PMI *Populus trichocarpa* and *Populus deltoides* Exhibit Different Metabolomic Responses to Colonization by the Symbiotic fungus *Laccaria bicolor*

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Background

• The goal of the study was to investigate the metabolic signaling responses, and the timing of the molecular factors involved in the establishment of the *Populus-Laccaria* mutualistic association in two poplar species with contrasting ease of colonization.

Science

- *P. trichocarpa* is readily colonized, whereas *P. deltoides* maintains a defense response with accumulations of salicin, tryptophan, and 1-*O*-caffeoylquinate.
- Colonization of *P. trichocarpa* leads to accumulations of glycerol and fatty acids, a decline in the plant-derived phenolic-based defense network, substituted with a fungal-derived network based on hydroquinone, arbutin, its glucoside, and alkaloids.
- MiSSP7-defective *L. bicolor* with impaired symbiosis still accumulate arbutin, mannitol, and alkaloids, but not trehalose

Significance

• Coupling transcript responses with metabolomic data indicates that L. bicolor uses the benzoate degradation pathway to generate succinate and fumarate and drive the main aromatic responses associated with the establishment of symbiosis

Arbutin, a key metabolite accumulating with symbiosis



L. bicolor uses benzoate degradation pathway to generate succinate and accumulate phenolic metabolites



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Tschaplinski et al. In Press. *Molecular Plant-Microbe Interactions*.

MPMI, 2014, In Press

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Abstract

Within boreal and temperate forest ecosystems the majority of trees and shrubs form beneficial relationships with mutualistic ectomycorrhizal fungi (ECM) that support plant health through increased access to nutrients as well as aiding in stress and pest tolerance. The intimate interaction between fungal hyphae and plant roots result in a new symbiotic 'tissue' called the ECM root tip. Little is understood concerning the metabolic re-programming that favors the formation of this hybrid tissue in compatible interactions and what prevents the formation of ECM root tips in incompatible interactions. We show here that the metabolic changes during favorable colonization between the ECM fungus *Laccaria bicolor* and its compatible host, *Populus trichocarpa*, are characterized by shifts in aromatic acid, organic acid, and fatty acid metabolism. We demonstrate that this extensive metabolic re-programming is repressed in incompatible interactions and that more defensive compounds are produced or retained. We also demonstrate that *L. bicolor* can metabolize a number of secreted defensive compounds and that the degradation of some of these compounds produce immune response metabolites (e.g., salicylic acid from salicin). Therefore, our results suggest that the metabolic responsiveness of plant roots to *L. bicolor* is a determinant factor in fungal:host interactions.

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