Dissimilar pigment regulation in *Serpula lacrymans* and *Paxillus involutus* during interkingdom interactions.

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Abstract

Production of basidiomycete atromentin-derived pigments like variegatic acid (pulvinic acid-type) and involutin (diarylcyclopentenone) from the brown-rotter Serpula lacrymans and the ectomycorrhiza-forming Paxillus involutus, respectively, is induced by complex nutrition, and in the case of S. lacrymans, bacteria. Pigmentation in S. lacrymans was stimulated by 13 different bacteria and cell-wall-damaging enzymes (lytic enzymes and proteases), but not by lysozyme or mechanical damage. The use of protease inhibitors with Bacillus subtilis or heat-killed bacteria during co-culturing with S. lacrymans significantly reduced pigmentation indicating that enzymatic hyphal damage and/or released peptides, rather than mechanical injury, was the major cause of systemic pigment induction. Conversely, no significant pigmentation by bacteria was observed from P. involutus. We found additional putative transcriptional composite elements of atromentin

synthetase genes in P. involutus and other ectomycorrhiza-forming species that were absent from S. lacrymans and other brown-rotters. Variegatic and its precursor xerocomic acid, but not involutin, in return inhibited swarming and colony biofilm spreading of Bacillus subtilis, but did not kill B. subtilis. We suggest that dissimilar pigment regulation by fungal lifestyle was a consequence of pigment bioactivity and additional promoter motifs. The focus on basidiomycete natural product gene induction and regulation will assist in future studies to determine global regulators, signalling pathways and associated transcription factors of basidiomycetes.

Involved units

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