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Título	Análise genômica e transcritômica de agrupamentos gênicos envolvidos na biossíntese de metabólitos secundários no fungo fitopatogênico Gaeumannomyces tritici
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The disease “Take-all” (TAD) is one of the most important in cereals and grasses, and it is caused by the fungus *Gaeumannomyces tritici* (Magnaporthaceae: Magnaporthales). In the last decade several species of the order Magnaporthales had their genome sequenced, thus allowing for comparative analysis to highlight putative virulence determinants. Among such determinants are the secondary metabolites (SM) that are small molecules, which can play fundamental roles in the infection process of phytopathogens. The characterization of genes responsible for the biosynthesis of SM in the genome of *G. tritici*, as well as the analysis of the expression, the conservation, and the evolution of these genes are fundamental for a better understanding of the molecular mechanisms involved in the development of the TAD. Here we describe the identity of 35 putative gene clusters potentially involved in SM biosynthesis (BGCs) in the genome of *G. tritici*. We also evaluate the conservation of these genes amongst 10 species of the Magnaporthales order. Notably, most of the BGCs identified in *G. tritici* were conserved in these species, but GtPKS1, GtPKS3, and GtTERP4, are exclusively found in the genome of *G. tritici*. Furthermore, the expression of identified BGCs was evaluated in a comparative analysis, exploring a mimicked infection condition. Seven BGCs were up-regulated in this condition, including the GtPKS1. Moreover, through comparative genomic analysis, GtPKS1, GtPKS10 and GtPKS-NRPS3 were putatively linked to the production of an isocoumarin/alternariol-like compound, ACR-toxin and trichosetin, respectively. These BGCs were further explored through phylogenetic inference, which highlighted the distribution of orthologous sequences among several plant-associated fungi. This further supports the hypothesis that these genes are important in host-pathogen interactions. Finally, the detailed identification of several genes enrolled in SM biosynthesis provides the foundation for future in-depth research, supporting the potential impact of small molecules on the lifecycle of *G. tritici*.