

Bacteria induce pigment formation in the basidiomycete *Serpula lacrymans*.

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Abstract

Basidiomycete fungi are characterized ecologically for their vital functional role in ecosystem carbon recycling and chemically for their capacity to produce a diverse array of small molecules. Chromophoric natural products derived from the quinone precursor atromentin, such as variegatic acid and involutin, have been shown to function in redox cycling. Yet, in the context of an inter-kingdom natural system these pigments are still elusive. Here, we co-cultured the model saprotrophic basidiomycete *Serpula lacrymans* with an ubiquitous terrestrial bacterium, either *Bacillus subtilis*, *Pseudomonas putida*, or *Streptomyces iranensis*. For each, there was induction of the gene cluster encoding a non-ribosomal peptide synthetase-like enzyme (atromentin synthetase) and an aminotransferase which together produce atromentin. Correspondingly, during co-culturing there was an increase in secreted atromentin-derived pigments, i.e., variegatic, xerocomic, isoxerocomic, and atromentic acid. Bioinformatic analyses from 14 quinone synthetase genes, twelve of which are encoded in a cluster, identified a common promoter motif indicating a general regulatory mechanism for numerous basidiomycetes.

Beteiligte Forschungseinheiten

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