Specific regulation of Botrydial and Botcinic acid gene clusters in Botrytis cinerea

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Botrytis cinerea is responsible for the gray mold disease on more than 200 plant species. Among the virulence factors identified in this Ascomycete are two non-host specific toxins (and their derivatives): botrydial (BOT, a sesquiterpene) and botcinic acid (BOA, a polyketide). The genes responsible for their biosynthesis are clustered in AT-rich subtelomeric regions of chromosome 1 (*BOA* genes) and chromosome 12 (*BOT* genes). Previous studies pointed out their co-regulation by conserved signalling pathways as well as by global transcription factors (TFs) like the calcineurin-dependent BcCrz1. A strong link between secondary metabolism gene expression and light-dependent development has been showed in *B. cinerea*, notably by the characterization of Velvet complex members BcVel1 and BcLae1. Global regulation data are available for *BcBOT* and *BcBOA* genes, but their direct regulators have not been characterized so far. A TF encoding gene present within a secondary metabolism cluster usually specifically regulates genes of this cluster. Amongst *BcBOA* genes, *BcBOA13* is predicted to encode a Zn(II)2Cys6 TF. In addition, a new version of *B. cinerea* genome annotation allowed adding new putative *BcBOT* genes to this cluster, including a gene predicted to encode a Zn(II)2Cys6 TF (*BcBOT6*). In our study, we functionally characterized *BcBOT6* and *BcBOA13*. Our hypothesis is that these TFs are specific regulators of their respective cluster. The data accumulated so far through the generation of deletion mutants and the analysis of gene expression by RT-qPCR support this hypothesis. In order to investigate the putative direct interaction between BcBot6 and BcBoa13 with promoters of genes from *BcBOT* and *BcBOA* culsters, a Yeast One Hybrid strategy was carried out. We searched for regulators of *BcBOT6* and *BcBOA13* to make the link between these TFs and known regulatory pathways. In parallel, we tested the role of epigenetic modifications in the transcriptional control of these clusterss. We generated deletion mutants of the orthologs of chromatin modifiers known to affect secondary metabolism gens expression in fungi (Hp1, Dim-5 and Kmt6). The expression profiles of *BcBOT* and *BcBOA* genes will be assessed in these mutants. Altogether, these results give a more precise view of the regulatory network controlling the expression of Bc*BOT* and Bc*BOA* gene clusters in *B. cinerea*.