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## Clues to Understand the Regulatory Metabolisms Governing the Biosynthesis of Fungal Secondary Metabolites

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Fungi are of particular interest due to their capacity to produce an extensive array of secondary metabolites. While many secondary metabolites have no known functions to the producing fungal organisms, these metabolites have tremendous importance to humans with beneficial (e.g., antibiotics) or detrimental (e.g., mycotoxins) properties. In this study, two important filamentous fungi, *Fusarium verticillioides* and *Mycosphaerella graminicola* were selected as target species and the genes regulatory functions on the biosynthesis of secondary metabolisms were studied. Functional genomics including forward and reverse genetics, and proteomics were utilized to better understand the complex secondary metabolism regulations in both *F. verticillioides* and *M. graminicola*. Identified genes in either *F. verticillioides* or *M. graminicola* background were *CPP1* (a putative protein phosphatase gene), *GAC1* (encoding a GTPase activating protein), *MCCI*(encoding c-type cyclin), and the velvet gene, *MVE1*. Our data suggest that there are diverse regulatory genes on fungal secondary metabolites with distinct or overlapping functional roles.