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RESEARCHARTICLE

Trends in Biotechnology and Plant Sciences

Integrating Genomics and Metabolomics for Quality Traits in Rice

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Abstract

More than half of the world's population depends on rice (Oryza sativa L.) as their main food supply, so improving its quality attributes is essential for both market value and nutritional security. Breeding has been completely transformed by developments in genomics and metabolomics, which have made it possible to precisely dissect complex features and hasten the creation of high-yielding, stress-tolerant, and quality-enhanced cultivars. While metabolomics highlights the biochemical alterations underlying grain quality, nutritional composition, and stress resilience, genomic methods like GWAS, QTL mapping, and genome editing show the genetic foundation of important features. Trait prediction is increased, metabolite–gene networks are found, and the creation of molecular markers and pathway biomarkers for marker-assisted selection is facilitated by the integration of multi-omics datasets. Improvements in nutrient content, fragrance, pigment production, and abiotic stress tolerance are highlighted in case studies. The management of environmental variability and the conversion of sensory characteristics into reliable biomarkers are the remaining difficulties. The development of climate-resilient rice varieties that satisfy a range of producer and consumer demands will be accelerated by future breeding that uses high-throughput phenotyping and machine learning-driven multi-omics integration.

KEYWORDS
Rice breeding, Genomics, Metabolomics, Multi-omics integration, Quality traits.

1 | INTRODUCTION

A staple food for more than 50% of the world's population, especially in Asia and Africa, is rice, a cereal grain that has been domesticated. Oryza sativa is the seed of the grass species, which is frequently referred to as Asian rice, and Oryza glaberrima, which is less commonly known as African rice. About 13,500 to 8,200 years ago, Oryza glaberrima was domesticated in Africa and Oryza sativa was domesticated in China, and about 3,000 years ago (Fairhurst & Dobermann, 2002). Almost 480 million metric tons of milled rice grains are produced annually, according to Muthayya and associates. Rice is crucial for calorie intake and nutritional sustenance for populations in the Asia-Pacific area, as well as in some Caribbean and Latin American countries (Muthayya et al., 2014). In contrast to 72% for wheat and 19% for maize, about 85% of all rice production is used for human consumption.

Plant breeding has been essential to increasing global agricultural productivity and food security since the early 20th century (Shiferaw et al., 2013). Although, new issues with food quality and quantity have emerged as a result of the world's population growth and consequent acceleration of food consumption. To produce crop varieties with desired qualities, such as increased yields, stress tolerance, and better nutritional profiles, plant breeding is still a potent technique. For the purpose of ensuring food and nutritional security, breeding for improved quality features is very important. Despite their success in enhancing specific agronomic qualities, traditional breeding techniques frequently face obstacles because complex traits are polygenic and environmental variability has an impact. Comprehensive profiling of the rice genome and metabolome has been made attainable by recent developments in high-throughput sequencing and mass spectrometry, which have yielded new insights into the molecular mechanisms fundamental phenotypic variation (Wenefrida et al., 2013).

Numerous agronomic and nutritional

characteristics of rice are controlled by complex genetic networks that synchronize metabolic pathways, such as those involved in amino acid biosynthesis, carbohydrate metabolism, flavonoid and anthocyanin production, and micronutrient accumulation, according to integrated analyses of genomic and metabolomic data (Zhang et al., 2022). Notably, forecasts based solely on genomic data are outperformed by using multi-omics data, which greatly increases the predictive accuracy for complex variables like yield heterosis and nutritional qualit y (Koller et al., 2002). The development of rice varieties with improved agronomic performance and nutritional value, tailored to a range of environmental conditions and consumer demands, is aided by these integrative approaches, which also speed up the identification of functional genes.

In this review, we synthesize recent advances in the integration of genomics and metabolomics for rice trait improvement. We examine methodological frameworks, highlight key discoveries that elucidate the genetic and metabolic determinants of vital traits, and explore emerging opportunities for translational research in rice breeding. By providing a comprehensive overview of this evolving field, we aim to guide future strategies for leveraging multi-omics data to meet global challenges in rice production and quality enhancement.

2. Advances in Genomics and Metabolomics Technologies in Rice Research

2.1. Genomics Revolutionizing Rice Research

Rice research has changed dramatically as a result of the quick development of genomics, which has made it possible to investigate the genetic foundation of important agronomic features in greater detail. Comprehensive analyses of the rice genome are now possible thanks to high-throughput sequencing technologies, which also help identify genes related to grain quality, yield, and stress tolerance. Breeding efficiency has increased and trait discovery has hastened thanks to technologies like marker-assisted selection (MAS), quantitative trait locus (QTL) mapping, and genome-wide association studies (GWAS) (Razzaq et al., 2022). Breeders may now track advantageous alleles for traits including submergence tolerance (SUB1A), bacterial blight resistance (Xa21), and scent (badh2) thanks to marker-assisted selection (MAS), a crucial genomics tool (Jena & Mackill, 2008). The deconstruction of polygenic traits that are challenging to enhance through conventional phenotypic selection, such as drought resistance, grain shape, and amylose content, has been made possible by quantitative trait locus (QTL) mapping (Wang & Xiang, 2025).

By taking advantage of natural variation among various germplasm collections, genome-wide association studies (GWAS) have proved especially successful in discovering single nucleotide polymorphisms (SNPs) associated with complex phenotypes (Cao et al., 2022; Zhao et al., 2011). By utilizing genome-wide marker effects to estimate breeding values, the incorporation of genomic selection (GS) into rice breeding pipelines has transformed predictive breeding and allowed for early selection prior to phenotypic evaluation (Shan et al., 2014). For qualities that need large multi-location trials or have poor heritability, like yield stability in various climates, GS is particularly useful (Sasaki & Burr, 2000).

2.2. Genome Editing in Rice Improvement

Rice improvement has been transformed by genome editing, which makes it possible to quickly and precisely alter the genes governing yield, quality, and stress tolerance. In contrast to traditional breeding, CRISPR/Cas9 and its derivatives (base editors, prime editors) have been utilized to accelerate trait deployment by deleting susceptibility genes, changing promoter activity, and generating targeted nucleotide modifications without introducing foreign DNA (Yang et al., 2024). Successful uses include base changes that give herbicide resistance by altering ALS alleles, promoter tweaks that fine-tune expression, and edits to grain-size and heading-date genes that boosted yield components (Wang et al., 2022). Additionally, by multiplexing, genome editing can stack advantageous alleles in elite germplasm and enable quick functional confirmation of candidate genes for biotic and abiotic tolerance. Global regulatory environments have an impact on rollout speed;

Nonetheless, recent evidence of heritable, off-target-minimized alterations and field tests suggest usefulness for practical breeding. Although there are still issues with effective delivery, off-target evaluation, polygenic trait engineering, and fair access in smallholder systems, advancements in promoter engineering, tissue-culture-free delivery, and precision editors make genome editing a game-changing technique for sustainable rice production (Zegeye et al., 2022). In order to translate genome editing into agronomic advantages under field circumstances and ensure resistance to climate change and global food security, ongoing research published in peer-reviewed publications focuses on merging genome editing with speed breeding, genomic selection, and phenomics. Additionally, the capacity to precisely modify target genes has been made possible by genome editing technologies such as CRISPR-Cas9, which has accelerated the development of rice varieties with increased resilience and productivity (Iqbal et al., 2021). By providing a glimpse of the plant's metabolic phenotype, metabolomics enhances genomics. This field records dynamic metabolite changes that are a reflection of physiological states, environmental reactions, and gene activity. Researchers can now profile hundreds to thousands of metabolites in rice tissues thanks to recent developments in nuclear magnetic resonance (NMR) spectroscopy and high-resolution mass spectrometry, as well as robust bioinformatics tools (Dan et al., 2021).

2.3. The Role of Metabolomics in Rice Functional Genomics

Understanding nutritional composition, stress reactions, and flavor/aroma profiles is made possible by these metabolic fingerprints. A thorough understanding of the relationships between genotype and phenotype in rice is provided by the convergence of genomics and metabolomics. Scientists can find biomarkers that predict traits like stress adaptation and grain nutritional quality by connecting particular metabolites to their genetic determinants (Ullah et al., 2022). The production of climate-resilient, nutritionally enhanced rice varieties that are suited to producer needs and customer preferences is made possible by this integration, which is essential to the growth of precision breeding (Shende et al., 2025). By offering dynamic, quantitative snapshots of the metabolite landscape in response to genetic, developmental, and environmental changes, metabolomics plays a crucial role in bridging the gap between genotype and phenotype in rice functional genomics (Chen et al., 2021). The control of various rice traits, from stress tolerance to grain quality, has been clarified by integrated metabolomics with transcriptomics and metabolite-based QTL mapping (phytochemical genomics), providing abundant prospective pathways for breeding (Okazaki & Saito, 2016). In a rice population, for example, coupled omics analysis identified important metabolic QTLs across tissues, reassembling regulatory networks for primary and secondary metabolism and connecting candidate genes to metabolite variation(Heuberger et al., 2010).

Metabolomic analysis of tolerant and susceptible cultivars under salt circumstances in the context of stress tolerance showed distinct accumulation patterns, especially of lipids, polyamines, and phenolamides—the building blocks of adaptive reactions(Heuberger et al., 2010). Metabolomics has also uncovered compositional variety in cooked rice varieties, linking variations in bioactive compounds (such vitamin E and phenolics) to underlying SNP diversity and assisting in the direction of nutritional improvement initiatives(Horgan & Kenny, 2011). Functional genomics in rice is becoming more accurate in identifying gene functions and revealing metabolic networks essential for agronomic and nutritional features by combining metabolomic datasets with genetic, transcriptomic, and phenotypic data (Jha et al., 2025; Ullah et al., 2022).

2.4. Proteomics and Metabolomics in Precision Rice Breeding

Proteomics and metabolomics integration is essential for precision rice breeding in order to analyze complex variables like as yield, stress tolerance, and quality. By connecting metabolite profiles to field-tested results, metabolomic profiling of parental lines allows predictive modeling of hybrid performance, especially yield heterosis, and directs selection prior to costly trials starting (Dan et al., 2020). Mechanisms of drought tolerance under different nitrogen regimes have also been clarified by multi-omics techniques that combine proteomics and metabolomics with physiological features, demonstrating how protein and metabolic adaptations promote resilience under stress (Du et al., 2020). By identifying distinct patterns in protein expression, phytohormone levels, and specialized metabolites that distinguish resistant from susceptible cultivars, proteomic and metabolomic analyses have shed additional light on rice's responses to biotic pressures, including viruses and insect pests. These analyses have also provided biomarkers and molecular targets for breeding (Iqbal et al., 2021). In a larger sense, integrated omics such as genomics, In general, integrated omics—which includes transcriptomics, proteomics, metabolomics, and genomics—provide a strong foundation for comprehending how traits are regulated in ideal and stressful circumstances, hastening the identification of important breeding regulators (Shende et al., 2025).

By connecting molecular changes to agronomic performance, these methods improve precision and allow for data-driven selection techniques that improve yield stability, nutritional quality, and stress resilience in rice breeding projects while saving time and money.By detecting allergenic proteins crucial for food safety and identifying tissue-specific enzyme isoforms and regulatory mechanisms, such as those involved in starch biosynthesis, the combination of proteomic and metabolomic analyses improves our understanding of rice metabolism. The development of high-yielding, stress-tolerant, and nutritionally enhanced rice varieties to address global food security challenges is accelerating thanks to these insights, as well as advancements in genomics and analytical technologies, which are enabling more accurate phenotype prediction, improved molecular breeding strategies for yield and resilience, and quicker regulatory assessments(Razzaq et al., 2022).

3. Synergistic Use of Genomic & Metabolomic Data

3.1. Multi-omics Data Integration for Trait Prediction

Integrating multi-omics data, including transcriptomics, metabolomics, methylomics, and genomes, into trait prediction improves model accuracy and expands biological knowledge. While adding transcriptome data (G + M + T) may result in overfitting without enhancing performance, combining genomic and metabolomic data (G + M) frequently produces the strongest predictive power for parameters like yield, grain weight, and tiller number in rice (Feizi et al., 2025). The improvement in predictive accuracy achieved through the integration of genomic and metabolomic datasets for different rice traits is summarized in Table 1. Similarly, in Arabidopsis, integrative modeling across genotype, expression, and methylation datasets identified both known and unknown genes, emphasized accession-specific gene contributions, and improved predictions for flowering time and other variables. In order to create trait-relevant networks, general multi-omics integration techniques—like random forest regression in conjunction with QTL mapping (eQTL, mQTL, pQTL)—have effectively identified predictive genes, proteins, and metabolites outside of plants. With the help of developing big-data analytics and machine-learning techniques, recent studies highlight the growing significance of multi-omics integration in rice trait development by providing insights into how these integrated datasets facilitate understanding yield and stress-related features(Shende et al., 2025). An overview of the integrated genomics–metabolomics breeding framework is illustrated in Fig. 1.

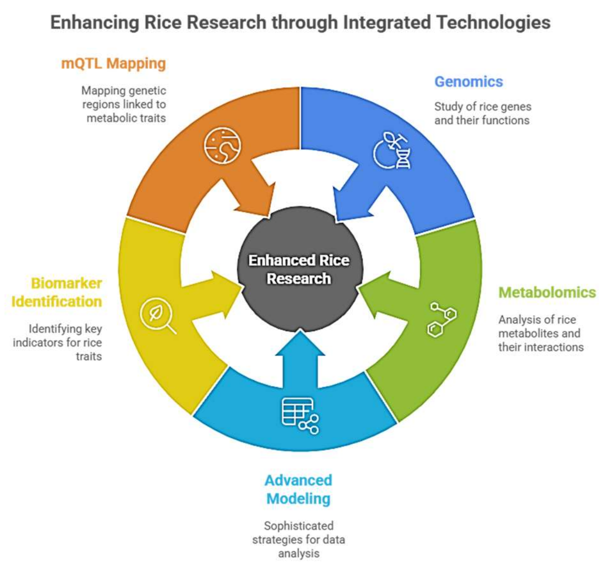

Fig. 1*:* Integrated platform that uses cutting-edge technologies, such as metabolomics, genomics, mQTL mapping, biomarker identification, and advanced modeling, to improve rice research. Improved knowledge, forecasting, and creation of desired rice features are facilitated by each element.

Note: Adapted from Razzaq et al. (2022), Dan et al. (2021), and Okazaki & Saito (2016), illustrating the integration of metabolomics, genomics, mQTL mapping, biomarker identification, and modeling in rice research.

Researchers used six models, including LASSO, BLUP, PLS, and SVM kernels, to integrate genomic and metabolomic data in a seminal work on hybrid rice. They discovered that while genomics alone worked well for high heritability variables, the predicted accuracy for hybrid yield was almost doubled when metabolite profiles were added. In simulated breeding, choosing the best hybrids solely based on metabolomic predictions resulted in an output gain of about 30% (Feizi et al., 2025). Because they function as in vivo integrative markers that represent genotype-to-phenotype cascades, metabolites most likely record the composite effect of numerous genetic networks, which accounts for their high predictive value.

3.2 Identification & Validation of Biomarkers

Developments in omics technologies and molecular diagnostics are driving the search for rice biomarkers, which are chemicals that consistently indicate characteristics like stress tolerance, quality, or genetic validity. Simple sequence repeats (SSRs) and SNP-based techniques are still essential for variety identification since they allow for the detection of adulterated rice and guarantee grain origin. High sensitivity and specificity are provided by methods like multiplex-SSR, droplet digital PCR (ddPCR), and KASP tests, which can identify varietal admixtures at concentrations as low as 1%. Reproducibility and consistency are essential for analytical validation (Xiao et al., 2022). To provide reliable biomarker quantification, reference proteins such heat shock protein (HSP) and elongation factor 1-α (eEF-1α) were verified as stable controls for western blot normalization across rice tissues and developmental phases (Vieira et al., 2022).

Important compounds—amino acids, sugars, and flavonoids—that have a substantial correlation with grain yield heterosis and quality attributes have been identified using untargeted metabolomic screens in maize and rice. As a metabolic trait marker, trehalose levels in rice grains under high night temperature (HNT) stress, for instance, slightly but significantly improved the prediction of grain width. Colocalized SNPs that affect metabolic characteristics and hyperspectral indices were found in polished rice genome-wide association studies (Jacobs et al., 2005). In order to map candidate genes within the carbohydrate and amino acid pathways linked to grain metabolism and yield traits, machine learning techniques (such as PLSR, LASSO, LGBM, RF, CNN, and SVM) assisted in filtering predictive metabolites and spectral traits. Last but not least, more accurate biomarker identification in rice systems has been made possible by integrative omics, which combines transcriptomics, proteomics, and metabolomics to uncover molecular markers connected to characteristics like stress tolerance or metabolic control (Li et al., 2011).

3.3. Advanced Modeling Strategies

In order to predict qualities like yield and stress resilience, recent studies emphasize the use of Random Forest, XGBoost, and SVM to combine genomes, transcriptomics, metabolomics, and environmental variables. These models perform better than single omics frameworks and can manage high-dimensional relationships. Through the automatic learning of structured representations from multi-modal input, deep learning (such as CNNs, LSTMs, and autoencoders) further improves performance. In comparison to PLSR or PCA-based methods, a novel architecture known as the compositional autoencoder (CAE) separates genotype-specific from environment-specific latent features, improving yield and phenology forecasts in maize by 5–10×. For soybean yield prediction, Long Short-Term Memory (LSTM) and attention-based architectures that use weather and genotype data have outperformed conventional models (Random Forest, LASSO), offering explicable insights into crucial growth times. When dealing with complicated, high-dimensional data, advanced modeling techniques offer improved performance, flexibility, and interpretability (Razzaq et al., 2022). The correct mix of ensemble learning, Bayesian approaches, XAI, or optimization techniques can improve your modeling efforts, regardless of your objectives: predictive accuracy, transparency, or model robustness.

The use of metabolomics has greatly improved our knowledge of the molecular underpinnings of rice quality, especially with regard to its nutritional content, sensory appeal, and ability to withstand stress. The complete profile of metabolites made possible by metabolomics, an emerging omics technology, provides important insights into the metabolic processes that determine the composition and qualitative attributes of rice grains.

3.4. Profiling Nutritional and Sensory-Related Metabolites

A vast range of nutritional and sensory-related metabolites, including as amino acids, sugars, organic acids, and secondary metabolites like flavonoids and phenolics, can be profiled using metabolomics. The flavor, texture, aroma, and nutritional content of rice grains are all directly influenced by these substances (Saeed et al., 2025). Researchers have created metabolic fingerprints that distinguish different types of rice according to their nutritional and organoleptic characteristics by using methods like nuclear magnetic resonance (NMR) spectroscopy, liquid chromatography–mass spectrometry (LC-MS), and gas chromatography–mass spectrometry (GC-MS) (Kusano et al., 2015). Anthocyanins, flavonoids, amino acids, and vitamins were identified as the main contributions to the nutritional quality of rice in a widely focused metabolomic analysis of 114 rice varieties (landraces vs. cultivars), which found 985 metabolites.

Potential glycosyltransferase genes that alter anthocyanins were discovered using transcriptomic integration, opening the door to better nutrition (Zhang et al., 2022). Using LC-MS to compare the metabolomics of common and glutinous rice (black and white), hundreds of metabolites were found (about 441 in black rice and about 343 in white), including seven vitamins (B3, B5, B6, and B13) and components of central metabolism like the citrate cycle and amino acids. This highlighted the nutritional differences between the two types of rice (Zhao et al., 2024). Rice breeding lines' nutritional and sensory qualities (such as digestibility and cooking quality) are driven by flavonoids, resistant starch, non-starch polysaccharides, tocopherols, and lipids, particularly in bran, according to LC-MS and multi-omics (Mumm et al., 2016). These findings are further supported by metabolite–gene networks.

3.5. Discovery of Metabolite Markers for Rice Subspecies and Quality Types:

The identification of quality-linked metabolites and the differentiation of rice subspecies—indica, japonica, and aus—have been made possible thanks in large part to metabolomics: Researchers found 3,097 metabolites in ten different types of cooked brown rice, with 763 exhibiting notable variance (Zhang et al., 2022). Using PLS-DA, metabolite profiles were clearly clustered by subspecies, identifying 194 metabolites that consistently distinguished between the indica, japonica, and aus groups PMC. Profiling 121 metabolites in mature seeds of indica and japonica cultivars showed not only varying abundances of different chemicals but also unique metabolic network associations, indicating metabolic adaption particular to subspecies and providing markers for breeding and quality (Zhou et al., 2024). These metabolite signatures not only reflect subspecies genetic diversity but also underpin traits relevant to nutritional, sensory, and agronomic quality—making them valuable targets for breeding and authentication efforts (Subramanian et al., 2024).

Additionally, metabolomics has made it easier to identify metabolite markers that can differentiate between various rice subspecies (like indica and japonica) and quality kinds (like aromatic versus non-aromatic rice). The identification of important discriminatory metabolites using untargeted metabolomic research has made it possible to precisely classify and choose rice lines with desired characteristics. For example, different concentrations of the major aroma molecule 2-acetyl-1-pyrroline (2AP) are closely linked to fragrant rice types and can be used as a molecular indicator of quality.

Table 1: Improvement in Trait Predictability with Multi-Omics Integration (Genomics + Metabolomics) (Wu et al., 2022).

Trait Type	Performance: Genomics Only	Improvement by Adding Metabolomics
High-heritability yields (rice hybrids)	Strong (~baseline)	2× improvement in predictability
Grain traits (width, size under stress)	Moderate	Modest gains via integration (for e.g., trehalose)
Derived metabolite-phenotype traits (rice core collection)	0.59 (GBLUP) for BLUP; 0.46 for metabolomics alone	Integrated models not detailed, but BLUP > metabolic alone

Note: Adapted from Wu et al. (2022), summarizing how metabolomics enhances trait predictability in rice breeding, especially for high-heritability and stress-related traits.

3.6. Metabolomic Signatures of Nutritional Differences Between Landraces and Cultivars

Different metabolomic fingerprints between contemporary cultivars and traditional landraces have been identified by comparative metabolomic analysis. Landraces frequently have higher concentrations of bioactive substances and metabolites linked to stress, which is indicative of their genetic diversity and environmental adaptation (Nam et al., 2015). These variations highlight the potential of landraces as stores of nutritional diversity and health-promoting substances that are frequently lacking in contemporary high-yielding cultivars. Secondary metabolites (anthocyanins, flavonoids), vitamins, and lipid-related substances are the main drivers of the constant nutritional differences between rice landraces and contemporary cultivars, according to metabolomic comparisons. Widely-targeted metabolomics of 114 rice accessions (35 landraces, 79 cultivars) produced a seed metabolome of approximately 985 compounds and demonstrated distinct landrace versus cultivar clustering; the main metabolites elevated in many landraces were flavonoids and anthocyanins, which accounted for a large portion of the nutritional variation. Glycosyltransferases and other putative genes associated with anthocyanin modification were also discovered using integrated transcriptome–metabolome networks from that investigation, corroborating a genetic foundation for metabolite enrichment in landraces (Gupta & De, 2017). Amino acids, sugars, and fatty-acid derivatives also vary by genotype, according to multiplatform and untargeted research. These variations impact the protein content, starch composition, and lipid profiles that support nutritional quality and processing characteristics. Functionally, these metabolomic signatures are important for breeding because, without sacrificing agronomic performance, markers derived from differential metabolites can direct selection for improved antioxidant capacity, dietary fiber interactions, and aroma/nutritional balance (Al-Khayri et al., 2023). Nevertheless, postharvest processing and environment × genotype effects alter metabolite levels, requiring integration with transcriptome loci and multi-environment validation to guarantee marker stability. In order to convert metabolite profiles from landraces into improved cultivars, recent studies recommend integrated multi-omics pipelines and focused validation (e.g., candidate enzyme tests, marker-assisted selection).

3.7. Identification of Stress-Associated Metabolites and Quality Impacts

Rice is subject to a variety of stresses, most notably salt and pathogen infection, which cause significant metabolomic changes that affect grain quality and stress resilience. 1H-NMR Five conserved markers were identified through profiling of rice root metabolites in 38 genotypes under extended moderate salinity: reduction of glutamine and alanine, accumulation of sucrose, allantoin, and glutamate (Yang et al., 2022). Growth potential and salt tolerance were positively connected with elevated glutamine and allantoin, indicating that reprogramming of nitrogen metabolism promotes survival and maybe quality preservation under stress (Pecoraro et al., 2023). Comparing salt-tolerant (Nonabokra, Bhutnath) and sensitive cultivars revealed variations in reactions to 91 identified metabolites, which included amino acids, organic acids, sugars, fatty acids, phenols, and polyols, in a distinct study that used leaf metabolomics (Chen et al., 2023). Notably, tolerant types have higher levels of gentisic acid and serotonin, suggesting functions in signaling and stress reduction.

Comparative metabolomic study has shown distinct metabolomic fingerprints between modern cultivars and traditional landraces. Because of their genetic diversity and environmental adaptation, landraces often exhibit higher amounts of bioactive chemicals and metabolites associated with stress. These differences demonstrate the potential of landraces as repositories of nutritional variety and health-promoting compounds that are often absent from modern high-yielding cultivars. Metabolomic changes brought on by stress can affect important quality metrics. Phenolic chemicals (such as ferulic and gentisic acids) might influence antioxidant activity and possible flavor profiles, whereas osmolyte buildup (such as sugars and amino acids) may change the texture and flavor of food. Hormonal and secondary metabolite changes under biotic stress could modulate aroma and nutritional value through altered phenolic and volatile profile (Li et al., 2022).

4. Integrative Approaches: Genomics Meets Metabolomics

Integrating genomics with metabolomics provides a powerful strategy for understanding the genetic basis of complex quality traits in rice. This approach enables the identification of metabolite-associated loci and regulatory networks that influence grain composition and sensory attributes (Wang, 2009). The conceptual relationship between genomics, metabolomics, data synergism, and modeling strategies is depicted in Fig. 2.

4.1. Strategies for Data Integration

Conceptually, effective data integration techniques fall into three categories: late (model-level), intermediate (latent/representation-based), and early (concatenation). For downstream modeling (which is straightforward but sensitive to size and missing data), early integration combines preprocessed features from many modalities into a single matrix; late integration fits distinct models for each modality and combines their results (Chen et al., 2014). Intermediate methods frequently strike the optimal balance between interpretability and performance by learning joint latent representations that capture both shared and view-specific variation. Unsupervised discovery of biological axes is made possible by latent-factor and matrix-factorization techniques, which estimate a limited number of hidden factors that account for covariance across omics layers (technical factors can be described explicitly). Prior to grouping or association testing, these techniques are particularly helpful for exploratory studies and dimensionality reduction (Handoko et al., 2011).

When the objective is the finding of biomarkers associated with known classes, supervised latent-component techniques like DIABLO (mixOmics) are excellent because they use discriminant analysis across datasets to choose feature panels that jointly discriminate phenotypes. DIABLO creates compact, multi-modal signatures by enforcing covariance between feature sets during variable selection. In addition to being excellent at patient/sample stratification and subtype discovery, network fusion is resilient to noise and heterogeneous feature scales (Kumar et al., 2015).

Although they necessitate meticulous regularization and frequently larger sample sizes, machine-learning and deep multi-view techniques such as autoencoders, graph neural nets, canonical correlation analysis (CCA) variants, and multi-view kernels can integrate very high-dimensional data and learn complex non-linear cross-modal relationships (Liu et al., 2020). No single approach dominates all tasks, according to comparative benchmarks; the selection should be in line with the objectives of the study and the size of the sample. Genomic tools such as GWAS and QTL mapping are combined with metabolomic profiling to dissect the biochemical basis of grain quality (Swamy et al., 2016). For example, linked natural variation in rice metabolites with genomic loci using metabolite-based GWAS, offering insights into biosynthetic pathways. This approach enables breeders to select rice varieties with better nutritional and sensory properties using genetic markers (Okazaki & Saito, 2016).

4.2. Metabolite–Gene Correlation Networks

A comparison of transcriptomics and metabolomics during germination between landraces and cultivars produced 1,982 differentially expressed genes (DEGs) and 358 differentially accumulated metabolites (DAMs). Metabolite–gene correlation networks identified potential genes associated with structural changes in anthocyanins, particularly glycosyl-transferases (Wang et al., 2012). By bridging the gap between metabolite variations and gene function, functional tests validated the roles of these enzymes. 42 metabolites and 101 genes were found to be associated when metabolomic and transcriptome data were integrated using Pearson correlation (PCC > 0.9) in rice grains. Key pathways such as carbon, lipid, amino acid, phenylpropanoid, hormone signaling, and oxidative phosphorylation were covered by networks, shedding light on the regulatory relationships influencing grain quality. Using Pearson correlation (PCC>0.9) to integrate transcriptome and metabolomic data in rice grains, 42 metabolites and 101 genes were shown to be associated (Yang et al., 2021).

The networks revealed regulatory relationships influencing grain quality and covered important pathways such as carbon, lipid, amino acid, phenylpropanoid, hormone signaling, and oxidative phosphorylation.

The reaction of rice to the root-knot nematode A combination of transcriptome and metabolome analysis was used to study Meloidogyne graminicola. The resistant variety ZH11 exhibited elevated levels of flavonoid metabolites, including quercetin, kaempferin, and apigenin, which mirrored the activation of genes involved in flavonoid production (Yang et al., 2021). The coordinated response between genes and metabolites during defense was demonstrated by correlation networks. Network analysis helps uncover gene–metabolite relationships. Correlation-based methods (e.g., Spearman, sparse CCA) are used to build networks, while causal models like G-DAG trace regulatory pathways from gene to metabolite (Safo et al., 2018). These networks help identify key regulatory genes, which can be targeted to improve rice grain quality.

4.3. mQTL Mapping

In order to connect metabolic characteristics to genetic variation, metabolite QTL (mQTL) mapping looks for genomic loci that affect metabolite abundance. The genetic architecture of grain metabolomes in rice has been clarified by mQTL investigations, which have provided targets for breeding nutritional and quality traits as well as hotspots for particular metabolite classes. Metabolite-based QTL (mQTL) mapping identifies loci controlling the accumulation of key metabolites. Recent studies have used meta-QTL analysis to refine genomic regions associated with rice quality traits like aroma, amylose content, and protein composition (Feizi et al., 2025). The identification of potential loci supporting desired nutritional profiles is one way that mQTL results support marker-assisted selection. For example, breeding for flavor, antioxidant capacity, or digestibility might be guided by metabolic hotspots for flavonoids or amino acids.

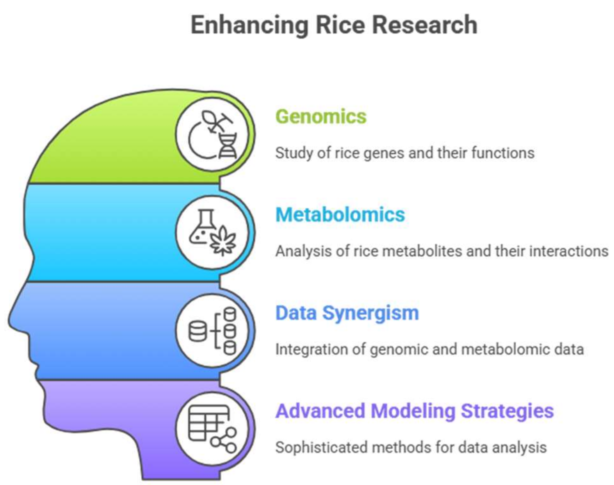

Fig. 2: Conceptual representation of how improved modeling techniques, data synergism, metabolomics, and genomics might improve rice research. Each element stands for a crucial layer in the comprehension, integration, and analysis of rice metabolic and genetic data for better trait development.
Notes: Inspired by Feizi et al. (2025), Shende et al. (2025), and Zhao et al. (2024), showing how multi-omics and advanced modeling enhance rice trait prediction and integration.

Multiple QTL investigations are combined in meta-QTL (MQTL) analysis to improve discovery robustness and fine-tune locus placements. Examples include MQTLs for iron and zinc concentrations, where 90 documented QTLs merged into 22 genomic areas of refined rice, with up to 75% fewer confidence ranges. Likewise, MQTL mapping of drought-tolerance traits across 563 QTLs revealed 61 stable MQTLs, emphasizing putative genes and narrowing areas, many of which are environment-conservative (Sun et al., 2021). For distinct inheritance patterns, bi-parental populations (such as recombinant inbred lines) continue to be the norm in mQTL mapping. sophisticated genotyping (such as sequence-based, high-density SNPs. In breeding programs these loci can be used to select for desired traits more efficiently

4.4. Enhancing Prediction with Multi-Omics

Integrating transcriptomics, metabolomics, and genomics improves trait prediction. In this used hyperspectral imaging, metabolomic data, and GWAS to identify candidate genes for lipid and flavonoid metabolism, validated by gene editing. This integrative framework supports marker-assisted selection and the development of rice varieties with superior nutritional and sensory profiles(Feng et al., 2025). The workflow of multi-omics integration for marker development and trait prediction is presented in Fig. 3. By capturing the multi-layered biological processes driving phenotypic variation, the integration of multi-omics datasets—such as transcriptomics, proteomics, metabolomics, and genomics—improves the predictive accuracy for complex traits in rice. For variables like grain production, quality, and stress tolerance, in particular, genomic selection models that incorporate transcriptomic and metabolomic indicators perform better than single-omics techniques. By integrating heterogeneous omics data, machine learning methods like random forests and deep neural networks might enhance breeding population trait prediction (Zhao et al., 2024). Additionally, by identifying molecular biomarkers associated with desired phenotypes, multi-omics frameworks provide genomic and marker-assisted selection procedures. Breeding for climate resilience and nutritional quality in rice can be accelerated by researchers using high-resolution genotyping data in conjunction with metabolite profiles and gene expression patterns to more accurately predict trait performance across settings.

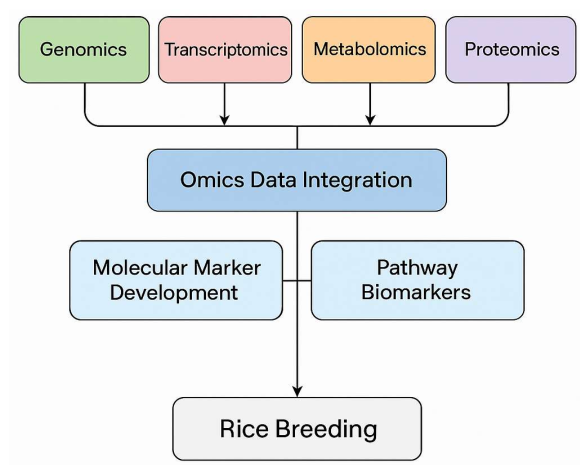

Fig. 3: Process flow showing how to combine many omics techniques (genomics, transcriptomics, metabolomics, and proteomics) to create molecular markers and pathway biomarkers for rice breeding. Integrating omics data speeds up the creation of better rice cultivars and permits accurate trait mapping.

Note*:* Based on Zhang et al. (2022), Chen et al. (2014), and Feng et al. (2025), depicting the role of GWAS, QTL mapping, and metabolomics in identifying biochemical markers and genes for rice quality traits.

5. Case Studies in Rice Quality Trait Improvement

5.1. Nutritional Quality Enhancement

Differently pigmented rice (black, red, and white) was profiled transcriptomically and proteomically. This revealed the roles of important enzymes (CHI, F3H, ANS) and metabolites (naringenin, dihydroquercetin, and cyanidin) in pigmentation and nutritional value. A gene–metabolite co-expression network during seed germination showed correlations between candidate genes including PAL, CHI, and 3GT and flavonoid metabolites like procyanidin A3 and malvidin (Yang et al., 2022). The function of five glycosyltransferases in catalyzing anthocyanin glucosides was functionally verified, showing their significance in nutritional quality (Yazdani et al., 2018). mQTL mapping is another complimentary method that links metabolic characteristics to genetic locations. Recombinant inbred lines were used for QTL analysis, which revealed three QTLs for protein content and seventeen for amino acid content. Specifically, when present together, two unique QTLs—qAAC6.1 and qAAC7.1—significantly boosted the amount of amino acids (Salari et al., 2021). The ability of targeted genetic selection to improve nutrition was established by near-isogenic lines with these advantageous alleles, which showed improved nutrient profiles. The foundation for varietal biofortification was laid by a subsequent investigation into aromatic rice germplasm that found QTLs linked to protein, amylose, iron, and zinc content (Mao et al., 2020). The breeding potential via ploidy manipulation was further highlighted by comparisons between autodiploid and autotetraploid rice, which revealed that tetraploid seeds contain higher levels of flavonoids, such as hesperidin, naringenin, and others—compounds linked to antioxidant and anti-inflammatory benefits.

5.2. Sensory and Physical Quality Traits

Phospholipids are strong markers for geographic discrimination, exceeding sugars and fatty acids in predicting accuracy, according to untargeted metabolomics of white rice from China and Korea. Complex metabolic patterns influenced by genotype and storage circumstances were revealed by multi-platform metabolomics spanning fragrant (e.g., basmati, jasmine) and non-fragrant rice types (Li et al., 2022). Although distinct biochemical differences were noted, overlapping metabolite patterns make reliable germplasm classification difficult.

Further, metabolomic profiling revealed that lysophosphatidylcholine and free fatty acids were elevated, whereas sugars, flavonoids, amino acids, and phenolics were downregulated. These changes demonstrated how metabolic reprogramming directly affects physical quality attributes, as they showed a substantial correlation with chalkiness, grain weight, and head rice yield (Mumm et al., 2016). A pilot study that characterized six high-eating-quality rice types using GC-IMS and texture analysis to record volatile profiles on the sensory front. Among the 39 primary volatiles, stickiness associated with 5-methyl-2-furanmethanol and dimethyl trisulfide, while hardness connected positively with E-2-hexenal, 2-hexanol-monomer, 1-propanol, and E-2-pentenal, connecting physical mouthfeel to aromatic chemicals. Additionally, by comparing fragrant (like basmati and jasmine) and non-fragrant rice varieties, a multi-platform metabolomics study identified metabolite variables that define fragrance and flavor profiles, demonstrating the biochemical complexity that underlies sensory quality.

5.3. Stress Resilience and Quality Maintenance

Resilience and quality maintenance under stress were indicated by increased levels of antioxidant-related metabolites, including sinapate, benzoate, glucuronate, ribitol, threitol, and threonine. In rice cultivars with high phosphate utilization efficiency (PUE), efficient lines maintained photosynthetic performance under P deficiency by modifying their metabolite profile (Xiang et al., 2023). These phenotypic advantages were linked to particular metabolite patterns: stable or increased grain levels of lactose, nicotinoylcholine, sucrose (m150), choline, and lactose, together with decreased levels of several stress-response metabolites (e.g., m72, m98). Even in situations where water is scarce, the synthesis of starch, protein, and phenolics is supported by metabolic pathways such as the metabolism of galactose, glycine-serine-threonine, and starch and sucrose (Wan et al., 2019). Metabolite markers were found in developing seeds and flag leaves in a different example that focused on combined drought and heat stress in several cultivars. In several organs, the baseline levels of compatible solutes such as glucose, fructose, raffinose, and 1-kestose were greater in tolerant cultivars (e.g., N22, Dular). Conversely, spikelets from sensitive cultivars (like Anjali) had higher levels of the polyamines putrescine and spermidine, which rose even more under stress and were associated with decreased resilience (Carey et al., 2019). Three seed metabolites (A237001, A237002, and ribitol) stood out in particular because they were early predictors of grain quality degradation, and their constitutive levels in flag leaves positively linked with an increase in the chalky grain fraction under stress.

6. Harnessing Omics for Molecular Marker Development and Pathway Biomarkers in Rice Breeding

Through the use of metabolite predictors for accurate phenotyping, marker-assisted selection (MAS), and their smooth integration into high-throughput breeding pipelines, molecular markers and pathway biomarkers produced from omics research have completely changed rice breeding. The creation of high-yielding, stress-resistant, and quality-enhanced rice cultivars has been sped up by these developments (Jena & Mackill, 2008). The application of genomics and metabolomics for rice quality trait improvement is illustrated in Fig. 4.

6.1. Omics-Driven Molecular Marker Development

In order to identify and map the genes linked to important agronomic features in rice, a large body of biological data has been produced by the development of genomics, transcriptomics, proteomics, and metabolomics (Ontoy & Ham, 2024). Genes that confer resistance to biotic and abiotic stressors, as well as yield and grain quality attributes, were precisely localized thanks to the completion of the rice genome sequencing (Jena & Mackill, 2008). Molecular markers have been used to map genes closely associated with features like increased grain quality, bacterial blight tolerance, blast resistance, submergence, and salinity tolerance (Jena & Mackill, 2008). In rice breeding projects, marker types such RFLP, SSR, SNP, and other PCR-based techniques are frequently employed.Target genes can be effectively monitored throughout breeding cycles thanks to MAS. Major gene or QTL integration into elite rice varieties has been made possible by MABC; noteworthy examples include improved cultivars that were released in Indonesia due to their high yield, stress tolerance, and higher nutritional quality (Jena & Mackill, 2008). Additionally, MAS makes it easier for several resistance genes to stack together (gene pyramiding), which produces long-lasting and broad-spectrum resistance to infections and pests (Jena & Mackill, 2008). Targeting complicated qualities like illness resistance and stress tolerance makes this strategy particularly effective. Precision and speed have significantly increased because to molecular techniques, particularly Marker-Assisted Selection (MAS).

Multiple QTLs from donor parents can be efficiently introgressed into elite cultivars in a few generations through the use of marker-assisted backcrossing (MABC). Researchers employed KASP SNP markers in MAS to accurately pyramid drought- and nitrogen-related QTLs (qDT3.9, qDT6.3, qGY1, qSF8) into the elite variety HHZ in a groundbreaking study. The resulting pyramided lines, like as PL6 and PL36, showed markedly better resistance to drought and low nutrients without sacrificing grain quality or yield.

Stepwise transfer (one gene at a time), simultaneous transfer (many genes), and a hybrid strategy combining both for quick fixation and low linkage drag are common pyramiding techniques.

6.2. Pathway Biomarkers and Metabolite Predictors for Accurate Phenotyping

Omics techniques include metabolite-based indicators for increased phenotyping accuracy in addition to DNA-level variation. Genetic loci governing metabolite accumulation in rice grains have been identified by Metabolome Quantitative Trait Loci (mQTL) investigations. Breeders can select for desired metabolic profiles associated with yield, nutritional value, and stress resilience by identifying mQTL hotspots. For instance, flavonoid glycosylation characteristics are highly genetically determined (Matsuda et al., 2012). Integrating proteomics, metabolomics, transcriptomics, and genomes provides a comprehensive understanding of intricate features and regulatory networks. OsPIL1, for instance, was found to be a transcription factor that controls growth, grain development, and blast resistance by coordinating the regulation of downstream genes and metabolites (Zhao et al., 2024). Certain metabolites, including vitamin E, trigonelline, and linolenic acid, function as pathway indicators for nutritional characteristics, pathogen resistance, and grain size (Zhao et al., 2024). The accuracy and speed of trait evaluation are increased by these direct molecular readouts. Metabolic data outperformed genetic data alone in predicting hybrid performance for yield-related variables.

Compared to genomic-only models, metabolomic models in one study nearly quadrupled hybrid yield predictability, and predictive ability rose by up to 13.6% when specific metabolic markers were used. Grain-width prediction benefited slightly from metabolic profiling under high night-temperature stress. Although genomic prediction performed better than metabolic models, accuracy for grain width and perimeter traits was increased by integrating the two datasets (genomic + metabolite) (Steinfath et al., 2010). Because they represent both genetic and physiological states, metabolites are powerful predictors of phenotypic features in agricultural plants. Strong correlations between metabolite profiles and 10 of the 17 grain-quality characteristics, including amylose ratio, were found in rice using untargeted metabolomics across wild cultivars. This allowed for reliable trait predictions that applied to different independent trials and fields.

6.3. Integration into High-Throughput Breeding Pipelines

Early hybrid performance prediction is made possible by genomic selection models that incorporate multi-omic datasets (genomic, transcriptomic, metabolomic, and phenotypic data), frequently prior to field experiments. Predictive accuracy for yield-related characteristics is further improved by using parental phenotypic data (Xu et al., 2021). Rapid target marker screening is made possible by high-throughput genotyping platforms, and large-scale, effective evaluation of complex traits is made possible by phenotyping technologies in conjunction with omics-based biomarkers (Sehgal et al., 2023). Prioritizing candidate genes in rice entails employing integrative techniques to identify possibly causative genes inside QTLs or GWAS regions. 206 high-priority genes, including transcription factors from MADS-box, WRKY, MYB, and other families, were extracted from 99 yield-related QTLs using an efficient workflow that integrated several omics sources, including sequence variation, gene expression, functional annotations, co-expression, and protein–protein interactions (Hu et al., 2018). With a candidate gene reduction of almost 21 times, validation revealed that LRR family protein (LOC_Os03g28270) and cytochrome P450 (LOC_Os02g57290) were important candidates underpinning grain- and panicle-length QTLs GL1 and pl2.1, respectively.

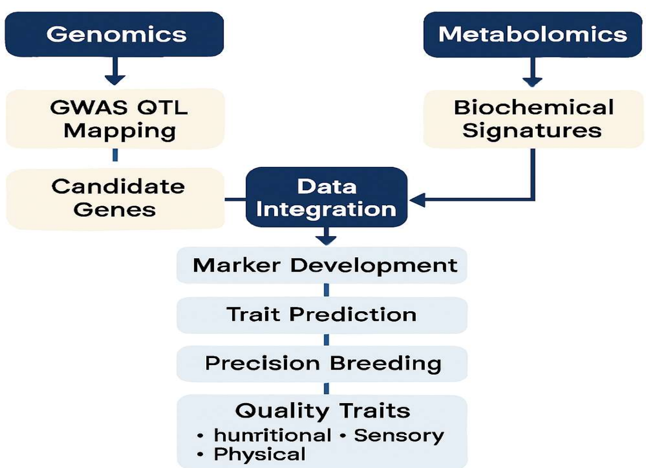

Fig. 1.3: An illustration of how to use genetics and metabolomics to improve rice quality traits. While metabolomics finds important biochemical markers connected to physical, sensory, and nutritional characteristics, genomic techniques like genome-wide association studies (GWAS) and QTL mapping find potential genes. Molecular marker creation, predictive modeling, and targeted breeding for superior rice cultivars are made possible by combined multi-omics data.
Note: Adapted from Zhang et al. (2022), Feng et al. (2025), and Chen et al. (2014), illustrating the integration of genomic and metabolomic data for precision breeding and trait enhancement in rice.

Another powerful strategy focused candidate genes using QTL data and gene functions generated from sequencing and expression information: gene lists were ten times smaller when prioritizing was based on the over-representation of biological processes. When compared to fine-mapping and GWAS datasets, this approach showed statistical and biological relevance. Integrated multi-omics workflows narrow down candidate genes underlying major QTLs, reducing the validation workload and focusing on the most promising targets for yield improvement (Keerthi et al., 2024). In contemporary rice breeding pipelines, MAS and omics-driven selection are now commonplace elements. Higher production potential, enhanced stress tolerance, greater grain quality, and increased market value are all displayed by rice varieties created using these techniques (Xu et al., 2021).

7. Challenges and Future Perspectives

The conversion of sensory attributes like flavor, texture, and scent into measurable omics characteristics is still very difficult because human sensory reactions are subjective by nature and impacted by contextual and psychological variables. Correlated substances are frequently found using metabolomics; nevertheless, sensory-guided methods and reconstitution studies are necessary to confirm causal relationships (Kusano et al., 2011). Additionally, trait-associated biomarkers are susceptible to fluctuation across locations and seasons due to the high sensitivity of metabolite profiles to environmental conditions, including as temperature, soil type, water status, and post-harvest treatment. In order to find stable, heritable biochemical indicators, multi-environment trials are necessary (Sampaio et al., 2016).

Transcriptomics, proteomics, metabolomics, and epigenomics are several omics layers that can be integrated to uncover pathway-level regulation and close the gap between genotype and phenotype, However, there are still difficulties in bringing disparate scales, dynamic ranges, and missing values into harmony (Ullah et al., 2022). In order to predict traits, machine learning (ML) advances provide strong tools for integrating heterogeneous omics data, capturing complex interactions and non-linear correlations. The creation of explainable models to aid with breeding decisions, strong feature selection, and access to huge, carefully curated datasets are necessary for machine learning to succeed (Nam et al., 2024).

8. Conclusion

Molecular markers, pathway biomarkers, and metabolite signatures associated with yield, quality, and stress resilience have all been identified thanks to the combination of genomics and metabolomics, which has greatly improved our capacity to analyze complex agricultural attributes. These methods have improved cultivar development and shortened breeding cycles by speeding up marker-assisted selection, making it easier to find new alleles, and increasing phenotyping precision (Gupta & De, 2017). Present-day successes—like metabolite-based predictive models, flavoromics-informed quality improvement, and multi-environment metabolite QTL mapping—showcase the usefulness of this integration in contemporary breeding initiatives.

Proteomics, transcriptomics, and epigenomics should be added to multi-omics integration in future studies to provide a more comprehensive understanding of genotype-phenotype interactions(Y. Chen et al., 2023). Standardized phenotyping procedures, machine learning-based data integration, and high-throughput metabolite profiling will all be crucial for forecasting trait performance in a variety of settings (Zhao et al., 2024). Ultimately, there is a lot of potential for speeding up the creation of high-quality, climate-resilient crop varieties that meet the needs of both producers and consumers thanks to the combination of genomes and metabolomics and strong computational frameworks (Chen et al., 2023).

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