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Editorial: Plant-microbe omics

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Editorial on the Research Topic Plant-microbe omics

Omics-based studies have evolved over the past two decades to provide rich datasets from which deeper system-level understanding can be unraveled. Omics technologies (e.g., genomics, transcriptomics, proteomics, and metabolomics) can provide specific molecular insights into plant and microbe fitness, disease states, stress, cell signaling/cell-cell communication, and nutrient exchange, and these molecular observations can be correlated with system phenotype and function. The overall health of plant-microbe systems and their surrounding environments can be assessed, and a greater understanding of processes related to nutrient exchange/cycling, plant disease, and ecosystem homeostasis can now be achieved via the latest approaches to plant-microbe omics analysis.

Plant-microbe interactions have traditionally been some of the most technically challenging sample types for omics analysis. Plant tissues, which contain recalcitrant cell wall polymers, make the extraction of biomolecules (i.e., proteins, transcripts, and metabolites) more involved compared to samples such as those analyzed in human/animal systems or clinical samples. Plant samples notoriously contain high levels of polyphenolics or other reactive compounds that, if not treated and removed properly from the protein samples, can negatively react with and alter metabolite and protein structure. Samples extracted from the rhizosphere often contain high levels of humic and fulvic acids, which are difficult to remove from the sample biomolecules of interest and which can negatively interfere with successful mass spectrometric or sequencing analyses, such as those used in proteomics and transcriptomics, for example. The aim of this Research Topic, therefore, was to cover current research in multi-omics applied specifically to elucidating plant-microbe interactions. This Research Topic, consisting of four articles, includes omics studies on plants interacting symbiotically or antagonistically (i.e., through pathogenic infection) with microorganisms. The research encompasses metatranscriptomics analyses of rhizosphere soils, bottom-up proteomic approaches, along with more specialized proteomic analyses such as top-down proteomics analyses that investigate post-translational modifications, and single-cell omics analyses to probe biomolecular changes at the cellular level to elucidate various plant-microbe interactions.

Hewitt et al. performed a metatranscriptomics analysis of bacterial and fungal communities in the rhizosphere and bulk soils surrounding tomato roots, comparing those grown with or without biochar augmentation. This research revealed that the growth parameters of shoot or fruit yields did not change significantly. However, the rhizosphere microbiomes were found to be enriched with beneficial bacteria, leading to a suppression of pathogenic fungi populations.

Using a bottom-up proteomics approach, Lenz et al. characterized the temporal pathogen-induced changes in resistant and susceptible *Populus trichocarpa* genotypes inoculated with the fungal pathogen *Sphaerulia musiva* (Septoria canker). This research highlighted genotype-specific pathogen defense responses in poplar trees.

By studying LC-MS and MALDI-MSI top-down proteomics on soybean nodules infected with either a symbiotic wild-type *B. japonicum* or a *Bradyrhizobium japonicum nifH* mutant, which is unable to fix nitrogen, Zhou et al. characterized novel post-translational modifications (PTMs). Multiple intact proteins, biopolymers, and over 1,600 plant and bacterial proteomes were detected. Many of the observed PTMs were previously uncharacterized in UniProt, showcasing how this proteomics approach provided novel PTM information on the soybean-rhizobium symbiosis.

Our fourth research article, by Vallet et al., demonstrated how single-cell metabolomics analysis, coupled with classification analyses, can be used as a reliable diagnostic tool to track metabolic changes in infected algae. Using LDI-HRMS on *Coscinodiscus granii*, *Coscinodiscus radiatus*, and the toxic dinoflagellate *Alexandrium minutum* infected by the oomycete *Lagenisma coscinodisci* and the alveolate *Parvilucifera* spp., novel insights into the important dynamics of cell-resolved infection, metabolism, and physiology of algae under pathogenic influence were discerned.

The articles contained in this Research Topic highlight the vast array of dynamic strategies and recent technological advances in omics analyses with the purpose of demystifying plant-microbe interactions.

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Conflict of interest

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