environmental stress is slow and difficult. When developing abiotic stress-tolerant or resistant cultivars, yield potential is a major factor. However, secondary physio-morphological traits also influence resistance to harsh environments. It's important to consider secondary traits and grain yield when developing stress-tolerant cultivars(Hossain *et al.,* 2021; Pandey *et al.,*

Table 1: Climate resilient crop varieties for various stresses (modified from Boraiah *et al.,* 2021)

Sr. No.	Crop	Type of Stress	Varieties
1.	Rice	Drought	DRR Dhan 47, DRR Dhan 50, Tripura Khara 1, CR Dhan 801, Sahbhagi, Birsa Vikas Dhan 111, Bahadur Sub-1
		Submergence/ Flooding	CR Dhan 802 (Subhas), Ksheera, CSR43, Tripura Jala, DRR Dhan 50, BahadurSub-1, MTU 1140, Samba sub-1
		High temperature	DRR Dhan 52, DRR Dhan 47
		Low temperature	NE Megha Rice 1, NE Megha Rice 2, Gizza-14 K-39, K-343, K-448, HPR 2143, HPR1068, RP2421, Varun Dhan
		Salinity	CARI Dhan 5, Panvel 3, CSR 56, CSR 52, CSR 56, CSR 60, CSR 46, GNR-5, Luna Sankhi (CR Dhan 405)
2.	Wheat	Drought	Sabour Nirjal, HUW 669, DBW 252, HI 1654, MACS 4100(d), HI 1628, HD 3293, NIDW 1149 (d), DBW 296, HUW 838, HI 8823(d), MP 1358, HD 3369, HI 1653, HI 8830(d), DDW 55(d), CG 1036, HI 1655, HI 1653
		Submergence/ Flooding	KRL 19, KRL 210, KRL-213, KRL 283
		High temperature	DBW 73, DBW 173, DBW 107, WH 1124, K 0307, DWR17
		Low temperature	RSP 561, Shalimar wheat-1, Man Sarovar, Buland
		Salinity	KRL-213, KRL 283, KRL 210, KRL 19, KRL 1-4
3.	Maize	Drought	HQPM-5 2020, NAH-1147, PEHM-1
		Submergence/ Flooding	KRL 19, KRL 210, KRL-213, KRL 283
		High temperature	RCRMH2, PMH-7, Suwan
4.	Pigeon pea	Drought	GRG 811, BDN-708, PRG 176, Prakash, GRG 811, LRG 52, GT- 102, BDN 716, BDN 711,
		Submergence/ Flooding	ICPL 84023, Mal 13, Asha, Maruti
		High temperature	UPAS-120, Rajeev Lochan, Bahar
		Low temperature	Bahar
		Salinity	C 11, Jagriti (ICPL 151), UPAS 120
5.	Black gram (Urd)	Drought	BDU-1, Pant Urd-35, Pratap Urd-1 (KPU 07-08), Azad-3, Shekhar-2
6.	Chickpea	Drought	JG 16, Nandyal Gram 49, Indira Chana 1, Pant gram-4, Pant Kabuli, gram-2, JG 36, NBeG 3, PKV Harita (AKG 9303-12)
		Submergence/ Flooding	GNG16, DCP92-3, GNG 1581, Pusa240
		High temperature	JG-14, JAKI 9218, JG -6, JG-11, Pant G 186, JG-315
		Low temperature	PDG 4
		Salinity	Karnal chana-1
7.	Groundnut	Drought	Dheeraj (TCGS 1073), DH-257, Dh 256 2020
		High temperature	Kadiri-6 (K-1240), Vemana (K-134), Ambar (CSMG-84-1), TG- 22, ICGV-86031
8.	Soybean	Drought	Pratap Soya 45 (RKS 45), RKS-24, Pratap Soya-2 (RKS-18), PS-1225, JS-95-60, JS-9305
		Submergence/ Flooding	Jawahar Soybean 97-52 (JS 97-52), AHILYA-4 (NRC-37)
		High temperature	JS-335
9.	Sorghum (Fodder)	Salinity	CSV- 44F (SPV-2445/ S713)

2017).The roots of a plant serve as its primary defence against abiotic stress, and the plant's ability to withstand challenging conditions is greatly enhanced if the soil it grows in is rich in biological diversity. Root traits, such as root length density, root hair length, and cortical root aerenchyma (a type of tissue that facilitates root growth under oxygen-limited conditions), were essential for tolerance and plant productivity(Comas *et al.,* 2013). The deeper roots can access water in deeper soil layers, which is critical for drought tolerance. Genetic variation for root traits exists within crop species that can be exploited through breeding to improve drought tolerance(Chai and Schachtman, 2022). In this context, the careful evaluation of various traits, including grain yield, biomass, harvest index, and root system architecture (RSA), is a complex process that requiresthe selection of the best hybrid progeny through crossbreeding to improve a trait such as stress tolerance (Mondal *et al.,* 2016). Desired traits can be introduced into a selected 'best' recipient line by backcrossing the selected progeny with the recipient line for several generations, thereby reducing unwanted phenotype combinations(Ahmar *et al.,* 2020). The number of instances in which introgression of traits from genetic resources and possible improvement through conventional breeding has been reported in several reports (Brozynska *et al.,* 2015; Bohra *et al.,* 2022).

3.2. Molecular techniques and plant biotechnological tools

3.2.1. Use of DNA-based markers and Genomics assisted breeding

Continued breeding efforts are necessary to tackle the problem of climate change and the projected food demand of an ever-growing population. Hence, past conventional breeding approaches are insufficient to match the speed with which crop improvement is necessary. Therefore, novel approaches like bi-parental QTL mapping using structured population and genome-wide association analysis using unstructured population enable us to dissect and detect genomic regions responsible for stress resilience and achieve a rapid genetic gain. The identification of the precise position of genes in the genomic areas responsible for important traits related to abiotic stress from the vast array of germplasm can be possible with whole genome sequencing and genotyping-by-sequencing (GBS)approaches (Fig. 2). As abiotic

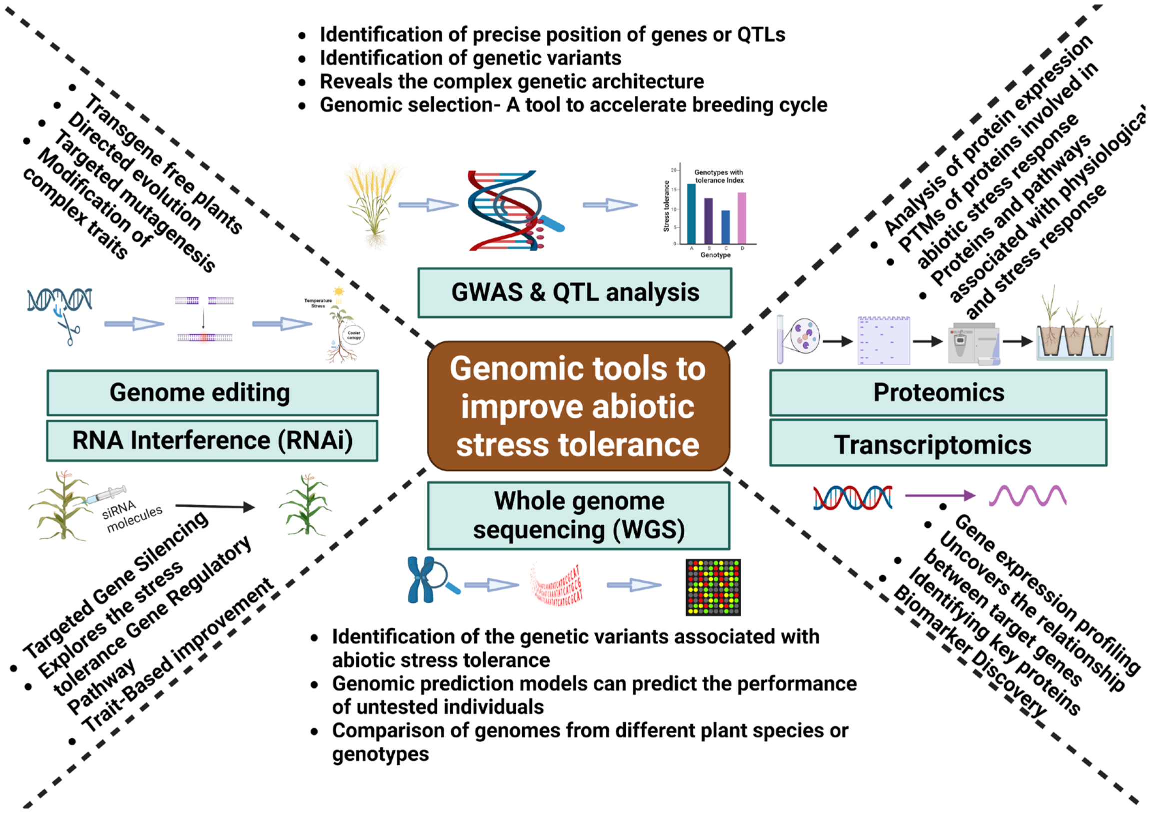


Fig. 2: A wide variety of genomics and biotechnology advances to increase tolerance to abiotic stress. Created with BioRender.com

stresses are complex traits, and to analysethe genetics of thismolecular marker like SNPs associated with stress tolerance enables the streamlining of the selection of plants carrying desired traits, reducing the need for extensive phenotypic screening and allowing the introgression of beneficial traits from wild or exotic germplasm into elite cultivars(Tuberosa and Salvi, 2006). The GWAS and QTL mapping are the two important techniques that provide valuable insights into the genetic basis of abiotic stress tolerance and aid in developing stress-tolerant crop varieties. With the help of biparental linkage mapping, success has been achieved in mapping and identifying major genomic regions associated with stress tolerance. However, this technique failed to identify minor alleles responsible for tolerance to abiotic stresses.

On the other hand, GWAS allows a genome-wide analysis of markers associated with traits, and it is more powerful than the former method in detecting *QTLs*, for example, in rice (Anilkumar *et al.,* 2022), oilseeds(Kadirvel *et al.,* 2021), Wheat(Phuke *et al.,* 2022),and Maize (Sahito et al. 2024). These techniques can be successfully applied to improve abiotic stress tolerance in crops such as maize, wheat, and Rice. Once gene/QTL is identified and fine-mapped, it can be transferredto other backgrounds using marker-assisted backcross breeding. For instance, throughmarker-assisted backcross breeding major QTL, i.e., Saltol for seedling stage salinity tolerance and the gene *OsHKT1*; 5 located in the Saltol region was transferred in many of the rice varieties(Yadav *et al.,* 2020),and Sub1A QTL confers tolerance to submergence in deep water rice was another notable example for marker-assisted breeding for climate resilience(Wu *et al.,* 2020)showed higher expression levels under stress indicating its role in conferring salinity tolerance (Yadav *et al.,* 2020). Hence, the application of genomics for abiotic stress tolerance can lead to the introduction of economically viable crop types, which will boost productivity and adaptability under stress conditions.

Most economically significant traits are intricate, controlled by minor genes, and susceptible to epistatic interactions. Traditional breeding or MAS to improve these traits falls short of meeting the anticipated food demand. With the passage of time, advancements in sequencing technologies, decreased costs, and increased accessibility of genome sequences have contributed to the development of an enhanced version of MAS, known as genomic selection (GS). This innovation aids plant breeders in selecting lines according to genomic estimated breeding values (GEBV) for desired traits and provides the opportunity to utilise GS. Genomic selection (GS) can be regarded as a potent instrument that expedites the breeding cycle, decreases the expense of developing breeding lines, facilitates the selection of superior genotypes, and achieves rapid genetic gain. The genomic selection process begins with developing a training population (TP), which is then genotyped and phenotyped for the desired traits after integrating data with pedigree information (a kinship square matrix that quantifies pair-wise relationships among population individuals) to construct a GS prediction model that establishes a connection between genome-wide marker data and phenotypes. Subsequently, the model is implemented on an additional group of individuals, referred to as the breeding population (BP), which consists of genotyped but phenotyped individuals, to obtain genomic estimated breeding value (GEBV) information. Determining the GEBV of a breeding population undoubtedly enables selection to be hinged on marker data, obviating the necessity for laborious and expensive phenotyping. In the context of wheat, GS models were predominantly constructed to identify accessions that are most susceptible to the adverse effects of climate change. This was achieved using various GS methods and phenotypic data obtained from high-throughput phenotyping platforms. Phenotypic data ofheat and drought stress effects were examined across over a thousand advanced wheat lines on grain yield in two distinct environments. These lines are accessible through the International Maize and Wheat Improvement Center (CIMMYT). Integrating GS with high-throughput genotyping and phenotyping methodologies enhanced the precision of wheat breeding predictions and selections. Successful examples of applications of GS in rice(Anilkumar *et al.,* 2022) for various biotic and abiotic stresses, wheat (Phuke *et al.,* 2022), and maize (Sahito *et al.,* 2024).

3.2.2. Transcription Factors (TFs) Engineering and Genome Editing

Engineering transcription factors, which bind to specific DNA sequences and regulate gene expression, is a precise and efficient way to improve a plant's abiotic stress resilience(Farooq *et al.,* 2014; Zhuang *et al.,* 2014). TFs, such asMYB, WRKY, NAC, bZIP, and AP2/EREBP,were reported as master regulators in many crop plants in response to various environmental stimuli. These imply that transcriptional regulation of stress-responsive genes is a crucial step in understanding the mechanisms that underlie plant stress responses and abiotic stress tolerance(Wang *et al.,* 2016). TF engineering enables targeted gene regulation, improving stress tolerance and potentially increasing crop yields by overexpressing or modifying TF genes. For example, *MYB TFs* are involved in drought and cold tolerance.(Fang *et al.,* 2008) and(Le *et al.,* 2011)found an association of upregulated 40 NAC TFs in response to drought and salinity in the rice and soybean crop. Recent advances in molecular genetics have demonstrated the critical role of transcription factor (TF) engineering in improving plant tolerance to abiotic stresses. In a recent study, overexpression of the *TaWRKY2* gene in wheat (*Triticum aestivum* L.) significantly enhanced drought tolerance compared with non-transgenic plants, indicating that WRKY transcription factors play a pivotal role in activating drought-responsive pathways (Gao *et al.,* 2018). Similarly, members of the AP2/ERF transcription factor family, particularly *DREB2A* from *Arabidopsis thaliana*, have been shown to regulate the expression of multiple stress-inducible genes, thereby enhancing plant tolerance to drought and other abiotic stresses (Yoon *et al.,* 2020).

The functional versatility of AP2/ERF transcription factors has been validated across several crops. In *Phaseolus vulgaris*, AP2/ERFs confer tolerance to drought and salinity, while in soybean (*Glycine max*), *GmDREB* genes enhance resistance to cold, salt, and drought. In wheat, *ERF1-V* plays a key role in drought tolerance. In rice (*Oryza sativa*), multiple DREB family members, including *OsDREB1B* (temperature response), *OsDREB1E*, *OsDREB1G*, and *OsDREB1I* (drought response), have been functionally characterised for their regulatory role in abiotic stress adaptation. Likewise, in maize (*Zea mays*), *ZmEREB3* is associated with responses to cold, salt, and drought stress, whereas *ZmEREB46*, *ZmEREB60*, *ZmEREB137*, and *ZmEREB240* are primarily linked to drought tolerance (Ma *et al.,* 2024).

In addition to these, the overexpression of the wheat heat-shock factor gene *TaHsfA6bT* in barley (*Hordeum vulgare* L.) was confirmed through RNA-seq and qRT-PCR analyses, which demonstrated enhanced thermotolerance, underscoring the interspecies applicability of TF-based genetic improvement (Goche *et al.,* 2025). The adaptability of transcription factor engineering allows the tailoring of plant responses to specific stressors, reducing dependence on chemical inputs and supporting sustainable agricultural systems.

However, transcription factor engineering also presents several challenges. The approach is technically complex and may lead to off-target effects due to the pleiotropic nature of gene regulation. Moreover, large-scale adoption faces obstacles such as regulatory restrictions, high development costs, and unpredictable environmental interactions, particularly in resource-limited regions. Therefore, a comprehensive and balanced strategy–integrating molecular, physiological, and field-based evaluations–is essential to effectively harness transcription factor engineering for the development of abiotic stress-tolerant crops (Fig. 2).

With genome editing, specific genomic loci can be precisely modified to introduce desired traits linked to resistance to abiotic stress. Site-directed nucleases (SDNs) and oligonucleotide-directed mutagenesis (ODM) are two categories that fall under the broader umbrella of new plant breeding techniques (NPBT). Both enable exactly directed mutagenesis, gene transfer, and expression control. A potent and frequently used genome editing technique, clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated protein 9 (Cas9), enables the rapid development of abiotic stress-tolerant plants by making precise changes in the DNA sequence(Zafar *et al.,* 2020). The CRISPR/*Cas9* system enables the removal of deleterious alleles and the introduction of beneficial alleles into elite cultivars, thereby avoiding linkage drag. The efficiency of the CRISPR system relies on a specifically designed single-guide RNA (sgRNA) complementary to the specific genomic regions under study. However, off-target deletions could occur due to the binding of sgRNA to unintended sites. Likewise, Zafar et al. (2020) introduced two new terms: sensitivity genes (S genes) and tolerance genes (T genes), which determine the positive or negative response of plants to abiotic stresses. For instance, abiotic stress increases the activity of papain-like cysteine proteases (PLCPs) in various plant species, including wheat and sweet potatoes *(SPCP2*). S genes, which negatively regulate abiotic stresses, have been underexplored so far. Thus, knocking out S genes may contribute towards stress tolerance by disrupting the pathways involved. For instance, the E3 ubiquitin ligase *Oryza sativa* stress-related RING finger protein 1 (*OsSRFP1*) increases the production of H2O2 (a significant ROS species) and decreases the activity of antioxidant enzymes in plant tissues, acting as a negative regulator for a variety of abiotic stresses(Fang *et al.,* 2008). Scientists have utilised the CRISPR-Cas9 tool to inactivate sensitivity genes (S genes) and enhance tolerance genes (T genes), thereby developing crops with improved tolerance to abiotic stress. It boosts yield potential under abiotic stress by producing non-transgenic plants with the required characteristics. Likewise, the development of chickpea transgenic lines by knockout of *4CL* and *REV7* genes exhibits drought tolerance and paves the way for future research in chickpeas. Although this system is relatively easy to use and more precise compared to other genome editing technologies, there are still some issues, including the potential for off-target mutations, regulatory hurdles, public perception and ethical concerns surrounding genetically modified organisms (GMOs), and the need for ongoing research to understand the long-term environmental and health consequences and impacts on biodiversity and ecosystems(Kim *et al.,* 2018). Considering its potential benefits and drawbacks, a balanced approach is crucial for the responsible and effective use of this technology in agriculture. Applications to abiotic stresses are still primarily limited to model species, such as Arabidopsis. Still, soybean and cocoa have shown promising drought and salt tolerance results by disrupting the *Drb2a* and *Drb2b* genes. Complex genetic mechanisms control abiotic stresses, which may require the simultaneous tuning of different genes (i.e., regulatory sequences and SNP editing); for biotic stresses, knocking out single genes (i.e., susceptibility genes) may produce the desired phenotype. New target genes, technical development for *SDN1* and *SDN2* approaches, and harmonised edited crop laws are needed to inspire a new generation of breeders.

3.2.3. Targets Induced Local Lesions In Genomes (TILLING)

Traditionally, TILLING protocols screened the population and selected mutagenised lines using enzymatic or physical methods. Loss-of-function, gain-of-function, and hypomorphic alleles can be associated with specific phenotypes. TILLING, next-generation sequencing, and multidimensional pooling can accelerate the identification of rare alleles in a population. Tilling by sequencing has found allelic variants underlying climate-responsive agronomic traits. TILLING identified new allelic variants of the Hsp26 gene family related to wheat heat stress and thermal tolerance. TILLING was used to create barley mutants to study nucleotide variations in the era1 (enhanced response to ABA1) gene, which is regulated differently in wheat and soybean in relation to drought tolerance. Modifications to traditional or sequencing-based TILLING have been proposed. A reverse-genetic method termed De-TILLING (Deletion Targeting Induced Local Lesions IN Genomes) has been developed to identify knockout mutations, facilitating the detection of extensive gene deletions or null alleles resulting in complete loss of function. EcoTILLING is utilised to identify natural allelic variation among individuals within a species, including humans. It is particularly effective for evaluating genetic diversity and identifying adaptive alleles associated with environmental resilience. Both techniques enhance traditional TILLING by aiding in the identification of allelic variants that contribute to crop adaptation to extreme agro-climatic conditions, as well as both biotic and abiotic stresses.

TILLING has been effectively employed in rice (*Oryza sativa* L.) to generate stress-tolerant mutants. Mutagenized lines from the rice variety BINA-7 demonstrated improved salt tolerance due to modifications in genes associated with ion transport and homeostasis, specifically *OsAKT1, OsHKT6, OsNSCC2, OsHAK11*, and *OsSOS1*, which are responsible for potassium uptake, sodium exclusion, and cellular osmotic balance. The functional characterisation of these genes illustrates the effectiveness of TILLING in identifying novel allelic variants associated with mechanisms of abiotic stress tolerance.

TILLING has been effectively utilised in various crop species to identify both induced and naturally occurring mutations linked to significant agronomic traits. In barley (*Hordeum vulgare* L.), novel alleles have been identified in key genes, including *HvCO1, Rpg1, eIF4E, HvHox1, BMY1, GBSS1, LDA1, SSI, SSIIa, mlo,* and *Mla,* which are linked to the regulation of flowering time, disease resistance, and starch metabolism. Mutations in chromatin modification and epigenetic regulatory genes, such as *DMT101, DMT102, DMT103, DMT106, HAC110,* and *HDA105,* have been identified in maize (*Zea mays* L.). In wheat (*T. aestivum* L.), TILLING has identified allelic variation in *Ppd-1*, which is associated with photoperiod sensitivity, as well as in *Rubisco activase A* and *Rubisco activase B*, genes essential for photosynthetic efficiency and thermal tolerance (Dwivedi et al, 2017; Siyal *et al.,* 2024)

TILLING and its derivative methods, De-TILLING and EcoTILLING, serve as effective non-transgenic tools for functional genomics, allelic mining, and precision breeding. The application enables the identification and utilisation of advantageous genetic variations, thereby expediting the development of stress-resilient and climate-adapted crop cultivars.

3.2.4. Other biotechnological approaches

Plants with enhanced abiotic stress tolerance have been developed using biotechnological technologies, including genetic engineering, proteomics, metabolomics, and transcriptomics (Villalobos-López *et al.,* 2022). The transfer of genes from one organism to another to confer a specific trait is known as genetic engineering, whereas proteomics and metabolomics are the studies of proteins and metabolites, respectively (Anwar and Kim, 2020; Raj and Nadarajah, 2023). Researchers have utilised these techniques to identify the genes, proteins, and metabolites involved in abiotic stress tolerance and generate plants with enhanced tolerance. Researchers have employed this technique to identify genes involved in abiotic stress tolerance and generate plants that are more resistant to stress (Zhuang *et al.,* 2014). Other methods, such as Gene pyramiding, RNA Interference (RNAi), Microbiome Engineering, and tissue culture-assisted breeding, have also been utilised to enhance tolerance to multiple abiotic stresses simultaneously, providing a broader spectrum of resistance in crops(Chen *et al.,* 2021; Younis *et al.,* 2020).

3.3. Integration of Speed breeding technologies with other breeding tools to enhance climate resilience in crop plants

Classical plant breeding methods enabled the achievement of the Green Revolution during the 1960s. However, the current growth of agricultural production is not in pace with future food demand. Hence, there is a need to breed new crop varieties that are multi-stress tolerant, climate-smart, and high-yielding. However, asignificant hurdle with traditional plant breeding methods is the time required for the generation's advancement, which is line fixation (making segregating lines nearly homozygous). At least it takes 10-12 years to releasea variety for commercial cultivation. Breakthroughs in molecular and genomics tools can accelerate the breeding process and handle large populations with precise gene transfer, trait introgression, and pyramiding or stacking of multiple genes with high efficiency, which is now a reality. "*Speed breeding*" is one such approach that drastically reduces generation time to advance to the next generation, thereby achieving accelerated breeding cycles. The main principle behind speed breeding is the use of an optimised photoperiod, combined with high-quality light, temperature, and nutrients, which can enhance the rate of photosynthesis, early flowering, and early seed harvest (Ahmar *et al.,* 2020). However, speed breeding alone is not sufficient to achieve all the success. Therefore, holistic breeding approaches must include novel breeding and biotechnological tools and techniques that enable rapid line development, efficient evaluation and an overall enhanced rate of genetic gain.

A combination of speed and marker-assisted breeding is a promising approach for delivering products rapidly. Speed breeding can be integrated with high-throughput genotyping and phenotyping to accelerate line development and trait introgression,thereby fast-tracking trait introgression in breeding programs. Additionally, speed breeding can be combined with genome editing to accelerate product development (Abdul Fiyaz *et al.,* 2020).The classical breeding method takes 10-12 years to develop and release new varieties, whereas marker-assisted selection approaches require 4-5 years to achieve the same goal. However, the integration of marker-assisted breeding with a speed breeding approach reduces the time required for product development by half, as rapid genetic gain can be achieved(Samantara *et al.,* 2022).

Another improved version of MAS is genomic selection. This technique can eliminate all genetic variation in the breeding material and achieve high selection accuracy based on GEBV, without requiring any phenotypic dataset. This enables the rapid selection and intercrossing of individuals in the early generation with higher breeding value. With speed breeding, there is an opportunity to accelerate line development and product delivery.

Further, speed breeding can also be integrated with genome editing tools called "express edit" to boost the breeding process. Genome editing tools can precisely modify the targeted gene, and subsequent mutants developed through genome editing can be advanced through speed breeding to select desirable plants rapidly (Hickey *et al.*, 2019). Some of the fundamental limitations include the high initial cost of establishing a speed breeding facility and the need for additional trained personnel to operate and maintain this facility. Nevertheless, low-cost, LED-based protocols can now be modified to meet our specific needs.

3.4. Phenotyping approaches

The economically significant trait yield reached a plateau in most food crops. By 2050, crop productivity must double to meet the projected food demand of the ever-growing population (Hunter *et al.*, 2017). Plant breeding primarily relies on the phenotype, the function of the genotype (G), the environment, and genotype-by-environment (GxE) interactions. As a result, significant efforts have been made in recent years to incorporate trait-based genomic techniques into traditional approaches to crop improvement (Fig. 3). Nevertheless, phenotyping remains an essential element of plant breeding, as the effectiveness of these genomics approaches largely depends on the phenotypic expression of the targeted trait. Phenotyping remains a significant limitation in understanding the genetic basis of complex traits that contribute to productivity, biotic stress, abiotic stress, and quality, despite the availability of genomic techniques and genomic data generated for breeding populations. There is a need for dependable, precise, automatic, and high-throughput phenotypic technologies to eliminate these phenotyping bottlenecks and improve the efficiency of breeding programs (Mir *et al.*, 2019).

3.4.1. Conventional approaches

Although traditional phenotypic selection can be a demanding and time-consuming process, it has helped develop new crop varieties that perform better in diverse environments and can aid in feeding a growing world population. It has been effectively utilisedto develop cultivars with better resilience to various stresses. Utilising phenotypic selection, several different

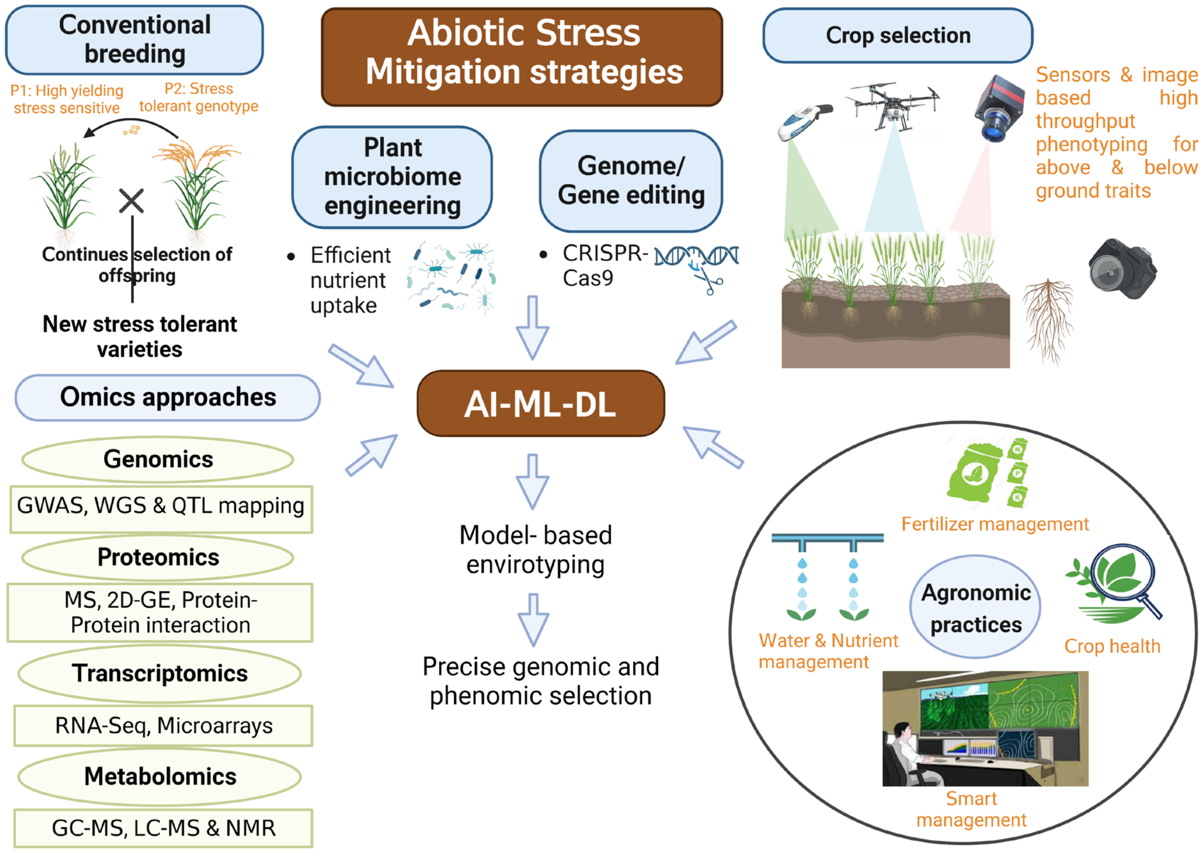


Fig. 3: Range of strategies that consider the effects of climate change to reduce the impact of abiotic stresses on the development of future crops. Created with BioRender.com

phenotypic traits, such as root traits, osmotic adjustment, canopy temperature, glycine betaine content, and potassium uptake and utilisation efficiency, have been evaluated(Cakmak, 2005; Richard *et al.,* 2015; Sukumaran *et al.,* 2021). In response to various environmental stimuli, plant physiological parameters such as chlorophyll content, the efficiency of PS II, net assimilation rate, transpiration, stomatal conductance, and intercellular CO2 concentration are modified, leading to reduced growth, development, and ultimately, decreased crop productivity. Different crop varieties and their wild relatives may possess unique physiological traits that can confer stress tolerance. So, by screening their diversity, every researcher or breeder wants to explore and utilise the novel source of stress tolerance in a breeding program. Physiological traits, such as canopy temperature (CT) and the normalised difference vegetation index (NDVI), have successfully assessed critical physiological responses in abiotic stress tolerance. Because of their direct association with crop water uptake and stay green type traits, which significantly contribute to the grain yield of the crop. Advanced breeding lines can be developed using CT, NDVI, and SPAD to stay green, as well as biomass potential and grain yield component characteristics in breeding for abiotic stress tolerance(Ramya *et al.,* 2016). Similarly, Infrared (IR) and chlorophyll fluorescence imaging enable the differentiation of stress response mechanisms through pixel-wise thermal image analysis for canopy temperature, which is significant for plant improvement perspectives in the days ahead(Taria *et al.,* 2020).However, the genetic dissection of crucial traits and understanding of the underlying mechanism requires comprehensive phenotyping of a large population, which varies from thousands to millions of plants. Traditional screening methods are expensive, time-consuming, and tiresome for such a large population. Further, trait expression is also influenced by environmental and management factors (G × E × M) (Dwivedi *et al.,* 2016, 2021).Thus, using modern tools and technologies, such as high-throughput phenotyping, can accelerate the phenotypic selection process and enable the evaluation of many traits(Araus and Cairns, 2014; Khan *et al.,* 2018).

3.4.2. High throughput phenotyping

Recent advances in phenomics have enhanced phenotyping protocols, making them more effective than ever in dissecting complex traits into easily scoreable components(Basavaraj *et al.,* 2023; Basavaraj and Rane, 2020). Some of the robust tools and phenotyping platforms available for various traits are described in Tables 2 and 3.

Table 2. Phenotyping tools and high throughput platforms for phenotyping of various crops

Phenotyping tools	Trait Measured	Applications	Reference
Above ground traits			
Plot Harvester	Grain yield	Yield measurement	Araus *et al.* (2012)
IR camera	Canopy temperature	Transpiration, stomatal behaviours	Fuchs (1990)
NDVI meter	Vegetation	Plant Health status, canopy greenness	Xia *et al.* (2016)
SPAD Meter	Greenness of leaves	Chlorophyll content and leaf nitrogen status	Ghimire *et al.* (2015)
Phenocart	Spectral signatures and plant Height	Phenotyping of large number of plants	Crain *et al.* (2016)
Drone	Digital area, canopy, canopy greenness, plant height	Large scale field phenotyping	Wan *et al.* (2019)
RGB Camera	Digital biomass, Canopy architectural traits	Proportion of green, blue, red colours, senescence pattern, canopy colour	Li *et al.* (2023)
LiDAR	Architecture of canopy	Structure of canopy	Jin *et al.* (2020)
IRGA	Gas exchange parameters	Stomatal conductance, respiration, net photosynthesis	Douthe *et al.* (2018)
Ceptomete	Leaf dimensions	Measuremnt of leaf area and leaf area index	Pokovai and Fodor (2019)

	Below Ground traits		
RADIX	Root system architecture	Monitoring and measurement of roots, distribution	Le Marié *et al.* (2016)
RhizoTubes	Measurement of root traits	Root system architecture	Jeudy *et al.* (2016)
Rhizoponics	Root system architecture	Monitoring and measurement of roots, distribution in *Arabidopsis*	Mathieu *et al.* (2015)
GROWSCREENRhizo	Root and shoot phenotyping	Monitoring and measurement of roots, distribution in *Arabidopsis*	Nagel *et al.* (2012)

Table 3. Controlled Phenotyping platforms available for different crops and traits (Modified from Li *et al.,* 2021)

Phenotyping platform and Institute	Sensors available	Traits measured	Crop (s)	Reference
Lemna Tech, ICAR-National Institute of Abiotic Stress Management, Baramati, India	RGB, IR, NIR	Senescence, tissue water content, Canopy temperature, growth rate, biomass	Major grain legumes	Personal Communication with Basavaraj PS
Lemna Tech, ICAR-Central Research Institute for Dryland Agriculture, Hyderabad, India	RGB, IR, NIR	Senescence, tissue water content, Canopy temperature, growth rate, biomass	Sorghum, maize	Personal Communication ICAR-CRIDA
Lemna Tech, ICAR-Indian Institute of Horticulture Research, Benagaluru, India	RGB, IR, NIR	Senescence, tissue water content, Canopy temperature, Biomass, plant height, width, compactness, drought stress	Tomato and other horticulture Crops	Personal Communication Laxman HR
Lemna Tech, ICAR-Indian Agricultural Research Institute, New Dehli, India	RGB, IR, NIR, Flouro	Senescence, tissue water content, Canopy temperature, PSII Efficiency	Wheat and Rice	Personal Communication IARI
LemnaTec Scanalyzer 3D, Germany	RGB, NIR, FLUO	Biomass, plant height, width, Growth rate, drought tolerance	Barley	Chen *et al.* (2014); Neumann *et al.* (2015)
LemnaTec Scanalyzer 3D, USA	Hyperspectral, RGB, NIR, FLUO	Tissue water content, Biomass, growth rate, senescence	Barley, corn, sorghum	Miao *et al.* (2020)
LemnaTec Scanalyzer 3D, Austrelia	RGB, NIR, FLUO, hyperspectral	Salinity tolerance, leaf water content, N content,	Chickpea, wheat	Atieno *et al.* (2017); Bruning *et al.* (2019)
Bellwether, USA	RGB, NIR, FLUO	Shoot length, water content, biomass, growth rate	Millets	Fahlgren *et al.* (2015)
HRPF platform, China	RGB, CT	Water stress tolerance, tillers count	Rice	Duan *et al.* (2018)
LemnaTec Scanalyzer HTS, USA	RGB, FPUO, NIR	Drought stress	Arabidopsis	Acosta-Gamboa *et al.* (2017)

Additionally, this helps reveal the underlying genetic processes involved in the expression of traits. In this section, we described the importance of phenotyping for climate-smart agriculture. More recent techniques involving the reflectance of electromagnetic spectra across different ranges promise to facilitate the development of high-throughput phenotyping tools for assessing various adaptive features of plants that exhibit differential physiological and metabolic responses to stress. These techniques and protocols can bridge the gaps in the conventional evaluation of stress-tolerant traits, which are laborious, time-consuming, and prone to error when assessing thousands of germplasm or breeding lines. Technological advancements and high-throughput techniques have made it possible to collect extensive data on plant genotypes and phenotypes, which requires additional effort to derive meaning from these measurements and integrate different datasets.

Machine vision holds considerable promise in the field of plant phenotyping, particularly in evaluating plant responses to stressors. Many imaging techniques are employed in machine vision to automatically record plant responses, often within a framework known as high-throughput plant phenomics (Buckner *et al.,* 2021). These devices can detect electromagnetic radiation at various wavelengths, including visible, infrared, and near-infrared. Hyperspectral imaging systems primarily provide spectral signatures of the observed items, designed to record the reflectance characteristics of objects across different wavelengths (Elvanidi *et al.,* 2018).There is ample proof that these cutting-edge imaging techniques help analyse how plants react to stress situations and identify relevant genes using phenotypic data.

Imaging, as mentioned above, produces either accurate or false images, which must be processed using the proper algorithms to extract the characteristics and create the necessary parameters for evaluating the plant reactions. These characteristics can serve as surrogate traits for the efficient screening of many genotypes, as they consistently correlate with stress responses and adaptability. For example, biomass, a standard shoot metric used to evaluate plant stress responses, can be revealed in the region of plant photos recorded from various angles using high-resolution cameras in the visible electromagnetic spectrum (Rane *et al.,* 2021). Further, surrogate traits such as digital plant area, which represents plant biomass, have been utilised to distinguish plant responses across genotypes(Rahaman *et al.,* 2017). Modifications in shoot architecture, such as reduced leaf area or size, mainly due to reduced cell elongation, can be captured by imaging systems combined with appropriate algorithms for image analysis (Amal *et al.,* 2020).Therefore, image-derived parameters, *viz*, calliper length, compactness, eccentricity, and boundary point ratio, can serve as surrogate indicators elucidating stress-induced morphological changes in plants(Feng *et al.,* 2020).

These imaging systems generate large datasets that require appropriate computational algorithms to extract physiologically relevant traits. When image-derived traits exhibit consistent correlations with stress responses and adaptability, they can serve as surrogate traits for efficiently and objectively screening large numbers of genotypes.

Biomass estimation, a commonly used parameter for assessing stress tolerance, can be obtained from multi-angle images captured by high-resolution RGB cameras operating in the visible spectrum (Rane *et al.,* 2021). Derived indices, such as digital plant area, have been effectively used to distinguish genotype-specific stress responses in crops like rice, wheat (*T. aestivum*), and barley (*H. vulgare*) (Rahaman *et al.,* 2017). Structural modifications in shoots, including reduced leaf area, rolling, or folding, which occur as adaptive responses to drought or salinity, can be detected through imaging systems integrated with automated algorithms (Amal *et al.,* 2020). Image-derived geometric features such as calliper length, compactness, eccentricity, and boundary point ratio are also useful for quantifying morphological alterations under stress (Feng *et al.,* 2020).

Near-infrared enhanced the crop's root and shoot length (in f water status and classified genotypes based on relative water content (Chen *et al.,* 2020). Thermal imaging, widely applied in rice, wheat, and maize (*Zea mays*), provides an effective means to monitor canopy temperature and transpiration efficiency under drought and heat stress (Ninanya *et al.,* 2021). Similarly, chlorophyll fluorescence imaging has been employed in crops such as barley and wheat to evaluate photosynthetic efficiency and the performance of photosystem II (PSII) and electron transport components under stress conditions (Faseela *et al.,* 2020).

In rice, RGB and thermal imaging systems, such as those from LemnaTech and FLIR-SC-620, have been used to quantify shoot biomass, ion concentration, canopy temperature, relative water content, and stomatal conductance under salinity stress. In barley, multi-angle RGB imaging using the Plant Accelerator platform has characterised shoot biomass, ion concentration, and performance indices under both drought and salt stress. In wheat, hyperspectral imaging with LemnaTech has been used to measure Na uptake, K /Na ratio, root biomass, and harvest index under salinity stress. Meanwhile, thermal and hyperspectral imaging systems have assessed relative growth rate, plant height, tiller number, and water-use efficiency under drought stress. In maize, hyperspectral imaging using PHENOVISION has been used to evaluate root architecture, anthesis-silking interval, drought tolerance index, and grain yield. In sorghum (*Sorghum bicolor*), UAV-based multispectral and hyperspectral imaging has captured canopy traits such as NDVI, stay-green value, chlorophyll content, leaf rolling, and biomass under drought stress. Additionally, root phenotyping systems such as GrowSCREEN-Rhizo and WinRHIZO Pro have been applied to barley, wheat, and rice to analyse nodal root angle, root biomass, and architectural traits crucial for water and nutrient uptake under limiting conditions (Islam et al. 2021)

Integrating multiple imaging modalities–RGB, thermal, hyperspectral, NIR, and chlorophyll fluorescence–provides a multidimensional understanding of plant stress physiology. When combined with artificial intelligence and machine learning algorithms, these systems enable automated genotype classification, stress prediction, and trait quantification with high precision. Collectively, imaging-based high-throughput phenotyping bridges the gap between genomics and physiology, accelerating the identification of stress-resilient genotypes in crops such as rice, wheat, barley, maize, and sorghum, and supporting sustainable crop improvement under climate change.

3.5. Exploring Artificial Intelligence (AI) and Machine Learning (ML)

AI and machine learning have advanced rapidly and are now extensively employed in plant genotyping and phenotyping. More importantly, genomics involves acquiring molecular data of phenotypes and usingpractical data mining tools to predict and describe them. Machine learning can gain new biological insights by predicting gene function and interactions among various cellular components (Fig. 3). Crop phenomics, enviromics, and other "omics" approaches reveal the complex biological mechanisms that drive crop functions in response to environmental threats. This review will discuss how AI and ML technology, used in breeding, help solve the problem of high-throughput phenotyping and gene functional analysis and how AI technology advances will open new breeding opportunities to use envirotyping data.

Current breeding methods make genotype-to-phenotype linking difficult, limiting high-throughput field phenotyping, genomics, and enviromics. AI has become a revolutionary field, offering substantial computational power and many new tools and strategies for crop breeding. This progress can be attributed to the increased development and availability of new technologies that enable high-throughput phenotyping of complex plant traits. In recent years, the use of AI in various scientific fields has expanded significantly, with the development of software and tools for data gathering and management in field phenotyping. For example, using AI-powered agricultural drones enables farmers to perform necessary crop management practices and monitor their fields from above using non-invasive imaging. Through the use of ML for robust image analysis, this integration steadily enhances the efficiency of data gathering and analysis. Machine learning algorithms(MLA) can create climate change models by evaluating vast datasets from multiple sources (e.g., satellite imagery and weather stations). Based on these algorithms, scientists can predict the patterns and correlations of climate change and its impact on agriculture(Saxena *et al.,* 2023).These technologies can accelerate the elucidation of genotypic differences in adaptive traits and potentially revolutionise crop breeding strategies, leading to improved food security in a changing climate.Hence, AI and MLA are instrumental in researching and developing stress-resilient crop varieties by facilitating the rapid and precise analysis of plant stress responses(Kumar *et al.,* 2022; Rico-Chávez *et al.,* 2022).

Machine vision emerged as an invaluable ally, bridging the gap between the intricate visual data captured and the meaningful biological insights that can be derived.

Through the lens of machine vision, the seemingly ordinary pixels in plant images are transformed into a treasure trove of information, offering profound insights into plant responses to drought stress (Ramos-Giraldo *et al.,* 2020). Through the fusion of imaging technologies, data analytics, and AI-driven algorithms, machine vision unlocks the secrets hidden within plant pixels, revealing phenotypes that arecritical indicators of a plant's resilience to drought (Dirk *et al.,* 2021). This potent combination of phenotypes and pixels is a prime example of how machine vision canrevolutionise crop improvement in the future, ensuring food security and mitigating the effects of climate change(Ampatzidis and Partel, 2019).

Machine learning (ML) and deep learning (DL) have revolutionised modern crop breeding by enabling predictive phenomics and data-driven selection strategies. ML has significantly accelerated breeding pipelines through integrative platforms, such as TERRA-REF, which facilitate standardised data sharing, minimise redundant experimentation, and foster collaboration among experts worldwide. These computational approaches have resolved fundamental challenges in genomics and phenomics by enabling real-time, high-dimensional data analysis and trait prediction across diverse environments.

Various ML frameworks have been successfully implemented for stress detection and prediction in multiple crops. For instance, supervised ML algorithms such as Random Forest (RF), Support Vector Machine (SVM), and K-Nearest Neighbour (KNN) have been used for classification and prediction of real-time terahertz time-domain spectroscopic data (THz-TDS) to detect water stress in basil (*Ocimum basilicum*), coriander (*Coriandrum sativum*), parsley baby leaf (*Petroselinum crispum*), coffee (*Coffea arabica*), and pea (*Pisum sativum*). Similarly, SVM and Gaussian Processes Classifiers (GPC) have been applied for abiotic stress identification in spinach (*Spinacia oleracea*) using visible and thermal imaging data (Table 5). In wheat (*Triticum aestivum*), supervised ML models such as Relief and SVM have been utilised for image-based identification and classification of genotypes under salt stress conditions. Additionally, the Dirichlet Aggregation Regression (DAR) framework has been employed to predict abiotic stress responses in barley (*Hordeum vulgare*) using hyperspectral imaging datasets (Gou et al. 2023). Collectively, these examples highlight the increasing potential of ML and DL frameworks in deciphering complex stress–response networks and enabling rapid, non-destructive evaluation of plant phenotypes. Integration of such computational models with high-throughput phenotyping platforms promises to enhance selection accuracy, reduce breeding cycle duration, and accelerate the development of climate-resilient crop varieties.

Furthermore, the Integration of AI into genome editing is currently being exploited to identify target prediction and design sgRNAs with increased specificity and improved efficiency. Abadi et al, (2017)designed a computer algorithm using an ML framework called CRISPR Target Assessment (CRISTA) to predict the genome's target. The predictions made with CRISTA were found to be more accurate and precise compared with other available methodologies. Increasingly, ML methodology has been used in genomic prediction, genomic selection, and marker-assisted selection. Many agricultural companies, such as Monsanto and John Deere, have invested hundreds of millions of dollars in developing technologies that utilise extensive data on soil type, seed variety, and weather to help farmers reduce costs and enhance yields. Additionally, they may access farm equipment data that is wirelessly transmitted to the cloud. Summit, the world's most powerful supercomputer, was recently unveiled with the potential to hold 27,000 GPUs, paving the way for a bright future. AI has the potential to be a game-changer in the near future, potentially bringing about an agricultural revolution and enhancing global food security.

3.6. Crop Agronomy and Improving Nutrients

The adoption of best and appropriate agronomic management practices, such as timely sowing, effective nutrient and water management, conditional crop planning, and protective control measures at sensitive periods of crop growth, is the main focus of the climate-smart (CS) technological approach.

3.6.1. Improving nutrient and water use efficiency

Amongst the modern approaches, the use of plant growth-promoting rhizobacteria (PGPR) under abiotic stress conditions has demonstrated improved root growth, soil productivity and soil fertility. Hence, engineering the plant microbiome through the introduction of stress-tolerant

Table 4: Recent studies published for abiotic stress tolerance using genomics approach in major cereals

Crop	Method	Stress	Population	Parentage	Targeted trait	Marker	Reference
Rice (***Oryza sativa***)	QTL mapping	Drought	39 CSSLs	Sasanishiki X Habataki	Grain yield Flowering time Spikelet fertility	SSR	Zhu *et al.* (2017)
	QTL mapping	Cold stress	F 2:3 progenies	BR1 X Habiganj Boro VI	Low-temperature tolerance	SNP	Biswas *et al.* (2017)
	QTL mapping	Flooding stress	Recombinant inbred lines	Indra X AC39416A	Submergence tolerance	104 SSR marker	Girija Rani *et al.* (2023)
	QTL mapping	Salinity stress	181 BC1F2	indica landrace Wujiaozhan X japonica Nip	High germinability	157 SSR or InDel markers	Zeng *et al.* (2021)
	GWAS	Heavy metal stress	276 accessions	Global-wide rice diversity panel	Accumulation of toxic heavy metals and metalloids	416 K SNPs	X. Liu *et al.* (2019)
Maize (***Zea mays***)	GWAS	Nitrogen starvation	410 inbred lines	Association panel	Grain yield and quality	26 K SNPs	Ndlovu *et al.* (2022)
	GWAS	Salinity	305 inbred lines	Association panel	Flowering and yield related trait	96 K SNPs	Zaidi *et al.* (2022)
	GWAS	Drought and heat stress	300 inbred lines	Association panel	Flowering and grain yield	38 K SNPs	Yuan *et al.* (2019)
	GWAS	Trace element deficiency and toxicity stress	489 inbred lines	Association panel	trace element accumulation in kernels	1.25 million (M) SNPs	Zhao *et al.* (2022)
Wheat (Triticum sp.)	GWAS	Salt Stress	153 diverse wheat genotypes	Diverse wheat genotypes	leaf chlorophyll content (CC) canopy temperature (CT) and specific leaf area (SLA)	11 K SNPs	Said *et al.* (2022)
	QTL mapping	Drought stress	183 backcross inbred lines (BILs)	HD2733 X 2*C306	14 physiological and yield related traits	35K Axiom SNP array and 86 SSR	Puttamadanayaka *et al.* (2020)
	GWAS	Cold stress	543 accessions	Association panel	Seedling stage low temperature tolerance	90K Illumina iSelect SNP array	Zhao *et al.* (2020)

	QTL mapping	Heavy metal stress	181 doubled haploid lines (DHLs)	UI Platinum X LCS Star	Grain Cd content	90k SNP assay	Qiao *et al.* (2021)
	QTL mapping	Heat stress	134 backcross inbred lines	WH730 X HD2733	Physiological and yield related traits	1350 SSRs	Sunil *et al.* (2020)
Chickpea (*Cicer arietinum*)	GWAS	Drought stress	Multi-parent advanced generation intercross (MAGIC)	Eight founder parents	Days to flowering maturity plant height biomass 100 seed weight and harvest index	57K SNPs	Thudi *et al.* (2023)
	GWAS	Salinity stress	138 genotypes	ICARDA	Salinity tolerance	2500 SNP and 3031 DArT markers	Ahmed *et al.* (2019); Ahmed *et al.* (2021)
	QTL mapping	Heat Stress	RILs	DCP 92-3 X ICCV 92944	Physiological and yield related traits	788 SNP markers	Jha *et al.* (2021)
Soybean (*Glycine max*)	GWAS	Drought stress	259 released cultivars	Chinese soybean cultivars panel	Seed germination	4616 SNPs	Liu *et al.* (2020)
	GWAS	Flooding stress	384 soybean plant introductions	Soybean Germplasm Collection	Flooding tolerance	31125 SNPs	Wu *et al.* (2020)
	GWAS	Salinity stress	305 soybean accessions	255 Cultivated and 50 wild soybeans	Leaf scorch score chlorophyll content ratio leaf sodium content and leaf chloride content	37573 SNPs	Do *et al.* (2019)

Table 5: Machine learning-based approaches for the identification classification quantification and prediction of abiotic stress responses in plants (Modified from Gou et al. 2024)

AI Techniques	Algorithms	Application	Datasets	Model plant	Stress
Deep Learning	Convolutional Neural Networks (CNN) Alex Net Google net InceptionV3 Least PLS-DA LSVSM.	Identification	1200 photos taken by camera under stress and non-stress conditions	Maize okra soybean	Water tension
SVM and Gaussian processes classifier (GPC)	SVM and Gaussian processes classification	Identification	Visible and thermal images	Spinach (*Spanicia oleraceae*)	Abiotic stress
Unsupervised Machine Learning	Convolutional Neural Networks (CNN) AlexNet Google net PLSDA Least squares support vector machine LS-VSM	Identification	Hyperspectral images of canopy of tobacco plants	Tobacco	Heavy metal stress

Unsupervised Machine Learning (Video Imaging)	Hidden Markov's model (HMMs)	Identification and Classification	Chlorophyll fluorescence digital profiles from Grow Tech Inc.	*Phaseolus vulgaris*	Stressor level groups (Low medium and high stressed) and drought nutrient and chemical stress
Unsupervised Machine Learning Partial Least Square Regression Principal Component Analysis	CNN	Identification and Classification	Spectral signature of leaf samples obtained with a visible near infrared spectrometer	Rice	Salt stress
Supervised Machine Learning	Relief Support vector machine	Identification and Classification	Images from four wheat lines	Wheat	Salt stress
Deep Learning		Identification and Classification	Hyperspectral images	*Bromus inermis*	Drought stress
Supervised Machine Learning	Random Forest (RF) Support Vector Machine (SVM) KNN	Classification and prediction	Real-time tetrahertz time-domain spectroscopic data (THz-TDS)	Basil coriander parsley baby-leaf coffee pea	Water stress
Supervised Machine Learning	RF Artificial neural network (ANN) and confident multiple-choice learning	Classification	Multispectral images	Maize	Water stress
Supervised Machine Learning	Confident multiple-choice learning	Identification and prediction	Gene expression time series datasets	*Arabidopsis thaliana*	Heat cold salt and drought
Single Ventricle Interactive Model (SViM)	SViM	Identification	Hyperspectral	Tomato	Water stress
Deep Learning (Image)	CNN	Classification	Images of Sorghum plant shoot from the Donald. Danforth Plant ScienceCentre	Sorghum plants	Nitrogen deficiency
Supervised Machine Learning	Decision tree (DT) SVM Naïve Bayes (NB)	Classification	Metabolite and protein content	*Arabidopsis thaliana*	Metabolic stress
Supervised Machine Learning	SVM	Classification	Biweekly RBG stereo and hyperspectral spatio-temporal images	Sugar beet plants	Drought and weed stress nitrogen deficiency
Linear discriminant analysis (LDA) and K-means	Linear discriminant analysis (LDA) and K-means	Identification and Classification	RGB images	Clover (*Trifolium subterraneum L.)*	Pollution

Supervised Machine Learning	Hierarchical models	Classification	5916 RGB images plant introduction accessories (PI) in different time points	Soybean (*Glycine max*)	Iron deficiency chlorosis
Supervised Machine Learning	ANN CNN Optimum path stress KNN and SVM	Classification	Electrical signal under cold low light and osmotic stimuli	Soybean plants	Cold low light and osmotic stimuli
Supervised Machine Learning	RF	Classification	Hyperspectral dataset acquired from Indian Agricultural Research Institute (IARI)	Wheat	Water stress
Deep Learning (Image)	CNN SVM	Classification	65184 labeled images from GitHub resource	Soybean	Biotic and abiotic stresses
Supervised Machine Learning	MLP and probabilistic neural network (PNN)	Classification	16 maize and 17 wheat genomic and phenotypic datasets with different trait-environment combinations	Maize and wheat	Drought
Supervised machine Learning	Decision tree (DT) and NB	Prediction	miRNA concentration	*Arabidopsis thaliana*	Drought salinity cold and heat
Supervised Machine Learning	Ridge regression LASSO elastic net RF reproducing kernel Hilbert space Bayes A and Bayes B	Prediction	A set of 29619 cured single nucleotide polymorphisms. Genotyped across a panel of 240 maize inbred lines	Maize	Drought stress
Deep Learning	CNN	Prediction	Three maize arid and six wheat datasets	Maize and wheat	Environmental stress
Dirichlet aggregation regression (DAR)	Dirichlet aggregation regression (DAR)	Prediction	Hyperspectral images	Barley	Abiotic stress
Supervised machine learning	Genomic random regression	Prediction	Complete genotypes molecular markers and phenotypic traits of stressed and control groups	Wheat	Environmental stress

microbial strains, such as Rhizobium spp., Azotobacter spp., and Trichoderma spp., can improve plant resilience and help control pollution and ecosystem degradation generated by chemical fertilisers (Hoque *et al.,* 2022). Similarly, supplying calcium and magnesium fertilisers in sodic soils and nitrogen to crops in areas with frequent rainfall is another important strategy to alleviate low metabolic activity and nitrate leaching. Several studies have reported that using nitrogen in the form of nitrate benefits the growth of waterlogged wheat and delays the symptoms of anoxia in tomatoes (Ferrante and Mariani, 2018).The supply of iron in agriculture can increase crop output and yield while also helping to control environmental pollution and alleviate the harmful effects of excessive salt accumulation in roots caused by salinity stress (Huang *et al.,* 2015). Proper irrigation and drainage management are found to mitigate the adverse effects of drought, flood and salinity stress in structurally weak soil.

To bridge the gap between resource-poor fields and farmers when incorporated into functional and sustainable farming systems, future breeding strategies should focus on genetic modification or identifying potential donor genotypes with high nutrient and water use efficiency to develop efficient crop varieties/hybrids. For example, genotypes can be screened with the help of colour-based visual reporter systems. It is possible to monitor the nutrient status with the naked eye and for accurate assessment by spectral reflectance (Li *et al.,* 2014). Other significant technologies that enable precise investigation of a plant's nutritional status at various developmental stages include co-expression analysis of comprehensive transcriptome data, indicator gene sets, and ionomic analysis (Takehisa and Sato, 2019). Biological Nitrification Inhibition (BNI) is a mechanism through which plant roots exude bioactive compounds that inhibit soil nitrifying microorganisms, enhancing nitrogen use efficiency and reducing nutrient loss during abiotic stress. The process is intricately associated with root exudation, which regulates plant–microbe interactions and soil nutrient dynamics within the rhizosphere. Recent studies indicate that drought and alkaline stress can significantly modify the composition and function of root exudates. Drought stress in pearl millet (*Pennisetum glaucum*) resulted in genotype-dependent alterations in root exudate profiles, which increased BNI activity in tolerant genotypes and facilitated root elongation, thereby enhancing soil microbial adaptation and nutrient retention (Ghatak *et al.,* 2022). *Leymus chinensis* demonstrated significant BNI capacity, as its root exudates inhibited soil nitrification by 72.44%, exceeding the effectiveness of the synthetic inhibitor dicyandiamide (DCD). The accumulation of ammonium (NH_4^+–N) via BNI satisfied nitrogen needs and enhanced adaptation to alkaline stress by modulating rhizosphere pH (Wang *et al.,* 2023).

The introgression of the Lr#n-SA chromosome region from *Leymus racemosus* into wheat (*T. aestivum*) resulted in increased BNI activity in elite cultivars 'ROELFS' and 'MUNAL'. This resulted in a reduction of ammonia-oxidising bacteria by up to 60% and enhanced ammonium assimilation, while maintaining yield performance. The BNI-isogenic lines showed synergistic effects when paired with synthetic nitrification inhibitors, offering a sustainable and cost-effective approach to mitigate nitrogen loss and enhance resilience under stress (Bozal-Leorri *et al.,* 2022). These findings highlight the potential of BNI-mediated root exudation as a natural strategy for enhancing nitrogen efficiency, improving soil health, and promoting climate-resilient crop production under abiotic stress conditions.

Research has also focused on identifying genes and molecular mechanisms that regulate nutrient uptake, transport, and utilisation under abiotic stress conditions, which can help to develop molecular markers and genetic tools (Mittler, 2006). For this, a large amount of data produced by ionomic analysis can be used to identify the complex and undetectable minor QTLs involved in nutrient uptake and utilisation (Takehisa and Sato, 2019). However, more accurate and sensitive strategies are needed to assess nutrient status and its effect on plant development and yield under the highly dynamic soil and environmental conditions in the field. In the near future, excess use of fertiliser use might be reduced by careful selection of diverse genotypes, utilisation of natural variation, investigation of root architecture, high-throughput precise phenotyping, standardised field trials, new methods for efficient fertiliser application, appropriate field management practises, and identification of new QTL/genes/nitrogen transporters and signalling molecules (Sandhu *et al.,* 2021).

3.6.2. Conditional crop planning

The newly developed crop management strategies, such as soil testing, adjusting sowing time, and crop rotation, have proven effective in improving yield and quality by reducing soil-borne diseases, pests, and weeds (Degani *et al.,* 2019). In agriculture,achieving higher yields is the primary objective of farmers; to accomplish this, economically and socially sustainable agronomic strategies are necessary to combat adverse climatic conditions. Sowing the crop at its recommended time is one of the most essential factors in agronomic management, as early or delayed sowing can harm germination, seedling development, and crop yield potential. A study by Panhwar et al. (2018) reported a 34% reduction in grain yield due to a one-month delay inwheat sowing. At the same time, early or timely crop sowing can significantly benefit yield potential due to crops' exposure to favourable climatic and edaphic conditions (Mariani and Ferrante, 2017). As crops are grown in different parts of the world and in various environments, it is challenging for farmers to determine a universal sowing time. Many modified agronomic tools are available, and farmers need to adopt them to fight climate change. For example, crop simulation models have the potential to select suitable cropping windows and, in this context, (Bai *et al.,* 2017) successfully utilised APSIM-Oryza and wheat models for rice-wheat rotation for sowing, irrigation and fertilizer application,Planting crops at wider spacing or during different times of the year can also help alleviate the impact of abiotic stresses (Sade *et al.,* 2018). Ultimately, it is of utmost importance to use crop varieties that are more tolerant to abiotic stresses and manage the crop in a way that reduces the effects of environmental stresses.

3.7. Nanotechnology

Alternative strategies are needed to mitigate abiotic stresses and develop stress-tolerant crops, given the complexity of stress tolerance traits and the limited genetic variability of yield components. Recent advancements underscore the potential of nanotechnology in mitigating the impacts of drought. The application of nanoparticles to crops is a promising method. It improves nutrient solubility, stability, and uptake while also scavenging ROS to assist plants in maintaining physiological functions and stress tolerance(Abdelsalam *et al.,* 2023). Foliar application of zinc–chitosan–salicylic acid (ZCS) nanoparticles at a concentration of 100 mg L^{-1} in wheat resulted in improved relative water content (RWC) and enhanced activities of superoxide dismutase (SOD), ascorbate peroxidase (APX), glutathione reductase (GR), and guaiacol peroxidase (GPOX), alongside increased levels of proline, ascorbate, and flavonoids under drought stress conditions. The biochemical enhancements reduced oxidative damage, maintained membrane integrity, and enhanced osmotic balance. As a result, the application of ZCS increased grain yield by 63% in drought-tolerant varieties and by 50% in susceptible varieties, illustrating the effectiveness of nanoparticles in facilitating drought recovery and maintaining productivity. The mechanism includes enhanced osmotic regulation, activation of reactive oxygen species-scavenging enzymes, and preservation of photosynthetic stability (Das *et al.,* 2023).

Synthetic or organic fertilisers take only 4–10 days to release their nutrients, while NFs can release their nutrients more slowly and steadily for up to 50 days. Likewise, several studies revealed that the use of nanohybrids of urea (i.e. a modified form of hydroxyapatite), P-enriched hydroxyapatite NPs and K-loaded NPs have been shown to improve crop growth, development, yield and quality, under unfavourable environmental conditions in rice, soybean and Cucurbita pepo, respectively (Kottegoda *et al.,* 2017; Liu and Lal, 2014; Seleiman *et al.,* 2021).

Similarly, ZnO nanoparticles have been found to mitigate heavy metal stress by enhancing antioxidant metabolites and enzymes, as well as promoting plant growth (Pokhrel *et al.,* 2013; Venkatachalam *et al.,* 2017). Similarly, TiO2 nanoparticles have been shown to significantly impact crops at physiological, morphological, and biochemical levels (Bhatt *et al.,* 2020; Mishra *et al.,* 2014).Therefore, nanotechnology holds the potential to advance sustainable agriculture mainly by improvingnutrient use efficiency and stress tolerance in plants. Although there are many advantages to NF applications for sustainable agriculture, concerns exist regarding the safety, bioavailability, and toxicity of released NPs (Seleiman *et al.,* 2021). Hence, there is a need to carefully evaluate the unintended and long-term effects of nanomaterials on plant growth, development, and the overall ecosystem. By better understanding the potential of nanotechnology in agriculture, farmers and customers could benefit from an economic driving force that has no negative impact on the environment or human health (Saxena *et al.,* 2023).

3.8. Microbiome engineering

The plant microbiome refers to the microbial community that inhabits and surrounds plants. It is a rapidly evolving field that focuses on improving nutrient availability and plant stress tolerance by manipulating plant-associated genes. The nearby region of plant roots contains a diverse microbial community, which promotes the water and nutrient uptake by the plants. For example, plant growth-promoting rhizobacteria (PGPR), Phosphate-Solubilising bacteria, and Nitrogen-fixing bacteria (rhizobia and Azotobacters) play a crucial role in phosphorus (P) solubilization, the fixation of atmospheric nitrogen, and the production of plant growth hormones, which contribute to improved plant growth and yield(Phour and Sindhu, 2022). PGPR can improve the germination rate, growth characteristics, thousand-grain weight, and grain output (Abbaspoor *et al.,* 2009; Nabti *et al.,* 2010). By improving salt tolerance, PGPR for seed inoculation enhanced the crop's root and shoot length (in tomato, pepper, canola, bean, and lettuce) and increased dry biomass, fruiting, and grain production (Egamberdieva and Lugtenberg, 2014).

Similarly, mycorrhizal fungi have been shown to have a positive effect on extending the plant root system, thereby enhancing nutrient and water absorption from the soil. The metagenomic high-throughput sequencing technique helps identify key microbial taxa and functional genes associated with nutrient solubilisation, cycling, and stress tolerance. Combining these beneficial microbes with complementary functions can synergistically improve nutrient acquisition and plant performance.

3.9. Precision agriculture and remote sensing

As discussed, crop improvement approaches only focus on developing new crop varieties with improved traits by genetic modification and conventional breeding. However, due to our limited capacity to phenotype plants precisely and efficiently, the dissection of complex quantitative traits has remained a significant challenge (Negrão *et al.,* 2017). Here, the development of remote sensing and precise agriculture technology has opened the door to creative methods for controlling the effects of abiotic stresses. As part of a precision-farming experiment in Romania, companies such as Nippon Electric Company, Limited (NEC; headquartered in Minato, Tokyo, Japan) and Dacom (headquartered in Santa Clara, USA) utilised environmental sensors and advanced data analytics tools to increase yields. Plant breeders are increasingly developing advanced systems to enhance the understanding of plant behaviour under diverse climatic conditions. The integration of such technologies into real-time stress monitoring, targeted intervention, and precision agriculture offers promising alternatives to conventional methods that often lack scalability and responsiveness (Berger *et al.,* 2022). Weather extremes–such as heatwaves, droughts, and excessive rainfall pose significant threats to global crop productivity. Remote sensing technologies have emerged as powerful tools for detecting crop damage and estimating yield losses caused by these climatic events over extensive spatial and temporal scales.

A recent study introduced a scalable remote sensing-based framework to predict in-season yield losses at the sub-field level and to attribute these losses to specific weather extremes (Duan *et al.,* 2024). Using data from 2017 to 2022 across winter cereal paddocks in South Australia, the study employed the Enhanced Vegetation Index (EVI2) time series derived from Sentinel-2 satellite imagery, aligned with thermal time rather than calendar days, to detect crop growth anomalies. The deviation between expected and observed EVI2 values was quantified as a Crop Damage Index (CDI), which served as a sensitive indicator of stress-induced yield loss.

The CDI, when analysed within distinct phenological stages, showed high predictive power for yield reduction–achieving R^2 values of 0.83 for wheat and 0.91 for barley, with accurate yield loss prediction possible up to two months before harvest. Furthermore, the combination of CDI trends with extreme weather indicators enabled effective identification of the specific weather events responsible for crop stress, while also capturing spatial variations in damage across sub-field regions.

This framework demonstrates the potential of remote sensing and time-series modelling to deliver early warning systems for crop damage, offering a powerful decision-support tool for breeders and farmers. Such predictive insights enable timely management interventions and adaptive breeding strategies, contributing to climate-resilient and sustainable agriculture.

The available remote sensing technologies are satellite imagery, aerial drones, and ground-based sensors, whichprovide real-time data on vegetation indices, temperature gradients, and soil moisture level scans, allowing farmers and scientists to get timely and accurate information about stress-prone areas within fields more accurately (Sawant *et al.,* 2019; Hossain *et al.,* 2021). The advanced precision agriculture and remote sensing technologies offered data-driven decision-making for the non-destructive assessment of existing and new crop varieties, evaluating them without altering their genetic makeup. Accurate phenotyping and real-time decision-making in the natural environment will provide advantages to farmers and researchers in implementing targeted management strategies to mitigate the consequences of abiotic stresses.

Conclusion and a way forward

Agricultural productivity and sustainability face considerable challenges from abiotic stresses, particularly in light of climate change and its associated environmental impacts. Nevertheless, recent advancements in understanding the mechanisms of abiotic stress tolerance in plants, combined with innovative agricultural practices and technologies, offer promising opportunities for mitigating the effects of these stresses. For instance, genetic engineering and genome editing techniques have shown promise in developing stress-tolerant crop varieties, such as wheat and rice, which can withstand abiotic stresses like drought and salinity. High-throughput phenotyping and crop sensors also offer opportunities for optimising crop inputs and decreasing the impact of abiotic stresses on crop productivity. Moreover, efficient agronomic strategies can help farmers prepare for and mitigate the effects of climate change and extreme weather events on crop production. AI algorithms can be used to address comparative genomics investigations or transfer information from a model plant to a crop of interest. Farmers and breeders can feed data into cloud-based AI applications via portable devices, drones, and agricultural equipment platforms, making AI applications more widely accessible.

Authors Contributions

Yashavanthakumar KJ: Original draft, conceptualisation, planning, monitoring; Prawin Pawar: Manuscript writing; Basavaraj PS: editing, writing, revisions; Manoj Oak: Conceptualisation, planning, monitoring, fund acquisition, review of the draft. Chandra Nath Mishra: editing, reviewing original draft;Mamrutha HM: editing, reviewing original draft; Suma Biradar: editing, reviewing original draft; SA Desai: editing, reviewing original draft. Sudhir Navathe: Conceptualisation, planning, monitoring; All authors read and approved the final draft.

Conflict of Interest statement

The authors declare that the research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

Ethical Compliance Statement

NA

Declaration on the use of Generative AI or AI-assisted technologies

The authors declare that no generative AI or AI-assisted technologies were used in the preparation of this manuscript. All text, data interpretation, and analysis were conducted entirely by the authors.

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