Editorial

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Multi-omics interventions in plant-microbiome interaction research

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Rhizosphere reflects a dynamic interface between plant roots and soil and represents one of the most complex and functionally active agricultural ecosystems. Within this micro-environment, plants orchestrate intricate chemical conversations with diverse microbial species comprising bacteria, fungi, archaea, and other microorganisms. Plant-microbiome interactions in the rhizosphere shape highly regulated partnerships due to precise molecular signaling, selective nutrient exchange, and co-evolutionary dynamics [1]. Beneath the visible manifestations of plant vigor, disease resistance, stress tolerance, and nutrient status lies an intricate molecular mechanism that is largely inaccessible to conventional analytical approaches. Emergence of multi-omics technologies that simultaneously integrate phenomics, genomics, transcriptomics, proteomics, metabolomics, and microbiomics with other biological data layers is fundamental to decoding the hidden molecular dialogue that drives interaction patterns and results in ecosystem functions [2,3]. The approach is now established as a shift from a reductionist paradigm to systems integration for simultaneous investigation of multiple layers of biological organization [4]. Genomics provides the genetic blueprint of protein-encoding genes, transcriptomics reveals actively expressed genes showing dynamic responsiveness, proteomics quantifies proteins performing cellular functions, and metabolomics captures the repertoire of small molecules reflecting metabolic activity and chemical signals, producing a holistic view of biological systems in plant-microbiome functionality [5]. This systems-level perspective is essential for understanding how microbial communities influence plant phenotypes and, conversely, how plant physiology shapes microbial community assembly and function.

1. MULTI-OMICS UNRAVEL PLANT-MICROBIOME INTERACTION MECHANISMS

Multiple layers of multi-omics technologies have catalyzed breakthrough studies in understanding the molecular mechanisms underlying plant-microbiome interactions [Figure 1]. The integration of multifaceted studies has provided an unprecedented systems-level view of how plants and their associated microbial communities interact, communicate, co-evolve, and co-regulate biological processes in the rhizosphere and how omics strategies decipher plant responses toward stresses and microbial interactions [6]. These approaches have deciphered that plants actively shape their rhizosphere microbiome communities through the secretion of root exudates composed of antimicrobial substances, organic compounds, and signaling molecules that selectively recruit beneficial microorganisms [7]. Transcriptomic analyses have uncovered how plant gene expression is dynamically reprogrammed in response to microbial colonization, particularly in pathways governing immunity, nutrient acquisition, and stress tolerance. Metagenomic and metatranscriptomic profiling have simultaneously captured the functional potential and active gene expression of entire microbial communities residing in the rhizosphere, phyllosphere, and endosphere. Metabolomic studies have further illustrated the chemical cross-talk between the plant and its microbiome, identifying key bioactive compounds such as phenolics, flavonoids, strigolactones, and organic acids that serve as molecular bridges between host and microbe. Proteomic investigations have complemented these findings by mapping protein-level interactions and post-translational modifications that mediate microbial recognition and downstream signaling cascades within plant tissues. The advent of single-cell multi-omics has added a new dimension of resolution, enabling researchers to dissect cell-type-specific responses within root and shoot tissues during the events of microbial colonization [8]. Computational integration frameworks, including machine learning (ML) and network-based modeling, have remained instrumental in synthesizing these heterogeneous datasets to identify key regulatory hubs and predictive biomarkers of beneficial plant-microbiome outcomes [9]. Collectively, multi-omics applications have capabilities to transform our system-level mechanistic understanding of the multiphasic interactions of plants and microbiome, initiating groundwork for microbiome-driven strategies for sustained agricultural practices under ecosystem resilience.

2. ROOT EXUDATE CHEMISTRY AND MICROBIAL RECRUITMENT

Plants actively manage their rhizosphere microbiome through strategic release of root exudates, a complex mixture of sugars, amino acids, organic acids, phenolic compounds, and secondary metabolites that collectively comprise 10–20% of photosynthetically fixed carbon of plants [10]. Metabolomic analyses have documented numerous distinct chemical molecules in root exudates, revealing remarkable species-specificity and developmental stage-dependent variation [11]. Integrated multi-omics studies combining exudate metabolomics using liquid chromatography-mass spectrometry and gas chromatography-mass spectrometry in combination with transcriptomics (RNA-Seq) and epigenomics analysis of root tissues have identified specific plant genes encoding transporters and biosynthetic enzymes controlling exudate composition [12]. Furthermore, genomic and metagenomic sequencing of rhizosphere microbial communities has revealed preferential utilization of specific exudate components by distinct

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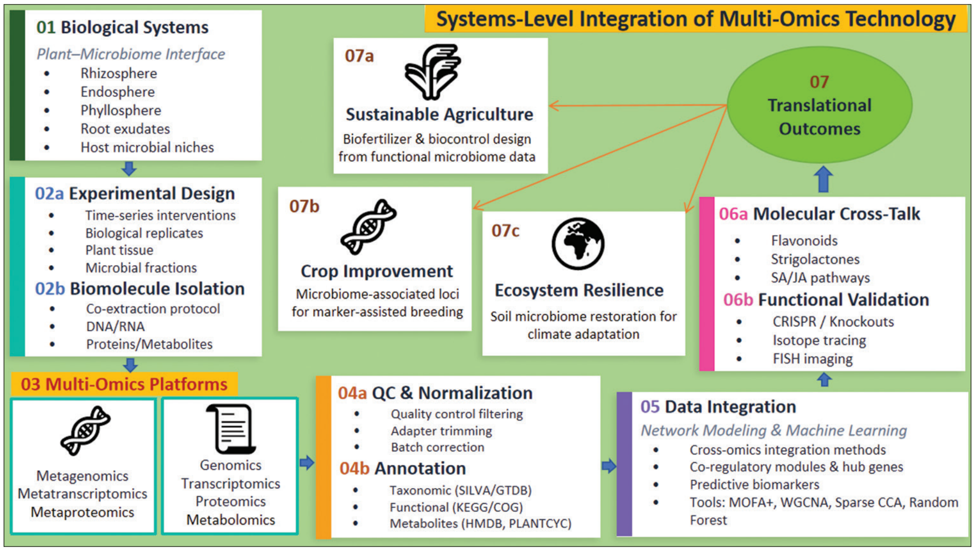

Figure 1: Multi-omics layers in the system level mechanistic framework of plant-microbiome interactions.

microbial taxa, enabling researchers to map chemical signals to microbial responses [13]. These integrated insights have demonstrated that plants strategically facilitate growth-promoting bacteria with preferred carbon sources while simultaneously releasing antimicrobial compounds to suppress pathogenic competitors.

3. NUTRIENT ACQUISITION AND BIOAVAILABILITY ENHANCEMENT

Soil nutrients, particularly phosphorus (P) and potassium (K), are limiting factors in many agricultural soils and create constraints in crop productivity globally. Multi-omics approaches facilitated studies on specific microbial taxa that enhance nutrient bioavailability through secretion of organic acids and phosphatases that solubilize mineral-bound nutrients [14]. Proteomic studies have identified specific enzyme complexes and membrane transporters that are involved in solubilizing inorganic P and mineralizing organic P, which facilitate phosphate acquisition by plant growth-promoting bacteria (PGPR) [15]. Transcriptomic profiling showed dramatic upregulated expression of nutrient transporter genes in plants colonized by PGPRs, indicating that the plants recognize and respond to microbial nutrient-acquisition activities [16]. In addition, metabolomic analyses revealed that colonization by nutrient-mobilizing microbes alters metabolite diversity and composition of plant tissues, increasing the content of nutritionally important microelements and secondary metabolites associated with crop quality [17]. Thus, multi-omics-based findings can drive the development of next-generation microbial inoculant products rationally designed to maximize nutrient-acquisition efficacy, with rigorous biochemical understanding.

4. DISEASE SUPPRESSION AND SYSTEMIC IMMUNITY

One of the most significant plant-microbiome interaction phenomena in agriculture is the capacity of certain microbial communities to suppress plant diseases through both direct antagonism and priming of plant immune responses. Multi-omics approaches have dramatically advanced the mechanistic understanding of these processes in plants [18]. Genomic studies of disease-suppressive soils have identified specific bacterial taxa, particularly dominated by *Bacillus* and *Pseudomonas* species, consistently enriched in suppressive versus non-suppressive soil environments [19]. Soil suppressiveness was found due to the presence of *Bacillus* and *Streptomyces* as dominant species, making the agricultural soils antagonistic against *Sclerotinia sclerotiorum*, a wide-spreading and devastating fungal plant pathogen [20]. Proteomic and genomic analyses have catalogued the specialized antimicrobial compounds produced by these bacteria, including polyketides, non-ribosomal peptides, and volatile organic compounds [21]. Colonization of plant roots by beneficial microbial species revealed activation of induced systemic resistance pathways, a form of systemic immunity in transcriptomic profiling, wherein beneficial microbes prime plant defense responses, resulting in enhanced resistance to diverse pathogenic threats [22]. Priming of beneficial microbial species involves upregulation of jasmonic acid and ethylene signaling pathways, as documented through coordinated transcriptomic and metabolomic studies [23]. The molecular sophistication of such interactions in plants at the cellular level, wherein microbes produce specific chemical or proteinaceous signals recognized by plant pattern recognition receptors, represents an inter-kingdom communication [24] which can be decoded by multi-omics approaches. Based on such methodological pipelines, the design of synthetic microbial consortia with multiple multi-trait organisms and bioprotectant formulations can be enabled with predictable disease-suppression efficacy to substantially reduce crop losses while decreasing dependency on synthetic fungicides [25].

5. STRESS RESILIENCE AND CLIMATE ADAPTATION

As climate change intensifies, understanding how plant-microbiome partnerships enhance crop resilience to abiotic stresses has become critically important. Multi-omics approaches have revealed that specific soil microbes enhance plant drought tolerance through multiple complementary mechanisms, including (i) modification of root architecture to maximize soil water acquisition, (ii) production of osmolytes that increase cellular water retention, and (iii) modulation of plant stress hormone biosynthesis to optimize resource allocation under water limitation [26]. Transcriptomic analyses of roots colonized by drought-alleviating bacteria demonstrate coordinated upregulation of genes encoding aquaporins (water channel proteins) and abscisic acid biosynthetic enzymes [27]. Metabolomic profiling has identified microbial-derived metabolites, including phenolics, amino acids, organic acids, proline analogs, and polysaccharides that accumulate in plants (tomato) under high temperature [28] and drought stress conditions to enhance osmotic tolerance [29]. Such multi-omics applications are illustrating mechanisms of enhanced heavy metal tolerance [30] and salinity resilience mediated by microbial species [31]. These findings are valuable for developing climate-ready crop varieties that maintain productivity under changing climatic conditions, incorporating both the genetic improvements and microbial strategies.

6. CHALLENGES IN MULTI-OMICS PLANT-MICROBIOME RESEARCH

Despite the extraordinary work using multi-omics approaches, significant challenges limit their widespread adoption and practical applications. Current multi-omics studies suffer from limited standardization in sampling protocols, sample preservation, DNA/RNA extraction procedures, and analytical methodologies [32]. The rhizosphere ecosystem, which is spatially heterogeneous, temporally dynamic, and accessible only through destructive sampling, presents exceptional technical challenges. Requirements for the depth of genome sequencing for accurate community analysis vary substantially based on soil and plant type and microbial diversity, along with the research objectives, and create difficulties in designing appropriate studies [33]. In addition, metagenomic and metatranscriptomic approaches generate an enormous volume of data, which requires high-end computational infrastructure, data handling capabilities, and expertise in bioinformatics and computational biology for information processing and interpretation. Computational infrastructure is a substantial limiting factor that restricts research capabilities in many regions where agricultural challenges are more acute.

Perhaps the most significant challenge in contemporary multi-omics research is the conceptual complexity in computational data integration. Genomic, transcriptomic, proteomic, and metabolomic datasets are generated using distinct technologies, normalized using multiple statistical methods, and characterized with different measurement errors and artifacts [32]. Integrating these heterogeneous data types into coherent biological meanings requires sophisticated bioinformatic pipelines and, more importantly, a deep understanding of the underlying biological systems [34]. This methodological heterogeneity severely impedes cross-study meta-analyses and limits reproducibility. Furthermore, the interpretation of integrated multi-omics data remains challenging, and correlation among multiple overlapping omics layers does not necessarily imply causation. Network analyses and systems biology modeling can address specific and pertinent challenges, but the field lacks optimal approaches for converting high-dimensional omics data into actionable biological insights [35]. Validation gap is another fundamental challenge in multi-omics research. Omics data suggest functional predictions, but these predictions require experimental validation through biochemical assays, genetic manipulation, or phenotypic assessment [36]. For example, identifying that a particular bacterial gene is upregulated in the rhizosphere does not establish whether that gene is functionally important for plant growth promotion. This is why functional validation through complementary approaches is essential, although it substantially imposes additional cost and temporal requirements. This limits the predictive power of multi-omics approaches and constrains their application in the rational design of agricultural interventions [35].

7. FUTURE-READY MULTI-OMICS-LED APPROACHES FOR AGRICULTURAL INNOVATION

The ultimate value of multi-omics research in plant-microbiome biology rests upon its capacity to generate actionable insights for their translation into improved agricultural practices, crop varieties, and management strategies that enhance productivity. Only limited multi-omics studies design research explicitly to address farmer-relevant questions or incorporate feedback from end-users in hypothesis formulation [36]. Agricultural advisory systems for farmers and crop improvement programs often lack engagement with cutting-edge multi-omics research. Bridging this translation gap requires designing translational research platforms that integrate multi-omics discovery with agronomic experimentation, farmer engagement, and crop breeding programs [37]. Multi-omics approaches may be standardized and deployed to address specific and defined agricultural problems such as optimizing biofertilizer formulations for particular soil-crop combinations, identifying microbial consortia for plant growth promotion, maximizing disease suppression in specific pathosystems, or selecting crop genotypes forming superior partnerships with native soil microbiota [38]. Such problem-driven multi-omics research will generate knowledge directly applicable to yield improvement, input reduction, and climate adaptation, translating scientific insights into tangible benefits for agricultural producers and consumers.

Several emerging perspectives in this leading area of research promise to enhance the utility and impact of multi-omics approaches in the complex biology and chemistry of plant-microbiome interactions. Long-read sequencing technologies (PacBio, Oxford Nanopore) are beginning to resolve complex genomic regions that short-read sequencing cannot adequately assemble, enabling more complete reconstruction of microbial genomes and detection of structural variants relevant to phenotypic variation [39]. Single-cell sequencing approaches, including single-cell genomics and single-cell RNA sequencing can help to illustrate heterogeneity within microbial populations and resolve spatial relationships among microbes within micro-aggregates and potentially reveal inter-microbial interactions obscured in bulk community analyses [40]. ML and artificial intelligence methodologies are increasingly being applied for the integration and interpretation of multi-omics datasets to enable the discovery of non-obvious patterns and generation of predictive models linking microbial community composition to ecosystem functions [41]. Emerging spatially-resolved multi-omics techniques that preserve spatial context while providing molecular resolution represent a frontier that can enable understanding of plant-microbe interactions at the plant root surfaces [7]. Collectively, these technological advances will expand the resolving and dissecting power of multi-omics approaches and enhance their capabilities to decode molecular mechanisms governing plant-microbiome interactive partnerships.

The intrinsic molecular complexity of plant-microbiome interactions is known to engage hundreds of metabolites, thousands of genes, and millions of distinct microbial cells engaged in synchronized biological activities. Approaches, tools, and emerging technologies in the area of multi-omics studies provide unprecedented capabilities to decipher plant-microbe interactions at a refined level to reveal multiple molecular mechanisms through which microbial species help to enhance plant nutrition, activate immunity, and confer stress resilience in crop plants. Global agriculture must simultaneously increase productivity to meet food security demands, reduce input usage to enhance environmental sustainability, and enhance crop resilience to climate variability. Strategic manipulation of plant-microbiome partnerships, guided by rigorous multi-omics understanding, offers a pathway toward achieving these seemingly contradictory objectives. However, realizing this potential requires overcoming significant technical, computational, environmental, and equity challenges. We welcome research submissions tackling multi-omics-enabled innovation in crop microbiome management, employing rigorous mechanistic approaches alongside field-validated agronomic outcomes. Through coordinated, translational multi-omics research, we can transform plant-microbiome science from molecular description to practical innovation, ultimately advancing sustainable, resilient, and productive agriculture capable of nourishing a growing global population within planetary boundaries.

8. USE OF ARTIFICIAL INTELLIGENCE (AI)-ASSISTED TECHNOLOGY

The authors declare that they have not used artificial intelligence (AI)-tools for writing and editing of the manuscript, and no images were manipulated using AI.

9. CONFLICTS OF INTEREST

The authors report no financial or any other conflicts of interest in this work.

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