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## Regulation of secondary metabolism in the anthracnose fungus *Colletotrichum higginsianum*

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**POSTER SESSION ABSTRACTS**  
**Session CS7 Metabolism and physiology**  
**CS7W25**

**Wednesday 6th April**  
**14:00 - 16:00**

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**Regulation of secondary metabolism in the anthracnose fungus *Colletotrichum higginsianum***

Species of the genus *Colletotrichum* cause devastating anthracnose or blight diseases on numerous crop plants worldwide. *C. higginsianum* uses a hemibiotrophic strategy to infect Arabidopsis and other Brassicaceae. Its genome contains a large number of genes (87) encoding secondary metabolism (SM) key enzymes. As in other fungi, these key genes are organized into clusters that may also contain genes encoding accessory enzymes of the same biosynthetic pathway, efflux transporters and pathway-specific transcription factors. A remarkable finding from RNA-Seq transcriptome profiling was that 27 SM clusters are specifically expressed only in planta by appressoria and/or biotrophic hyphae. Since each cluster potentially synthesizes one final metabolite, this suggests appressoria and biotrophic hyphae deliver a cocktail of different metabolites to the first infected host cell. To identify and characterise these metabolites we need to mass-produce them from in vitro cultures. We therefore deleted histone-modifying enzymes controlling chromatin status and over-expressed global transcriptional regulators (e.g. Dim5, Hp1, Kmt6, CclA, Sge1). This led to the discovery of metabolites which are not produced by wild type mycelia in vitro. Bioassays are ongoing to evaluate their biological activities against plants, bacteria and fungi.

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