

INTEGRATING AGRONOMY AND MOLECULAR RESEARCH FOR SUSTAINABLE CROP IMPROVEMENT: EXPLORING PLANT–ENVIRONMENT INTERACTIONS, STRESS RESPONSES, MOLECULAR MECHANISMS AND PRECISION CROP MANAGEMENT

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ABSTRACT

Sustainable crop production is increasingly challenged by climate variability, soil degradation, water scarcity, emerging pests and diseases, declining resource-use efficiency, and the need to produce more food with fewer environmental inputs. Conventional agronomic management and crop improvement have contributed substantially to agricultural productivity; however, their effectiveness under increasingly heterogeneous and rapidly changing environments is often constrained by complex plant–environment interactions. Integrating agronomic science with molecular biology, genomics, phenomics, microbiome research and precision agriculture provides an opportunity to develop crop production systems that are both productive and resilient. Plant responses to environmental stress involve coordinated morphological, physiological, biochemical and molecular mechanisms, including changes in root architecture, stomatal regulation, osmotic adjustment, antioxidant metabolism, hormone signalling, transcriptional regulation and stress-responsive gene expression. Recent advances in genomics-assisted breeding, quantitative trait locus mapping, genome-wide association studies, transcriptomics, proteomics, metabolomics and genome editing have expanded the ability to identify and manipulate genes and pathways associated with stress adaptation. At the same time, precision agriculture technologies, including remote sensing, proximal sensors, geographic information systems, unmanned aerial systems, artificial intelligence and variable-rate management, enable site-specific crop management. Plant-associated microbiomes provide an additional biological dimension by influencing nutrient acquisition, stress signalling, disease suppression and soil health. Recent literature indicates increasing convergence among molecular breeding, microbiome engineering, phenotyping and precision agronomy. This review examines the integration of these approaches, emphasizing plant–environment interactions, abiotic and biotic stress responses, molecular mechanisms, genomics-assisted crop improvement and precision crop management. It further discusses research gaps and proposes an integrated framework for developing climate-resilient, resource-efficient and sustainable cropping systems.

Keywords: Agronomy, Crop Improvement, Plant–Environment Interaction, Abiotic Stress, Molecular Breeding, Genomics, Plant Microbiome, Precision Agriculture, Climate Resilience, Sustainable Agriculture

1. INTRODUCTION

Agriculture is undergoing a major transformation driven by climate change, population growth, resource constraints, soil degradation and changing demands for food quality and environmental sustainability. Crop productivity can no longer be considered solely as a function of genetic potential or agronomic management under optimal conditions. Instead, productivity is the outcome of complex interactions among genotype, environment, management practices, soil properties, microorganisms and climatic conditions. Consequently, sustainable crop improvement requires approaches that simultaneously address the biological mechanisms underlying plant adaptation and the agronomic practices used to manage production environments. Traditional agronomy has primarily focused on optimizing crop establishment, nutrient management, irrigation, planting density, weed control, pest management and harvesting. These practices remain fundamental to agricultural productivity. However, the increasing frequency of drought, heat waves, salinity, flooding and other stresses has highlighted

the importance of understanding how crops respond to environmental variability at physiological and molecular levels. Genomics-assisted breeding has emerged as an important approach for identifying genes, alleles and quantitative trait loci associated with stress adaptation and other complex traits.

Plant responses to environmental stress are highly complex. Drought, salinity, temperature extremes, nutrient deficiencies and flooding can disrupt photosynthesis, membrane stability, water relations, nutrient acquisition and reproductive development. Plants respond through interconnected signalling networks involving reactive oxygen species (ROS), phytohormones, calcium signalling, mitogen-activated protein kinases, transcription factors and stress-responsive genes. These molecular responses ultimately influence physiological and agronomic traits such as root growth, water-use efficiency, flowering, biomass accumulation and yield. At the same time, developments in molecular biology have created opportunities to complement rather than replace agronomic approaches. Marker-assisted selection, genomic selection, transcriptomics, metabolomics and genome editing can accelerate the development of improved cultivars, while precision agriculture can ensure that genetic potential is appropriately expressed through site-specific management.

The plant microbiome represents another important component of this integrated system. Beneficial microorganisms can influence nutrient acquisition, hormone regulation, antioxidant activity and plant defence. Recent research increasingly emphasizes the potential of microbiome-based approaches for improving crop resilience while reducing dependence on synthetic inputs. Therefore, the future of sustainable crop improvement lies in the convergence of **genetics, molecular biology, agronomy, soil science, microbiology, phenomics, digital agriculture and data science**. This review examines this convergence and its potential contribution to productive, resource-efficient and climate-resilient agriculture.

2. PLANT–ENVIRONMENT INTERACTIONS IN CROP PRODUCTION

Plant growth and productivity are determined by continuous interactions between genetic characteristics and environmental conditions. The same genotype may express substantially different phenotypes when grown under contrasting soil, climatic and management environments. Understanding these interactions is therefore fundamental to sustainable crop production.

2.1 Soil–Plant Interactions

Soil provides plants with water, nutrients and physical support while simultaneously serving as a habitat for diverse microbial communities. Soil texture, structure, organic matter, pH, salinity, moisture and nutrient availability influence root development and nutrient acquisition. Root systems actively modify their surrounding environment by releasing organic compounds, recruiting microorganisms and altering nutrient availability. Root exudates can influence microbial communities and nutrient cycling, creating a dynamic rhizosphere in which plant and microbial processes are closely interconnected.

Improved soil organic matter management, conservation agriculture, balanced fertilization and biological amendments can enhance soil structure and biological activity. At the molecular level, nutrient availability also regulates transporter genes, transcription factors and signalling pathways associated with root development and nutrient-use efficiency.

2.2 Plant–Water Relationships

Water availability is one of the major determinants of crop productivity. Plants regulate water uptake and loss through root architecture, stomatal behaviour, osmotic adjustment and hydraulic characteristics. Under drought conditions, plants may increase root allocation, reduce stomatal conductance and accumulate osmoprotective compounds such as proline, soluble sugars and compatible solutes. Absciscic acid (ABA) plays a major role in coordinating stomatal closure and other drought responses.

The integration of irrigation scheduling with knowledge of crop water-use physiology can improve water productivity. Precision irrigation systems can further enable application of water according to spatial and temporal variation in crop demand.

2.3 Temperature and Light

Temperature affects virtually every physiological process in plants. High temperatures can impair pollen viability, photosynthesis, membrane stability and grain or fruit development, while low temperatures can cause chilling or freezing injury.

Plants possess sophisticated temperature-sensing and signalling mechanisms involving heat-shock proteins, heat-shock transcription factors, antioxidant systems and membrane modifications. Molecular research has identified numerous regulatory components associated with heat and cold tolerance, providing opportunities for breeding climate-adapted cultivars.

3. ABIOTIC STRESS AND CROP PRODUCTIVITY

Abiotic stresses are among the major constraints limiting agricultural productivity and stability across diverse agroecosystems. Drought, salinity, heat, cold, flooding, waterlogging, nutrient imbalance and heavy-metal toxicity can individually or collectively interfere with plant growth, development and reproductive success. The severity of stress depends not only on its intensity and duration but also on crop species, genotype, developmental stage and environmental conditions. In field situations, plants are frequently exposed to combinations of stresses rather than a single stress, making adaptation particularly complex. Abiotic stress can disrupt water relations,

photosynthetic activity, membrane integrity, nutrient acquisition, cellular metabolism and reproductive development, ultimately resulting in reductions in biomass accumulation and yield. Plants have consequently evolved a sophisticated network of morphological, physiological, biochemical and molecular mechanisms that enable them to perceive environmental changes and adjust their growth and metabolism accordingly. These mechanisms include modification of root architecture, stomatal regulation, osmotic adjustment, accumulation of compatible solutes, activation of antioxidant defence systems, regulation of ion transport, changes in hormone signalling and expression of stress-responsive genes [1–4].

Drought stress is one of the most important environmental limitations to crop production, particularly in rainfed and water-limited agricultural systems. Reduction in soil moisture decreases plant water potential and can restrict cell expansion, stomatal conductance, photosynthesis and nutrient transport. Prolonged drought may cause oxidative stress because the imbalance between energy capture and metabolic utilization promotes excessive accumulation of reactive oxygen species (ROS). Plants respond to drought through several mechanisms, including deeper root development, changes in root-to-shoot allocation, stomatal closure, osmotic adjustment and enhanced antioxidant activity. The phytohormone abscisic acid (ABA) plays a central role in drought responses by regulating stomatal closure and activating downstream stress-responsive pathways. Accumulation of osmoprotective substances such as proline, soluble sugars and certain amino acids can help maintain cellular water balance and protect macromolecules and membranes. At the molecular level, drought tolerance is controlled by interconnected regulatory networks involving transcription factors such as DREB, NAC, WRKY, MYB and bZIP families, which regulate the expression of numerous downstream stress-responsive genes [2,5]. The complex genetic architecture of drought tolerance makes conventional breeding challenging, and therefore molecular markers, quantitative trait locus (QTL) mapping, genomic selection, transcriptomics and genome editing are increasingly being integrated into breeding programmes. However, the effectiveness of these approaches depends on field validation because drought responses observed under controlled conditions may not always translate into stable yield advantages under diverse production environments.

Salinity represents another major abiotic constraint, particularly in irrigated agriculture, coastal regions and areas with poor drainage. Excessive concentrations of soluble salts impose both osmotic and ionic stress on plants. The osmotic component restricts water uptake, whereas excessive accumulation of sodium and chloride ions can disturb cellular ion homeostasis and interfere with essential nutrient uptake. Plants have evolved mechanisms involving selective ion transport, ion exclusion, sequestration of toxic ions into vacuoles, osmotic adjustment and antioxidant defence to minimize salinity-induced damage. Transport systems such as the SOS pathway and sodium transporters contribute to the maintenance of intracellular ion balance, while compatible solutes and antioxidant enzymes provide additional protection against cellular damage [6]. Agronomic interventions such as improved drainage, appropriate irrigation management, balanced fertilization, organic matter addition and selection of salt-tolerant cultivars can reduce the adverse effects of salinity. Integrating these practices with molecular breeding provides an opportunity to develop cultivars capable of maintaining productivity under saline conditions. Similarly, heat stress has become increasingly important because rising temperatures and more frequent heat waves can adversely affect crop growth and reproductive development. High temperatures can impair photosynthesis, accelerate senescence, destabilize cellular membranes and reduce pollen viability, leading to substantial yield losses when stress occurs during flowering and grain or fruit development. Plants respond to heat stress through heat-shock proteins, heat-shock transcription factors, antioxidant systems, membrane lipid modification and changes in metabolic activity [7]. Genetic variation in these mechanisms can be exploited through conventional and molecular breeding to develop heat-resilient cultivars.

Cold stress, flooding and waterlogging represent additional environmental constraints affecting crop establishment, nutrient uptake and productivity. Low temperatures can impair membrane function, enzymatic activity and photosynthesis, whereas freezing conditions can cause cellular damage through ice formation. Plants respond to cold stress through changes in membrane composition, accumulation of protective metabolites and activation of cold-responsive genes, including those regulated through CBF/DREB pathways. Flooding and waterlogging, in contrast, primarily create oxygen deficiency in the root zone, disrupting aerobic respiration and nutrient uptake. Some crops possess adaptive mechanisms such as aerenchyma formation, adventitious root development and metabolic adjustment that improve survival under hypoxic conditions [8]. Nutrient stress also interacts strongly with environmental stress because deficiencies or excesses of nitrogen, phosphorus, potassium, iron and other elements can influence plant growth and stress tolerance. Nutrient availability affects antioxidant capacity, osmotic regulation, root development and metabolic activity, while stress itself can alter nutrient acquisition and transport. Consequently, sustainable crop improvement requires a combined consideration of genetic tolerance, soil fertility, water management and crop husbandry rather than treating individual stresses independently. The integration of physiological screening with molecular markers, high-throughput phenotyping and precision field management can facilitate the identification and deployment of genotypes with stable performance under variable environments [9–12].

Table 1. Major plant stresses, physiological effects and molecular responses

Stress type	Major environmental causes	Major effects on plants	Important physiological responses	Representative molecular responses
Drought	Low rainfall, high evapotranspiration, soil-water deficit	Reduced growth, leaf expansion and yield	Stomatal closure, osmotic adjustment, deeper rooting	ABA signalling, DREB/AREB transcription factors, osmoprotectant accumulation
Heat	High temperature, heat waves	Reduced pollen viability, photosynthesis and grain filling	Heat-shock response, membrane stabilization	Heat-shock proteins, HSFs, antioxidant enzymes
Salinity	Salt accumulation in soil or irrigation water	Ionic toxicity, osmotic stress and nutrient imbalance	Ion exclusion, osmotic adjustment	SOS pathway, NHX transporters, antioxidant responses
Flooding	Excess rainfall, poor drainage	Oxygen deficiency, root damage and reduced respiration	Anaerobic metabolism, adventitious rooting	ERF transcription factors, fermentative enzymes
Cold	Low temperature, frost	Membrane injury, reduced metabolic activity	Membrane stabilization, cryoprotection	CBF/DREB pathways, cold-responsive genes
Nutrient deficiency	Low soil fertility or nutrient imbalance	Reduced biomass, chlorosis and low yield	Enhanced nutrient acquisition	Nutrient-responsive transporters and transcription factors
Biotic stress	Pathogens, insects and nematodes	Tissue damage, reduced photosynthesis and yield	Defence activation, systemic resistance	PR proteins, phytohormone signalling, resistance genes

Table 2. Major molecular and genomic approaches used in crop improvement

Approach	Principal objective	Major information generated	Application in crop improvement
QTL mapping	Identify genomic regions controlling quantitative traits	QTLs and linked markers	Stress tolerance, yield, quality traits
GWAS	Identify marker–trait associations	SNP–trait associations	Complex trait dissection
Marker-assisted selection	Track favourable alleles	Diagnostic molecular markers	Rapid selection of breeding lines
Genomic selection	Predict breeding value	Genome-wide marker profiles	Accelerated breeding cycles
Transcriptomics	Study gene expression	Differentially expressed genes	Stress-response mechanisms
Proteomics	Study protein abundance and modification	Stress-associated proteins	Functional characterization
Metabolomics	Characterize biochemical changes	Metabolite profiles	Biomarker discovery
Genome editing	Modify specific genomic sequences	Targeted genetic changes	Trait improvement and functional validation
Multi-omics	Integrate multiple molecular layers	Integrated biological networks	Complex trait prediction

Table 3. Plant–microbe interactions relevant to sustainable crop production

Microbial group	Major interaction with plants	Potential benefits
Plant growth-promoting rhizobacteria	Root colonization and signalling	Growth promotion, nutrient acquisition and stress tolerance
Arbuscular mycorrhizal fungi	Symbiotic root association	Improved phosphorus and water acquisition
Endophytic bacteria	Internal plant colonization	Growth promotion and stress mitigation

Beneficial fungi	Rhizosphere/endosphere association	Disease suppression and nutrient mobilization
Nitrogen-fixing bacteria	Biological nitrogen fixation	Improved nitrogen availability
Phosphate-solubilizing microorganisms	Mineral phosphate solubilization	Enhanced phosphorus availability
Biocontrol microorganisms	Antagonism and induced resistance	Suppression of plant pathogens

Table 4. Precision agriculture technologies and their applications in crop management

Technology	Information obtained	Major agricultural application
Remote sensing	Vegetation indices, canopy condition	Crop monitoring and stress detection
UAV/drone imaging	High-resolution field images	Disease, biomass and phenotyping assessment
GIS	Spatial variability	Field zoning and site-specific management
GNSS/GPS	Precise geographical position	Machinery guidance and variable-rate application
Soil sensors	Moisture, EC, temperature and nutrients	Irrigation and fertilizer management
Weather stations	Temperature, rainfall, humidity and wind	Crop forecasting and stress prediction
Multispectral imaging	Spectral crop signatures	Nutrient and disease assessment
Thermal imaging	Canopy temperature	Water-stress detection
IoT systems	Real-time field measurements	Automated monitoring and decision support
AI/ML	Pattern recognition and prediction	Yield prediction and management optimization

4. BIOTIC STRESS AND PLANT DEFENCE

Biotic stresses caused by insects, pathogens, nematodes, viruses, bacteria, fungi and other biological agents represent major threats to crop productivity and food security. Unlike abiotic stresses, which are primarily associated with physical and chemical environmental conditions, biotic stresses involve dynamic interactions between plants and living organisms. The outcome of these interactions depends on the genetic characteristics of both the host and the attacking organism, environmental conditions and agricultural management practices. Plants have developed sophisticated defence systems that include constitutive physical and chemical barriers as well as inducible immune responses. The plant cell is capable of recognizing conserved molecular patterns associated with pathogens through pattern-recognition receptors located at the cell surface. Recognition of these signals initiates a series of downstream events involving calcium influx, reactive oxygen species production, protein phosphorylation, mitogen-activated protein kinase signalling and transcriptional reprogramming. These processes activate defence-related genes and biochemical pathways that restrict pathogen invasion and spread [13,14].

Plant defence is strongly regulated by phytohormones, particularly salicylic acid, jasmonic acid and ethylene. Salicylic acid is generally associated with defence against biotrophic pathogens, whereas jasmonic acid and ethylene have important roles in responses to necrotrophic pathogens and herbivorous insects. However, these signalling pathways are interconnected and their relative contribution depends on the pathogen, tissue, developmental stage and environmental conditions. Plants can also activate systemic defence mechanisms, allowing tissues distant from the initial site of attack to acquire enhanced resistance. Systemic acquired resistance and induced systemic resistance demonstrate the ability of plants to coordinate defence at the whole-plant level. The interaction between defence signalling and plant growth is particularly important because excessive allocation of resources towards defence can reduce biomass accumulation and reproductive output. Therefore, an important objective of modern crop improvement is to achieve a balance between growth and defence, allowing plants to maintain productivity while possessing adequate resistance against major pests and pathogens.

Genetic resistance remains one of the most effective and environmentally sustainable approaches to controlling crop diseases. Resistance genes, quantitative resistance loci and susceptibility genes have been identified in numerous crop species through conventional genetic analysis, QTL mapping, genome-wide association studies and genomic approaches. Molecular markers linked to resistance loci can accelerate breeding through marker-assisted selection, while genomic selection can facilitate the accumulation of multiple resistance alleles. Advances in genome sequencing have further enabled the identification of candidate resistance genes and pathogen-interacting proteins. Genome-editing technologies, particularly CRISPR/Cas systems, have introduced additional possibilities for targeted modification of genes involved in plant immunity. Editing susceptibility genes can potentially enhance resistance without introducing resistance genes from unrelated genetic backgrounds [15,16]. Nevertheless, the durability of resistance remains a major concern because pathogen populations can evolve rapidly. Therefore, pyramiding multiple resistance genes, combining qualitative and quantitative resistance,

maintaining genetic diversity and integrating resistant varieties with agronomic and biological management strategies are important for long-term disease management.

Integrated pest management provides an important bridge between biological understanding and practical agronomy. Crop rotation, resistant varieties, biological control, cultural practices, monitoring and judicious pesticide use can collectively reduce pest and disease pressure while minimizing environmental impacts. The plant microbiome further contributes to plant defence because beneficial microorganisms can compete with pathogens, produce antimicrobial compounds, stimulate plant immunity and modify hormone signalling. Rhizobacteria and mycorrhizal fungi may enhance induced systemic resistance and improve plant tolerance to both biotic and abiotic stresses [17,18]. Consequently, modern approaches to crop protection increasingly recognize the plant as part of a larger biological system consisting of the host plant, pathogens, beneficial microorganisms, soil and surrounding environment. Molecular research can identify the mechanisms underlying these interactions, whereas agronomic management can create conditions that favour beneficial interactions and suppress harmful organisms. Combining host resistance, beneficial microbiomes, biological control, precision monitoring and targeted intervention may therefore provide a more sustainable alternative to reliance on chemical control alone.

Climate change further complicates biotic stress management because temperature, precipitation and atmospheric carbon dioxide influence pathogen development, insect population dynamics, host susceptibility and plant defence. Changes in cropping systems and the movement of agricultural pests into new geographical regions may also alter disease and pest risks. Consequently, future breeding programmes need to consider not only resistance to existing pathogen populations but also the potential for changing pest and disease environments. Integration of molecular surveillance, pathogen genomics, field phenotyping and predictive modelling could improve the ability to anticipate emerging threats. Such approaches can contribute to more responsive crop protection systems in which resistant cultivars and management recommendations are adjusted according to local environmental and biological conditions.

5. MOLECULAR MECHANISMS OF PLANT STRESS RESPONSES

Plant responses to environmental stresses are regulated through highly interconnected molecular networks that coordinate perception, signal transduction, gene expression, metabolism and physiological adjustment. Stress perception represents the first stage of this response and may involve changes in cellular water potential, membrane properties, ion concentrations, reactive oxygen species, calcium levels and other cellular signals. These primary signals activate complex downstream pathways involving protein kinases, transcription factors, phytohormones and stress-responsive genes. Rather than operating as independent pathways, these mechanisms interact extensively, allowing plants to integrate information from multiple environmental signals. This molecular plasticity is particularly important under field conditions where drought, heat, salinity, nutrient stress and biotic stresses can occur simultaneously. Understanding these regulatory networks is therefore essential for identifying molecular targets that can be used to improve crop resilience without imposing excessive penalties on growth and yield [3,19].

Reactive oxygen species are central components of plant stress signalling. Molecules such as superoxide radicals, hydrogen peroxide and hydroxyl radicals are continuously produced during normal cellular metabolism, particularly in chloroplasts, mitochondria and peroxisomes. Under stress conditions, their production may increase substantially. Excessive accumulation can damage proteins, lipids, nucleic acids and cellular membranes, but controlled ROS production also functions as an important signalling mechanism. Plants maintain ROS homeostasis through enzymatic and non-enzymatic antioxidant systems. Major antioxidant enzymes include superoxide dismutase, catalase, ascorbate peroxidase, glutathione reductase and various peroxidases, while non-enzymatic antioxidants include ascorbate, glutathione, carotenoids, tocopherols and phenolic compounds. The balance between ROS generation and detoxification therefore determines whether ROS act primarily as signalling molecules or cause oxidative damage. Enhanced antioxidant capacity has been associated with tolerance to drought, salinity, heat, cold and other stresses, making antioxidant metabolism an important component of molecular breeding programmes [20,21].

Calcium signalling represents another important mechanism through which plants perceive and respond to environmental changes. Stress conditions can produce rapid changes in cytosolic calcium concentration, which are subsequently decoded by calcium-binding proteins and protein kinases. Calcium-dependent protein kinases, calmodulins and calcineurin B-like proteins participate in downstream signalling pathways that regulate ion transport, gene expression and metabolic adjustment. Calcium signalling interacts with ROS, ABA and other hormonal pathways, creating an interconnected signalling network. Absciscic acid is particularly important in responses to drought and salinity because it regulates stomatal closure, root growth and expression of stress-responsive genes. ABA biosynthesis, transport and perception involve several molecular components, including PYR/PYL receptors, protein phosphatase 2Cs and SnRK2 kinases. Activation of this pathway ultimately influences transcription factors and genes involved in osmotic adjustment, antioxidant protection and cellular stress tolerance [22]. Such signalling networks illustrate why stress tolerance cannot generally be attributed to a single gene or biochemical pathway.

Transcription factors constitute a major regulatory layer in plant stress responses. Members of the DREB, NAC, WRKY, MYB, bZIP and AP2/ERF families regulate groups of genes involved in water relations, antioxidant

metabolism, osmoprotection, defence and cellular protection. DREB transcription factors, for example, are associated with regulation of dehydration- and cold-responsive genes, whereas NAC and WRKY proteins participate in broader responses to abiotic and biotic stresses. The ability of a transcription factor to regulate multiple downstream genes makes such regulators attractive targets for crop improvement. However, constitutive activation of some stress-responsive genes can result in growth retardation or yield penalties under favourable conditions. Consequently, current research increasingly focuses on tissue-specific, stress-inducible or precisely edited regulatory mechanisms that can activate protective responses when required while maintaining normal growth under non-stress conditions [23–25].

Plant hormones form another central component of molecular stress regulation. In addition to ABA, salicylic acid, jasmonic acid, ethylene, auxins, cytokinins, brassinosteroids and strigolactones participate in coordinating growth and stress responses. Hormonal crosstalk enables plants to prioritize different physiological processes according to environmental conditions. For example, drought may stimulate ABA-mediated stomatal regulation while simultaneously modifying auxin-dependent root growth. Biotic stress can activate jasmonic acid and salicylic acid pathways, which may interact with growth-related hormonal pathways. This complex interaction creates an important challenge for molecular crop improvement because enhancing one stress-response pathway may influence other traits. Therefore, systems biology and multi-omics approaches are increasingly being used to understand the relationships among genes, proteins, metabolites and hormones.

Epigenetic regulation provides an additional layer of control over stress responses. DNA methylation, histone modifications, chromatin remodelling and non-coding RNAs can influence gene expression without changing the underlying DNA sequence. Environmental conditions may alter epigenetic states, potentially contributing to stress memory and acclimation. Small RNAs and microRNAs can also regulate stress-responsive genes at the post-transcriptional level. Although the stability and heritability of many stress-associated epigenetic changes remain under investigation, these mechanisms provide an important area for future crop improvement research. Integrating epigenomics with transcriptomics, metabolomics and phenomics could help identify regulatory mechanisms that contribute to stable adaptation.

Recent advances in molecular technologies have made it possible to investigate these mechanisms at unprecedented resolution. Transcriptome sequencing can identify genes that are differentially expressed under specific environmental conditions, while proteomics can reveal changes in functional proteins and metabolomics can characterize the biochemical consequences of stress. When integrated with genomic information and high-throughput phenotyping, these datasets can help establish relationships between genetic variation, molecular responses and field-level traits. Genome editing further provides an opportunity to test the functional role of candidate genes and regulatory regions. However, successful translation from molecular discovery to crop improvement requires validation across diverse genetic backgrounds and environments. The future of molecular stress biology will therefore depend increasingly on combining laboratory experimentation with field phenotyping, agronomic management and predictive modelling.

Table 5. Integration of molecular breeding, phenotyping and precision agronomy

Research component	Data generated	Role in crop improvement	Expected outcome
Genomics	SNPs, haplotypes, QTLs	Identify genetic variation	Selection of superior alleles
Transcriptomics	Gene-expression profiles	Identify stress-responsive genes	Candidate gene discovery
Proteomics	Protein profiles	Identify functional responses	Mechanistic understanding
Metabolomics	Metabolite profiles	Identify biochemical signatures	Stress biomarkers
Phenotyping	Morphological and physiological traits	Quantify genotype performance	Accurate trait assessment
Remote sensing	Spatial and temporal crop data	Monitor field performance	High-throughput field evaluation
Soil sensing	Soil moisture and nutrient variability	Characterize growing environment	Site-specific management
Weather monitoring	Environmental conditions	Characterize stress exposure	Improved G × E analysis
AI/ML	Predictive models	Integrate complex datasets	Genotype and management prediction
Field validation	Multi-location performance	Confirm biological relevance	Deployment of improved cultivars

6. PLANT–MICROBE INTERACTIONS AND THE CROP MICROBIOME

Plants exist in close association with diverse microbial communities that colonize the rhizosphere, phyllosphere, endosphere and seed-associated environments. Collectively, these microorganisms constitute the plant

microbiome and represent an important component of plant growth, nutrition, health and adaptation to environmental stress. The composition and activity of the plant microbiome are influenced by plant genotype, soil properties, climate, developmental stage and agricultural management. Root exudates containing sugars, amino acids, organic acids, phenolics and other metabolites provide substrates that influence microbial recruitment and community structure in the rhizosphere. In turn, microorganisms can modify nutrient availability, synthesize phytohormones, produce siderophores, solubilize minerals, suppress pathogens and stimulate plant defence mechanisms. Consequently, the plant should not be considered an isolated biological entity but rather as part of a dynamic plant–microbe–soil system in which microbial communities influence plant phenotype and productivity [1–3].

Plant growth-promoting rhizobacteria and beneficial fungi have received considerable attention because of their potential to improve crop performance under both favourable and stressful conditions. Beneficial bacteria belonging to genera such as *Bacillus*, *Pseudomonas*, *Azospirillum* and *Rhizobium* can promote plant growth through biological nitrogen fixation, phosphate solubilization, siderophore production, phytohormone synthesis and modulation of root architecture. Arbuscular mycorrhizal fungi can increase the effective soil volume explored by plant roots and improve the acquisition of phosphorus and other nutrients, particularly under nutrient-limited conditions. Microbial associations may also enhance plant tolerance to drought, salinity and temperature stress by modifying root growth, regulating antioxidant activity, influencing osmolyte accumulation and stimulating stress-responsive signalling pathways. Some beneficial microorganisms can trigger induced systemic resistance, thereby preparing plants for subsequent pathogen attack. These mechanisms demonstrate that the microbiome represents a potentially valuable biological resource for sustainable crop improvement and reduced dependence on synthetic agricultural inputs [4–6].

The relationship between plants and their microbiomes is highly dynamic and genotype dependent. Different crop genotypes can recruit distinct microbial communities from the same soil, suggesting that genetic variation influences microbial assembly. Conversely, microorganisms can influence plant phenotypes through effects on nutrient metabolism, hormone signalling and stress responses. This reciprocal relationship creates opportunities to incorporate microbiome traits into crop improvement programmes. However, the effectiveness of microbial inoculants is often inconsistent across environments because introduced microorganisms must compete with established native communities and respond to differences in soil chemistry, climate and management. Therefore, future research should move beyond the evaluation of individual microbial strains and increasingly investigate microbial consortia, functional microbial networks and plant genotype–microbiome interactions. Advances in metagenomics, metatranscriptomics, metabolomics and synthetic microbial community design can help identify microorganisms and functional pathways associated with beneficial plant phenotypes [7,8].

Microbiome engineering represents an emerging approach in which microbial communities are deliberately manipulated to improve plant performance. This may involve the application of microbial inoculants, modification of agricultural practices to favour beneficial microorganisms, seed microbiome management or selection of crop genotypes capable of recruiting beneficial microbial communities. Such approaches could be particularly valuable in drought-prone, saline and nutrient-deficient environments. Nevertheless, successful microbiome-based agriculture requires a better understanding of microbial stability, ecological compatibility and field-level performance. Integration of microbiome science with molecular breeding and agronomy may ultimately allow breeders and agronomists to consider both plant genetic potential and the microbial environment in which that potential is expressed. This represents an important transition from conventional crop improvement towards a more holistic approach to sustainable agricultural production.

7. MOLECULAR BREEDING FOR SUSTAINABLE CROP IMPROVEMENT

Molecular breeding has significantly expanded the ability of crop improvement programmes to identify, characterize and utilize genetic variation associated with agronomically important traits. Conventional breeding depends largely on phenotypic selection, whereas molecular breeding incorporates information obtained from DNA markers, genome sequences and genomic prediction into the selection process. This is particularly valuable for complex traits such as drought tolerance, heat tolerance, nutrient-use efficiency, disease resistance and yield stability, where phenotypic expression can be strongly influenced by environmental conditions. Molecular breeding can improve selection efficiency by identifying genomic regions associated with desirable traits and enabling breeders to track these regions across generations. The development of high-density molecular markers, reference genomes and increasingly affordable sequencing technologies has further accelerated the application of genomic approaches in crop improvement [9–11].

Marker-assisted selection has been one of the most widely adopted molecular breeding approaches. In this strategy, molecular markers closely linked to genes or QTLs controlling target traits are used to identify individuals carrying favourable alleles. Marker-assisted selection has been particularly effective for traits controlled by major genes, including several forms of disease resistance and quality characteristics. QTL mapping extends this approach to quantitative traits by identifying genomic regions that contribute to phenotypic variation. However, many QTLs have relatively small effects and may exhibit strong genotype $\times$ environment interactions, limiting their direct application across diverse environments. The integration of QTL information with high-

throughput phenotyping and multi-environment testing can improve the reliability of marker-based selection and help distinguish stable genetic effects from environmentally induced variation [12,13].

Genome-wide association studies have further expanded the capacity to dissect complex traits by exploiting naturally occurring genetic variation in diverse germplasm collections. Unlike traditional biparental mapping populations, GWAS can provide higher mapping resolution and allow researchers to investigate a wider range of alleles. GWAS has been used to identify genomic regions associated with flowering time, yield components, grain quality, nutrient-use efficiency, drought adaptation, disease resistance and other agronomic traits. However, population structure, linkage disequilibrium and environmental variation can influence the interpretation of GWAS results. Therefore, candidate loci identified through association studies require validation through independent populations, functional experiments or genome-editing approaches before they can be confidently incorporated into breeding programmes.

Genomic selection has emerged as another important strategy for improving complex quantitative traits. Instead of selecting plants based only on markers linked to individually detected QTLs, genomic selection uses genome-wide marker information to predict the breeding value of individuals. This approach is particularly attractive for traits controlled by many genes with small effects, where conventional marker-assisted selection may be inefficient. Genomic selection can potentially shorten breeding cycles and increase selection intensity by allowing promising individuals to be identified before extensive phenotypic evaluation. Its effectiveness depends on the quality and size of the training population, marker density, trait heritability, population relatedness and similarity between training and prediction populations [14,15]. Combining genomic selection with high-throughput phenotyping, environmental characterization and machine learning may further improve prediction accuracy under complex production conditions.

The integration of molecular breeding with gene-editing technologies provides an additional pathway for targeted crop improvement. CRISPR/Cas systems and related technologies allow researchers to modify specific genes or regulatory regions associated with agronomic and stress-related traits. Genome editing has been investigated for improving disease resistance, plant architecture, nutritional quality, drought tolerance, salinity tolerance and other characteristics. Base editing and prime editing have expanded the range of possible genetic modifications by enabling more precise sequence changes. Nevertheless, molecular breeding should not be viewed as a substitute for conventional breeding or agronomy. Genotypes identified through molecular approaches must ultimately demonstrate consistent performance under realistic field environments. Therefore, the integration of molecular breeding, physiological screening, multi-environment testing, phenomics and precision agronomic management is essential for translating genomic discoveries into practical improvements in crop productivity and sustainability.

8. TRANSCRIPTOMICS, PROTEOMICS AND METABOLOMICS

The development of high-throughput omics technologies has transformed the study of plant biology by enabling researchers to investigate biological processes at multiple molecular levels. Genomics provides information about the genetic potential of an organism, whereas transcriptomics, proteomics and metabolomics provide information about how that potential is expressed and translated into cellular functions. These technologies are particularly valuable for investigating complex plant responses to environmental stresses because stress adaptation involves coordinated changes in gene expression, protein abundance, enzyme activity and metabolite accumulation. The integration of these datasets can provide a more comprehensive understanding of the molecular mechanisms underlying crop adaptation and productivity [16,17].

Transcriptomics is widely used to identify genes that are differentially expressed under contrasting environmental conditions. RNA sequencing technologies enable researchers to investigate thousands of transcripts simultaneously and identify candidate genes involved in drought, salinity, heat, nutrient deficiency and pathogen responses. Transcriptomic studies can reveal stress-responsive transcription factors, signalling components, transporters, metabolic enzymes and regulatory RNAs. Comparisons between tolerant and susceptible genotypes can further help identify genes associated with contrasting stress responses. However, changes in transcript abundance do not necessarily correspond directly to changes in protein abundance or metabolic activity. Consequently, transcriptomics provides an important but incomplete representation of the biological response and should ideally be integrated with other molecular datasets.

Proteomics provides information about proteins that are actually present and functioning within cells and tissues. Since proteins represent the functional machinery of many cellular processes, proteomic analysis can reveal changes in enzymes, transport proteins, structural proteins, signalling components and stress-related proteins. Under drought and salinity, for example, plants may alter the abundance of proteins involved in antioxidant defence, carbohydrate metabolism, photosynthesis and cellular protection. Comparative proteomics between tolerant and sensitive genotypes can therefore identify candidate proteins associated with stress adaptation. Protein modifications, including phosphorylation and other post-translational changes, provide additional information about signalling processes that cannot be obtained from transcriptomic analysis alone [18].

Metabolomics complements transcriptomics and proteomics by characterizing changes in the small molecules produced during plant metabolism. Environmental stress can alter primary metabolites such as sugars, amino acids and organic acids as well as secondary metabolites including phenolics, flavonoids, terpenoids and alkaloids. Some metabolites function as osmoprotectants, antioxidants, signalling molecules or defence compounds.

Metabolic profiles can therefore provide important indicators of plant physiological status and stress adaptation. Metabolomics may also help identify biochemical markers that can be used in breeding programmes for selecting stress-resilient genotypes. When combined with high-throughput phenotyping, metabolic signatures may provide an intermediate bridge between molecular responses and observable plant traits.

Multi-omics integration represents a major future direction in crop improvement. Combining genomic variation with transcript abundance, protein profiles and metabolite concentrations can help establish relationships between genotype, molecular mechanisms and phenotype. For example, a genomic region identified through GWAS can be examined through transcriptomics to determine whether candidate genes are differentially expressed, through proteomics to determine whether their encoded proteins are altered, and through metabolomics to determine whether the associated biochemical pathways are affected. Such integrative approaches can help move research from simple gene identification towards functional understanding. However, multi-omics datasets are highly complex and require advanced statistical, computational and bioinformatic approaches. Artificial intelligence and machine learning may increasingly assist in identifying meaningful patterns within these datasets and predicting phenotypic outcomes.

The integration of omics technologies with agronomy is particularly important because molecular responses observed under controlled laboratory conditions may not accurately represent responses under field environments. Environmental heterogeneity, soil properties, crop density and management practices can substantially influence gene expression and metabolism. Therefore, future research should increasingly combine molecular profiling with field-based phenotyping and detailed environmental characterization. Such approaches can help identify molecular signatures that remain predictive across environments and can ultimately contribute to more efficient breeding and precision crop management.

9. GENOME EDITING AND PRECISION CROP IMPROVEMENT

Genome editing has emerged as an important technology for accelerating targeted crop improvement and complementing conventional and molecular breeding approaches. Earlier genetic engineering approaches often involved the introduction of foreign genes, whereas genome-editing technologies can modify specific sequences within an existing genome. CRISPR/Cas systems have become particularly prominent because of their relative simplicity, versatility and ability to target multiple genomic regions. The technology has been investigated for modification of genes controlling disease resistance, plant architecture, flowering, nutritional composition, yield components and tolerance to environmental stresses. Genome editing therefore offers an opportunity to directly test the function of candidate genes identified through QTL mapping, GWAS and multi-omics studies [19–21].

One important application of genome editing is the improvement of abiotic stress tolerance. Candidate genes associated with drought response, ion homeostasis, root development, antioxidant metabolism and stress signalling can potentially be modified to alter plant responses to environmental stress. Editing regulatory regions rather than completely disrupting genes may allow breeders to fine-tune gene expression and reduce undesirable effects on growth. Similarly, susceptibility genes involved in pathogen infection can be targeted to improve disease resistance. Multiplex editing, in which several genes are modified simultaneously, is particularly attractive for complex traits controlled by multiple pathways. Nevertheless, the biological consequences of simultaneous modification of multiple genes can be difficult to predict because plant traits are governed by interconnected networks rather than independent pathways.

Recent advances in base editing and prime editing have expanded the precision of genome modification. Base editors can facilitate specific nucleotide changes without necessarily creating double-stranded DNA breaks, while prime editing provides the potential for a broader range of targeted sequence alterations. These technologies may eventually allow breeders to reproduce naturally occurring favourable alleles or introduce precise modifications associated with stress tolerance and nutritional traits. However, challenges remain regarding editing efficiency, delivery methods, tissue regeneration, genotype dependence and potential unintended effects. Comprehensive molecular and phenotypic characterization is therefore essential before edited plants are advanced to agricultural production.

The effectiveness of genome editing ultimately depends on integration with agronomic evaluation. A molecularly modified plant may exhibit improved performance under one stress condition but show limited advantage under another environment or management system. For example, modifying a gene involved in stomatal regulation may improve water conservation but potentially reduce carbon assimilation under favourable conditions. Similarly, enhancing disease resistance may alter plant growth or resource allocation. Consequently, edited genotypes should be tested across multiple environments, seasons and management regimes. Combining genome editing with genomic prediction, physiological phenotyping, remote sensing and precision agronomy could help identify genetic modifications that provide stable benefits at the field scale.

Ethical, regulatory and biosafety considerations must also accompany the technological development of genome editing. Regulatory approaches differ among countries and depend partly on the type of genetic modification produced. Public understanding, transparency and appropriate risk assessment are important for the responsible deployment of genome-edited crops. Future research should therefore integrate technological innovation with ecological evaluation, food and environmental safety assessment and stakeholder participation. Genome editing

has considerable potential, but its greatest contribution to sustainable crop improvement is likely to occur when it is used as one component of a broader breeding and agronomic framework rather than as an isolated technology.

10. PRECISION CROP MANAGEMENT

Precision crop management represents a transition from uniform field management towards site-specific and data-driven agricultural decision-making. Conventional agricultural practices often apply seed, fertilizer, irrigation and crop-protection inputs uniformly across fields despite substantial spatial and temporal variation in soil properties, crop growth and environmental conditions. Precision agriculture seeks to characterize this variability and adjust management accordingly. Geographic information systems, global navigation satellite systems, remote sensing, unmanned aerial vehicles, proximal sensors, soil sensors and variable-rate application technologies provide tools for collecting and utilizing spatially explicit information. By matching inputs more closely with crop requirements, precision management has the potential to improve productivity, input-use efficiency and environmental sustainability [22–24].

Remote sensing is particularly valuable because it enables rapid assessment of crop conditions over large areas. Satellite and unmanned aerial vehicle imagery can provide information about vegetation indices, canopy temperature, biomass, plant density, crop growth and stress distribution. Changes in spectral characteristics can be associated with nutrient deficiencies, water stress, disease development or differences in crop vigour. When combined with ground observations, remote sensing can support the identification of areas requiring targeted intervention. High-resolution imagery from unmanned aerial systems is particularly useful for research plots and commercial fields because it can capture spatial variation at relatively fine scales. These technologies are also increasingly being incorporated into high-throughput phenotyping programmes for evaluating large numbers of breeding lines under field conditions.

Precision irrigation is another important application of site-specific crop management. Traditional irrigation systems may apply similar amounts of water throughout a field even when soil moisture, crop demand and root-zone characteristics vary spatially. Soil-moisture sensors, weather stations, evapotranspiration estimates and remote-sensing information can be integrated to determine when and where irrigation is required. Similarly, precision nutrient management can use soil sampling, crop sensing and yield maps to determine spatial patterns of nutrient availability and crop demand. Variable-rate fertilizer application can then be used to adjust nutrient inputs according to field variability. Such practices can potentially reduce nutrient losses while maintaining crop productivity, although the economic benefits depend on crop value, field heterogeneity, equipment cost and management expertise.

Precision crop protection is also developing rapidly. Remote sensing, machine vision and artificial intelligence can assist in detecting weeds, insect damage and disease symptoms before they become widespread. Site-specific application of herbicides or pesticides can reduce the amount of chemical input applied to unaffected areas. Automated systems equipped with cameras and machine-learning algorithms can distinguish crops from weeds and potentially facilitate targeted mechanical or chemical control. Early detection can also improve disease management by enabling intervention before pathogen populations reach economically damaging levels. However, reliable field-level performance requires robust datasets covering different cultivars, environmental conditions, disease stages and production systems.

The integration of precision agriculture with molecular crop improvement provides an important opportunity for sustainable agriculture. Genetically improved cultivars may possess enhanced tolerance to particular environmental conditions, while precision management can ensure that soil, water, nutrient and crop-protection resources are supplied according to actual crop requirements. This interaction can be conceptualized through a genotype $\times$ environment $\times$ management framework in which genetic potential is evaluated under specific environmental and management conditions. High-throughput phenotyping can connect molecular breeding with precision agriculture by generating detailed information on how different genotypes respond across field environments. Artificial intelligence and machine-learning models can then integrate genomic, phenotypic, soil, weather and management datasets to predict crop performance and recommend site-specific interventions [25,26]. Despite its potential, precision crop management faces several challenges, including high initial investment, limited digital infrastructure, data interoperability, sensor calibration, technical expertise and accessibility for smallholder farmers. Data quality and interpretation are also critical because inaccurate sensor measurements or poorly trained predictive models can result in inappropriate management recommendations. Future precision agriculture systems therefore need to be affordable, reliable, interoperable and adapted to local farming conditions. Greater integration of farmer knowledge with digital technologies will also be important. The long-term objective should not simply be the increased use of digital tools but the development of decision-support systems that translate complex environmental and biological information into practical, economically viable and environmentally responsible management decisions.

11. ARTIFICIAL INTELLIGENCE AND DIGITAL AGRICULTURE

Artificial intelligence (AI), machine learning and digital agriculture are increasingly influencing the development of modern crop production systems by enabling the analysis of large and complex datasets generated through genomics, phenomics, remote sensing, soil monitoring and field experimentation. Conventional agricultural

decision-making often depends on generalized recommendations, historical experience and limited field observations. However, the increasing availability of high-resolution environmental, physiological and molecular data provides opportunities to develop more precise and adaptive management systems. Artificial intelligence can assist in identifying relationships between crop genotype, environmental conditions and management practices that may not be readily apparent through conventional statistical approaches. By integrating information from weather stations, satellite imagery, soil sensors, crop growth models, genomic databases and field observations, AI-based systems can support prediction of crop performance, early identification of environmental stress and optimization of agricultural inputs. These applications are particularly relevant to sustainable crop improvement because they can help connect genetic potential with field-level performance and resource-use efficiency [27–29]. Machine-learning algorithms, including random forests, support vector machines, artificial neural networks, deep learning and ensemble models, have been used in agricultural research for yield prediction, disease detection, crop classification, soil-property estimation and irrigation management. These approaches can process complex and nonlinear relationships among environmental variables and crop responses. For example, remotely sensed information on canopy temperature, vegetation indices and plant biomass can be combined with soil moisture and weather data to identify regions experiencing water stress. Similarly, spectral and image-based technologies can assist in distinguishing healthy crops from plants affected by nutrient deficiencies, insect damage or disease. In crop breeding, machine-learning methods can be used to integrate genomic markers, environmental variables and phenotypic measurements to improve genomic prediction. This is particularly important for complex traits such as drought tolerance, yield stability and nutrient-use efficiency, which are influenced by numerous genes and environmental factors. However, the usefulness of AI models depends on the quality, representativeness and accuracy of the data used for model development.

Digital agriculture also offers opportunities to improve the efficiency of agricultural extension and farmer decision-making. Mobile applications, digital advisory platforms, satellite-based monitoring and connected sensor systems can provide farmers with information related to weather conditions, crop health, irrigation requirements, pest risks and nutrient management. When appropriately designed, these tools can facilitate timely and site-specific recommendations. Nevertheless, the adoption of digital agriculture is influenced by internet connectivity, digital literacy, affordability, availability of technical support and the suitability of technologies for local farming systems. Smallholder farmers may face additional challenges because of fragmented landholdings, limited access to machinery and inadequate access to reliable digital services. Therefore, the development of AI-based agricultural systems should emphasize affordability, transparency, ease of use and compatibility with local knowledge and farming practices. AI should be considered a decision-support technology rather than a replacement for agronomic expertise or farmer experience [27,30].

An important future direction involves the integration of artificial intelligence with molecular breeding and high-throughput phenotyping. Breeding programmes generate large amounts of information from genomic markers, field trials, physiological measurements and environmental observations. AI can assist in identifying patterns within these datasets and predicting the performance of breeding lines across different environments. Such integration may improve the identification of genotypes with stable performance under drought, heat, salinity and other environmental stresses. In addition, AI-based models can support the optimization of planting dates, irrigation schedules, fertilizer application and crop-protection strategies. However, models trained under one geographical, climatic or management condition may not perform reliably in another. Independent validation, model interpretability, data standardization and continuous updating are therefore essential. The long-term contribution of AI to sustainable agriculture will depend on the successful integration of computational tools with biological knowledge, field experimentation and practical agronomic decision-making.

12. INTEGRATING MOLECULAR BREEDING WITH PRECISION AGRONOMY

The integration of molecular breeding and precision agronomy represents an important advancement in the development of sustainable and climate-resilient agricultural systems. Molecular breeding focuses on identifying and utilizing genetic variation associated with desirable traits, whereas precision agronomy aims to manage environmental and production factors according to spatial and temporal variability. Although these disciplines have traditionally developed through relatively separate research pathways, their integration can provide a more comprehensive understanding of crop performance. The expression of a crop genotype is strongly influenced by soil conditions, temperature, water availability, nutrient supply, pest pressure and management practices. Therefore, the development of improved cultivars must be accompanied by an understanding of the environments and management systems in which their genetic potential can be effectively expressed. This relationship is commonly described through the genotype $\times$ environment $\times$ management framework, which recognizes that crop productivity is determined by the interaction of genetic characteristics, environmental conditions and agronomic practices [31,32].

Molecular breeding can identify genotypes with desirable characteristics such as improved root development, water-use efficiency, nutrient-use efficiency, disease resistance and tolerance to environmental stresses. However, the performance of these genotypes may vary considerably across locations and seasons. For example, a drought-tolerant genotype may perform well under water-limited conditions but may not provide a substantial advantage under adequate irrigation. Similarly, a cultivar with high nutrient-use efficiency may respond differently

depending on soil fertility and fertilizer management. Precision agronomy can help identify such interactions by collecting detailed information on soil properties, crop growth, weather conditions and management practices. High-throughput phenotyping platforms, remote sensing and field sensors can be used to evaluate breeding materials across heterogeneous environments. These observations can then be combined with genomic information to identify genotypes that perform consistently under specific production conditions.

The integration of molecular and agronomic approaches is particularly important for improving complex traits. Yield, drought tolerance, heat adaptation, nutrient-use efficiency and resource productivity are generally controlled by multiple genes and influenced by environmental conditions. Molecular markers and genomic prediction can assist in identifying promising breeding lines, while precision field evaluation can determine whether these lines maintain their advantages under different management systems. Multi-environment trials conducted using detailed environmental characterization can improve the understanding of genotype $\times$ environment interactions. In addition, crop growth models can be integrated with genomic and phenotypic information to predict the performance of genotypes under future climate scenarios. Such approaches may assist breeders in selecting cultivars suitable for particular agroecological regions and help agronomists develop management recommendations tailored to specific genetic materials.

Precision agronomy can also improve the practical value of molecularly improved cultivars. For example, cultivars with improved nutrient-use efficiency may perform more effectively when fertilizer application is adjusted according to soil nutrient variability and crop demand. Similarly, genotypes with improved water-use efficiency may benefit from irrigation schedules based on soil moisture, evapotranspiration and crop developmental stage. Disease-resistant cultivars can be integrated with disease forecasting and targeted crop protection to reduce unnecessary pesticide applications. These examples illustrate that genetic improvement and agronomic management should be considered complementary components of sustainable crop production. The future of crop improvement will therefore require stronger collaboration among plant breeders, molecular biologists, agronomists, soil scientists, microbiologists, data scientists and farmers.

13. SUSTAINABLE CROP MANAGEMENT AND CLIMATE RESILIENCE

Sustainable crop management involves the efficient use of natural resources while maintaining crop productivity, soil health, biodiversity and long-term agricultural viability. Modern agricultural systems face increasing pressure to produce sufficient food while reducing environmental degradation and dependence on non-renewable resources. Climate change has further intensified these challenges by increasing the frequency of droughts, heat waves, irregular rainfall, flooding and other environmental disturbances. Under these conditions, sustainable crop improvement requires the combined application of improved genetic resources, appropriate agronomic practices, biological inputs and precision management technologies. The objective should not be limited to increasing yield under favourable conditions but should also include improving yield stability, resource-use efficiency, nutritional quality and resilience under variable environments [33,34].

Soil health is a central component of sustainable crop production because soil properties influence nutrient availability, water retention, root development and microbial activity. Practices such as crop rotation, conservation tillage, residue retention, cover cropping, organic matter addition and integrated nutrient management can improve soil structure and biological functioning. These practices may also contribute to carbon sequestration and reduce soil erosion. Molecular research can complement soil management by identifying crop genotypes with improved root traits, nutrient-use efficiency and beneficial interactions with soil microorganisms. Root architecture, root exudation and plant–microbe interactions influence nutrient acquisition and soil biological processes. Therefore, breeding programmes that consider root traits and rhizosphere interactions may contribute to more efficient utilization of soil resources. Combining these genetic improvements with site-specific nutrient management and biological soil amendments may improve productivity while reducing nutrient losses.

Water management is another major component of climate-resilient agriculture. Efficient irrigation, rainwater harvesting, soil-moisture conservation and drought-adapted cropping systems can reduce the adverse effects of water scarcity. Precision irrigation technologies can support the application of water according to crop demand, soil moisture and environmental conditions. At the genetic level, improved root systems, stomatal regulation, osmotic adjustment and efficient water transport may contribute to drought adaptation. However, water-use efficiency must be evaluated carefully because reduced water loss does not always result in increased yield. A successful drought-resilient cultivar should ideally maintain productivity while using available water efficiently. This requires the integration of physiological screening, molecular breeding, crop modelling and field-level irrigation management.

Sustainable crop protection also requires a combination of genetic resistance, biological control, cultural practices and precision monitoring. Excessive dependence on chemical pesticides can contribute to environmental contamination, resistance development and disruption of beneficial organisms. Resistant cultivars, crop diversification, biological control agents and integrated pest management can reduce pest and disease pressure. Molecular approaches can help identify resistance genes and develop cultivars with improved protection against important pathogens. Precision technologies can support early detection of disease and insect infestations, enabling targeted interventions. The use of microbial inoculants and beneficial plant-associated microorganisms may further contribute to crop health and stress adaptation. Nevertheless, the performance of biological and

molecular interventions must be evaluated under diverse field conditions to determine their consistency, economic feasibility and long-term environmental effects.

Climate-resilient agriculture also requires attention to crop diversification and production-system design. Diversified cropping systems, intercropping, agroforestry and the use of locally adapted varieties can reduce production risks and improve ecosystem services. Molecular breeding can contribute by developing varieties suitable for different climatic conditions and cropping systems, while precision agronomy can support the optimization of planting dates, crop combinations, irrigation and nutrient management. The integration of climate information, crop models and farmer knowledge can further improve adaptation planning. Sustainable crop management should therefore be understood as a systems-level approach that combines genetic improvement, soil and water conservation, biological interactions, efficient input use and climate-informed decision-making.

14. CHALLENGES IN INTEGRATING AGRONOMIC AND MOLECULAR APPROACHES

Although the integration of agronomy and molecular research offers substantial opportunities for sustainable crop improvement, several scientific, technical, economic and institutional challenges remain. One of the major challenges is the complexity of plant responses to environmental stresses. Traits such as drought tolerance, heat resilience, nutrient-use efficiency and yield stability are generally controlled by multiple genes and influenced by environmental conditions. A gene or QTL that contributes positively to a particular trait under one environment may have a smaller effect or even an undesirable effect under another. Furthermore, plants frequently experience multiple stresses simultaneously, and the molecular mechanisms involved in combined stress responses may differ from those activated by individual stresses. Consequently, identifying genetic factors that provide stable benefits under realistic field conditions remains a major challenge.

The genotype $\times$ environment $\times$ management interaction presents another important limitation. Breeding programmes often evaluate genotypes under specific experimental conditions, whereas farmers cultivate crops across diverse soils, climates, input levels and management systems. The performance of a cultivar under experimental conditions may therefore differ from its performance in farmers' fields. Multi-environment trials, participatory breeding, detailed environmental characterization and improved field phenotyping are required to address this problem. High-throughput phenotyping technologies can generate valuable information, but differences in sensor calibration, data quality, experimental design and analytical methods can limit comparisons across studies. Standardization of phenotyping protocols and greater integration of field and molecular datasets are therefore necessary.

A further challenge concerns the translation of molecular discoveries into practical agricultural technologies. The identification of candidate genes through genomics, transcriptomics or metabolomics does not necessarily guarantee improved yield or stress tolerance. Candidate genes must be validated through functional studies, genetic transformation or genome editing and evaluated across diverse genetic backgrounds. In addition, the expression of a desirable trait may be associated with trade-offs involving plant growth, reproductive development, nutritional quality or susceptibility to other stresses. Molecular improvement must therefore be accompanied by extensive physiological and agronomic evaluation. The time, cost and infrastructure required for these activities can be considerable, particularly in crops with long breeding cycles or complex reproductive systems.

The use of advanced technologies also raises challenges related to infrastructure, expertise and accessibility. Genomic sequencing, high-throughput phenotyping, precision sensors, remote sensing and artificial intelligence require technical facilities, computational resources and trained personnel. These resources may not be readily available to small research institutions or farming communities. In many developing agricultural regions, farmers face limitations related to internet connectivity, access to machinery, financial resources and digital literacy. Therefore, technological development should be accompanied by efforts to create affordable, user-friendly and locally adapted solutions. Participatory research involving farmers, extension professionals and local institutions can help ensure that technologies address actual production challenges.

Data management and interoperability represent additional concerns. Molecular, phenotypic, environmental and agronomic datasets are often generated using different platforms, formats and measurement protocols. Integrating these datasets requires standardized terminology, reliable databases and appropriate computational tools. Privacy, data ownership and equitable access to agricultural information also require consideration, particularly when digital platforms and commercial technologies are involved. Similarly, the deployment of genome-edited crops and microbial products must be supported by appropriate biosafety assessment, regulatory compliance and transparent communication. Addressing these challenges will require interdisciplinary collaboration, investment in agricultural research infrastructure, capacity building and stronger links between scientific institutions and farming communities.

Table 6. Major challenges and potential research directions

Challenge	Current limitation	Suggested research direction
Genotype $\times$ environment interaction	Inconsistent genotype performance	Multi-environment testing

Complex stress tolerance	Multiple genes and pathways involved	Multi-omics and systems biology
Phenotyping bottleneck	Labour-intensive measurements	High-throughput phenotyping
Microbiome variability	Inconsistent field performance	Genotype–microbiome studies
AI model transferability	Models may be location-specific	Multi-location model validation
Data integration	Different platforms and formats	Standardized agricultural databases
Genome-editing adoption	Regulatory and biosafety considerations	Robust validation and transparent assessment
Technology accessibility	High cost and technical requirements	Affordable farmer-oriented technologies
Climate uncertainty	Increasing environmental variability	Climate-resilient breeding and modelling

Table 7. Future research priorities for sustainable crop improvement

Priority area	Key objective	Potential contribution
Climate-resilient breeding	Develop stress-resilient cultivars	Yield stability
Multi-omics integration	Understand complex regulatory networks	Improved trait discovery
Precision phenotyping	Rapidly measure complex traits	Faster breeding
Plant microbiome engineering	Utilize beneficial microorganisms	Improved nutrient and stress efficiency
Genome editing	Precisely modify target genes	Trait enhancement
AI-assisted breeding	Integrate genomic and environmental data	Improved selection accuracy
Precision nutrient management	Match nutrients with crop demand	Reduced nutrient losses
Precision irrigation	Optimize water application	Improved water-use efficiency
Digital agriculture	Provide real-time crop information	Better farm-level decisions
Participatory research	Integrate farmer knowledge	Improved technology adoption

15. FUTURE PERSPECTIVES

The future of sustainable crop improvement is likely to be shaped by the increasing convergence of molecular biology, agronomy, microbiology, phenomics, artificial intelligence and precision agriculture. Traditional crop improvement has often focused on individual traits, such as yield, disease resistance or drought tolerance. However, the complexity of agricultural environments requires a broader approach that considers multiple traits and their interactions. Future breeding programmes will need to identify genotypes capable of maintaining productivity, nutritional quality and resource-use efficiency under changing environmental conditions. This will require greater emphasis on yield stability, root system architecture, nutrient acquisition, water-use efficiency, stress recovery and interactions with beneficial microorganisms. Molecular technologies can help identify the genetic basis of these traits, while agronomic research can determine how they are expressed under practical production conditions.

Multi-omics approaches are expected to contribute substantially to the understanding of complex plant responses. Integrating genomics, transcriptomics, proteomics, metabolomics, epigenomics and microbiome data can provide a more comprehensive view of the regulatory networks underlying crop adaptation. Such integration may help identify candidate genes, molecular markers and biochemical indicators associated with stress resilience. However, the development of effective analytical frameworks will be necessary to distinguish causal relationships from simple correlations. Machine learning and systems biology may assist in interpreting large datasets and developing predictive models of plant performance. The use of multi-omics information in breeding should nevertheless be supported by functional validation and field-based evaluation.

High-throughput phenotyping is another important area for future research. Conventional phenotyping is often labour-intensive, time-consuming and limited in scale. Remote sensing, automated imaging, robotics, drones and sensor networks can provide detailed information on crop growth, canopy temperature, biomass, disease symptoms, root traits and stress responses. When combined with genomic data, these technologies may improve the efficiency of genomic selection and help identify genotypes with stable performance across environments. Future phenotyping platforms should be designed to capture dynamic responses rather than relying solely on measurements taken at harvest. Monitoring stress development, recovery and reproductive responses may provide more useful information for identifying climate-resilient genotypes.

Genome editing is likely to remain an important component of future crop improvement. Advances in base editing, prime editing, multiplex editing and regulatory-region modification may expand the range of genetic changes that can be introduced into crop genomes. These technologies may facilitate the improvement of complex traits by modifying several genes or regulatory pathways. However, their application should be accompanied by careful

evaluation of unintended effects, ecological interactions, nutritional characteristics and field performance. Genome editing should be integrated with conventional breeding, genomic selection and physiological screening rather than used as an isolated strategy.

Plant microbiome research also offers promising opportunities. Future studies may identify crop-specific microbial communities that improve nutrient acquisition, stress tolerance and disease resistance. Microbiome-based crop improvement could involve the selection of plant genotypes that recruit beneficial microorganisms, the development of microbial consortia and the use of management practices that support microbial diversity. However, microbial functions are strongly influenced by soil and environmental conditions, and therefore field-level consistency remains a major research priority. Combining microbiome research with molecular breeding and precision agronomy may help develop more reliable biological solutions.

Digital agriculture and AI-based decision-support systems are expected to become increasingly important in connecting biological information with farm management. Future systems may integrate genomic data, soil properties, weather forecasts, crop models, remote sensing and farmer observations to provide site-specific recommendations. Digital representations of agricultural fields, sometimes described as agricultural digital twins, could support simulation of alternative management strategies under different climatic conditions. Nevertheless, such systems must remain accessible, transparent and relevant to farmers. The development of sustainable agriculture will ultimately depend not only on technological innovation but also on effective extension services, supportive policies, farmer participation and equitable access to improved technologies.

16. RESEARCH GAPS AND PRIORITY AREAS

Despite significant advances in agronomic science and molecular biology, several research gaps continue to limit the development of fully integrated crop improvement systems. One major gap is the limited understanding of how crops respond to combinations of environmental stresses under field conditions. Most molecular studies have traditionally focused on individual stresses under controlled environments, whereas agricultural crops frequently experience drought, heat, nutrient deficiency, salinity and biotic stresses simultaneously. The molecular, physiological and agronomic responses to these stress combinations may differ considerably from responses to individual stresses. Future research should therefore prioritize realistic stress combinations, stress timing, stress recovery and the effects of repeated environmental disturbances.

Another important gap concerns the limited integration of molecular information with field-level agronomic performance. Although large numbers of genes, QTLs and molecular markers have been identified, relatively few have been translated into broadly useful crop improvement products. This limitation is partly associated with genotype $\times$ environment interactions, insufficient field validation and inadequate understanding of trait trade-offs. Greater collaboration between molecular researchers, breeders and agronomists is required to ensure that candidate genes and markers are evaluated for their practical contribution to yield, resource-use efficiency and stress resilience.

Phenotyping remains a major bottleneck in many crop improvement programmes. Genotyping technologies can generate extensive information at relatively high speed, but accurate measurement of complex traits under diverse field conditions remains difficult. There is a need for standardized, affordable and scalable phenotyping platforms capable of measuring root traits, canopy temperature, water status, nutrient acquisition, disease progression and stress recovery. The integration of sensor-based measurements with conventional field observations and farmer assessments could improve the relevance of phenotyping systems.

The role of the plant microbiome in crop improvement also requires further investigation. Although beneficial microorganisms have been associated with improved plant growth and stress tolerance, the mechanisms responsible for consistent field performance are not fully understood. Future research should examine plant genotype–microbiome interactions, microbial community stability, soil-specific responses and the effects of agronomic practices on microbial functions. Greater attention is also needed to the development of standardized methods for evaluating microbial inoculants and microbial consortia.

The application of artificial intelligence and machine learning in agriculture presents both opportunities and limitations. Many existing models are developed using datasets from specific locations, crop varieties or environmental conditions. Their performance may decline when applied to new regions or production systems. Future research should emphasize model validation, interpretability, data sharing, uncertainty estimation and integration of biological knowledge. AI-based systems should also be evaluated for their economic and practical usefulness rather than solely on predictive accuracy.

Finally, sustainable crop improvement requires greater attention to socioeconomic and institutional factors. Technologies developed through molecular biology and precision agriculture must be affordable, accessible and suitable for diverse farming communities. Smallholder farmers should be involved in the design and evaluation of technologies to ensure that innovations address local needs. Research institutions, universities, extension agencies, private organizations and farmers must work together to facilitate the transfer of scientific advances into practical agricultural systems.

17. CONCLUSION

The integration of agronomy and molecular research provides a comprehensive framework for addressing the increasingly complex challenges facing modern agriculture. Crop productivity and sustainability are determined by interactions among genetic potential, environmental conditions, soil properties, microbial communities and management practices. Therefore, improvements in agricultural production cannot be achieved effectively through genetic or agronomic interventions considered in isolation. Molecular research provides valuable information about the genes, regulatory pathways, metabolites and physiological mechanisms involved in plant growth, stress tolerance and adaptation. Agronomy, in contrast, provides the practical foundation for managing soil, water, nutrients, crops and environmental variability under field conditions.

Advances in molecular breeding, QTL mapping, genome-wide association studies, genomic selection, transcriptomics, proteomics, metabolomics and genome editing have created new opportunities for developing crops with improved productivity, nutritional quality and resilience to environmental stresses. At the same time, plant microbiome research has expanded the understanding of beneficial interactions among plants, microorganisms and soils. Precision agriculture, remote sensing, sensor technologies, artificial intelligence and digital decision-support systems provide additional opportunities to improve the efficiency of agricultural inputs and to manage field variability.

The successful application of these technologies requires a shift towards integrated research based on the genotype $\times$ environment $\times$ management framework. Molecularly improved cultivars must be evaluated under diverse field conditions, while agronomic practices should be adapted to the genetic characteristics of individual crops. High-throughput phenotyping, multi-omics integration, crop modelling and AI-assisted analysis can help connect molecular mechanisms with practical agricultural performance. However, challenges related to complex stress responses, genotype $\times$ environment interactions, phenotyping, infrastructure, technology accessibility, regulatory requirements and farmer adoption must be addressed.

Future crop improvement should therefore focus on developing productive, resource-efficient and climate-resilient cropping systems rather than concentrating exclusively on yield enhancement. Greater collaboration among breeders, agronomists, molecular biologists, soil scientists, microbiologists, data scientists, extension professionals and farmers will be essential. By combining molecular innovation with field-based agronomic knowledge and precision management, agricultural research can contribute to improved food security, efficient resource utilization, soil health and environmental sustainability. The integration of these disciplines represents an important pathway towards resilient agricultural systems capable of meeting future food demands under changing climatic and ecological conditions.

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