



OPEN ACCESS

EDITED AND REVIEWED BY
Ernesto Satoshi Nakayasu,
Pacific Northwest National Laboratory
(DOE), United States

*CORRESPONDENCE

Kim K. Hixson,
✉ kim.hixson@pnnl.gov

RECEIVED 15 August 2023

ACCEPTED 17 August 2023

PUBLISHED 07 November 2023

CITATION

Hixson KK, Dhingra A, Dini-Andreote F,
Doktycz MJ, Tschaplinski TJ and
Paša-Tolić L (2023), Editorial: Plant-
microbe omics.
Front. Anal. Sci. 3:1278170.
doi: 10.3389/frans.2023.1278170

COPYRIGHT

© 2023 Hixson, Dhingra, Dini-Andreote,
Doktycz, Tschaplinski and Paša-Tolić.
This is an open-access article distributed
under the terms of the [Creative
Commons Attribution License \(CC BY\)](#).
The use, distribution or reproduction in
other forums is permitted, provided the
original author(s) and the copyright
owner(s) are credited and that the original
publication in this journal is cited, in
accordance with accepted academic
practice. No use, distribution or
reproduction is permitted which does not
comply with these terms.

Editorial: Plant-microbe omics

Kim K. Hixson^{1,2*}, Amit Dhingra³, Francisco Dini-Andreote⁴,
Mitchel J. Doktycz⁵, Timothy J. Tschaplinski⁵ and
Ljiljana Paša-Tolić²

¹Physical and Computational Sciences Directorate, Pacific Northwest National Laboratory, Richland, WA, United States, ²Environmental Molecular Sciences Laboratory, Earth and Biological Sciences Directorate, Richland, WA, United States, ³Department of Horticultural Sciences, College of Agriculture & Life Science, Texas A&M, College Station, TX, United States, ⁴Department of Plant Science and Huck Institutes of the Life Sciences, The Pennsylvania State University, University Park, PA, United States, ⁵Oak Ridge National Laboratory, Biosciences Division, Oak Ridge, TN, United States

KEYWORDS

plant-microbe interactions, multi-omics, metabolomics, proteomics, pathogen, plant-microbe

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.

Author contributions

KH: Conceptualization, Writing–original draft, Writing–review and editing. AD: Writing–review and editing. FD: Writing–review and editing. MD: Writing–review and editing. TT: Writing–review and editing. LP-T: Writing–review and editing.

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.

The author(s) declared that they were an editorial board member of Frontiers, at the time of submission. This had no impact on the peer review process and the final decision.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.