Integrating Omics Approaches for Climate-Resilient Crops: A Comprehensive Review

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

Review Article

ABSTRACT

Climate change is a looming threat to global agriculture, impacting temperature, rainfall patterns, pest dynamics, and soil quality. These challenges transcend numerous crops vital for global food security. Drought, soil acidity, and nutrient fluctuations induced by climate change impede crop productivity, necessitating the development of breeding strategies to produce climate-resilient varieties. This review delves into the integration of omics approaches, including genomics, transcriptomics, proteomics, and metabolomics, to bolster breeding programs across diverse crops. By harnessing high-throughput technologies, researchers gain insights into the genetic and molecular mechanisms underlying traits such as stress resistance, yield, and disease tolerance. The cultivation of elite cultivars with enhanced stress tolerance is paramount for sustainable agriculture in the face of climate change. Various breeding approaches, encompassing functional

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genomics and mutagenomics, are explored alongside the application of genome editing tools like CRISPR/Cas9 and TALEN for targeted trait enhancement. Through the integration of multi-omics data, novel genetic targets are unearthed, facilitating the development of crop varieties resilient to climate-induced stressors beyond maize. This review underscores the significance of multi-omics in crop breeding and highlights strides made toward climate-resilient crop production. Understanding crop responses to abiotic stresses induced by climate change is imperative for the development of resilient varieties. The integration of modern genetics into classical breeding methods aims to cultivate stress-resistant cultivars, mitigating food security risks. Multi-omics approaches play pivotal roles in unraveling crop performance and stress tolerance mechanisms under diverse environmental conditions. Moving forward, the integration of multi-omics approaches will pinpoint candidate genes and pathways, enabling precision breeding to enhance crop performance amidst changing climates. These endeavors will propel the advancement of climate-resilient crops, safeguarding global food security in the face of climate change's challenges.

1. INTRODUCTION

In the 21st century, scientists face the monumental task of optimizing climate-change adaptation, agricultural productivity, food security, and environmental protection. Climate change is unmistakably altering our environment, with rising average temperatures, global warming, unpredictable rainfall patterns, and an increase in areas affected by floods or water deficits [1]. These changes are leading to the expansion of regions prone to drought or salinity, resulting in reduced plant growth and crop productivity. Variations in climatic conditions disrupt agro-ecosystems and the food supply chain. Agriculture heavily relies on prevailing climatic conditions, subjecting crops to external environmental and abiotic stresses due to climate variations [2,3]. Crop plants often face multiple abiotic stresses simultaneously, including salinity, chilling, drought, waterlogging, heavy metals, and temperature fluctuations, significantly impeding growth and development and reducing agricultural productivity globally. Furthermore, global warming caused by greenhouse gas emissions has led to increased temperatures and drought conditions, posing threats to crop productivity. For example, a 20–30% yield loss was observed in two major cereals, wheat, and maize [4,5]. While traditional plant breeding techniques have produced several high-yielding crop cultivars over the years, their implementation is hindered by the longer time required for various development and breeding cycles.

High-throughput omics technologies have revolutionized crop breeding by providing detailed insights into the molecular processes that govern plant development and how they respond to environmental stresses [6]. Genomics, in particular, has played a central role in crop breeding, allowing researchers to pinpoint key genetic traits and speed up the creation of improved plant varieties. With an increasing number of crop genomes being sequenced, the amount of genetic data available for agricultural research has grown significantly [7]. This genomic data boom is complemented by advances in epigenomics and transcriptomics, which reveal the mechanisms of gene regulation and help identify traits that breeders find valuable. The establishment of robust genomic databases has been a key factor in advancing crop breeding. These databases compile information about genetic structure, gene expression patterns, and other crucial biological data, serving as comprehensive resources for researchers. Alongside genomics, proteomics and metabolomics have gained traction, offering deeper insights into protein functions and the metabolic pathways involved in plant growth and response to stress [8].

These omics technologies work in tandem to pinpoint genes and pathways linked to desired traits, enabling breeders to create new plant varieties with enhanced characteristics [9]. Combining multi-omics data is crucial for unlocking the full potential of these technologies. By integrating diverse datasets, researchers can gain a broader understanding of the biological processes behind crop traits and how they interact [7]. This integration allows for the development of predictive models to forecast crop performance under various environmental conditions, enabling breeders to select promising plant varieties for further development [2,3]. Additionally, integrating omics data speeds up breeding cycles, reducing the time and resources

needed to produce new varieties with improved traits.

Omics technologies have transformed crop breeding by providing insights into the genetic and molecular underpinnings of plant traits [9]. This allows breeders to identify key genes and pathways that drive desirable characteristics, leading to more efficient development of new plant varieties. The growing importance of omics in agricultural research is reflected in the increasing volume of studies (Fig. 1) [10]. However, effective use of omics in crop breeding requires integrating diverse datasets, offering a comprehensive view of the biological processes underlying plant traits. This integration helps reduce breeding cycles, allowing breeders to quickly select and develop varieties with enhanced traits. Ultimately, it contributes to creating more robust and high-yielding crops, essential for addressing food security and climate resilience.

This review examines the role of integrated omics approaches in crop breeding and explores the current state of these integration efforts. We look at the different types of omics data used in crop breeding, including genomic, epigenomic, transcriptomic, proteomic and metabolomic information [11]. We also review the various databases that house these datasets, evaluating their features, strengths, and limitations. Additionally, the review addresses the challenges in integrating omics data, such as data heterogeneity, scalability, and interoperability, while showcasing recent advancements in the field. We highlight the benefits of omics integration, such as quicker breeding cycles, enhanced global food security, and the ability to develop more resilient and productive crops. Integrating omics databases and technologies is a critical step in advancing crop breeding [12]. It opens the door to creating new crop varieties that are more productive, resilient, and sustainable, which aligns with the broader goal of achieving global food security [13]. As the field of omics integration evolves, we expect further breakthroughs that will bolster our capacity to meet the demands of a changing climate and an expanding global population.

2. BREEDING FOR CLIMATE-RESILIENT CROPS

Predicting future conditions for maize cultivation is becoming increasingly challenging due to a variety of factors, including emerging diseases and environmental stresses, which can disrupt breeding pipelines and impact crop yields [12,14]. The key to developing climate-resilient maize lies in reducing breeding cycle times and providing improved maize varieties more quickly to meet evolving environmental challenges. To ensure maize varieties are resilient to climate change, breeders focus on traits such as smaller anthesis-silking interval (ASI), stay green characteristics, smaller tassels, erect leaves, and high grain yield (Fig. 2) [15]. Several approaches are employed in plant breeding to improve crop traits and achieve desired characteristics in maize:
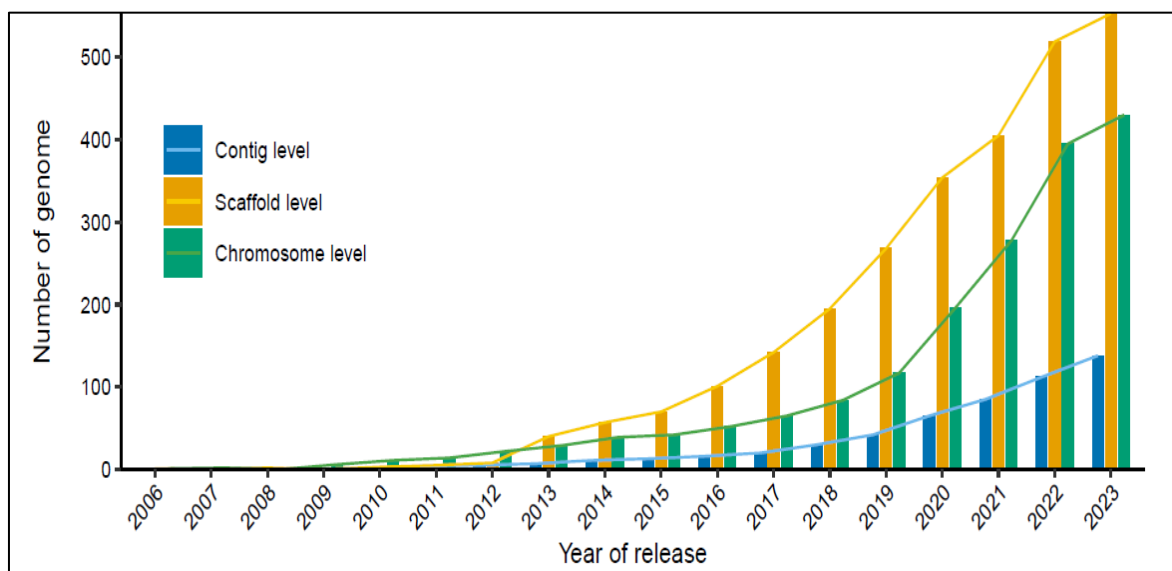

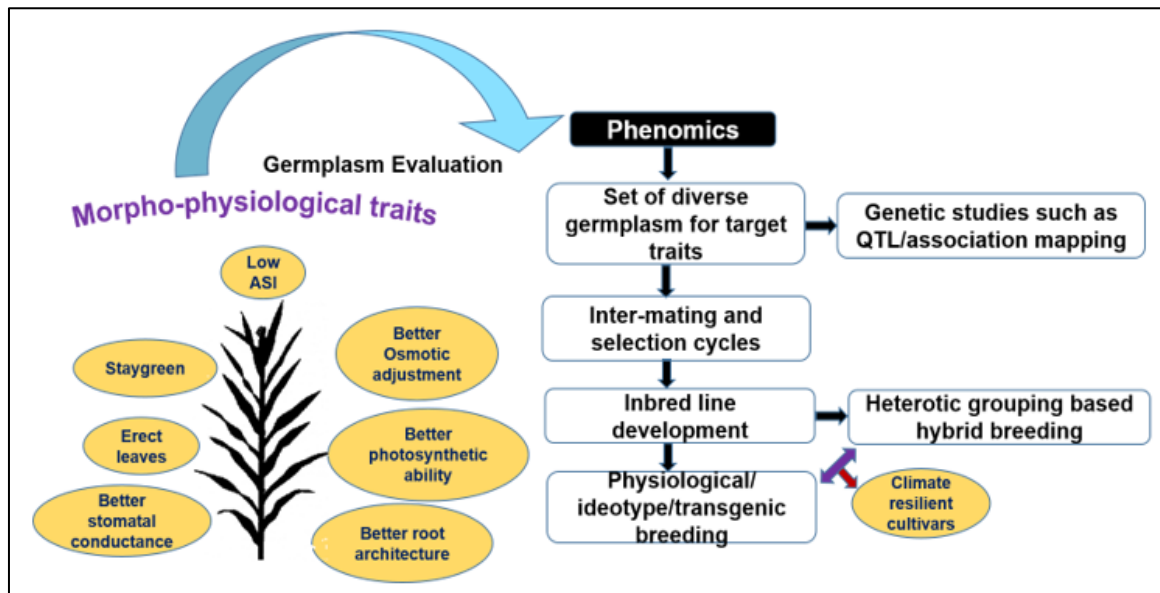**Fig. 1. The number of completed genome assemblies for land plants [10]**

Fig. 2. Target traits and breeding approaches for improvement of climate resilience [15]

Conventional and Population Improvement: This traditional approach involves selecting the best-performing plants and cross-breeding them to enhance desirable traits. It relies on a broad genetic base and aims to improve overall population quality.

Ideotype Breeding: This method focuses on breeding plants with a specific "ideal" set of traits that best suit particular environmental conditions or production systems. It often includes traits like plant architecture, leaf shape, and grain yield.

Physiological Breeding: This approach targets specific physiological traits that contribute to plant performance, such as photosynthesis efficiency, water use, or nutrient uptake.

Distant Hybridization: This involves crossing different species or distantly related varieties to introduce new genetic material and enhance diversity. This approach can lead to the introduction of unique traits and increased resilience to stress.

Genetic Engineering: Utilizing advanced biotechnology, this method introduces specific genes into maize to confer desired traits, such as resistance to diseases or pests, tolerance to abiotic stresses, or improved nutritional content.

These diverse breeding methods provide a toolkit for developing climate-resilient maize varieties that can withstand unpredictable environmental conditions while maintaining high yield and quality. By employing a combination of these approaches, breeders can address the challenges posed by climate change and ensure the continued productivity and sustainability of maize crops.

Precise phenotyping is a critical component in achieving significant genetic gains, particularly in breeding programs focused on drought stress resilience [16]. Phenomics- the comprehensive study of phenotypes through advanced imaging and analytical technologies provides a powerful tool for assessing plant traits with greater accuracy and at larger scales [17]. When combined with conventional breeding, physiological breeding, Ideotype breeding, and molecular breeding approaches, phenomics can significantly enhance the success of drought stress breeding programs [18]. Using precise phenotyping techniques, breeders can monitor plant growth, stress responses, and other critical traits in real-time, allowing for a deeper understanding of how plants adapt to drought conditions (Fig. 2). This detailed phenotypic data, when integrated with conventional and molecular breeding methods, offers several advantages:

Early Detection of Traits: Phenomics enables the early detection of key traits related to drought tolerance, such as root architecture, water-use efficiency, and photosynthesis rates [55]. This early detection helps breeders identify promising candidates for further breeding.

Improved Selection Accuracy: By utilizing phenomics, breeders can select plants with the

most favourable traits with greater precision. This reduces the risk of selecting suboptimal plants, thereby increasing the likelihood of achieving higher genetic gains.

Acceleration of Breeding Cycles: Integration of phenomics with conventional and molecular breeding approaches allows breeders to rapidly evaluate a large number of plants, accelerating the breeding cycles. This speed is crucial for responding to the urgent challenges posed by climate change and water scarcity.

Enhanced Understanding of Plant Physiology: Phenomics can help researchers understand the physiological mechanisms that underlie drought tolerance. This knowledge can guide Ideotype breeding, where specific plant architectures or growth patterns are targeted for development.

Data-Driven Breeding Decisions: Phenomics provides a wealth of data that can be used to make more informed breeding decisions. The integration of this data with conventional and molecular breeding strategies creates a comprehensive approach to developing drought-resistant maize varieties [19].

3. APPLICATIONS OF FIVE OMICS IN CROP BREEDING

Omics data have revolutionized crop science, providing an unprecedented understanding of plant biology at various levels. This detailed information has paved the way for significant improvements in crop shape, including higher yield, enhanced nutrient uptake through improved root systems, better adaptability to environmental changes, resistance to adverse conditions, and even flavour [20]. Here are some key omics domains and techniques contributing to these advancements (Fig. 3) [10].

3.1 Genome

Genome sequencing allows breeders to identify genetic regions responsible for key traits. It forms the basis for more targeted breeding and genetic engineering approaches.

- ***Genome-Wide Association Studies (GWAS):*** GWAS identifies genetic markers linked to specific traits, such as high yield or stress tolerance [21]. By analyzing genetic variations across a large plant population, breeders can find associations with desirable characteristics.
- ***Genetic Mapping:*** Genetic mapping locates genes on chromosomes and explores their interactions, providing insights into complex traits that affect crop structure and performance [22].
- ***Structural Variation:*** This involves studying large-scale changes in the genome, such as insertions, deletions, and duplications. Structural variation analysis can reveal novel genes or pathways influencing crop shape, root efficiency, or environmental adaptability.
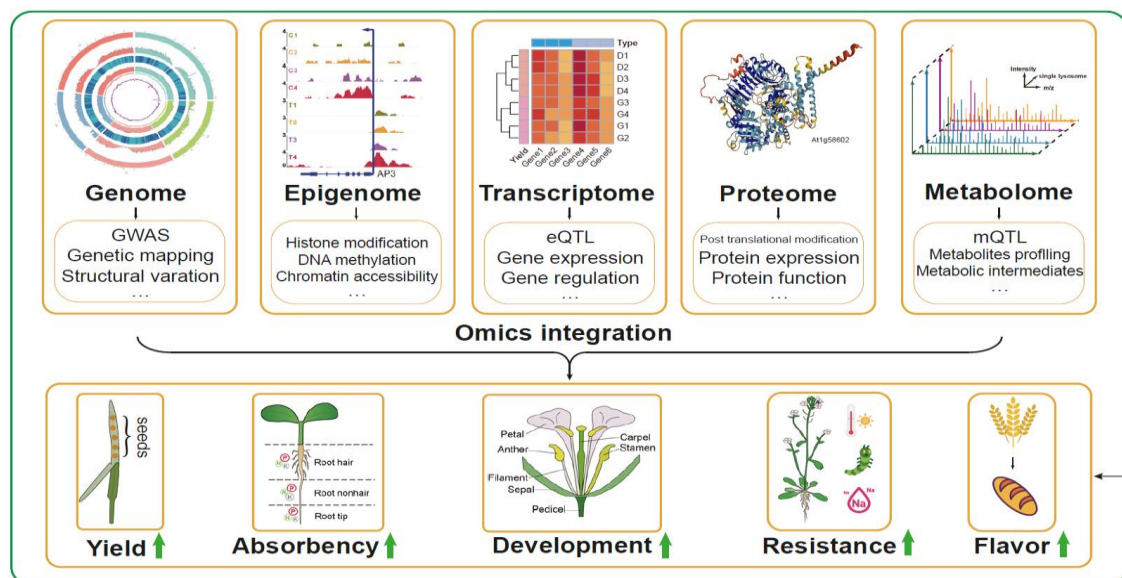

Fig. 3. Applications of five omics technologies in crop breeding [10]

3.2 Epigenome

Epigenetics studies changes in gene expression without altering the DNA sequence. Techniques like histone modification, DNA methylation, and chromatin accessibility analysis reveal how these changes affect traits like stress resistance and adaptability [23].

3.3 Transcriptome

Transcriptomic analysis focuses on gene expression patterns, allowing researchers to understand how genes are regulated and expressed under different conditions. eQTL (expression quantitative trait loci) studies link genetic variations to changes in gene expression, providing a deeper understanding of regulatory mechanisms [24].

3.4 Proteome

Proteomics examines protein expression and function, including post-translational modifications. This provides insights into how proteins control plant development, stress responses, and other critical processes [25].

3.5 Metabolome

Metabolomic studies analyse metabolic pathways by profiling metabolites and metabolic intermediates. mQTL (metabolite quantitative trait loci) analysis identifies genetic factors influencing metabolite levels, shedding light on plant growth, flavour, and stress resistance [26,27].

By integrating data from these omics domains, breeders can gain a comprehensive view of the factors influencing crop shape and performance. This holistic understanding is key to developing improved crops with higher yields, better resilience, and other desirable traits.

4. STRUCTURAL GENOMICS FOR CROP BREEDING PROGRAMS

Structural genomics relies on molecular markers to tag and map genes of interest, providing a foundation for crop breeding programs. Different types of marker techniques are used in this field, each offering unique benefits for understanding and manipulating plant genomes. Non-PCR techniques such as restriction fragment length polymorphisms (RFLP) were among the first methods used to identify DNA variations [28].

RFLP involves digesting DNA with restriction enzymes and then using a labeled DNA probe to detect differences in the resulting fragment patterns. This technique has been pivotal in early studies of genome structure and gene mapping. PCR-based techniques have expanded the capabilities of structural genomics by allowing more rapid and versatile DNA amplification [29]. Random amplified polymorphic DNA (RAPD), for example, uses a single primer of arbitrary sequence to amplify random segments of DNA, revealing polymorphisms. Amplified fragment length polymorphisms (AFLP) selectively amplify restriction fragments from digested genomic DNA, providing a robust method for detecting genetic variations [30]. Single nucleotide polymorphisms (SNPs) represent single-nucleotide changes in the genome and can be detected through genomic sequencing, offering a high-resolution approach to identifying genetic differences.

High-throughput techniques like diversity array technology (DArT) leverage microarray hybridization to genotype numerous polymorphic loci across the genome, providing a comprehensive view of genetic diversity [31]. The advent of next-generation sequencing (NGS) has further simplified the identification and utilization of SNPs, enabling deeper and more extensive genomic analysis. In crop genetics, quantitative trait loci (QTL) mapping and genome-wide association studies (GWAS) are crucial for exploring complex traits. QTL mapping uses statistical methods to connect phenotypic traits with genotypic data, typically employing molecular markers like SNPs and AFLPs [30,31]. This approach allows researchers to identify and map QTLs associated with important crop traits, facilitating targeted breeding strategies. GWAS examines the entire genome for associations between genetic variants and specific traits, providing broader insights into the genetic architecture of complex traits [21,32]. Structural variants (SVs), including insertions, deletions, and duplications, also play a significant role in controlling agronomically important traits. The combination of marker-assisted selection (MAS) and genotyping-by-sequencing (GBS) has proven valuable in improving hybrid breeding, enabling breeders to enhance crop quality and yield. Multiparent mapping approaches, like multiparent advanced generation intercrosses (MAGIC) and nested association mapping (NAM), have revealed the potential for considerable phenotypic diversity through experimental breeding [33]. These approaches

offer robust resources for breeding improvement and can help identify and validate QTLs through functional genomics studies.

5. FUNCTIONAL GENOMICS AND MUTAGENOMICS

Functional genomics leverages the vast resources and insights provided by structural genomics to study gene function on a global scale. The term refers to the development of comprehensive experimental approaches that aim to assess the roles of specific genes. This field has greatly benefited from a variety of biotechnological tools that help identify and isolate genes of interest, as well as create overexpression or knockout lines for functional transgenic studies. Before the advent of next-generation sequencing (NGS), traditional methods like suppression subtractive hybridization (SSH), expressed sequence tag (EST), and cDNA-AFLP-sequencing were used to identify candidate genes, often involving time-consuming and labor-intensive procedures [34]. The introduction of NGS has significantly streamlined these processes, allowing researchers to identify genes related to traits like disease resistance, stress tolerance, and yield more efficiently. Genome editing tools such as clustered regularly interspaced short palindromic repeats (CRISPR/Cas9) and transcription activator-like effector nuclease (TALEN) have become instrumental in crop improvement [35]. These technologies offer precise gene editing capabilities without the need for inserting foreign DNA, enabling targeted modifications that can increase yield, confer pest and disease resistance, and improve stress tolerance. For instance, both TALEN and CRISPR/Cas9 have been used to create mutants with mildew resistance in bread wheat and tomato [36,37,56]. Other significant crops, including soybean, rice, maize, and sorghum, have also seen successful genome editing using these tools.

Mutagenomics, a subset of functional genomics, focuses on investigating gene function through the creation of mutants and the application of reverse genetic techniques. Methods such as Targeting Induced Local Lesions in Genomes (TILLING) have proven valuable for inducing and detecting mutations in a range of crops, including rice, maize, wheat, barley, tomato, and soybean [38]. Reverse genetic techniques, such as RNA interference (RNAi) and virus-induced gene silencing (VIGS), allow researchers to silence or knock down gene expression, enabling the study of gene function even when mutant alleles are not readily available [39]. These functional genomics and mutagenomics approaches have significantly contributed to crop improvement by providing a deeper understanding of gene function. They have been used to enhance crop growth, increase yield, and boost resistance to stress and diseases. By integrating these techniques into breeding programs, researchers can create crops with desirable traits that are better suited to meet the demands of modern agriculture. The ongoing advancement of these technologies holds the promise of further accelerating crop improvement, offering innovative solutions to global food security challenges.

6. TRANSCRIPTOMICS

Transcriptomics is the study of the transcriptome—the complete set of RNA transcripts produced by an organism's genome within specific cells or tissues. This field provides critical insights into gene expression patterns in response to various stimuli over time. Transcriptome profiling allows researchers to monitor gene expression changes and understand gene functions in a more dynamic context. Early transcriptomic studies used traditional profiling techniques like cDNAs-AFLP, differential display-PCR (DD-PCR), and suppression subtractive hybridization (SSH), but these methods had limited resolution [40]. With the advancement of robust techniques, RNA expression profiling has evolved through methods such as microarrays, digital gene expression profiling, next-generation sequencing (NGS), RNA-seq, and serial analysis of gene expression (SAGE) [41]. These techniques offer higher resolution and enable more comprehensive analyses of gene expression.

For instance, RNA-seq studies in maize have been used to identify genes responsive to drought stress. Comparative transcriptomics, which compares expression profiles across different crop species, has also proven useful. This approach identified common genes in response to heat stress among rice, wheat, and maize, demonstrating its potential to reveal conserved stress-response pathways. Additionally, alternative splicing (AS) transcriptomics has become a valuable tool for studying how plants generate multiple transcripts in response to abiotic stress conditions [42]. This approach has been employed in crops like rice,

maize, and sorghum to explore splicing factors' roles in controlling abiotic stress responses. Overall, transcriptomic techniques play a crucial role in elucidating gene regulation, which is key to improving crop species.

7. PROTEOMICS

Proteomics involves the profiling of the total expressed protein in an organism and is divided into different areas: sequence, structural, functional, and expression proteomics. These branches allow researchers to study proteins from various perspectives, including their amino acid sequences, structural configurations, and functions. Structural proteomics examines protein structure and can be analyzed using computational modeling and experimental methods like nuclear magnetic resonance (NMR), X-ray crystallography, and electron microscopy [43]. The goal is to understand the protein's physical conformation and how it relates to its function. Functional proteomics focuses on understanding the roles that proteins play within cells or tissues. This branch is critical for linking protein structure to biological function. Experimental techniques like affinity chromatography and interaction studies help elucidate protein functions.

Expression proteomics is concerned with profiling protein expression levels, which can be influenced by various factors, including environmental conditions or genetic modifications. Techniques like SDS-PAGE, two-dimensional gel electrophoresis (2-DE), and two-dimensional differential gel electrophoresis (2D-DIGE) are commonly used for separating proteins and analyzing their expression patterns [44]. Mass spectrometry (MS) has become a cornerstone of proteomics, allowing for the precise identification and quantification of proteins. Methods like MALDI-TOF, electrospray ionization (ESI), and collision-induced dissociation (CID) provide detailed information about protein molecular weights and structures [45]. These proteomic approaches have significantly contributed to advancing plant research by allowing researchers to study proteins at a deeper level, facilitating a more thorough understanding of plant biology, crop improvement, and stress responses [46]. This integrated understanding from both transcriptomics and proteomics provides a comprehensive view of plant functionality, offering pathways for innovation in crop breeding and agricultural sustainability.

8. METABOLOMICS

Metabolomics provides a comprehensive analysis of the complete set of metabolites—small molecules such as carbohydrates, lipids, proteins, vitamins, and amino acids—in an organism's cells or tissues [18,47]. It complements transcriptomics and proteomics, offering deeper insights into the molecular basis of stress tolerance and other complex plant traits. By studying the metabolome, researchers can identify and understand the biochemical pathways that underlie plant responses to environmental stresses, leading to more targeted breeding strategies [6,10]. The role of metabolomics in crop breeding is especially significant when breeding for traits like drought tolerance and nutrient uptake efficiency. By focusing on the metabolites involved in these processes, breeders can use metabolite-based markers for selection, providing an alternative to traditional phenotype-based selection. This approach has been used in major cereals like rice, wheat, and maize to identify the molecular mechanisms for stress tolerance. Metabolomics is also essential for understanding nutrient uptake in plants. Traits like nitrogen usage efficiency, which are crucial for plant growth and yield, largely depend on root characteristics. Studies have shown that certain metabolites, such as phosphatidylcholine and phosphatidylglycerol, are associated with increased root biomass growth under nitrogen-deficient conditions, leading to enhanced nutrient uptake [48].

The complex relationship between genes, proteins, and metabolites in maize during different developmental stages emphasizes the need for advanced analytical techniques. Methods such as gas chromatography-liquid chromatography (GC-LC), confocal microscopy, high-performance liquid chromatography (HPLC), and ion trap tandem mass spectrometry are used to explore the intricate connections between genomics and metabolomics [49]. This detailed analysis helps identify the interactions between genes, proteins, and metabolites that lead to specific physiological outcomes. Maize, for example, has high polyphenol content, which is known for its antioxidant and anticancer properties. Studying these phytochemicals, such as anthocyanins in the aleurone layer and various other compounds, can reveal the genetic regulatory mechanisms that drive phenotypic outcomes [50]. This deeper understanding of metabolites in maize and other crops provides a

strong foundation for developing more resilient and nutritionally valuable crop varieties.

The field of omics technologies has broadened as a result of the introduction of high-performance technologies in many study fields. To integrate data from genomics, transcriptomics, proteomics, and metabolomics studies, systems biology techniques are employed (Fig. 4).

9. FUTURE PERSPECTIVES

The future of crop breeding, particularly in maize, looks promising with the continued integration of advanced omics technologies. As transcriptomics, proteomics, and metabolomics evolve, breeders will gain deeper insights into the complex interactions between genes, proteins, and metabolites that drive plant growth, stress responses, and yield [50]. This multifaceted approach allows for more precise selection and accelerated breeding cycles, leading to the development of crops with enhanced stress tolerance, nutrient efficiency, and disease resistance. The potential applications of these technologies extend beyond traditional breeding. Genome editing tools like CRISPR/Cas9 and TALEN offer precise methods to introduce desired traits without relying on conventional genetic modification techniques [36,37]. These methods can be used to create crops with increased resistance to environmental stressors and improved nutritional profiles, contributing to global food security and sustainability.

As researchers continue to explore the plant metabolome, a deeper understanding of primary and secondary metabolites will emerge, shedding light on their roles in plant physiology and stress responses [54]. This knowledge could lead to the identification of novel biomarkers for stress tolerance, allowing breeders to create crops that are more resilient to changing climate conditions [51]. Furthermore, comparative studies across different crop species will help identify conserved stress-response pathways, enabling the development of crops that can thrive in a variety of environments. With advanced analytical techniques such as GC-LC, HPLC, and mass spectrometry, researchers can delve into the molecular mechanisms behind crop phenotypes [49], offering new avenues for breeding innovation. Overall, the integration of omics technologies in crop breeding promises to revolutionize the field, providing a pathway to develop crops that meet the demands of a growing global population while addressing the challenges posed by climate change and resource scarcity [52,53]. This forward-thinking approach to agriculture has the potential to transform food production, making it more efficient, resilient, and sustainable.
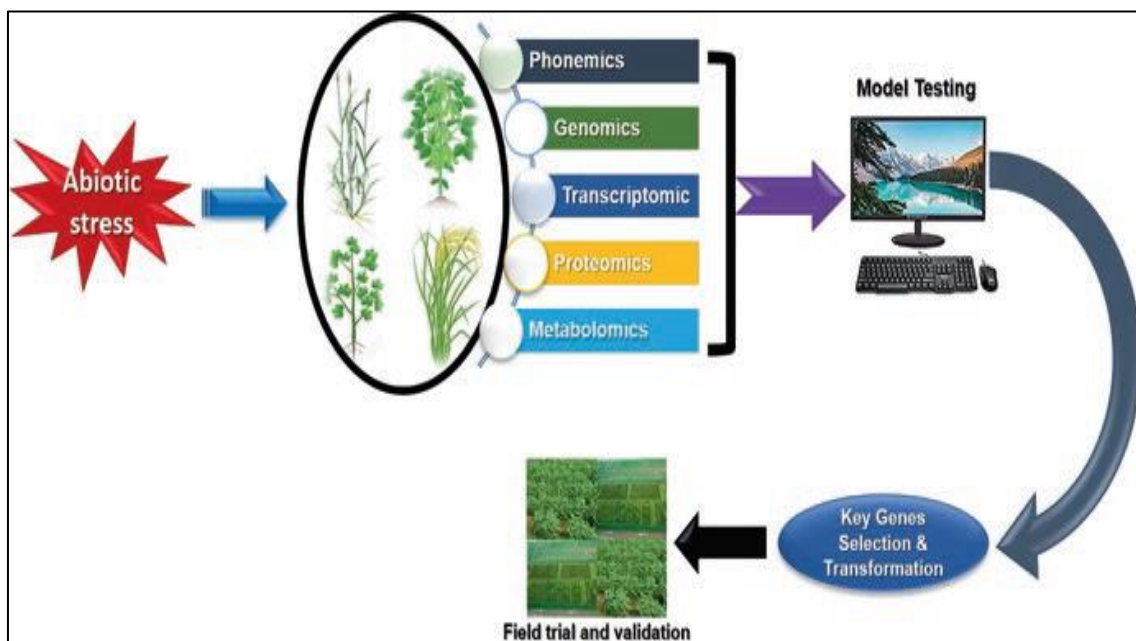

Fig. 4. Integration of different omics approaches for abiotic stress tolerance in crops [57]

10. CONCLUSION

The convergence of advanced omics technologies, including transcriptomics, proteomics, and metabolomics, is reshaping the landscape of crop breeding. These tools offer a comprehensive understanding of the complex molecular processes that govern plant traits, enabling breeders to make more informed and precise selections. The integration of these technologies has accelerated breeding cycles, paving the way for crops with enhanced stress tolerance, nutrient efficiency, and disease resistance. The emergence of genome editing techniques like CRISPR/Cas9 and TALEN further complements traditional breeding methods, allowing for precise trait modification. This has significant implications for developing crops that are more resilient to environmental stressors and better suited to a changing climate. The ability to introduce specific traits without conventional genetic modification is a major breakthrough in crop improvement, offering a pathway to address global food security and sustainability challenges. The ongoing advancements in omics technologies, coupled with high-throughput analytical methods, suggest a future where crop breeding becomes increasingly efficient, responsive, and tailored to meet global demands. This holistic approach to crop breeding is poised to drive innovation in agriculture, providing solutions that are not only productive but also sustainable, thereby contributing to a more secure and resilient food system.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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