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REVIEW ARTICLE

Revolutionizing fruit breeding through multi-omics approaches: From genomics to synthetic biology

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Abstract

Omics technologies have revolutionized fruit breeding by providing unprecedented insights into the genetic, molecular and biochemical mechanisms underlying desirable traits. The integration of genomics, transcriptomics, proteomics, metabolomics and epigenomics has enabled the identification of key genes, pathways and regulatory networks associated with fruit quality, shelf life and stress tolerance. Genomics-assisted breeding, including genome-wide association studies (GWAS) and marker-assisted selection (MAS), has accelerated the development of improved cultivars with enhanced traits. Transcriptomics and proteomics have shed light on the complex gene expression and protein dynamics during fruit development and ripening, while metabolomics has identified crucial metabolites influencing flavor, nutritional value and postharvest quality. Epigenomics has revealed the role of epigenetic modifications in regulating fruit-related processes and environmental adaptability. High-throughput phenotyping, coupled with omics data, has facilitated rapid and accurate trait assessment, enabling breeders to make informed decisions. The application of CRISPR/Cas genome editing has opened new avenues for precise manipulation of fruit traits. However, the ethical and regulatory aspects of omics-based breeding must be carefully considered to ensure responsible implementation and public acceptance. By harnessing the power of omics technologies and integrating them with traditional breeding approaches, researchers can develop climate-resilient, high-quality fruit crops that meet the growing demands of consumers and contribute to sustainable agriculture.

Keywords: epigenomics; fruit breeding; genomics-assisted breeding; metabolomics; omics technologies; proteomics; transcriptomics

Introduction

The current breeding technology merges omics technologies with systems biology to build an innovative system which elevates both precision and swift operations in modern breeding methods. Microbiology research uses the four analytical methods of omics technologies to reveal all gene-driven transformations which form fruit characteristics. The acquired knowledge enables breeders to choose better options due to information-based decisions instead of traditional visual selections.

The identification of quantitative trait loci (QTL) and genomic selection (GS) through genomics-assisted breeding (GAB) serves as an essential breeding method for fruit operations because it delivers more precise forecasting capabilities for breeding. Standard phenotypic observations do not sustain breeder performance forecasting as effectively as GAB techniques since they present time-consuming and inaccurate and costly drawbacks (1, 2). Genome-wide association studies (GWAS) now serve as a crucial tool for discovering genetic markers that link features including fruit quality alongside shelf life alongside biological and environmental stress resistance (2, 3). The analysis process is improved by high-throughput sequencing approaches that detect single nucleotide polymorphisms (SNPs) in conjunction with other genetic components affecting phenotypic diversity (2, 3).

Systems biology functions as an integrated system to analyse fruit developmental and quality aspects and genomic research capabilities. Scientists use multi-omics research models to understand the mutual influence of genetic and environmental elements on fruit characteristics (4, 5). The systematic organization provides superior benefits for studying hereditary characteristics acquired from various genetic components and environmental influences. Biological systems research has discovered fundamental regulatory pathways governing fruit development while identifying metabolic processes linked to essential gene activation patterns that increase production quality (3, 6).

The speed of research conducted in GAB and systems biology increases substantially thanks to machine learning (ML) and artificial intelligence (AI). Scientists use these technologies to analyse large genomic and phenotypic datasets to establish patterns for creating performance and inherited trait predictive models (1, 7). According to previous studies, breeders can enhance their crossbreeding decisions through trait selection using this methodology to obtain better cultivars (7).

Genomics and marker development for precision breeding

The integration of genomics and marker development into precision breeding has revolutionized the field of fruit crop improvement. By employing advanced genomic techniques such as GWAS and marker-assisted selection (MAS), breeders can enhance the efficiency and accuracy of selecting desirable traits in fruit crops. This approach is particularly beneficial given the complexities associated with breeding perennial crops, which often exhibit long juvenile phases and significant genetic variability.

One of the primary advantages of genomics-assisted breeding is the ability to identify and utilize molecular markers linked to important agronomic traits. For instance, studies have demonstrated that GWAS can effectively identify quantitative trait loci (QTL) associated with fruit quality traits, such as size, sweetness and disease resistance (8, 9). The combination of parental and breeding populations in these analyses has been shown to improve prediction accuracy and enhance the power of GWAS, thereby facilitating the identification of genes responsible for complex traits (9, 10). Furthermore, the declining costs of sequencing technologies have made it feasible to utilize a large number of DNA markers, which is crucial for overcoming the limitations imposed by the long juvenile periods of fruit trees (3, 9).

Table 1 illustrates genomic tools and their applications for fruit crop improvement and lists respective fruit species along with genomic methods. This complete review demonstrates how genomics modernizes global fruit breeding initiatives. Marker-assisted selection serves as an effective technology for improving multiple species of fruit plants. Geneticists developed SNP markers that help improve both apple and other fruit crops by picking traits that enhance quality and resistance to diseases (2, 11). Through MAS technology breeders select favorable gene traits instead of phenotypic traits because genetic information avoids outside environmental effects during the choice process. A molecular-based breeding strategy allows both accelerated breeding and increased precision of trait selection (2, 11).

The implementation of GS within breeding programs extends the prediction abilities for breeding lines genetic potential. GEBVs calculated from dense marker data allow GS to determine breeding candidates with best traits at early stages of breeding cycles (20, 21). Scientists have achieved success by using this approach for genetic improvement in citrus and papaya among other fruit crops to discover elite types with favorable characteristics (9, 21). Predicting plant performance through genomic analysis decreases the time and labor used in traditional breeding methods to develop improved varieties more efficiently (3, 11).

Table 1. Application of genomics in fruit crop improvement: techniques, fruits studied and key finding

Aspect	Description	Applications in fruit crops	Fruits studied	Genomic tools used	References
Genomic Mapping	The process of identifying and mapping the locations of genes within the genome	Identifying genes related to fruit quality traits such as flavor, color, texture and shelf-life	Apples, Grapes, Bananas	GWAS, QTL Mapping	(9, 10)
Genome Sequencing	The technique of determining the complete DNA sequence of an organism's genome	Full genome sequencing for understanding genetic basis of yield, disease resistance and fruit quality	Citrus, Papaya	Whole Genome Sequencing (WGS)	(12)
Gene Editing (CRISPR/Cas9)	A technology that allows for precise alterations of the genome by adding, removing, or altering sections of the DNA sequence	Developing genetically modified fruit varieties for improved disease resistance and better-quality traits	Tomatoes, Apples	CRISPR/Cas9	(13)
Quantitative Trait Loci (QTL)	Regions of the genome that are linked to specific traits and are inherited through generations	Identifying QTLs for traits like fruit size, sugar content and resistance to environmental stress	Apples, Citrus, Grapes, Bananas	GWAS, QTL Mapping	(2, 14)
Transcriptomics	The study of RNA molecules to understand gene expression patterns under different conditions	Studying genes responsible for ripening, flavor profile and disease resistance	Grapes, Apples, Citrus	RNA-sequencing, qRT -PCR	(15)
Metabolomics	The study of metabolites, such as sugars, acids and secondary metabolites, produced during plant growth and development	Identifying metabolites associated with flavor, disease resistance and shelf-life	Tomatoes, Grapes	Mass Spectrometry (MS), NMR	(16)
Gene Expression Profiling	Measuring the expression of genes at different stages of development or under varying environmental conditions	Studying the expression of genes involved in fruit quality, ripening and stress resistance	Apples, Grapes, Citrus	RNA-seq, Microarrays	(17)
Marker-Assisted Selection (MAS)	A technique where molecular markers linked to desirable traits are used to select plants for breeding	Selecting for traits like fruit quality, disease resistance and yield through SNP markers	Apples, Pears, Mangoes	SNP Markers, MAS	(2, 11)
Epigenomics	The study of changes in gene expression that do not involve alterations to the DNA sequence, often due to environmental factors	Understanding how environmental factors like temperature and water availability affect fruit development and quality	Apples, Grapes, Citrus	DNA Methylation Profiling	(18)
Comparative Genomics	Comparing the genomes of different fruit crops to identify conserved genes and pathways	Identifying genes that contribute to beneficial traits such as disease resistance and environmental tolerance	Apples, Grapes, Mangoes	Comparative Genomic Analysis	(19)
Genomic Selection (GS)	A technique that predicts genetic performance based on genomic data using genomic estimated breeding values (GEBVs)	Selecting breeding lines with superior traits early in the breeding cycle to accelerate cultivar development	Citrus, Papaya	GS, GEBVs	(20, 21)
High-Throughput Phenotyping	The use of advanced technology to rapidly assess phenotypic traits, often combined with genomics data for trait selection	Accelerating the identification of phenotypic traits like fruit size, color and disease resistance in breeding programs	Apples, Grapes, Citrus	Phenotypic Screening, Imaging Technology	(22)

Transcriptomics and proteomics: insights into gene and protein function

The combination of transcriptomics and proteomics has accelerated our knowledge of gene and protein activities resulting in improved breeding methods for high-quality resilient fruits. These omics technologies in Fig. 1 reveal molecular-level explanations about traits related to fruit development together with ripening while enlarging understanding of plant responses to environmental stresses.

During critical developmental stages transcriptomics studies RNA transcripts in detail to detect differently expressed genes (DEGs) through its analysis. Researchers have discovered that ripening processes in fruit are controlled by specific genes including elements of ethylene signalling as well as biosynthesis. Scientists have found that MADS-box transcription factors specifically fruitful homologs control both style abscission and tomato fruit ripening according to previous studies (23, 24). The control of ripening processes depends on gene expression dynamics because they offer vital pathways to improve fruit quality characteristics.

Transcriptomic assessments prove crucial for uncovering genomic factors which affect fruit dissolvable content and acid levels. Studies on PH genes in melons have shown their power to control acidic properties which led to the natural development of sweet melons during evolutionary periods (9). Such discoveries about fruit flavors guide the next generation of genetic manipulation efforts focused on improving consumer preferences.

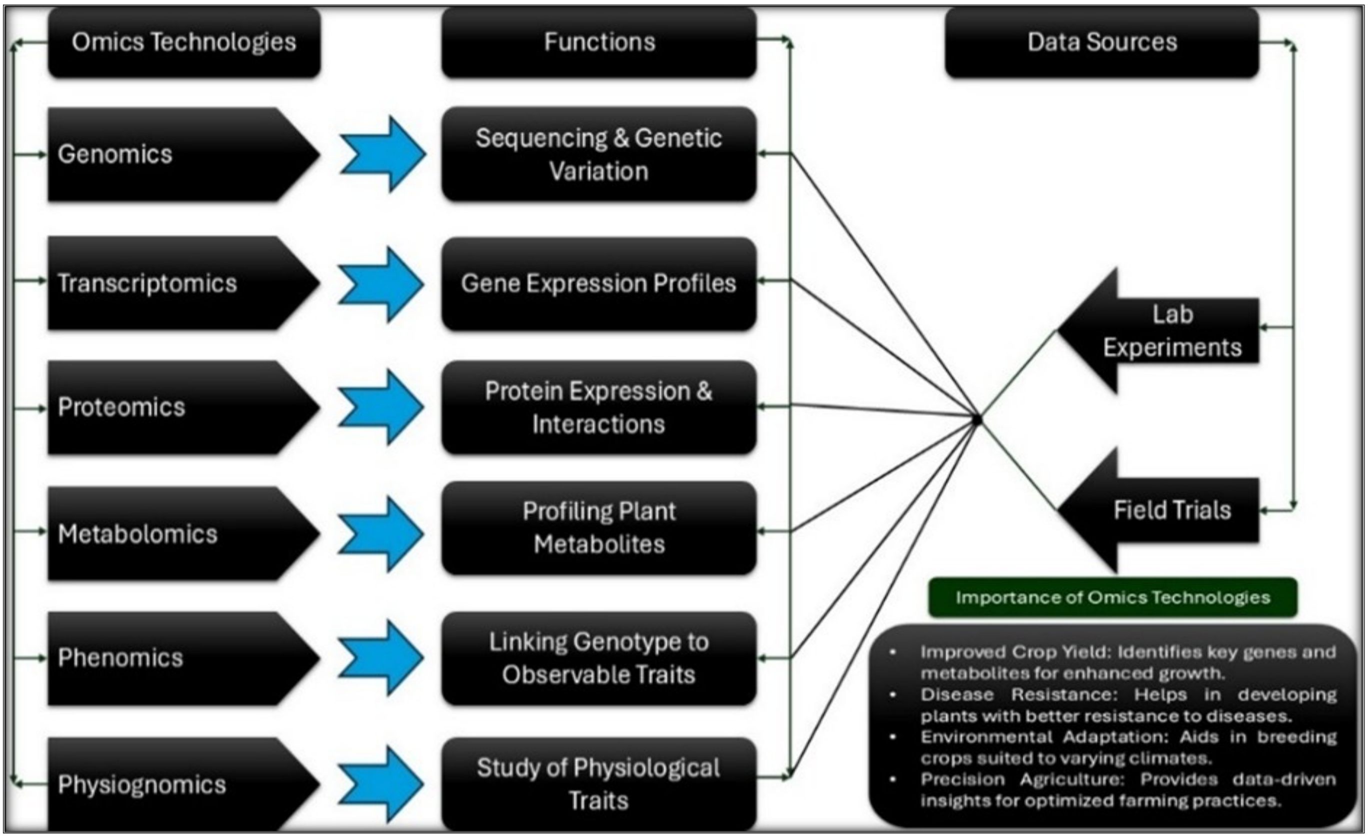
The field of proteomics enhances transcriptomic research through protein expression analysis alongside post-translational modifications crucial for determining developmental functional roles in fruits. Proteomic analysis enables scientists to discover metabolic proteins to study carotenoid biosynthesis regulation in watermelon as it demonstrates the important applications of proteomic methods for fruit trait understanding (10). The researchers examined POD genes from grapevine while studying their fruit development patterns because these genes appear to influence fruit quality and stress response mechanisms (12).

Through the merger of transcriptomic and proteomic data scientists can employ systems biology to understand the complete network of actions between genes and proteins and their associated metabolites. The combination of multi-omics approaches led to better identification of networks that regulate fruit ripening and development according to earlier research (14). Completion of an integrated perspective enables researchers to create strategies which improve fruit crop resilience against diverse environmental factors.

The progress in next-generation sequencing along with high-throughput proteomic technology has made the acquisition of large-scale datasets possible for tropical and subtropical fruit crops functional genomic research. The collection of these datasets offers important resources to discover genes linked with desirable features which enhances breeding speed (25). Researchers are using expressed sequence tags (ESTs) to understand gene expression patterns for fruit ripening of Chinese bayberry among other species (26).

Metabolomics and epigenomics: enhancing fruit quality and adaptability

Developing fruit crop research through the combination of metabolomics and epigenomics proves effective for improving both fruit quality and adaptation characteristics. By studying metabolites in biological systems through metabolomics scientists obtain insights on natural biochemical processes involved in fruit development and ripening and stress responses. The field of epigenomics uses heritable gene expression modifications that lack DNA sequence changes to control biological actions especially during environmental factor exposure.



- Improved Crop Yield: Identifies key genes and metabolites for enhanced growth.
- Disease Resistance: Helps in developing plants with better resistance to diseases.
- Environmental Adaptation: Aids in breeding crops suited to varying climates.
- Precision Agriculture: Provides data-driven insights for optimized farming practices.

Fig. 1. Omics technologies in crop improvement.

Metabolomics offers laboratories the capacity to detect and quantitate several metabolites consisting of sugars and organic acids alongside amino acids and secondary metabolites that constitute vital indicators for fruit quality evaluation through assessments of flavour and aroma as well as nutritional values. The levels of specific metabolites particularly flavonoids and carotenoids serve as markers for better fruit quality reception by consumers (27). Scientists have demonstrated that metabolic pathway manipulation leads to elevated beneficial compounds which generates better quality fruit products (27).

Epigenomic studies demonstrate that developmental processes of fruit alongside ripening phases heavily depend on epigenetic alterations including DNA methylation along with histone modifications. DNA demethylation leads to activation of ripening pathways in tomatoes which improves their quality according to previous studies (28, 29). The environment shapes epigenetic modifications through temperature and light regulation to influence fruit development as well as stress response thus helping fruit crops adapt to climate change (28, 30). Epigenetic manipulation represents a new technological approach for producing better fruits by extending their shelf life and improving taste profiles (28, 30, 31). The advancement of epigenomic research throughout time is visible through a line graph presentation showing rising interest in various epigenetic functions Fig. 2.

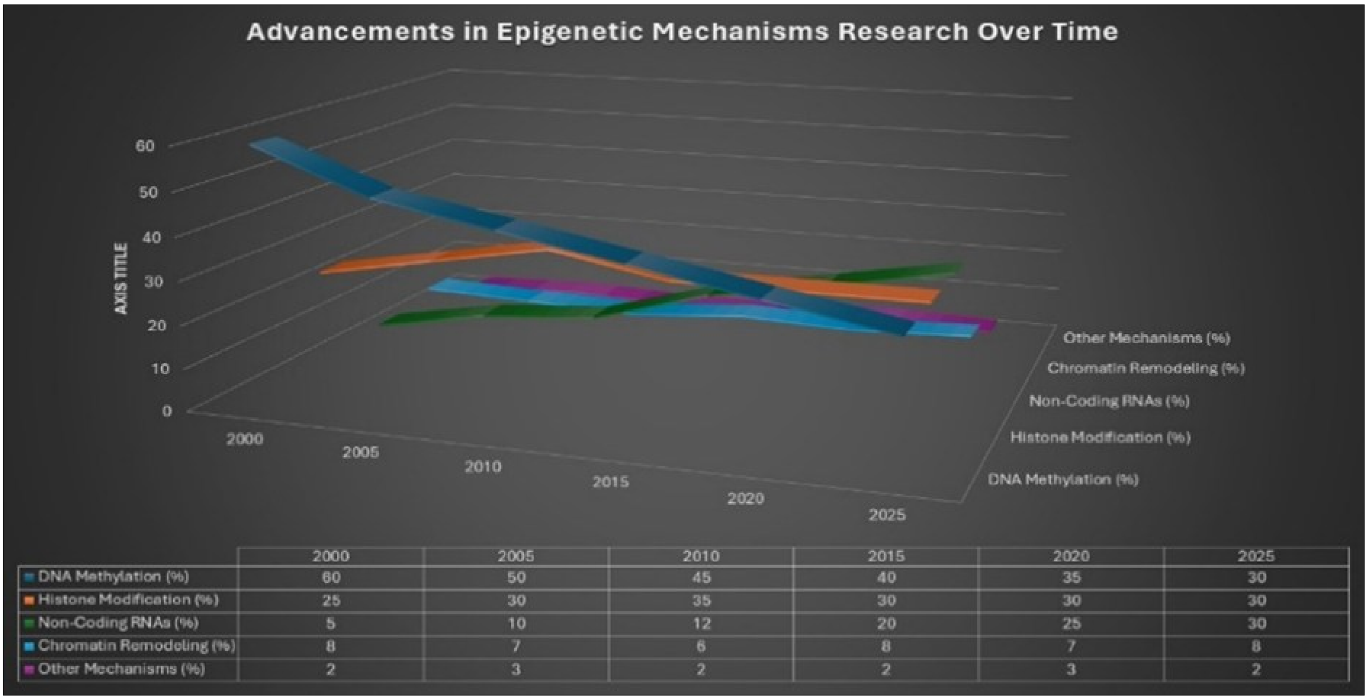
For instance, research based on metabolomics combined with epigenomics creates an advanced strategy to study interconnected regulatory systems which control both fruit quality characteristics and adaptation capabilities. The united application of omics technologies enables researchers to find crucial metabolites alongside their regulatory genes which benefits breeding strategy development for metabolism and epigenetic modification control (32, 33). Genetic selection programs benefit from epigenetic markers discovery which enables breeders to obtain cultivars showing enhanced quality compounds and strong environmental adaptability (32, 33).

High-throughput sequencing technologies have advanced to the point where researchers can fully analyse metabolomes and epigenomes simultaneously thus producing large datasets for fruit crop functional genomics (33). Through data-driven tactics researchers can detect genes along with metabolic pathways which prove beneficial for breeders to enhance genetics (27). The combination of transcriptomic and metabolomic data analysis improved fruit ripening knowledge alongside quality trait mechanisms thus leading to advanced breeding strategies (27, 34).

Integrative omics for trait discovery and stress tolerance

Integrative omics methods serve as efficient tools which help researchers discover new traits and improve stress resistance in fruit -production plants. Various omics disciplines such as genomics along with transcriptomics and proteomics and metabolomics form an integrated system that allows researchers to monitor complete fruit crop biological and chemical responses to both abiotic and biotic stress factors. Integrative omics puts specific emphasis on how plant hormones manage stress responses in plants. Hormones including abscisic acid (ABA) together with ethylene and jasmonates regulate plant responses to environmental stress by influencing growth and development as well as fruit production (35, 36). The stress response enhancement abilities of ABA result from its control of stomatal reactions and promotion of root elongation to sustain water needs (36). The identification of fundamental regulatory genes for crop improvement becomes possible by studying hormonal pathways through transcriptomic and proteomic methodologies (37).

Using CRISPR/Cas systems as part of genome editing applications now enables precise enhancements of beneficial characteristics in fruit crops. Through CRISPR precise genome changes in plants enable scientists to introduce stress tolerance traits without obtaining any additional unwanted features (38, 39). CRISPR technology has resulted in the manipulation of fruit maturation processes while simultaneously making fruits resilient against several environmental stressors which reinforces fruit quality and production levels (38, 39). The combination between genome editing techniques and omics data reveals crucial information about genetic regulations and provides importance for building new agricultural products which withstand environmental changes.



	2000	2005	2010	2015	2020	2025
■ DNA Methylation (%)	60	50	45	40	35	30
■ Histone Modification (%)	25	30	35	30	30	30
■ Non-Coding RNAs (%)	5	10	12	20	25	30
■ Chromatin Remodeling (%)	8	7	6	8	7	8
■ Other Mechanisms (%)	2	3	2	2	3	2

Fig. 2. Advancements in epigenetic mechanisms research over time

Using crop wild relatives (CWRs) presents a beneficial strategy for developing new fruit crops which resist various stresses. The extensive genetic composition found in CWRs enables breeders to transfer resistance characteristics into their cultivated counterparts. New findings from transcriptomic profiling allow researchers to find stress-regulatory genes in CWRs so breeding programs can integrate these genes to develop variety -specific tolerance against drought and salinity conditions (40, 41). By applying these techniques scientists expand the genetic variability of farming crops and enhance their development speed for stress-tolerant cultivars.

Metabolic profiling applications in fruit crop research enabled researchers to study both the biochemical pathways which influence fruit development and stress reactions. Tomato research has revealed key metabolic processes during fruit ripening by showing ways to enhance nutritional value and lengthen shelf life according to previous study (42). Metabolomic studies together with other omic methods enable researchers to monitor complete physiological transformations when stress occurs and this promotes better plant breeding strategies.

High-throughput phenotyping and omics integration

Crop breeding has experienced a fundamental change through the combination of high-throughput phenotyping with omics technologies because it improves both trait detection capability and plant tolerance to stress conditions. This combination expands analytical capabilities by uniting phenotypic trait inspections with genomic and transcriptomic and proteomic and metabolomic evaluations to achieve better knowledge about plant stress responses as well as desirable trait genetics.

Modern phenotypic data collection has experienced a significant transformation through high-throughput phenotyping technologies which now perform rapid multi-plant assessment with automated mechanisms instead of manual operations. A previous finding demonstrates how HTP platforms produce efficient phenotypic results using multiple sensors for obtaining vital measurements for broad-scale plant breeding (43). The new breeding framework boosts the breeding process by allowing fast trait assessment of growth rate and leaf area and stress response evaluation under standardized environments (44, 45).

Combining HTP with omics information leads to effective QTL identification for stress tolerance. Through research by Yang et al. HTP was successfully used in rice GWAS to discover genomic areas linked to changes in agronomic qualities (46). This approach improves genetic understanding of traits while enabling breeders to identify top-quality genotypes for their programs.

The merging machine learning technology with artificial intelligence systems helps process the large datasets resulting from HTP and omics technology applications. Similar studies (47) demonstrates that AI demonstrates effective capabilities for controlling and analysing diverse multi-omics datasets to lead breeding decisions and strengthen stress response programs. Predictive modelling combined with plant environmental response forecasting helps in creating climate-adapted crops.

The measurement of stress tolerance becomes more successful through the integration of HTP with omics. Stress-induced metabolic pathways become visible when metabolomics operates together with phenotypic measurements according to previous study (48) because the identification process reveals crucial metabolites which give plants resistance against abiotic stresses including drought and salinity. Using combined analysis methods produces better plant stress physiology comprehension which leads to findings about stress tolerance genetics for cultivation programs.

Improved high-throughput sequencing technologies now help researchers find favorable genes and alleles linked to stress tolerance characteristics. A study that uniting multi-omics methods brought major progress to breeding techniques that aim to increase abiotic stress tolerance in crops like maize (49). The combined system gives breeders access to complete knowledge of plant genetics and phenotypes when making their selections.

High-throughput phenotyping linked with omics technology drives quicker breeding strategies which produce resilient crop varieties that succeed in altering environmental conditions. Researchers obtain more detailed genetic information about traits and stress tolerance mechanisms by using phenotypic data with genomic and additional omics data sets such as transcriptomic and proteomic and metabolomic data.

Synthetic biology and omics in postharvest improvement

Synthetic biology and omics technologies now function as emerging research fields which target improvements in postharvest characteristics together with shelf-life extension and nutrition values of fruits and vegetables. The combination of advanced genetic engineering methods and omics research enables scientists to develop new approaches which reduce horticultural product wastage while improving their overall quality.

Through synthetic biology researchers obtain advanced technological methods which enable optimization of fruit metabolic pathways for improved desirable characteristics. Recent research demonstrates that brassinosteroids (BRs) enhance antioxidant compounds while decreasing chilling injuries across different fruit species during postharvest period. 24-Epibrassinolide solution treatments on blood oranges produced dual benefits by lowering chilling damage together with higher production of antitoxins which maintained product quality (50). According to previous studies, BR treatment enhanced mandarin fruit quality through an increase of total soluble solids together with antioxidants which establishes synthetic biology as a promising postharvest quality enhancer (51).

Postharvest biochemical changes receive valuable insights from combined use of omics technologies that include metabolomics and transcriptomics. The metabolomic profiling allows researchers to comprehend the modifications which affect fruit quality attributes including sugars and acids and polyphenols and their interaction during storage (52). The identified metabolites serve as breeding targets for biotechnology research which aims to enhance nutritious flavour content.

Postharvest improvement finds critical support from the combination of high-throughput phenotyping technologies with omics integration systems (53). Extensive phenotyping tests on Valencia oranges and Rustenburg navel oranges to build shelf-life forecasting systems for optimal warehousing solutions and loss reduction. Researchers can better identify factors that determine postharvest quality by linking omics information to collected phenotypic data thus they can create targeted solutions to extend fruit lifetime.

Biocontrol agents employed for postharvest disease management provide an opportunity for synthetic biology and omics scientific methods to work together. Scientists have tested Cryptococcus Laurentiis as antagonistic yeast which shows potential for controlling damage-causing postharvest diseases in peaches specifically blue mold (54). The stress challenges encountered by biocontrol agents but noted that omics research will help understand yeast metabolism better to boost their effectiveness in disease control. Biocontrol methods integrated with synthetic biology practices will enable more environment-friendly postharvest management methods.

Multi-omics approaches generate biomarkers for postharvest quality which enables precision agriculture programs to develop efficiently (55). Table 2 outlined how the combination of integrated omics enables researchers to understand fruit stress and defence reactions following harvest which benefits fruit product quality improvements and resilience development in breeding programs. The identification of genetic as well as metabolic markers for desirable traits enables breeders to choose those traits more efficiently.

Postharvest agricultural research makes significant progress through the combination of synthetic biology principles and omics technology exploration. The employment of progressive analytical methods permits researchers to establish modern techniques which optimizes both produce quality standards and shelf preservation stability and waste reduction effectiveness. A comprehensive approach as part of sustainability-aligned agriculture minimizes waste while maximizing resource utilization to provide food security simultaneously.

Omics-based breeding: ethical and regulatory aspects

Using omics technologies for crop breeding serves as a great opportunity to advance agricultural production but it requires addressing crucial ethical and regulatory challenges to gain public trust properly. The main ethical issue stems from how these changes affect native biodiversity together with surrounding ecological environments. Research has shown the development of omics-based genetically modified organisms (GMOs) might replace traditional crop varieties because these natural varieties contain essential genetic traits needed for food security (32). The need for extensive assessment exists because policymakers together with farmers and consumers must actively participate in making environmentally sustainable choices regarding crop variety implementation. Concerns exist about smallholder farmers and developing countries having access to omics data and genetic resources due to intellectual property rights related to these assets. The essential aspect of achieving global food security demands equitable access to these resources (56).

Strong oversight mechanisms in the field of omics-based breeding processes need to exist for testing the safety and effectiveness of newly developed plant varieties. According to previous studies, the evaluation procedure for genetically modified crops demands clear guidelines (57). The expanding speed of multi -omics technology demands regulatory bodies to create extensive evaluation protocols which address both environmental and non-target organism risks. The multidimensionality of multi-omics data prompts regulatory agencies to adopt assessment protocols that track complicated relationships between genotype-to-phenotype-to-environmental influences on crop performance (58).

When omics data enters breeding programs it creates new challenges regarding the handling of sample ownership and information security. According to previous studies, the deployment of large omics-generated datasets demands both ethinical data sharing protocols and protection of those who contribute to data collection (56). Public trust in omics-based breeding initiatives requires that ethical data usage practices and transparency standards must be achieved.

The implementation of omics technologies assists with climate-resilient crop development but produces additional hurdles in the process. The breeding techniques develop crop varieties for different conditions yet excessive focus on genetic traits makes crops susceptible to upcoming environmental threats (59). A sustainable agricultural practice requires proper management of omics-based breeding benefits together with careful preservation of genetic diversity.

Table 2. Integrative omics approaches for trait discovery and stress tolerance in fruit crops

Aspect	Fruit Crop	Type of Stress	Details	Suggestions	References
Omics Approaches	Various (e.g., Tomato, Citrus, Peanuts)	Abiotic & Biotic Stress	Integration of genomics, transcriptomics, proteomics and metabolomics helps understand stress responses at the molecular and biochemical level, enhancing resilience	1. Expand omics approaches to lesser-studied crops 2. Use advanced AI tools to predict stress responses 3. Develop crop-specific omics platforms	(22)
Role of Plant Hormones	Tomato, Citrus	Drought, Salinity, Heat Stress	ABA, ethylene and jasmonates regulate growth, root development and water uptake, enhancing drought and heat tolerance	1. Study hormone interactions in multi-stress conditions 2. Enhance hormone biosynthesis in crops 3. Develop stress-resilient varieties through hormone manipulation	(35, 36)
Genome Editing (CRISPR/Cas)	Tomato, Apple	Heat, Salinity, Disease Stress	CRISPR/Cas systems enable precise modifications, improving traits like stress tolerance, fruit ripening and disease resistance	1.Target stress-related genes for editing 2. Integrate CRISPR with omics data for better precision 3. Develop stress-resistant cultivars using genome editing	(38)
Crop Wild Relatives (CWRs)	Tomato, Peach	Drought, Salinity, Pest Stress	Wild relatives possess genetic diversity for stress tolerance, enabling the transfer of resilient traits to cultivated crops	1. Explore wild relatives from diverse regions. Cross-breed for resilience traits 2. Identify novel genes in CWRs for stress tolerance	(40, 41)
Metabolic Profiling	Tomato, Apple	Drought, Heat, Disease Stress	Metabolomics identifies metabolic shifts during stress, offering targets to improve fruit quality, nutritional content and shelf-life	1. Study metabolite changes under multi-stress conditions 2. Optimize metabolic pathways for improved yield 3. Enhance shelf-life through metabolic engineering	(42)

Conclusion

A novel development emerges in agricultural practices because omics technologies serve their essential role in breeding programs while improving plant quality during storage and giving plants resilience against environmental stress. Through genomics combined with transcriptomics as well as proteomics and metabolomics and epigenomics researchers discover extensive biological mechanisms associated with plant trait behaviour. The entire system provides two major benefits for scientists: essential genetic route identification and improved targeted breeding techniques development. High-throughput phenotyping along with these advances speeds up trait discovery which leads to more precise breeding methods that allow growers to develop crops suitable for quickly changing environments. The enormous benefits of omics-based breeding require monitoring and managing the ethical as well as regulatory difficulties that may arise. Which leads to responsible implementation of these technologies as well as public acceptance it requires proper attention to biodiversity issues alongside data ownership regulations and strong framework regulations. Navigating regulatory challenges together with transparent decisions and inclusive stakeholder participation and clear policies will help address these challenges. The combination between omics technologies and traditional breeding approaches will lead to resistant crops which combine superior quality with capabilities for addressing population growth requirements through sustainable agricultural operations. Moving ahead requires establishing proper equilibrium between technological progress and moral accountability because omics-based breeding methods need to support sustainable food production and ecological protection purposes.

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Authors' contributions

NS and NP conceived the concept and VT supported the idea. WAM collected all the literature and composed all the information and wrote the article. RR extensively edited the article and gave their valuable suggestion. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: The authors declare that there is no conflict of interest.

Ethical issues: None

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