Benjamin J. Garcia (Jacobson Team) Computational Biology Integrative Analysis

Novel approach: Parallelization of Kraken (ParaKraken) allows for high resolution taxonomic assignments by incorporating all kmers from whole genome sequences from all kingdoms of life into multiple databases, running each in parallel, and then resolving all database-read pairs to generate a single taxonomic assignment

	Objective	 identification of novel associations and responses in the poplar phytobiome during acute progressive drought and cyclic drought.
	New science	 Dual identification of host and phytobiome, utilizing the same RNA-Seq data, by creating a pipeline that couples traditional host transcriptomics with ParaKraken, allowing for identification of novel associations not possible with prior methods Development of a highly parallel taxa identification pipeline that can incorporate any number of species, including species without a taxonomy, for high resolution taxa assignments
	Impact	 The phytobiome is affected quite differently by the cyclic or acute nature of the drought rather than the severity of the drought, with an increase in taxa under cyclic drought that are often reported to have beneficial effects on the plants.
Phytobiome and Transcriptional Adaptation of Populus deltoides to Acute Progressive Drought and Cyclic Drought. 2018.		

Phytobiome and Transcriptional Adaptation of Populus deltoides to Acute Progressive Drought and Cyclic Drought. 2018. BJ Garcia, JL Labbe, P Jones, PE Abraham, I Hodge, S Climer, S Jawdy, L Gunter, GA Tuskan, X Yang, TJ Tschaplinski, DA Jacobson. Phytobiomes Journal 2018 (2): 249-260. https://doi.org/10.1094/PBIOMES-04-18-0021-R.













Interaction network of gene ontology (GO) terms and their

associated phytobiome taxa. Relationships between significantly differentially expressed genes and significantly differentially abundant taxa during drought were established using DUO. GO terms associated with each gene were then used to calculate modified Fisher's exact test enrichments in order to identify patterns of functional changes positively associated with taxa and negatively associated with taxa. *Rhizophagus* and *Trichinella* were positively associated with reactive oxygen species metabolism, giving support to the hypothesis that *Rhizophagus* may decrease oxidative stress in the plant host while the nematode may have effects on the host immune system.