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RECEIVED 09 December 2024  
ACCEPTED 16 December 2024  
PUBLISHED 07 January 2025

CITATION  
Naqvi RZ, Mansoor S and Amin I (2025)  
Editorial: Omics approaches to improve crops  
yields. *Front. Sustain. Food Syst.* 8:1541973.  
doi: 10.3389/fsufs.2024.1541973

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# Editorial: Omics approaches to improve crops yields

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## KEYWORDS

omics, genomics, metagenomics, transcriptomics, biotechnological application, crop plants, sustainable agriculture

## Editorial on the Research Topic Omics approaches to improve crops yields

Enhancing crop yield and superior traits is crucial in developing better crop varieties to address climate change and various environmental and biological challenges. Global warming driven by climate change can lead to a rise in insect pests and plant diseases, posing a risk to crop productivity (Pixley et al., 2023). Crop breeding is useful to improve crops yields and favorable traits, nevertheless, the introduction of modern biotechnological procedures and omics disciplines in conventional breeding widens the available tools to speed up the breeding programs (Naqvi et al., 2022). Recent decades have seen significant growth in omics technologies, driven by advancements in next-generation sequencing (NGS), and bioinformatics data analysis algorithms owing to abundance of biological data. The leading omics toolkit include genomics, transcriptomics, proteomics, and metabolomics. Several crop species' genomes have been successfully sequenced, and crucial genes linked to economic characteristics are now known. These genes reveal crop trait regulatory mechanisms and provide practical basis for molecular breeding (Naqvi et al., 2024). The focus of the current Research Topic was to illuminate the utilization of latest omics technologies for exploration of crops' genetic insights and identification of more important genes that will be helpful to develop climate-smart crops leading to zero hunger on the planet.

Zhan et al., investigated the molecular mechanisms triggering the phenotype variations among two diploid and autopolyploid varieties of banana by using transcriptomics. The researchers acquired non-chimeric autotetraploid plants from diploid banana "Pisang Berlin," that exhibits resistance to Fusarium wilt. The autotetraploids exhibited considerable enhancements in pseudostem diameter, plant height, and root length. Furthermore, genes related to area, thickness, and chlorophyll content in leaves were also upregulated. Transcriptomic analysis identified differential gene expression in hormonal signal transduction, the mitogen-activated protein kinase (MAPK) signaling, and carbon fixation pathways. Metabolomic study also identified variably accumulating compounds associated with plant hormonal signal transmission, indole alkaloid production, porphyrin and chlorophyll metabolism, and carbon fixation in photosynthetic organelles. The results indicate that the hormones ABA and IAA, along with regulation of photosynthesis, might significantly contribute to the improvement of autotetraploids, potentially facilitating the production of triploid offspring for cultivation.

Nwachukwu and Babalola, have reviewed and shed light on the important insights of metagenomics for its exploitation to improve crop plants. Metagenomics is a non-culture approach that captures the complete microbial community in ecological samples, enabling the laboratory analysis of whole genomes devoid of culturing. This non-culture method provides more genetic information than traditional methods. Understanding the interactions between microbes, soil, and plants stays crucial for improving crop yields for viable agriculture. Metagenomic techniques can help develop new bio-pesticides and bio-fertilizers that remain environmentally friendly, thereby improving plant development and sustainable crop production.

Robusta coffee cultivation is crucial due to its higher disease resistance and ability to withstand climate changes. Genetic resources from various gene banks can further improve quality and agronomic traits in coffee. Verleysen et al., utilized genotyping by sequencing (GBS) to identify genetic diversity in 730 Yangambi Coffee shrubs, identifying 263 unique accessions through a novel HiPlex screening assay. Eight accessions were preferentially used, corresponding to originators. This study described the genetic composition of the INERA Coffee Collection in Yangambi, the Democratic Republic of Congo. The findings unearthed that most accessions dispensed to a cultivar origin 'Lula', while four were assigned to subgroup A of Congolese. The study donates to the re-assessment and evaluation of Robusta coffee germplasm.

Lipidomics and metabolomics are essential tools for investigating crop lipids and metabolites. Cui et al., reveal dynamical changes in tea lipid and metabolic profiles during manufacture processes. Nonetheless, individual lipidomics or metabolomics cannot discern essential components for quality assessment and authenticity verification. Integrating lipidomics with metabolomics can broaden the breadth of composition analysis, wrapping both polar/non-polar molecules. A technique combining UPLC-Triple-TOF/MS-based lipidomics and metabolomics was established to distinguish early spring green tea (ET) from late spring green tea (LT). This work distinguished the chemical compositions of ET and LT by lipidomics and metabolomics. ET samples contained glycerophospholipids and acylglycerolipids, whereas LT samples comprised glycolipids, sphingolipids, and hydroxyphenylphytin. The reconstructed orthogonal partial least squares discriminant analysis (OPLS-DA) model demonstrated a 100% accuracy rate in classifying tea quality based on harvest time.

Song et al., investigated mepiquat chloride (DPC)'s regulation in soybeans via morphology and physiology, along with proteomic analyses. The study used Heinong44 and Heinong65 soybean varieties, sprayed with DPC solution at the seedling stage. The study used morphological and physiological experiments, tandem mass tag quantitative proteomics, followed by bioinformatics analysis to detect differentially expressed proteins and study changes in the soybean leaf proteome after DPC treatment. Proteomic analysis of 100 mg/L DPC treated leaves showed that numerous proteins associated with plant development and stress tolerance were differentially

expressed. Results show that DPC reduces shoot dry weight, plant height and decreases total flavonoids and malondialdehyde. Furthermore, it was found that DPC inhibits shoot growth and photosynthesis but promotes lateral root development, enhances protective enzymes, and improves plant resistance to abiotic stress.

Millets is a promising agricultural crop, that can help ensure global food security due to their resilience against climate change and increasing demand for nutritious food and feed. Sanku et al., narrated about innovations in NGS technologies like genome-wide expression analysis which can aid in genomic selection by predicting stress tolerance related genes in millet breeding populations. Transcriptomics is an NGS technology that is being utilized to study the impact of differentially expressed genes and transcription factors for millet improvement, potentially revealing breeding opportunities for climate resilience. Advancements in spatial transcriptomics, can further help decode cell transcripts and differentially expressed genes, evading complications instigated by large genomes. This data can be analysed using advanced bioinformatics algorithms to identify significant patterns and regulatory genes. This combined effort can be used in marker assisted selection or genetic transformations for development of crop varieties with climatic resilience. Overall, transcriptomics is essential for improving the resilience of millets and other cereal crops and promoting sustainable agriculture.

Contemporary advancements in NGS have transformed crop breeding and broadened the potential for enhancing agricultural traits. Accordingly, the articles published in this Research Topic portray the prospective of omics approaches for acquiring biological data and digging genes allied with agronomical traits in crop plants. The issue provides valuable information on current research in this area that will provide readers with up-to-date knowledge about mechanisms and genes mined by omics approaches that could be useful for smart breeding programs and forecast essential basis for future crop research.

## Author contributions

RN: Writing – original draft, Writing – review & editing. SM: Writing – original draft, Writing – review & editing. IA: Writing – original draft, Writing – review & editing.

## Acknowledgments

The authors appreciate and acknowledge the frontiers team members who supported and passionately helped the authors in setting up, launching, and gearing this Research Topic until its successful completion.

## Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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