

The tri-trophic interaction between plant, beneficial microorganisms, and pathogens have been understudied in the past. It is currently believed that plants are able to regulate the microbial composition inhabiting its root and rhizosphere by exuding distinct bioactive chemical compounds and possibly thereby acquire resistance to biotic stresses. In order to investigate the molecular mechanism underlying this interaction, 29 accessions (differences in genetic adaptation) of *Arabidopsis thaliana* (wild type) were grown in field soil under controlled conditions. The root (n=6) and its attached soil were harvested, snap-frozen, lyophilized, ground, and extracted in a monophasic solvent mixture. The fraction of extracted material was subjected to derivatization (methoximation + trimethylsilylation) for primary metabolites profiling by employing the GC-TOF MS platform. The raw data was processed by BinBase (Fiehn 2016) for metabolite annotation as well as post-processed to remove the redundant features. The remaining fraction was subjected to solvent-solvent extraction by utilizing a biphasic solvent mixture (Matyash et al. 2008). The non-polar phase was analyzed by using reverse-phase LC-MS/MS on a high-resolution Thermo Q Exactive HF mass spectrometer for lipid profiling (lipidomics). The data for the polar layer was acquired by using HILIC-TripleTOF to determine polar metabolite composition. Both lipidomics and HILIC raw data were processed by MS-DIAL (Tsugawa et al. 2015), followed by post-processing with MS-FLO (DeFelice et al. 2017) to remove the insignificant features. Furthermore, the microbial composition was determined by the Illumina MiSeq sequencing platform. The data from multiple platforms will be combined, and different statistical approaches such as one-way ANOVA, PCA, PLS-DA, HCA and heatmap will be employed to highlight the statistically significant features associated with a certain group of plant genotype as well as their significant impact on rhizosphere microbial community composition.