Plant Science Review

PLANT SCIENCE REVIEW

ISSN No: 3041-7279

Review Article

Journal homepage: https://psr.crcjournals.org/

Check for updates

Transcriptomics and Metabolomics as Integrative Tools for Modern Plant Breeding Programs

Madhuri Arya

Department of Plant Breeding and Genetics, TCA, Dholi (RPCAU, Pusa), India

Received 28 July 2021 | Revised 14 August 2021 | Accepted 12 September 2021 | Available Online 02 October 2021

*Corresponding Author: **Madhuri Arya** | Email Address: **madhuriaryatca@gmail.com**

Citation: Madhuri Arya (2021). Transcriptomics and Metabolomics as Integrative Tools for Modern Plant Breeding Programs. ***Plant Science Review***. **DOI: https://doi.org/10.51470/PSR.2021.02.02.01**

Abstract

Modern plant breeding faces unprecedented challenges driven by climate change, population growth, and the demand for sustainable agriculture. While traditional breeding and molecular marker technologies have significantly advanced crop improvement, the integration of high-throughput omics approaches provides new opportunities to accelerate genetic gains. Transcriptomics and metabolomics, in particular, serve as powerful complementary tools to unravel gene expression patterns and metabolic networks underlying complex agronomic traits. Transcriptomics reveals regulatory pathways through genome-wide gene expression profiling, while metabolomics captures the biochemical end-products of these processes, offering a direct link between genotype and phenotype. Together, these tools enable breeders to identify candidate genes, biomarkers, and metabolic signatures associated with stress tolerance, yield stability, and nutritional quality. This review highlights the applications of transcriptomics and metabolomics in plant breeding, including stress-resilience improvement, nutritional enhancement, and marker discovery. It further discusses integrative frameworks such as multi-omics analysis, systems biology, and machine learning to translate omics data into practical breeding pipelines. Challenges such as high costs, data complexity, and limited field validation are acknowledged, alongside future prospects for precision breeding and climate-resilient agriculture.

Keywords: *transcriptomics, metabolomics, plant breeding, systems biology, multi-omics integration, stress tolerance, biomarkers, crop improvement*

1. Introduction

The twenty-first century presents critical challenges for global agriculture, including climate variability, biotic and abiotic stresses, land degradation, and the need to feed an ever-growing population. Traditional breeding approaches have delivered remarkable success in developing improved crop varieties, but they are often time-consuming and limited in their ability to dissect complex traits governed by multiple genes and environmental interactions. Molecular marker technologies such as quantitative trait loci (QTL) mapping and genome-wide association studies (GWAS) have improved breeding precision, yet they provide only partial insights into the dynamic regulation of plant traits [2], omics technologies have emerged as transformative tools. Among them, transcriptomics and metabolomics are particularly promising because they capture different but interconnected layers of plant biology. Transcriptomics offers a snapshot of gene activity, revealing the networks that regulate physiological responses [2]. Metabolomics, on the other hand, identifies the small-molecule metabolites that act as functional intermediates and final products of gene expression, thus linking genotype to phenotype more directly. By combining these two approaches, breeders can obtain a holistic understanding of trait architecture, enabling the identification of novel biomarkers and breeding targets.This review discusses the role of transcriptomics and metabolomics in modern breeding programs, their integration with other omics and breeding tools, key applications in stress resilience and nutritional quality, and the future prospects of these technologies in precision agriculture.

Table 1. Applications of Transcriptomics in Plant Breeding

Trait/Target	Crop Examples	Transcriptomic Insights	Breeding Application
Drought tolerance	Rice, Wheat, Maize	Differential expression of DREB, NAC, aquaporins	Marker discovery for drought-resilient lines
Disease resistance	Tomato, Soybean	Pathogen-induced defense gene expression	Identification of resistance genes/QTLs
Yield-related traits	Cereals (maize, rice)	Regulation of starch biosynthesis, flowering genes	Gene-based selection for yield stability
Nutritional enhancement	Rice, Cassava	Upregulation of carotenoid biosynthesis genes	Development of biofortified varieties

Table 2. Applications of Metabolomics in Plant Breeding

Trait/Target	Crop Examples	Key Metabolites Identified	Breeding Application
Nutritional quality	Maize, Tomato, Rice	Carotenoids, flavonoids, anthocyanins	Biofortification for improved nutrition
Abiotic stress tolerance	Wheat, Sorghum	Proline, glycine betaine, antioxidants	Selection of stress-tolerant cultivars
Biotic stress resistance	Potato, Arabidopsis	Phenolics, alkaloids, terpenoids	Metabolite markers for pest/pathogen resistance
Quality traits	Tomato, Grapes	Sugars, volatiles, aroma compounds	Breeding for flavor and postharvest quality

Table 3. Integration of Transcriptomics and Metabolomics in Breeding Pipelines

Approach	Example Application	Outcome
Transcript–metabolite correlation	Linking drought-induced transcription factors with proline accumulation	Identification of stress biomarkers
eQTL–mQTL mapping	Combining expression QTLs and metabolite QTLs in maize	Pinpointing candidate genes for stress tolerance
Systems biology networks	Integration in rice and Arabidopsis	Revealed regulatory hubs for stress resilience
Machine learning models	Predicting yield under stress using multi-omics datasets	Improved accuracy of selection in breeding

2. Transcriptomics in Plant Breeding

Transcriptomics, the study of RNA transcripts, provides insights into gene activity under specific developmental stages or environmental conditions [3].

2.1 Applications in Stress Tolerance

- **Abiotic stress:** Transcriptome profiling has identified drought-responsive genes such as dehydrins, aquaporins, and transcription factors (e.g., DREB, NAC). These markers help breeders target genetic variation for stress tolerance.
- **Biotic stress:** Pathogen-induced transcriptome shifts reveal resistance genes, secondary metabolite pathways, and defense-related transcriptional regulators.

2.2 Yield and Developmental Traits

Transcriptome studies reveal gene expression patterns linked to flowering time, grain filling, and biomass accumulation. For example, differential expression of starch biosynthesis genes in cereals has been used to enhance yield stability [4].

2.3 Marker Discovery

RNA-sequencing facilitates the discovery of single nucleotide polymorphisms (SNPs) and expression QTLs (eQTLs), which can be used in marker-assisted or genomic selection.

3. Metabolomics in Plant Breeding

Metabolomics analyzes plant metabolites, the biochemical products that reflect both genetic makeup and environmental influences.

3.1 Nutritional Enhancement

Metabolite profiling has been widely applied to improve crop nutritional quality. For instance, carotenoids and flavonoids have been metabolically engineered in maize and tomato for biofortification.

3.2 Stress-Related Metabolites

Compatible solutes (proline, glycine betaine), antioxidants, and secondary metabolites (phenolics, alkaloids) are key metabolic markers of abiotic and biotic stress responses. Their identification enables breeding of stress-resilient cultivars [5].

3.3 Quality Traits

Metabolomics supports the improvement of flavor, aroma, and postharvest quality. For example, sugar and volatile compound profiling in fruits informs breeding programs for consumer-preferred varieties [6].

4. Integrating Transcriptomics and Metabolomics

Individually, transcriptomics and metabolomics provide valuable insights into plant biology, but their integration creates a powerful framework for modern breeding programs. Together, they enable researchers to move beyond single-layer observations and gain a systems-level understanding of how genes, pathways, and metabolites interact to shape complex agronomic traits.One important application is systems biology, where transcript and metabolite data are jointly analyzed to uncover regulatory gene–metabolite networks [7]. For instance, correlation analyses have revealed how drought-induced transcription factors influence the biosynthesis and accumulation of metabolites such as proline and antioxidants, which act as protective molecules under stress. Such network-based approaches identify both upstream regulators and downstream metabolic signatures, offering dual entry points for targeted breeding.

The use of multi-omics pipelines has further expanded the scope of plant improvement. By integrating transcriptomics, metabolomics, and genomic approaches such as genome-wide association studies (GWAS) and quantitative trait loci (QTL) mapping, researchers can identify not only causal genes but also the biochemical pathways that directly influence stress tolerance, yield stability, or nutritional quality [8]. This holistic perspective provides a stronger foundation for marker development and candidate gene validation compared to single-omics studies, machine learning and artificial intelligence tools are increasingly being employed to handle the complexity of multi-omics datasets. Predictive models trained on transcriptomic and metabolomic signatures can forecast phenotypic outcomes such as yield under drought or nutrient efficiency. These computational approaches enhance the precision of breeding decisions, helping breeders prioritize genotypes with the greatest potential for field success.

5. Challenges in Applying Omics to Breeding

Despite the promise, several limitations hinder widespread adoption:

- **Cost and infrastructure:** High-throughput sequencing and metabolite profiling remain expensive for large-scale breeding programs.
- **Data complexity:** Multi-omics datasets are large and computationally demanding, requiring bioinformatics expertise.
- **Environment-dependent variation:** Gene expression and metabolite accumulation vary under different conditions, complicating reproducibility.
- **Field validation gap:** Many discoveries remain at the laboratory stage, with limited translation into real-world breeding pipelines [9].

6. Future Perspectives

Future advancements in plant breeding will increasingly rely on the seamless integration of omics technologies with field-level applications. One of the most promising directions is the development of high-throughput phenotyping systems that can be directly linked with transcriptomic and metabolomic datasets, enabling faster and more precise selection of superior genotypes. To ensure the practical value of omics-based discoveries, greenhouse-to-field pipelines will play a central role in validating transcriptomic and metabolic markers under realistic agricultural conditions [10]. At the molecular level, CRISPR-Cas genome editing offers an unprecedented opportunity to functionally validate candidate genes identified through omics approaches, thereby bridging the gap between discovery and application. Moreover, the future of plant breeding lies in pan-omics platforms, where transcriptomics, metabolomics, proteomics, and epigenomics are analyzed collectively to capture the full complexity of plant responses to environmental challenges. To handle the vast datasets generated by these platforms, artificial intelligence and machine learning models will become indispensable, transforming raw omics data into actionable breeding targets with predictive accuracy [11]. Together, these innovations will not only accelerate crop improvement but also ensure that modern breeding strategies remain sustainable, resilient, and adaptive to climate change.

7. Conclusion

Transcriptomics and metabolomics have emerged as transformative tools in modern plant breeding, bridging the gap between genotype and phenotype. Transcriptomics provides a window into regulatory networks, while metabolomics reflects the biochemical fingerprints of plant adaptation and productivity.

When integrated, these approaches enhance the ability to identify biomarkers, dissect complex traits, and accelerate crop improvement. While challenges related to cost, data management, and field validation remain, advances in computational biology, systems integration, and genome editing promise to overcome these barriers. Ultimately, the strategic use of transcriptomics and metabolomics will be essential to developing resilient, nutritious, and high-yielding crop varieties capable of sustaining global food security in a changing climate.

References

1. Yandeau-Nelson, M. D., Lauter, N., &Zabotina, O. A. (2016). Advances in metabolomic applications in plant genetics and breeding. *CABI Reviews*, (2015), 1-15.

2. Alseekh, S., Bermudez, L., De Haro, L. A., Fernie, A. R., &Carrari, F. (2018). Crop metabolomics: From diagnostics to assisted breeding. *Metabolomics*, *14*(11), 148.

3. Choi, H. K. (2019). Translational genomics and multi-omics integrated approaches as a useful strategy for crop breeding. *Genes & Genomics*, *41*(2), 133-146.

4. Kumar, R., Bohra, A., Pandey, A. K., Pandey, M. K., & Kumar, A. (2017). Metabolomics for plant improvement: status and prospects. *Frontiers in Plant Science*, *8*, 1302.

5. Zivy, M., Wienkoop, S., Renaut, J., Pinheiro, C., Goulas, E., &Carpentier, S. (2015). The quest for tolerant varieties: the importance of integrating "omics" techniques to phenotyping. *Frontiers in plant science*, *6*, 448.

6. Arbona, V., Manzi, M., de Ollas, C., & Gómez-Cadenas, A. (2013). Metabolomics as a tool to investigate abiotic stress tolerance in plants. *International journal of molecular sciences*, *14*(3), 4885-4911.

7. Zabotina, O. A. (2013). Metabolite-based biomarkers for plant genetics and breeding. In *Diagnostics in plant breeding* (pp. 281-309). Dordrecht: Springer Netherlands.

8. Fernie, A. R., &Keurentjes, J. J. (2011). Genetics, genomics and metabolomics. *Annual Plant Reviews Volume 43: Biology of Plant Metabolomics*, *43*, 219-259.

9. Misra, B. B., Langefeld, C., Olivier, M., & Cox, L. A. (2019). Integrated omics: tools, advances and future approaches. *Journal of molecular endocrinology*, *62*(1), R21-R45.

10. Sumner, L. W., Lei, Z., Nikolau, B. J., & Saito, K. (2015). Modern plant metabolomics: advanced natural product gene discoveries, improved technologies, and future prospects. *Natural product reports*, *32*(2), 212-229.

11. Khalid, N., Aqeel, M., & Noman, A. (2019). System biology of metal tolerance in plants: an integrated view of genomics, transcriptomics, metabolomics, and phenomics. *Plant Metallomics and Functional Omics: A System-Wide Perspective*, 107-144.