

Using time-course metabolomics to characterize the early interchange of substrates and putative signals during the establishment of the *Populus-Laccaria* symbiosis

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Populus spp., including *P. trichocarpa* (black cottonwood), *P. deltoides* (eastern cottonwood), and interspecific hybrids, such as *Populus tremula x alba* 717-1-B4, are long-lived, woody perennial species that can form a symbiotic relationship with the ectomycorrhizal fungus, *Laccaria bicolor*. Establishment of the *Populus-Laccaria* symbiotic relationship requires the intricate exchange of mycorrhiza-induced small secreted proteins (MiSSPs) and metabolites that serve as signals and substrates between the two organisms. Our goal is to develop an integrated systems biology approach, coupling transcriptomics, metabolomics, and proteomics to identify key molecular factors (MiSSPs and diffusible signals) and gene networks involved in symbiosis formation and metabolism. The approach was to investigate the metabolic signaling responses, and the timing of the molecular factors involved in the establishment of the mutualistic association. Time-course studies of gene expression and proteomic responses were conducted by the Francis Martin Lab (INRA-Nancy), whereas GCMS-based metabolomic responses were conducted at ORNL. Early metabolomic responses indicate a substantial plant defense response is elicited by *L. bicolor*. Declines in metabolites in *Populus* roots with symbiosis, including glycerol, tryptophan, hydroxycinnamate-quinic esters, quinic, TCA cycle organic acids, and amino acids, likely indicate increased substrate utilization by *L. bicolor*. Symbiosis was associated with localization of MiSSP7 in the nucleus of poplar root cells and a massive reprogramming of the plant defense responses. Metabolomic analyses characterized the nature of that reprogramming and identified metabolites that are being tested in diffusible contact studies to establish the nature of their roles in plant-microbe metabolite exchange and communication.

Biography

Tim Tschaplinski completed his Ph.D. at the University of Toronto and postdoctoral studies at Oak Ridge National Laboratory, where he now serves as the Metabolomics Group Leader in the Biosciences Division. He is a plant molecular physiologist experienced in biochemistry, specifically the application of mass spectrometry to research problems in genomics, bioenergy crop production, environmental stress physiology, and plant-microbe signaling, including characterizing the molecular basis of plant-microbe symbiotic relationships in contrast with pathogenic relationships. He has published more than 65 papers in reputed journals and serves as an editorial review board member for *Tree Physiology* and *Environmental and Experimental Botany*.