

## 8 Lifestyle transitions in plant pathogenic Colletotrichum fungi deciphered by genome and transcriptome analyses.

O'Connell RJ, Thon MR, Hacquard S, Amyotte SG, ..., Schulze-Lefert P, van Themaat EV, Ma LJ, Vaillancourt LJ.  
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### Recommendations:

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MUST READ

This paper is a delightful example of how comparative and functional genomics can be applied to study molecular plant pathogenesis, evolution, and host specialization. Genome and transcriptome sequencing of two hemibiotrophic fungal pathogen of dicots and monocots provides new insights into pathogenesis strategies. Despite the roughly equal genome copy number of CAZY enzymes in *Colletotrichum higginsianum* and *C. Graminicola*, the fungi express considerably different patterns reflecting the carbohydrate compositions of the host cells. The effector protein repertoire is also wildly divergent and reflects independent diversification and a much larger inventory in *C. Higginsianum*, perhaps linked to the breadth of host plants it can infect in contrast to the narrower *Zea* range of *C. graminicola*. Further transcriptional profiling of infection was able to show three waves of genes that reflect the appresoria for host penetration, effectors as part of establishment of biotrophic phase, and lytic enzymes to support necrotrophic growth to degrade host tissue. The wealth of new genes that can be linked to these varied processes will provide fodder for many future studies in this important microbe-plant pathogen system.

### Disclosures

None declared

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### Abstract:

*Colletotrichum* species are fungal pathogens that devastate crop plants worldwide. Host infection involves the differentiation of specialized cell types that are associated with penetration, growth inside living host cells (biotrophy) and tissue destruction (necrotrophy). We report here genome and transcriptome analyses of *Colletotrichum higginsianum* infecting *Arabidopsis thaliana* and *Colletotrichum graminicola* infecting maize. Comparative genomics showed that both fungi have large sets of pathogenicity-related genes, but families of genes encoding secreted effectors, pectin-degrading enzymes, secondary metabolism enzymes, transporters and peptidases are expanded in *C. higginsianum*. Genome-wide expression profiling revealed that these genes are transcribed in successive waves that are linked to pathogenic transitions: effectors and secondary metabolism enzymes are induced before penetration and during biotrophy, whereas most hydrolases and transporters are upregulated later, at the switch to necrotrophy. Our findings show that preinvasion perception of plant-derived signals substantially reprograms fungal gene expression and indicate previously unknown functions for particular fungal cell types.

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