Processing sites involved in intron splicing of Armillaria natural product genes.


Abstract

We analysed the structure of four genes whose transcriptional products are likely to be involved in the small molecule metabolism of the homobasidiomycete Armillaria mellea with the aim of verifying splice sites. To this end we experimentally validated in silico predicted intron/exon junctions for accuracy. Based on 78 verified junctions, a consensus for donor and acceptor sites in Armillaria is presented, along with experimental evidence for non-canonical splice sites, introns with alternative donor or acceptor junctions, and allele-selective splicing. The investigated reading frames show significant homologies to: (1) antibiotic and other small molecule efflux transporter genes; (2) phenoloxidase/laccase genes; (3) genes for dual Cys2His2/Zn(II)2Cys6 transcriptional regulators. For all of these gene categories, this is the first report on examples from the genus Armillaria.

Involved Units and Groups

**Pharmaceutical Microbiology**

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Identifier