Review

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Climate-Resilient Crops: Integrating AI, Multi-Omics, and Advanced Phenotyping to Address Global Agricultural and Societal Challenges

Doni Thingujam , Sandeep Gouli , Sachin Promodh Cooray , Katie Busch Chandran , Seth Bradley Givens , Renganathan Vellaichamy Gandhimeyyan , Zhengzhi Tan , Yiqing Wang , Keerthi Patam , Sydney A. Greer , Ranju Acharya , David Octor Moseley , Nesma Osman , Megan E Brooker , Mary Love Tagert , Mark J Schafer , Changyoon Jeong , Kevin Flynn Hoffseth , Raju Bheemanahalli , J. Michael Wyss , Nuwan Kumara Wijewardane , Jong Hyun Ham , M. Shahid Mukhtar *

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Review

Climate-Resilient Crops: Integrating AI, Multi-Omics, and Advanced Phenotyping to Address Global Agricultural and Societal Challenges

Doni Thingujam [1], Sandeep Gouli [2], Sachin Promodh Cooray [3], Katie Busch Chandran [4], Seth Bradley Givens [3], Renganathan Vellaichamy Gandhimeyyan [5], Zhengzhi Tan [6], Yiqing Wang [6], Keerthi Patam [6], Sydney A. Greer [6], Ranju Acharya [7], David Octor Moseley [8], Nesma Osman [9], Megan E Brooker [10], Mary Love Tagert [3], Mark J Schafer [7], Changyoon Jeong [11], Kevin Flynn Hoffseth [12], Raju Bheemanahalli [5], J. Michael Wyss [13], Nuwan Kumara Wijewardane [3], Jong Hyun Ham [2] and M. Shahid Mukhtar [6,*]

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Abstract

Drought and excess ambient temperature intensify abiotic and biotic stresses on agriculture, threatening food security and economic stability. The development of climate-resilient crops is crucial for sustainable, efficient farming. This review highlights the role of multi-omics encompassing genomics, transcriptomics, proteomics, metabolomics, and epigenomics in identifying genetic pathways for stress resilience. Advanced phenomics, using drones and hyperspectral imaging, can accelerate breeding programs by enabling high-throughput trait monitoring. Artificial intelligence (AI) and machine learning (ML) enhance these efforts by analyzing large-scale omics and phenotypic data, predicting stress tolerance traits, and optimizing breeding strategies. Additionally, plant-associated microbiomes contribute to stress tolerance and soil health through bioinoculants and synthetic microbial communities. Beyond agriculture, these advancements have broad societal, economic, and educational impacts. Climate-resilient crops can enhance food security, reduce hunger, and support vulnerable regions. AI-driven tools and precision agriculture empower farmers, improving livelihoods and equitable technology access. Educating teachers, students, and future

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generations fosters awareness and equips them to address climate challenges. Economically, these innovations reduce financial risks, stabilize markets, and promote long-term agricultural sustainability. These cutting-edge approaches can transform agriculture by integrating AI, multi-omics, and advanced phenotyping, ensuring a resilient and sustainable global food system amid climate change.

Keywords: climate change; abiotic stress; machine learning; microbiome; epigenomics; genomics; proteomics; metabolomics

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1. Introduction

The accelerating impacts of climate change are profoundly altering agricultural landscapes worldwide, posing serious threats to food security, economic stability, and societal well-being [1]. Unpredictable weather patterns, including prolonged droughts, intense heat waves, devastating floods, and the proliferation of novel pests and diseases, are increasingly disrupting traditional farming practices and reducing crop yields [2]. These challenges are increased by the growing global population requiring more food, thus placing immense pressure on existing agricultural systems [3,4]. Agriculture is inherently dependent on stable environmental conditions and thus is one of the most vulnerable sectors to the multifaceted impacts of climate change [5]. Rising global temperatures are already leading to heat stress in many crops, disrupting vital physiological processes such as photosynthesis and pollination, and ultimately reducing yields [6]. Changes in precipitation patterns, characterized by increased frequency and intensity of droughts in some regions and floods in others, create water scarcity or waterlogged soils, both detrimental to plant growth and survival [7]. Furthermore, altered temperature and humidity conditions are facilitating the geographic expansion and increased virulence of agricultural pests and diseases, demanding new management strategies [8]. The increased frequency of extreme weather events, such as hurricanes, cyclones, and hailstorms, can cause catastrophic damage to crop and agricultural infrastructure, leading to significant economic losses and food shortages [9]. These climate-induced stresses adversely affect not only crop yields but also soil health, water resources, and the long-term sustainability of agricultural systems, presenting a multifaceted challenge for both farmers and policymakers.

Addressing these growing challenges, the development and widespread adoption of climate-resilient crops have become a critical global priority. Developing crops that possess enhanced tolerance or resistance to various abiotic and biotic stresses linked to climate change is crucial for ensuring future food security, protecting the livelihoods of vulnerable populations, and advancing a more sustainable and equitable agricultural future [10]. Climate resilience encompasses a range of desirable traits, including the ability to maintain yield stability under fluctuating environmental conditions, efficient resource utilization, and enhanced nutritional quality [11]. The quest for climate-resilient crops has been significantly accelerated by the integration of several powerful and rapidly evolving technologies. AI is playing an increasingly vital role in analyzing vast datasets from genomics, phenomics, and environmental monitoring to identify complex relationships and predict optimal breeding strategies for resilience [12]. AI algorithms can assist in identifying superior germplasm, optimizing resource management, and developing predictive models for pest and disease outbreaks under changing climate scenarios [13]. The analytical capabilities of AI complementing multi-omics approaches offer an integrated view of the molecular mechanisms that govern plant responses to environmental stresses [14]. Simultaneous analysis of these different biological layers can identify key genes, proteins, and metabolic pathways associated with resilience traits, enabling more targeted breeding efforts [15–17]. Nevertheless, advanced phenotyping technologies use high-throughput platforms with sensors, imaging, and automation to non-destructively measure complex plant traits across scales. When combined with genomic and environmental data, they provide insights into genotype-phenotype relationships, facilitating the selection of climate-resilient crop varieties [18,19]. This review emphasizes the key technological

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advancements, specifically AI, multi-omics, and advanced phenotyping, and how synergistic integration of these tools holds immense promise for accelerating our ability to cultivate crops fit for a changing world, thereby addressing critical agricultural and societal challenges.

2. Climate Change and Agricultural Stress

2.1. Abiotic Stress Factors

2.1.1. Drought and Water Scarcity

Water scarcity, exacerbated by global warming and human activities, poses a significant threat to ecosystems and human survival. Uneven precipitation patterns, predicted to worsen with increased Arctic stream flow and decreased subtropical rainfall, are driving hydrological and agricultural droughts [20]. According to the United Nations Convention to Combat Desertification [21] report, 44% of droughts have occurred on the African continent, with over 300 drought events recorded in the last 100 years, including 134 events between 2000 and 2019. Over the last century, Europe has experienced 45 drought events, affected millions of people and resulting in $27.8 billion in losses [22]. In terms of population, more than 2 billion people were affected by droughts in the 20th century, mainly in North Africa, the Middle East, and Australia [23]. These changes affect billions worldwide and pose a significant threat to food security and socioeconomic stability. Projections indicate a substantial expansion of arid regions, potentially displacing over 700 million people by 2030 [24]. Global freshwater withdrawals reached 3.9 trillion m^3 in 2017, up from 500 billion m^3 in 1900, largely due to population growth and resource-intensive consumption patterns [25]. Freshwater demand for food production is expected to double by 2050, supporting a population of 10 billion people, but its availability remains uncertain due to rising concerns about water scarcity and socio-economic impacts [26]. Additionally, emissions of CO2 and methane have increased global temperatures by 0.85°C from 1880 to 2012, with projections exceeding 1.5°C this century [20].

Drought poses a significant threat to animals and crops, affecting up to 45% of the world's agricultural land, which is home to 38% of the global population. In the US, drought is increasingly common, currently costing an average of $9.6B per year, and it is thus considered one of the most critical economic problems and natural threats to the planet. Drought, combined with heat stress, can severely impact agriculture, resulting in estimated losses of $200 billion in the USA between 1980 and 2012 [27]. Plants are vulnerable to moisture stress, particularly due to drought caused by limited water supply or high transpiration rates [28]. Prolonged drought leads to declining plant fitness and yield [29–31]. Major crops face significant yield risks due to water scarcity, with projected losses of 7 to 8.1 % for soybean, 9 to 12% for wheat, and 18.1 to 19.4% for rice by the end of the 21st century [9,32,33].

In semi-arid and drought-prone areas, the co-occurrence of drought and heat stress has a detrimental impact on plants [34,35]. Heino et al. [2023] noted that heat stress often coincides with drought worldwide during the reproductive stages of wheat, rice, and maize [36]. This combined stress affects gas exchange, photosynthetic pigments, enzyme activities, and biochemistry [37] [Figure 1]. Furthermore, concomitant drought and heat waves during reproductive stages cause abnormal anther development, reduced pollen viability, ovule abortion, and inhibited flowering [38,39]. In maize, the co-occurrence of drought and heat stress increases ROS and malondialdehyde levels, leading to reduced nutrient uptake and diminished growth [40]. Similarly, soybeans experience a 7% reduction in seed weight due to the interactive effects of drought and heat during flowering [34].

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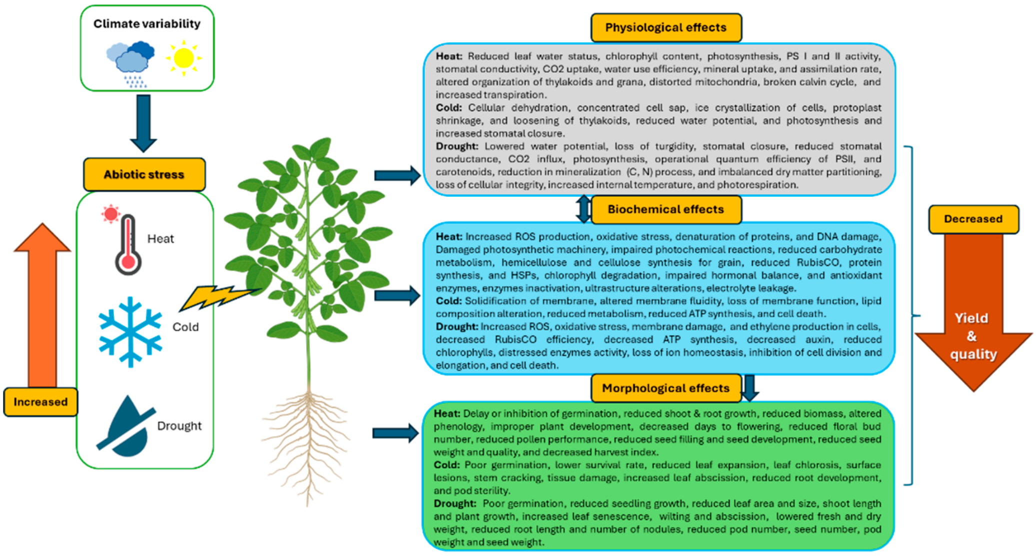

Heat: Reduced leaf water status, chlorophyll content, photosynthesis, PS I and II activity, stomatal conductivity, CO2 uptake, water use efficiency, mineral uptake, and assimilation rate, altered organization of thylakoids and grana, distorted mitochondria, broken calvin cycle, and increased transpiration.

Cold: Cellular dehydration, concentrated cell sap, ice crystallization of cells, protoplast shrinkage, and loosening of thylakoids, reduced water potential, and photosynthesis and increased stomatal closure.

Drought: Lowered water potential, loss of turgidity, stomatal closure, reduced stomatal conductance, CO2 influx, photosynthesis, operational quantum efficiency of PSII, and carotenoids, reduction in mineralization (C, N) process, and imbalanced dry matter partitioning, loss of cellular integrity, increased internal temperature, and photorespiration.

Heat: Increased ROS production, oxidative stress, denaturation of proteins, and DNA damage, Damaged photosynthetic machinery, impaired photochemical reactions, reduced carbohydrate metabolism, hemicellulose and cellulose synthesis for grain, reduced RubisCO, protein synthesis, and HSPs, chlorophyll degradation, impaired hormonal balance, and antioxidant enzymes, enzymes inactivation, ultrastructure alterations, electrolyte leakage.

Cold: Solidification of membrane, altered membrane fluidity, loss of membrane function, lipid composition alteration, reduced metabolism, reduced ATP synthesis, and cell death.

Drought: Increased ROS, oxidative stress, membrane damage, and ethylene production in cells, decreased RubisCO efficiency, decreased ATP synthesis, decreased auxin, reduced chlorophylls, distressed enzymes activity, loss of ion homeostasis, inhibition of cell division and elongation, and cell death.

Heat: Delay or inhibition of germination, reduced shoot & root growth, reduced biomass, altered phenology, improper plant development, decreased days to flowering, reduced floral bud number, reduced pollen performance, reduced seed filling and seed development, reduced seed weight and quality, and decreased harvest index.

Cold: Poor germination, lower survival rate, reduced leaf expansion, leaf chlorosis, surface lesions, stem cracking, tissue damage, increased leaf abscission, reduced root development, and pod sterility.

Drought: Poor germination, reduced seedling growth, reduced leaf area and size, shoot length and plant growth, increased leaf senescence, wilting and abscission, lowered fresh and dry weight, reduced root length and number of nodules, reduced pod number, seed number, pod weight and seed weight.

Figure 1. Effect of abiotic stress on crop plants.

2.1.2. Extreme Temperature Stress

Temperature significantly impacts organisms' distribution across latitudinal and altitudinal gradients [41]. Plant life exists within a limited temperature range, from -10°C [e.g., temperate woody trees] to a specific threshold for arid cacti. Each organism has an optimal temperature range that maximizes growth and function, while deviations can halt biological processes, leading to stress or death depending on intensity and duration [42]. Low or non-freezing temperatures [0-15°C] can induce substantial injury and mortality in tropical and subtropical plants [43]. Tropical and subtropical species, such as maize, soybeans, cotton, tomatoes, and bananas, exhibit rapid injury symptoms when exposed to temperatures below 10-15°C, due to their limited adaptation to temperate climates [44] (Figure 1). Cold stress disrupts plant growth and development. The severity of cold stress effects is modulated by plant cellular morphology, biochemistry, physiological functions, and developmental stage [45]. Symptom manifestation varies across plant species and tissues, reflecting differential sensitivities [46]. In rice, early-stage cold stress can have lasting impacts on later growth, leading to cellular membrane damage and growth retardation [47]. Visual symptoms of cold injury include tissue damage, surface lesions, stem cracking, metabolite leakage, leaf wilting, chlorosis, necrosis, leaf curling, and discoloration [48,49]

Temperature stress influences photosynthesis, nutrient cycling, protein synthesis, and phytohormone regulation [50]. Future projections indicate that heatwaves and extreme temperatures will become more frequent and intense, with the prediction of a temperature increase of 2 to 3 °C over the next 30 to 50 years [20]. Even with a 1°C increase, prolonged heat waves can result in up to 38% yield loss in wheat [51,52]. Global average temperatures have risen by 0.8°C since 1990, with nighttime temperatures rising 1.4 times faster than daytime temperatures [53]. This poses a significant threat to agriculture, resulting in reduced grain yields of up to 6% in wheat (*Triticum aestivum* L.), 3.2% in rice (*Oryza sativa*), 3.4% in maize (*Zea mays*) and 2.8% in soybean for every 1 ◦C rise in nighttime temperature from their control [54–56]. Heat stress particularly impacts reproductive stages in crops, reducing pollen viability and seed set [57,58]. For example, heat stress can disrupt the reproductive organs of both males and females, leading to significant yield losses [58]. Moreover, the effect of heat waves often coincides with high vapor pressure deficits (VPD), beyond a certain point, higher temperature with high VPD adversely affect the pollen development, thus reducing sexual reproduction and grain yield formation [59,60] [Figure 1]. Heat stress occurring for 2 to 5 days around flowering negatively impacts reproductive organ function and seed set in rice [61,62], affects the anthesis-silking interval in maize [63], and decreases pollen shedding in wheat [52,64], leading to irreversible yield loss through reduced floret fertility and seed number [38,65,66].

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2.2. Agricultural Management Strategies and Abiotic Stresses

Effective agricultural and water management strategies are essential for mitigating abiotic stresses such as drought, waterlogging, and salinity [67–69]. By enhancing water use efficiency and integrating conservation practices, farmers can ensure their crops receive adequate moisture, minimize water waste, and strengthen their resilience to environmental challenges [70]. Employing soil amendments, cover crop practices, and sound soil management, along with appropriate crop selection, enables farmers to maintain agricultural productivity despite changing climatic conditions [71–73].

The application of soil amendments using thermally and hydrothermally processed materials, such as biochar and hydrochar, represents an innovative strategy for enhancing soil health, particularly in the context of managing abiotic stresses like drought, salinity, and temperature extremes [74–76]. Biochar is produced through pyrolysis, a process involving high temperatures and limited oxygen, which transforms organic material into a stable, carbon-rich product. In contrast, hydrochar is generated via hydrothermal carbonization (HTC), where biomass is subjected to high pressure and temperature in the presence of water. Both biochar and hydrochar are rich in carbon and possess unique properties that distinguish them from conventional organic matter such as compost or manure. These materials are stable forms of carbon that can remain in the soil for decades, contributing to long-term organic matter and enhancing the soil's capacity to retain nutrients and moisture [77].

Furthermore, biochar and hydrochar have been shown to improve soil porosity and aggregate stability [78]. Their porous structure facilitates enhanced water infiltration, root penetration, and the overall physical structure of the soil, while also increasing cation exchange capacity (CEC) [79]. One significant advantage of applying biochar and hydrochar is their ability to alleviate drought stress by retaining moisture in the soil [80]. Additionally, these materials have demonstrated effectiveness in managing soil salinity by improving water retention capacity and promoting the movement of water and nutrients, ultimately helping to lower salt concentrations around plant roots [81,82]. Both biochar and hydrochar provide habitats for soil microbes, including beneficial bacteria and fungi. These microorganisms play a vital role in enhancing nutrient cycling and fostering plant growth, thus contributing to soil health and resilience under stress conditions. They also improve the availability of soil nutrients and aid in the decomposition of organic matter [82]. Importantly, hydrochar typically contains a higher concentration of water-soluble nutrients, such as nitrogen, phosphorus, and potassium, compared to biochar, offering more immediate benefits for plant growth [83].

Winter cover crops are a sustainable agricultural practice that can greatly enhance soil health and mitigate the impacts of abiotic stresses such as erosion, drought, and nutrient deficiencies [84,85]. There are several types of winter cover crops: legumes [such as clover, vetch, and winter peas] excel at nitrogen fixation and enhancing soil fertility; grasses [such as rye, oats, and barley] offer effective erosion control and contribute to organic matter; and brassicas [such as radishes] assist in breaking up compacted soil and improving soil structure [86,87]. Cultivating winter cover crops can enhance soil health and alleviate abiotic stresses by increasing organic matter content in the soil [86] Organic matter plays a crucial role in improving soil structure, nutrient retention, and microbial activity. As cover crops develop, their roots penetrate the soil, contributing to organic material that decomposes and enriches it. Notably, certain winter cover crops, especially legumes, have the ability to fix atmospheric nitrogen, enhancing soil fertility and decreasing the reliance on synthetic fertilizers [88].

During winter, soils are frequently left bare or only lightly covered, rendering them susceptible to erosion from wind and water. The dense root systems of winter cover crops act as a protective barrier for the soil surface, mitigating erosion and preserving valuable nutrients. Additionally, the presence of cover crops enhances water infiltration and reduces surface runoff [89]. As these cover crops decompose in the spring, they release nutrients back into the soil in a form that is more readily available to plants, thereby improving nutrient cycling and minimizing the risk of nutrient imbalances.

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Furthermore, the root systems of winter cover crops improve soil structure by creating channels that facilitate deeper water penetration and access to nutrients from lower soil layers, which helps prevent salt accumulation in the topsoil [90,91]. The decomposition process of winter cover crops provides a consistent supply of organic matter, nourishing beneficial microorganisms such as bacteria, fungi, and earthworms, thereby enhancing soil biodiversity [92].

3. Multi-Omics Approaches for Enhancing Crop Resilience

3.1. Genomics and Genetic Engineering

3.1.1. Genome-Wide Association Studies [GWAS]

GWAS have emerged as a fundamental approach for identifying genetic loci associated with complex traits by examining genome-wide variation across diverse natural populations [93]. For crop stress tolerance studies, GWAS enables the systematic association of single-nucleotide polymorphisms (SNPs) with key agronomic traits such as drought endurance, salinity resistance, and heat tolerance [94–96]. With engaging high-density genotyping platforms and extensive phenotypic datasets, GWAS provides insights into the polygenic nature of stress responses and uncovers allelic variants contributing to resilience. In maize, GWAS identified quantitative trait loci (QTLs) related to drought tolerance, emphasizing mechanisms of osmotic adjustment and root architecture modulation [97–99]. Similarly, in rice, loci associated with salinity tolerance have been linked to genes involved in ion transport, notably sodium and potassium homeostasis [100,101]. In wheat, GWAS has pinpointed genomic regions regulating traits critical for heat stress resilience, such as grain filling duration and membrane stability under high temperatures [94,96]. Moreover, GWAS has been instrumental in identifying candidate genes encoding transcription factors such as DREB (Dehydration-Responsive Element Binding), NAC (NAM: no apical meristem; ATAF: Arabidopsis Transcription Activation Factor; and CUC: *Cup-Shaped Cotyledon)*, and transporters including HKT1 that mediate stress adaptation [102,103]. These identified markers are invaluable for marker-assisted selection [MAS] and genomic selection (GS), facilitating early and efficient breeding of stress-tolerant varieties [104]. The integration of GWAS findings with functional genomics, such as transcriptomics (Figure 2) and CRISPR-based validation, further accelerates the translation of genetic discoveries into resilient crop cultivars.

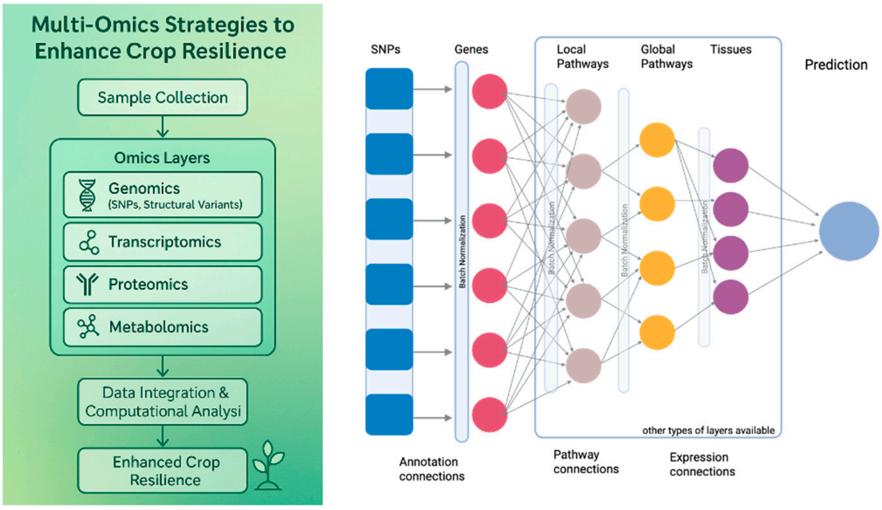

Figure 2. Integration approach of genomics, transcriptomics, proteomics, and metabolomics to enhance crop resilience to stress.

3.1.2. CRISPR and Gene Editing for Stress Tolerance

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CRISPR-Cas9 technology has revolutionized plant genetic engineering by enabling precise, efficient, and targeted modifications of plant genomes, providing a transformative platform for improving stress tolerance traits [105]. Through site-specific genome editing, CRISPR-Cas9 allows researchers to knockout, insert, or replace genes associated with plant stress responses, thereby facilitating the development of crops better suited to withstand environmental challenges. Targeted editing of key transcription factor genes, such as those in the DREB and NAC families, has been demonstrated to enhance resilience to abiotic stresses including drought, salinity, and heat [106–111]. In rice, CRISPR-mediated knockout of OsERF922, a negative regulator of abiotic stress tolerance, might result in improved drought and salt tolerance [112–114]. Similarly, in wheat, editing of ABA signaling components, including TaPYL1, has led to enhanced drought resilience through modulation of stomatal behavior and water-use efficiency [115]. Beyond gene knockouts, CRISPR-Cas9 facilitates base editing and prime editing, enabling the precise introgression of favorable alleles from wild relatives into elite cultivars without linkage drag, thus broadening genetic diversity and enhancing crop adaptability [116,117]. Furthermore, multiplex genome editing allows simultaneous modification of multiple genes, a strategy increasingly important for engineering complex traits such as combined drought and heat tolerance [118]. Overall, CRISPR-based genome editing holds enormous potential to accelerate the breeding of climate-resilient crops in an era of increasing environmental instability.

3.2. Transcriptomics: Gene Expression Under Stress

3.2.1. RNA Sequencing [RNA-Seq] for Identifying Stress-Responsive Genes

RNA-Seq has emerged as a powerful tool to capture dynamic transcriptional changes in plants subjected to environmental stress, enabling the identification of key regulatory genes that are activated or suppressed in response to specific cues [119,120]. Moreover, RNA-Seq facilitates the identification of differentially expressed genes (DEGs), providing insights into the molecular mechanisms underlying stress adaptation. These DEGs often encode proteins involved in stress perception, signal transduction, transcriptional regulation, defense responses, and metabolic reprogramming necessary for survival under adverse conditions [119,121]. For example, in soybeans exposed to drought and flooding stress, RNA-Seq revealed the differential expression of TF genes, including Basic Helix-loop Helix (bHLH), Ethylene Response Factors (ERFs), myeloblastosis (MYB), NAC, and WRKY amino acid motif (WRKY) type major families, highlighting the complexity of stress management mechanisms [122]. Similarly, in Arabidopsis under salt stress, transcriptomic analyses have shown the activation of LEA45, GSTF6, DIN2/BGLU30, TSPO, GSTF7, LEA18, HAI1, ABR, and LTI30 [123]. In wheat, RNA-Seq under heat stress conditions has identified heat shock proteins [HSPs] and transcription factors like HsfA2 as critical components of thermotolerance [124] Furthermore, time-course RNA-Seq studies enable the dissection of early versus late stress responses, offering temporal resolution to gene regulatory networks [19]. Overall, RNA-Seq provides a foundational resource for functional genomics, facilitating the identification of candidate genes and regulatory pathways for molecular breeding and genetic engineering aimed at enhancing crop stress resilience.

3.2.2. Regulatory Networks in Plant Stress Adaptation

Beyond the analysis of individual genes, transcriptomics enables the construction of gene regulatory networks (GRNs) that model the complex interactions among transcription factors (TFs), non-coding RNAs (ncRNAs), and their downstream target genes [125,126]. GRNs provide a holistic framework to understand how plants coordinate diverse molecular pathways during stress responses. Key TF families such as WRKY, MYB, NAC, DREB, and bZIP frequently emerge as central nodes, orchestrating the transcriptional activation or repression of multiple stress-responsive genes [127–129]. For instance, WRKY TFs are known to modulate genes involved in oxidative stress responses and pathogen defense, while MYB proteins regulate osmotic balance and secondary

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metabolite biosynthesis during abiotic stress. Moreover, the role of small non-coding RNAs, particularly microRNAs (miRNAs), has been increasingly recognized. miRNAs such as miR398 and miR169 are pivotal regulators of stress adaptation, mediating the cleavage or translational repression of transcripts encoding key signaling components [130,131]. Long non-coding RNAs (lncRNAs) also contribute by acting as molecular sponges or scaffolds to modulate gene expression under stress conditions [132,133]. By integrating transcriptomic data with bioinformatic network analyses, researchers can decipher hierarchical regulatory relationships and feedback loops, offering a systems-level perspective of plant stress biology (Figure 2). Such comprehensive network models are invaluable for pinpointing master regulators and hub genes, which represent promising targets for genetic engineering aimed at enhancing crop resilience.

3.3. Proteomics and Metabolomics

3.3.1. Stress-Induced Changes in Protein Expression

Proteomics provides a powerful platform to analyze global changes in the protein landscape of plants under stress conditions, offering direct insights into functional responses that are not always predictable from transcriptomic data alone. Stress exposures, such as drought, salinity, and heat, often result in significant shifts in protein abundance, localization, and post-translational modifications [134]. Key commonly identified stress-responsive prteins include HSP70 and HSP90, antioxidant enzymes such as superoxide dismutase (SOD) and catalase (CAT), and molecular chaperones that assist in protein folding and stabilization under adverse conditions [135,136]. Proteomic investigations of drought-stressed soybean have revealed upregulation of ion transporters, ROS-scavenging proteins, LEA proteins, and enzymes involved in osmotic adjustment, such as proline synthetase [137,138]. Furthermore, proteomics has proven instrumental in uncovering stress-induced post-translational modifications, including phosphorylation, ubiquitination, and sumoylation, which critically regulate protein stability, activity, and interactions during stress responses [139,140]. For instance, phosphorylation of signaling kinases such as MAPKs plays a crucial role in transducing environmental signals into appropriate cellular responses. Spatial proteomics can aid in studying complex protein-protein interaction [141] and offer several advantages over traditional methods such as Cytotrap [142]. Advanced quantitative proteomic techniques, such as iTRAQ and label-free LC-MS/MS, have further enhanced the ability to detect subtle but significant changes in stress-related proteins, thereby deepening our understanding of the dynamic proteome remodeling that underpins plant resilience mechanisms [143].

3.3.2. Metabolic Pathways Involved in Plant Defense

Metabolomics serves as a powerful approach for characterizing the comprehensive biochemical shifts that underpin plant survival and adaptation under environmental stress. Exposure to stresses such as drought, salinity, and heat often leads to the accumulation of compatible solutes, including proline, glycine betaine, and soluble sugars, which help maintain cellular osmotic balance and stabilize proteins and membranes [144,145]. Antioxidants such as glutathione, ascorbate, and tocopherols are also upregulated to mitigate the damaging effects of reactive oxygen species (ROS) generated under stress conditions [146,147]. In addition to primary metabolites, stress conditions stimulate the biosynthesis of a wide range of secondary metabolites, including flavonoids, terpenoids, and phenolic compounds, which contribute to ROS scavenging, pathogen defense, and modulation of plant signaling pathways [148,149]. Hormonal reprogramming is another hallmark of stress responses, with elevated levels of abscisic acid (ABA), jasmonic acid (JA), and salicylic acid (SA) fine-tuning growth regulation, stomatal behavior, and defense activation [150,151]. Recent integrated metabolomic and transcriptomic studies have illuminated key metabolic shifts, such as the enhanced flux through the phenylpropanoid pathway and tricarboxylic acid (TCA) cycle under stress, highlighting critical nodes for potential genetic or chemical intervention [152,153]. Thus,

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metabolomics not only provides a snapshot of plant physiological status but also uncovers potential metabolic engineering targets for improving crop resilience.

3.4. Epigenomics and Environmental Adaptation

3.4.1. Role of DNA Methylation in Stress Memory

Epigenomic modifications, particularly DNA methylation, represent crucial mechanisms that regulate gene expression without altering the underlying DNA sequence. These modifications play a pivotal role in plant responses to environmental stress, influencing gene expression patterns and contributing to plant adaptation [154,155]. DNA methylation, through the addition of a methyl group to the 5′ position of cytosine residues, can silence or activate genes involved in stress responses, often without permanent genetic changes [156]. Exposure to various stressors, including drought, salinity, and heat, has been shown to induce stable or transient changes in DNA methylation patterns at key regulatory loci [157–159]. These epigenetic alterations enable plants to "remember" previous stress events, which results in faster and more robust activation of defense mechanisms upon re-exposure to similar stress conditions, a phenomenon often referred to as "stress memory" [160–162]. For example, in wheat and rice, DNA methylation changes induced by drought stress were found to enhance recovery and survival following repeated drought cycles, indicating that these epigenetic modifications may contribute to improved resilience and long-term stress tolerance [163,164]. These findings highlight the potential of targeting epigenomic pathways to improve crop stress tolerance and ensure better yield stability in the face of increasing environmental variability.

3.4.2. Transgenerational Adaptation Through Epigenetic Modifications

Emerging evidence indicates that environmentally induced epigenetic changes can sometimes be inherited across generations, enabling plants to adapt to environmental stresses in ways that do not involve genetic mutations [161]. Epigenetic modifications, including DNA methylation, histone modifications, and small RNA profiles, can be passed down to offspring, effectively "priming" them for enhanced resilience to environmental challenges [165]. Such modifications can enhance the plant's ability to cope with stress, even in the absence of genetic mutations. This transgenerational epigenetic inheritance has been observed in several plant species, including Arabidopsis and rice, where progeny from stressed parents have demonstrated increased tolerance to drought, salinity, and other abiotic stresses [163,166].

Previous studies have also shown that exposure to salt and osmotic stress in Arabidopsis leads to DNA methylation changes that are inherited by the next generation, conferring enhanced tolerance without modifications to the primary sequence of the genome [167]. Similarly, in rice, salinity-induced epigenetic changes are passed on to offspring, improving their resilience to salinity stress [168]. The stability and mechanisms underlying transgenerational epigenetic inheritance are still being elucidated, but this phenomenon opens new avenues for crop breeding strategies aimed at enhancing stress tolerance [169]. Through the use of natural epigenetic processes, it may be possible to precondition crops to better withstand the increasing frequency and intensity of environmental stresses brought about by climate change.

4. Field-Based Phenomics: Advanced Trait Monitoring

4.1. High-Throughput Screening Technologies

Field-based phenomics, powered by advanced high-throughput phenotyping [HTP] technologies, is revolutionizing modern crop monitoring. The growing challenges of food security and climate resilience emphasize the need for innovative, data-driven solutions in agriculture. By integrating cutting-edge sensing technologies with machine learning, HTP enables large-scale, precise trait monitoring and facilitates genetic improvement and agronomic decision-making [170]. HTP relies on diverse sensor technologies, including red, green, and blue (RGB), multispectral,

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hyperspectral, Light Detection and Ranging (LiDAR), and thermal sensors. Each component plays a vital role in capturing plant morphology, canopy architecture, chlorophyll content, and stress responses with high precision. LiDAR-based 3D imaging further enhances structural analysis, allowing detailed measurements of plant height and biomass accumulation with minimal environmental disturbance [171]. RGB, multispectral, and thermal imaging enhance the estimation of important crop parameters such as yield, abiotic stress, and canopy height [172]. Additionally, hyperspectral imaging [HIS]provides high-resolution spectral data for plant phenotyping, nutrient content estimation, stress and disease detection [173]. Combining HSI with deep learning models has shown the potential to identify crop diseases before visible symptoms appear, improving response times and reducing yield losses [174]. These sensor technologies onboard uncrewed aerial vehicles (UAVs) and uncrewed ground vehicles (UGVs) have expanded the capacity for rapid, cost-effective data collection over large experimental plots, offering new opportunities for non-invasive crop assessment in field conditions [175]. Despite these advancements, challenges persist in standardizing data collection protocols and ensuring cross-platform interoperability. The vast amount of data generated by HTP systems necessitates robust computational tools and cloud-based storage solutions to streamline analysis and accessibility. Additionally, transforming phenotypic data into actionable insights requires close collaboration between geneticists, agronomists, agricultural engineers, and data scientists to optimize breeding strategies and field management practices [175]. By leveraging advanced phenotyping technologies and AI-powered analytics, researchers can accelerate genetic improvements, enhance crop resilience, and promote sustainable agricultural practices for future food security [170].

4.2. Integrating Multi-Omics and Phenomics

ML, a subset of AI, frequently employs applied statistical and computational techniques to enable the capacity to "learn" from data without explicit programming [176]. This characteristic is pivotal as it provides an unbiased approach to analyzing diverse data patterns for predictive modeling [177]. Once a set of patterns is learned, the model can predict a broad spectrum of outputs. Generally, ML methods fall into two categories—supervised and unsupervised learning [178]. Deep learning [DL], a promising approach, is a subset of ML grounded in artificial neural networks, which can be either supervised or unsupervised. Unlike traditional ML methods that rely on labor-intensive pre-processing engineering pipelines and visible feature extraction through data transformation, DL autonomously learns characteristics or patterns. It utilizes a cascade of multiple layers of nonlinear processing units for feature extraction, highlighting enhanced performance, particularly with large volumes of data [179–181]. Architectures of advanced deep learning-based convolutional neural networks (CNNs) have been used to develop SoyDNGP [182], a web-based deep learning framework for soybean breeding, as well as RiceSNP-BST [183] and RiceSNP-ABST [184], which predict biotic and abiotic phenotypes, respectively, from GWAS data. Specifically, SoyDNGP is developed based on genotype data from SoyBase database (42,509 SNPs from 20,087 soybean accession) and phenotype data associated with GRIN-Global. After filtering and data processing, 13,784 accessions were used to train the model. Unlike previous models such as DeepGS and DNNGP [185,186], which uses 1D SNP vectors, the SoyDNGP instead uses 3D input data (M×M×3) where SNP mutation types [0/0, 0/1, 1/1] are mapped across three separate channels to retain spatial and mutational context. Particularly, the architecture consists of twelve convolutional layers and a single fully connected layer, with stride-2 convolutions instead of max-pooling to reduce feature loss [182]. Stability and generalization are improved by utilizing Dropout, Batch Normalization, and L2 regularization techniques. Furthermore, Coordinate Attention (CA) mechanism is also added to enhance feature extraction by mainly focusing on both spatial and channel-level information. Smooth L1 loss for regression and Cross-Entropy loss for classification are employed during training, with the Adam optimizer employed for optimizing. SoyDNGP demonstrated exceptional performance in genomic prediction tasks, achieving 0.96 accuracy in classification tasks such as predicting flower color and a 0.87 correlation in regression tasks, including estimating seed weight. SoyDNGP's key advantage is

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its adaptability to multiple crops, including maize, rice, cotton, and tomato, showcasing its versatility. This scalability positions SoyDNGP as a powerful tool for genomic prediction across diverse agricultural research and breeding programs. To further validate its effectiveness, it should be tested using GWAS and phenomics data from other agronomically important crops under stress conditions.

RiceSNP-BST and RiceSNP-ABST [183,184] models, on the other hand, overcome the challenge of limited access to high-quality genome-level genotype data. They are specifically designed to support stress-tolerant rice breeding, enabling more efficient selection and improvement of resilient rice varieties. The models employ an automated CNN architecture search with the capability of multidimensional feature extraction, (i.e., utilizing One-hot, DNA2vec, DNABERT, and DNAshape encodings) to represent both DNA sequence and structural information. Feature importance is modeled using SHAP to increase interpretation. In this instance, a benchmarking dataset was developed using three negative sampling approaches (Random, Common, Rearranged) each across two sequence lengths (41 nt, 101 nt). These models outperform over some traditional ML and contemporary DL in terms of prediction performance, robustness, and generalization in independent and cross-species. To further improve biological interpretability, causal learning approach is applied, it identified important key DNA structural features (ProT, Roll, Buckle, etc.) that contribute to both SNP functionality and transcription factor binding [184]. Overall, RiceSNP-BST and RiceSNP-ABST demonstrate the power of integrating DNA sequence and structure with automated DL to enhance SNP detection. Their interpretability and scalability make them highly valuable for rice genomics and precision breeding, particularly under biotic and abiotic stress conditions. Both frameworks are accessible via web servers, ensuring broad usability in genome research and breeding applications, advancing next-generation crop improvement strategies.

Traditional GWAS identifies genetic associations but often lacks mechanistic explanations. While AI-driven models improve prediction by integrating multi-omics data, their limited interpretability hinders biological insights. To address this, interpretable AI is becoming increasingly important in GWAS and phenotype prediction, enhancing transparency and providing deeper insights into complex biological processes. GenNet [187] is a recently used open-source deep learning framework designed for interpretable phenotype prediction from genetic variants in human datasets, applied to seventeen phenotypes, including hair and eye color, as well as schizophrenia with high accuracy. It offers more interpretability and easier understanding in genetic studies. Gennet Framework constructs biologically informed neural network architectures by defining sparse, hierarchical connections between layers as SNPs to genes, and genes to pathways or tissue types based on curated annotations from databases such as NCBI RefSeq, KEGG, and GTEx. This biologically constrained architecture significantly decreases the number of trainable parameters by enabling efficient training of large-scale genomic data with limited computational resources. The architecture is built on the principle of biological interpretability, where each node in the model represents a true biological entity, meaning that the learned weights of a GenNet provide direct interpretations as effect sizes [187]. The generalized framework accommodates modularity and flexibility through distinct biologically meaningful layer types, including gene-based, exon-based, pathway-based, and tissue-expression based layers, that can be adapted according to standard phenotypic prediction tasks. Batch normalization is employed at each layer for input standardization, while L1 regularization promotes sparsity to allow the model to focus only on the most relevant biological features, improving interpretability. GenNet models are trained with binary cross-entropy loss for classification tasks. An Adam or Adadelta algorithm is used to perform gradient descent for optimization, with early stopping based on validation loss used to prevent overfitting. These methods ensure robust and interpretable modeling of complex genotype-to-phenotype relationships. Architecture allows for interpretation across layers, making GenNet a valuable tool for discovering functional insights into the genetics of complex traits [187]. While recently applied in human GWAS and phenotype prediction, it holds significant potential for future applications in plant GWAS and phenotype prediction. Its application in plant science could significantly improve breeding efficiency,

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trait selection, and precision agriculture, ultimately contributing to the development of more resilient and high-yielding crop varieties.

5. The Role of Artificial Intelligence and Machine Learning

5.1. AI in Data Analysis and Prediction

AI transforms data analysis and prediction across multiple disciplines, offering unprecedented capabilities in extracting meaningful insights from complex datasets. In agriculture, AI-driven methodologies enhance predictive modeling, optimize resource allocation, and accelerate breeding advancements by efficiently analyzing vast amounts of genetic, environmental, and phenotypic data [188]. Advanced ML algorithms, including deep learning and ensemble methods, have demonstrated remarkable success in predicting complex biological outcomes. For instance, AI-driven models have significantly improved the accuracy of yield forecasting and stress tolerance assessments in crops, outperforming conventional statistical techniques [189]. The ability of AI to process large-scale genomic data further enhances the efficiency of trait selection, reducing the need for extensive field trials while maintaining high predictive reliability [190]. In predictive modeling, AI refines data processing by identifying key variables and their interactions, enabling the optimization of breeding strategies and environmental adaptation. Convolutional neural networks and support vector machines have been successfully applied in HTP, automating the classification of plant traits and stress responses from imaging data [191]. These advancements streamline decision-making by providing real-time insights into crop performance, allowing researchers to develop adaptive strategies for improving agricultural resilience [188]. Despite its transformative potential, AI-driven data analysis faces challenges related to model generalization and interpretability, data standardization, and computational demands. The complexity of integrating heterogeneous datasets from genomics, phenomics, and environmental monitoring necessitates robust analytical frameworks and interdisciplinary collaboration [189]. AI technologies continue to evolve, and their integration into predictive modeling will further refine analytical precision, fostering advancements in diverse fields from agriculture and beyond [188].

5.2. AI in Precision Agriculture

Food security and maximizing crop production are growing challenges in the agriculture sector. Precision agriculture was driven to address spatial and temporal field variability while achieving economic savings and environmental benefits, and it has been transformed by AI technologies. The integration of AI with precision agriculture has resulted in a transformative shift in modern farming with enhanced crop monitoring and management and increased automation to accommodate these challenges [192]. The integration of AI with decision-support systems in precision agriculture is revolutionizing farm management by leveraging real-time data collected through Internet of Things (IoT)-based sensor systems [193]. IoT enables the storage of essential sensor data and crop management information in a centralized cloud system, enhancing cost efficiency and computational power [194]. These systems have the potential to be expanded with the integration of different platforms like UAVs and UGVs. Integrating UAVs and UGVs with different sensing technologies marks a significant breakthrough in robotics. UAVs can monitor vast agricultural fields from the air, detecting crop stress caused by pests, diseases, or water deficiencies, and relay this data to UGVs, which then execute precise interventions such as fertilization, pesticide applications, or irrigation [195]. The combination of satellite imagery, UAVs, UGVs, ground-based sensors, IoT-based systems, and AI algorithms equips farmers with real-time data, allows proactive decision-making in precision agriculture [196]. A summary of the modern agricultural system is illustrated in Figure 3.

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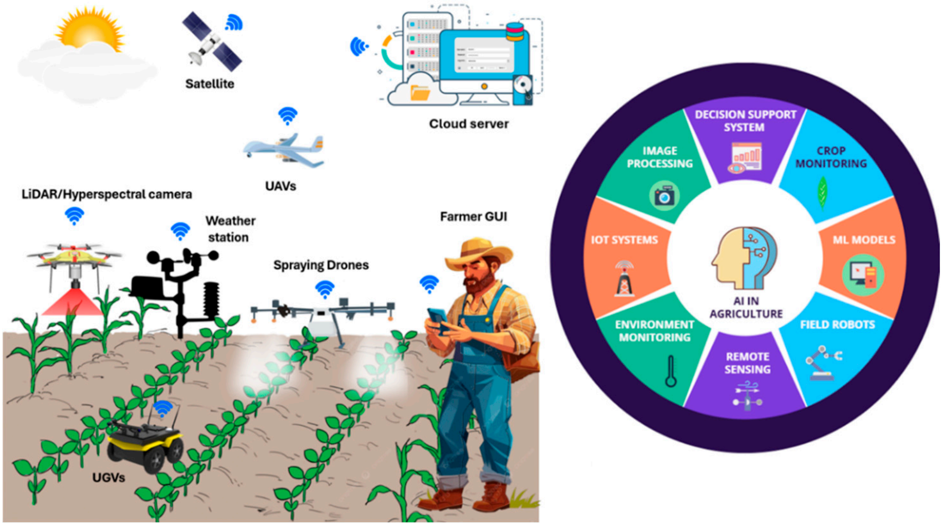

Figure 3. Visual illustrations of the role of artificial intelligence in agriculture: Monitoring, analysis, and precision agriculture.

5.3. AI and Automated Crop Management

The use of AI in crop management is reshaping modern agriculture, driving improvements in efficiency, sustainability, and resilience [197]. These digital technologies can boost productivity by optimizing the management of inputs such as irrigation, seed, nutrients, and pesticides to mitigate the issues of pests and diseases. In agriculture, plant protection plays a crucial role in maintaining crop health and boosting yields. Intelligent pesticide prescription spraying systems observe and identify pests, diseases, and weeds, utilize data-informed strategies to develop tailored precision management plans and employ smart tools to take preventive actions [198]. Recent developments in remote sensing and image analysis technologies have made it possible to accurately, instantly, and non-invasively identify pests and pathogens over extensive regions [199]. The use of AI-driven management strategies coupled with diverse sensing technologies can support the execution of disease control plans by leveraging early data on crop health and the precise location of diseases [200]. Common AI-based approaches for disease control include decision trees, random forests, k-nearest neighbors, support vector machines, and artificial neural networks [201]. Efficient irrigation and nutrient management are essential components of automated crop management. AI offers cutting-edge solutions to maximize resource use, improve crop health, and decrease environmental damage. Through the application of AI methods, farmers can improve irrigation and nutrient management, leading to increased yields, minimized resource use, and a smaller ecological impact [202]. AI algorithms can aid farmers in making better-informed choices, thereby minimizing the risks tied to climate variability and market changes.

6. Plant-Associated Microbiomes and Sustainable Agriculture

6.1.1. Role of Beneficial Microbes in Drought and Salinity Resistance

Beneficial microbes, particularly plant growth-promoting rhizobacteria (PGPR), are key to microbiome engineering for enhancing plant tolerance to drought and salinity stress, which threaten over 40% of global agricultural land [203–206]. It may not be the case that a specific PGPR has a unique beneficial activity for either drought or salinity stress. Instead, it is likely that a beneficial activity of PGPR contributes to tolerance for both stresses, although certain activities play a more crucial role for specific stresses. It has been reported that diverse PGPR can promote the resilience of crops to drought and salinity through multifaceted mechanisms. In maize, Bacillus megaterium enhances root hydraulic conductivity under salinity, while Pantoea agglomerans increases root

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conductance [207,208]. Certain Bacillus and Pseudomonas species improve drought and salinity tolerance by producing 1-aminocyclopropane-1-carboxylic acid (ACC)deaminase, solubilizing phosphate, and secreting siderophores [209–213]. Some PGPR secrete exopolysaccharides [EPS], forming biofilms that stabilize soil structure, improve moisture retention, and enhance microbial colonization [214]. Regulation of ion homeostasis and redox balance through the production of various antioxidizing enzymes and non-enzymatic antioxidants is also a crucial mechanism by which PGPR mitigate drought and salinity stresses [215–221]. These multifaceted mechanisms highlight PGPR as a sustainable strategy for improving plant adaptation to drought and salinity stress.

6.1.2. Synthetic Microbial Communities for Crop Resilience

The identification of microbial strains capable of producing different products that can assist in plant growth under stress condition can help in promoting sustainable agriculture [222]. Synthetic microbial communities (SynComs), a strategically designed multi-strain approach, represent a significant advancement in enhancing crop resilience against environmental stressors. Unlike single-strain inoculants, SynComs integrate functionally complementary microbes that interact synergistically to enhance nutrient acquisition, pathogen suppression, and abiotic stress tolerance through inter-microbial communication, such as quorum sensing and metabolite exchange [223,224]. The composition of a SymCom can be designed through experimental studies on microbial interactions or through computational approaches, such as genome-scale metabolic modeling [GEM], utilizing genomic databases of beneficial microbes to predict their metabolic roles in enhancing plant resilience [225,226].

SynComs strengthen plant resilience by utilizing metabolically diverse microbes. For instance, co-inoculation of Paenibacillus mucilaginosus and metal-resistant Sinorhizobium meliloti improved Cu uptake, enhanced soil microbial biomass, and increased antioxidant activity while reducing oxidative stress [225,227,228]. Additionally, co-culturing Pseudomonas koreensis and Microbacterium hydrothermale enhanced ACC deaminase, indole-3-acetic acid (IAA), and cytokinin production, reducing ethylene emissions by 20% and mitigating oxidative stress under salinity stress [229]; and a consortium of Ensifer adhaerens, Pseudomonas fluorescens, and Bacillus megaterium improved wheat resilience to salinity by enhancing shoot and root growth, chlorophyll content, and K/Na balance while reducing electrolyte leakage [230]. Combining multiple beneficial microbes can also lead to disease suppression and enhanced nodulation and nitrogen fixation. This is exemplified by mixtures of Bacillus spp. with species of Pseudomonas, Rhizobium, or Bradyrhizobium [231–235]. The integration of various microbial functions, such as ACC deaminase activity, osmolyte production, and biofilm formation, further enables SynComs to regulate phytohormones and improve stress adaptation. This approach supports SynComs' role in promoting sustainable agriculture and developing climate-resilient crops [230,236]. Nevertheless, the successful application of SynCom largely depends on the survivability of microbes during preservation and in non-native soils. Development of innovative encapsulation and coating techniques is crucial for the widespread use of SynComs [237,238].

6.2. Bioinoculants and Soil Health Improvement

6.2.1. Enhancing Nutrient Uptake and Root Development

Bioinoculants, primarily beneficial bacteria, play a crucial role in improving plant nutrition by facilitating nutrient uptake and optimizing root-system architecture (RSA). These microbial agents aid in nutrient solubilization, mobilization, and assimilation, thereby reducing dependency on synthetic fertilizers. Nitrogen-fixing bacteria, such as Rhizobium, Bradyrhizobium, Azospirillum, and Azotobacter, convert atmospheric nitrogen into ammonia, increasing nitrogen availability [239–241]. Phosphate-solubilizing bacteria, including Pseudomonas, Enterobacter, and Leclercia, produce organic acids that release phosphorus from insoluble compounds, improving its accessibility to plants [242–244]. Similarly, other nutrient elements can be better obtained through the action of

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beneficial bacteria, such as potassium by potassium-solubilizing bacteria [245,246], silicon by silicate-solubilizing bacteria like Burkholderia eburnea and Bacillus globisporus [247,248], iron by siderophore-producing PGPR, including Pseudomonas, Stenotrophomonas, and Enterobacter [249–251], manganese by certain Bacillus and Pseudomonas strains [252,253], and selenium [Se] by selenium-accumulating PGPR, such as Enterobacter and Bacillus [254,255]. The enhanced nutrient uptake mediated by bioinoculants helps mitigate various biotic and abiotic stresses.

Bioinoculants also influence root morphology by producing phytohormones, such as IAA and gibberellic acid (GA), promoting lateral root formation, elongation, and root hair proliferation [256,257]. This structural modification improves water and nutrient uptake efficiency, particularly under drought and salinity stress [258–260]. These microbes interact dynamically with plant roots by sensing and responding to root exudates, which regulate bacterial gene expression, metabolism, and colonization [261]. These interactions support microbial adaptation and plant resilience [262–265] and promote soil stability, organic matter decomposition, and microbial diversity, ultimately leading to sustainable agricultural practices and long-term soil health.

6.2.2. Imaging Methods for Evaluation of Root System Architecture

RSA is composed of the overall spatial and morphological features of the root system of a plant, with these features related to phenotypic traits. Investigating how RSA changes in response to different factors allows greater understanding of the connections between plants and environment [266]. Measurements of RSA features is pursued through application of a variety of imaging techniques [267,268], commonly defined by specific methods of plant and root cultivation and potential root harvesting [269]. These methods may be viewed as choices along a spectrum from destructive to non-destructive [270]. Destructive methods involve those seen generally in field-size and some greenhouse experiments, including harvesting of the entire root system through use of “shovelomics”, where the root crown is removed [271–273], exposure of the root system of plants by trenching alongside [274], and traditional coring, with removal of cylindrical cores containing whole roots, pieces or subnetworks of roots [275]. At the greenhouse level, roots may be extracted from pots. Generally, roots and root materials are washed after harvesting, and this washing step itself may be destructive. Roots are then imaged with various systems, including 2D imaging with RGB or monochrome flatbed scanners, DSLR cameras, machine vision cameras, or minirhizotron tube cameras [after coring in the field] [276]. Three dimensional imaging techniques may be applied as well including multi-camera setups with sample revolution [277], with 3D reconstructions of the root system possible after image processing.

Non destructive methods are seen at the greenhouse and bench levels, including use of various rhizotrons or rhizoboxes where roots are grown in boxes with visible windows [278,279], clear pots or boxes filled with soil [280], on germination paper [281], in agar filled petri dishes or containers [280], or hydroponically [282], at varying levels of plant maturity, and length scale. Imaging in 2D is possible through transparent windows and sides with systems including RGB/monochrome DSLR and machine vision cameras. With these types of methods 3D imaging is also more accessible, including magnetic resonance imaging [MRI] [283], x-ray computed tomography [283–285], and positron emission tomography [268]. Laser light has also been used in conjunction with gel medium [286]. MRI and tomographic methods are affected by challenges in imaging resolution, soil material opacity, and water interactions, amongst others. Choice of imaging method for evaluating RSA is often dependent on experiment size and hardware, and on subsequent image processing pipeline decisions.

6.2.3. Reducing Dependency on Chemical Fertilizers

The increasing reliance on synthetic fertilizers, particularly nitrogen-based formulations, has significantly contributed to soil degradation and greenhouse gas emissions, accounting for approximately 2.1% of anthropogenic emissions [287]. Bioinoculants offer an environmentally friendly approach to enhancing plant growth and nutrient acquisition through improved microbial

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metabolic networks [288–294]. The application of biofertilizers [or bioinoculants] has shown to enhance crop yields by 25% while significantly lowering the need for synthetic inputs, reducing nitrogen requirements by 50% and phosphorus needs by 25%. This reduction not only minimizes dependency on chemical fertilizers but also decreases soil and plant vulnerability to pests and diseases, thereby lowering the need for synthetic pesticides [295]. The shift toward biofertilizers is reflected in market trends, with the U.S. biofertilizer market projected to grow from $3.55 billion in 2024 to $4.47 billion by 2026 [294]. This growth is driven by various advantages of using microbial agents, including the enhancement of plant resilience against diverse environmental stresses [296–298].

7. Societal, Social, and Economic Impacts of Climate-Resilient Crops

7.1. Global Food Security and Hunger Reduction

Since the beginning of the 21st Century, the world has seen substantial reductions hunger and food insecurity, but both hunger and food insecurity continue to be major social challenges in all world regions, and particularly in sub-Saharan Africa [299]. Future population, agricultural land use, and climate projections suggest that between 2.5 and 4.2 billion people [51% of the world's population] will be at risk of undernourishment by 2050 without agricultural innovation for climate adaptation in the intervening years [300]. In the world's most vulnerable regions, hunger, food insecurity, and rapid food price increases have been linked to social unrest and food riots, most recently in 2008 and 2010 [301]. Weather volatility and higher temperatures have reduced crop yields and contributed to a rise in food shortages, hunger and food insecurity, and undernourishment is predicted to increase in countries with increasing populations [302] Climate-induced crop failure due to temperature increases and weather volatility has been a major contributor to both external and within-country migration, particularly in countries that rely more heavily on the agricultural sector [303]. Projected yield decreases from weather variability are greatest for oilseed crops, which include soybeans [304]. While intensive efforts in several other areas may also be needed to minimize the impact of extreme and volatile weather, learning more about the resilience of plants, soils, and microbial communities to improve crop yields in adverse and variable environmental conditions will constitute one crucial component of the global effort to meet reduce food insecurity [305]. The iPACERS project focuses efforts to understand biotic and abiotic stress tolerance of one of the most important food crops, soybeans [the King of Beans], one of the most important sources of protein for the world's population with a global market value projected to increase from $155 Billion in 2023 to $278 Billion by 2031 [306].

In the United States, soybean production has increased over the last 100 years from about 1.5 million acres in 1924 to nearly 90 million acres in 2024 [307]. Soybeans are currently the second largest row crop in the United States, and if demand continues to grow, soybeans could replace corn as the most planted crop [308]. Extreme weather events can cause crop failure or significantly lower yields that can influence farming strategies and decision-making strategies, farmer mental health, suicide rates, and community participation. A deeper understanding of how extreme and volatile weather conditions affect soybean plants, root systems, and soil microbiomes at the cellular level can empower soybean farmers to develop and implement more effective adaptation strategies. Farmers who perceive that climate change has increased risks to their own farm are more likely to explore adaption strategies, experiment with a wider variety of adaption strategies, and take more advantage of available support structures, such as crop insurance programs, community support through grower associations, and conservation programs [309].

Changing weather conditions over the past decades has resulted in decreasing production of corn and cotton in Louisiana, along with increasing production in rice and soybeans, and these trends are likely to continue in the future, increasing the need for research that specifically focuses on adaptation strategies related to soybean farming [310]. Effective strategies require both deeper understanding of biotic and abiotic stress of the soybean plant under extreme or volatile weather

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conditions and the willingness of farmers to implement the strategies. A recent study partially attributed Michigan farmers' willingness to adopt sustainable agricultural practices to both their understanding of the necessity and benefits of adopting a new variety or practice and their perceptions of the opinions and practices of other farmers in their social networks [311] Concerns about climate change, crop failure, and lower yields can have negative consequences for farmers' health and mental health [312] and suicide [313]. Advances in agricultural technologies and plant breeding have led to more climate-resilient crop varieties and more sustainable agricultural systems, even for smallholder farmers in developing nations, and show promise for additional mitigation strategies [314–316]. Climate resilient crops can potentially reduce risks [real or perceived] to farmers due to weather volatility and extreme weather. Extension and support communities play a vital role in building relationships and engaging farmer stakeholders in the coproduction of scientific and technical knowledge to increase resilience in rural communities [317].

The iPACERS project attempts to address the complex challenges related to soybean production in the southern United States by integrating scientific knowledge related to soybean stress tolerance, root system dynamics, and soil microbiome responses to extreme weather with environmental educational outreach to farmers, teachers, and students in communities where soybean production has been established and is forecasted to expand in the coming decades. Participating scientists will help develop future generations of researchers through their respective labs and research programs. Importantly, the practical challenges faced by farmers and rural communities cannot typically be addressed using the theoretical perspectives and methods of a single academic discipline or institution. Therefore, multi-institutional and multidisciplinary approaches to the complex agroecological and social challenges related to climate change will continue to lead the efforts to find adaptation strategies that strengthen agricultural communities, mitigate the negative effects of extreme weather and weather volatility, build agricultural research capacity, and lead toward more sustainable agricultural systems. Scientists and their research programs benefit from these large-scale collaborations by gaining access to equipment, expertise, data, and techniques to conduct research and generate meaningful data and findings that have practical relevance for stakeholders. Stakeholder communities both benefit from and contribute to the broad dissemination of research findings, and these communities provide critical feedback that researchers can use to make advances in climate adaptation more accessible and relevant to local populations.

7.2. Integrating Climate-Agriculture Education

Climate change education enables individuals and communities to understand the impacts of changing climates on agricultural systems and food security. It equips farmers, educators, policymakers, and students with knowledge and skills to mitigate climate change and adapt agricultural practices. Education has the potential to serve a critical role in addressing climate change by developing a population with climate literacy and offering potential solutions to mitigate the impacts of climate change [318–320]. A systematic review of environmental and climate education studies suggests that effective environmental education includes: (1)focusing on personally relevant and meaningful information and (2) using active and engaging teaching methods [321]. Specific to climate change, Monroe et al [2019] also found four themes related to successful education initiatives: (1) engaging in deliberative discussions, (2) interacting with scientists, (3) addressing misconceptions, and (4) implementing school or community projects [321]. Projects that focus on local and individual action may be especially effective [320,322]. The authors of another systematic review of climate change education call for the development of curriculum that "directly involve children and young people in responding to the scientific, social, ethical, and political complexities of the issue" [323]. An integrated, systems-based model for understanding both the impacts of climate change and potential to develop solutions can make the topic both more meaningful and empowering for students [324,325].

Both the Next Generation Science Standards (NGSS), used in the majority of the United States to guide science education, and The National Council for Agricultural Education's Agriculture, Food,

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and Natural Resources (AFNR) standards for K-12 agriscience education include standards related to understanding human impact on climate change and using biotechnology to adapt organisms (Table 1) [326,327]. However, neither set of standards has strong deliberate integration of the two ideas (i.e. using biotechnology to develop agricultural solutions to climate-change-driven problems) and in other parts of the world, there is a similar siloing of topics [328]. Teacher professional development (TPD) workshops could address this by training teachers in the use of CRISPR Cas-9 to develop drought-tolerant, heat-resistant, or other climate-change-resistant food crop plants. Commercial providers of K-12 biotechnology classroom kits have already begun to produce age-appropriate kits for classroom use. The AFNR standards could be an excellent resource for science educators to design biotechnology-driven climate education from, as they already consider the intersection of science, society, economic, and career applications. Our proposal of teaching climate change through the lens of agriscience and biotechnology solutions meets the extant literature's suggestions for meaningful and effective classroom-based climate education.

School-based agriscience educators are an often-overlooked group in consideration of climate change education [329]. Local Extension agents are also valuable as trusted sources of education and information for farmers [330]. Very few published studies have examined these educators' knowledge and attitudes regarding climate change and those that have report a range of knowledge, beliefs in the anthropogenic origins of climate change, and instructional time spent on the topic [331]. These educators should be considered for future research and professional development training. Among science teachers there is also a range of knowledge and beliefs regarding the inclusion of climate education in their curricula. For some teachers, teaching climate change aligns with personal beliefs about the importance of environmental education, their identity as scientists, and/or their feelings of hope in regard to solutions to climate-change-driven problems [332,333]. However, even among secondary science teachers who teach climate change, there may be misconceptions in their knowledge and a hesitancy to include social, political, economic contexts [334,335]. Future professional development opportunities should consider the range of potential educators, including science, agriscience, and Extension or other outreach teachers, the range of attitudes and beliefs, and the role that teacher science identity and actionable learning can play in effective climate education [336,337]. Integrating climate issues into biotechnology and agriscience education promotes sustainability and prepares future generations to tackle global challenges effectively. It also anchors a challenging and sometimes emotional topic in consideration of real-world impacts and engages learners in considering their ability to develop or support real, technology-driven solutions to global problems.

Table 1. NGSS and AFNR Standards Related to Climate Change and Biotechnology.

Standard Set	**Topic**	
	Climate Change	Biotechnology
NGSS	MS-ESS3-3. Apply scientific principles to design a method for monitoring and minimizing a human impact on the environment. MS-ESS3-4. Construct an argument supported by evidence for how increases in human population and per-capita consumption of natural resources impact Earth's systems. MS-ESS3-5. Ask questions to clarify evidence of the factors that have caused the rise in global temperatures over the past century.	MS-LS4-5. Gather and synthesize information about technologies that have changed the way humans influence the inheritance of desired traits in organisms. HS-LS2-7. Design, evaluate, and refine a solution for reducing the impacts of human activities on the environment and biodiversity.

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	HS-ESS3-4. Evaluate or refine a technological solution that reduces impacts of human activities on natural systems. HS-ESS3-5. Analyze geoscience data and the results from global climate models to make an evidence-based forecast of the current rate of global or regional climate change and associated future impacts to Earth's systems. HS-ESS3-6. Use a computational representation to illustrate the relationships among Earth systems and how those relationships are being modified due to human activity.	HS-LS4-6. Create or revise a simulation to test a solution to mitigate adverse impacts of human activity on biodiversity.
AFNR	NRS.01.03. Apply ecological concepts and principles [e.g., weather, air quality, UV protection, atmospheric pressure, etc.] to the interaction of atmospheric and natural resource systems. NRS.02.01. Examine and interpret the purpose, enforcement, impact, and effectiveness of laws, agencies, and private and public organizations related to natural resource management, protection, enhancement, and improvement [e.g., water regulations, game laws, environmental policy, local, state, and national conservation organizations, agricultural extension service, etc.]. NRS.02.03. Analyze how social perceptions of natural resource management, protection, enhancement, and improvement change and develop over time. ESS.03.01. Apply meteorology principles to environmental sustainability systems. ESS.03.01.03.c. Evaluate the potential impacts of global climate change on environmental sustainability systems. ESS.03.01.04.c. Create an action plan to mitigate the impact of climate change on environmental sustainability systems. FPS.02.02. Examine the impact of AFNR on the local, state, national, and global society and economy. FPS.04.02. Assess and explain the natural resource related trends, technologies and policies that impact AFNR systems.	PS.03.01. Demonstrate plant propagation techniques in plant system activities. PS.03.01.05.c. Evaluate the impact of using genetically modified agricultural and ornamental crops on other production practices. BS.03.04. Apply biotechnology principles, techniques, and processes to enhance plant and animal care and production [e.g., selective breeding, pharmaceuticals, biodiversity, etc.].

8. Future Directions

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8.1. Integrating AI, Multi-Omics, and Phenomics in Crop Breeding

The integration of AI, multi-omics, and phenomics can reshape the landscape of modern crop breeding. Multi-omics approaches encompassing genomics, transcriptomics, proteomics, metabolomics, and epigenomics enables comprehensive dissection of plant responses to environmental stresses at various biological levels. However, managing and interpreting the vast datasets generated from these methods require sophisticated computational tools. AI and ML algorithms are being increasingly deployed to uncover complex genotype-to-phenotype relationships, predict trait performance, and guide marker-assisted and genomic selection processes [177,338]. ML models have been used to predict yield under drought conditions by integrating SNP markers with high-throughput phenotypic data [339]. Deep learning, a subset of AI, can also identify novel gene–trait associations from large omics datasets, enabling trait prediction with higher accuracy than conventional statistical methods. Simultaneously, advances in phenomics especially HTP platforms using drones, imaging systems, LiDAR, and thermal cameras allow precise, real-time monitoring of plant traits like canopy temperature, chlorophyll fluorescence, and water-use efficiency under field conditions [18,340]. Integrating these phenomic datasets with multi-omics profiles and AI-driven modeling enables predictive breeding, accelerates the identification of superior genotypes, and improves selection accuracy across diverse environments. The combination of these technologies paves the way of 'data-driven breeding,' where identifying climate-resilient varieties becomes more efficient, cost-effective, cost-effective, and more reliable.

8.2. Investment in Climate-Smart Agricultural Technologies

To translate scientific innovations into on-the-ground impact, substantial and sustained investment in climate-smart agriculture (CSA) is essential. CSA technologies aim to increase productivity, adapt and build resilience to climate change, and reduce greenhouse gas emissions [341]. These include precision agriculture tools, resource-efficient irrigation systems, stress-resilient crop varieties, decision support tools, and gene-editing platforms like CRISPR-Cas9. Public and private investment is particularly critical in accelerating the development and deployment of technologies that benefit smallholder farmers, who are disproportionately affected by climate variability [342]. Precision technologies such as smart irrigation controllers, moisture sensors, and AI-based pest forecasting systems are increasingly adopted in industrial agriculture but remain underutilized in resource-limited settings. CRISPR genome editing transforms crop improvement by enabling precise, rapid trait integration under stress with minimal off-target effects, warranting broader agricultural adoption [343]. Additionally, mobile-based advisory services and digital platforms are enhancing farmers' access to climate and market information, empowering them to make informed decisions. Governments and development agencies must prioritize investments not only in technology but also in infrastructure, policy reform, and education. This includes supporting seed system development, strengthening biosafety regulations, and incentivizing private sector innovation. Importantly, investment must be inclusive, ensuring that women, indigenous communities, and marginalized groups benefit equitably from CSA advancements [344].

8.3. Strengthening Global Collaborations and Research Initiatives

The global nature of climate change and food insecurity calls for international collaboration and cross-sectoral partnerships. Strengthening global research networks can facilitate the sharing of germplasm, data, and best practices and reduce duplication of efforts. Major initiatives such as the CGIAR's OneCGIAR reform, the FAO Global Soil Partnership, and the Crop Wild Relatives (CWR) Project represent coordinated efforts to mobilize international expertise and resources toward sustainable crop improvement [345,346]. Collaborative breeding programs that integrate local knowledge with global science have shown success. For example, participatory breeding initiatives in Sub-Saharan Africa and South Asia have resulted in locally adapted, stress-tolerant varieties of rice, millet, and cassava. Similarly, North–South and South–South research alliances can enhance

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capacity building, particularly in developing nations facing the brunt of climate stress. To sustain and expand these efforts, policies must promote open data sharing, intellectual property transparency, and equitable access to genetic resources. Training the next generation of plant scientists in interdisciplinary, collaborative, and globally minded frameworks will also be critical. Furthermore, establishing regional centers of excellence in climate-resilient agriculture can drive locally tailored solutions while feeding into global innovation pipelines. These centers should focus not only on scientific excellence but also on socio-economic impacts and policy translation.

9. Conclusion

The challenges to global agriculture posed by climate change demand urgent and innovative solutions. Integrating multi-omics, AI-driven analytics, and advanced phenotyping in developing climate-resilient crops can bring unprecedented developments. By deciphering complex stress responses and accelerating precision breeding, these technologies bridge the gap between research and real-world agricultural resilience. Harnessing plant-microbe interactions to enhance crop adaptability and soil health becomes possible. Beyond scientific advancements, the widespread adoption of these tools can drive socioeconomic progress through strengthening food security, empowering farmers, and fostering sustainable economies. Achieving this vision demands coordinated action among scientists, policymakers, and educators. The path ahead demands scalable, equitable implementation while advancing fundamental science to outpace evolving climatic challenges. Together, these strategies can safeguard food systems, ensuring productivity and sustainability in an uncertain climate future.

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