

Decoding conserved and host-specific plant responses to root knot nematode infection

Advances in omics technologies and bioinformatic tools have made large-scale gene expression studies more accessible. However, RNA-seq datasets are typically analyzed within the narrow scope of their original experiment limiting our ability to identify gene expression patterns that are conserved across hosts, infection stages, and experimental conditions. This limitation is especially important for plant-parasitic nematodes which infect large and diverse host species and contain many genes with limited clear homology making biological interpretation from individual datasets challenging. Here, we integrated several publicly available *Meloidogyne incognita* transcriptomics-datasets from multiple host species to identify conserved and condition-specific gene expression patterns associated with nematode-host interactions. Raw datasets were first assessed for quality, and only high-quality datasets were retained for downstream analysis. We then grouped curated datasets into early infection, representing 2 to 7 days post inoculation, and late infection, representing 2 to 3 weeks post-infection. Integrated cross-host transcriptomes from multiple host species for early and late infection were generated. We identified 1,461 and 2,979 differentially expressed genes at early and late infection stage respectively. These results suggest that host responses to *M. incognita* infection shift strongly over time, with broader transcriptional reprogramming happening during later stage of infection. We also developed a co-expression gene network among host genes to identify group of genes and pathways that respond similarly across host species. Commonly induced pathways across hosts may provide targets for nematode management, while distinct host responses may help explain differences in host compatibility and infection outcomes. This integrated approach extends the value of existing transcriptomic datasets, support database management for sustained utility, and uncovers new biological insights into plant-nematode interactions.