

Proteomics approach for biological inspection of *Dendroctonus Frontalis* (Southern Pine bark Beetle) in loblolly pine (*Pinus taeda*)

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Abstract

The southern pine bark beetle (SPB), *Dendroctonus frontalis* (Coleoptera: Curculionidae: Scolytinae), is the most economically and ecologically important insect pest of southern forests in USA. Genomics solutions for the management of the SPB can be sought to identify molecular targets that are essential in the SPB's mutual interaction with two species of fungi that can serve as food and provide essential nutrients for larvae. Two of these fungi, *Entomocorticium* sp. A and *Ophiostoma ranaculosum*, are obligate mutualists with *D. frontalis*, and the third associate is a blue-staining fungus, *O. minus*, that is commonly introduced by beetles and phoretic mites. *O. minus* negatively affects beetle larvae and in high abundance can impact *D. frontalis* population dynamics. Size of lesions formed and quantity of secondary metabolites produced in response to fungal inoculations varied significantly among *Pinus* species. Such targets in the mycangial glands could be associated with metabolic pathways that are involved in the biosynthesis of defense chemicals to which the two fungus species have been adapted. To break the mutual interaction between the SPB and the two fungus species, pine trees can be engineered to induce effectors that interrupt the function of the molecular targets in the mycangium. For example, if an essential enzyme in this interaction is identified, such enzyme can be used as a molecular target for engineering the induced effectors which bind with the enzyme, so that the enzyme is not available for its function.

References

Hofstetter RW, Mahfouz JB, Klepzig KD, Ayres MP., Effects of tree phytochemistry on the interactions among endophloedic fungi associated with the southern pine beetle (2005), J. Chem. Ecol., 31(3):539-60.

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