

Functional analysis of mating type genes and transcriptome analysis during fruiting body development of *Botrytis cinerea*

ABSTRACT

Botrytis cinerea is a plant-pathogenic fungus producing apothecia as sexual fruiting bodies. To study the function of mating type (MAT) genes, single-gene deletion mutants were generated in both genes of the MAT1-1 locus and both genes of the MAT1-2 locus. Deletion mutants in two MAT genes were entirely sterile, while mutants in the other two MAT genes were able to develop stipes but never formed an apothecial disk. Little was known about the reprogramming of gene expression during apothecium development. We analyzed transcriptomes of sclerotia, three stages of apothecium development (primordia, stipes, and apothecial disks), and ascospores by RNA sequencing. Ten secondary metabolite gene clusters were upregulated at the onset of sexual development and downregulated in ascospores released from apothecia. Notably, more than 3,900 genes were differentially expressed in ascospores compared to mature apothecial disks. Among the genes that were upregulated in ascospores were numerous genes encoding virulence factors, which reveals that ascospores are transcriptionally primed for infection prior to their arrival on a host plant. Strikingly, the massive transcriptional changes at the initiation and completion of the sexual cycle often affected clusters of genes, rather than randomly dispersed genes. Thirty-five clusters of genes were jointly upregulated during the onset of sexual reproduction, while 99 clusters of genes (comprising >900 genes) were jointly downregulated in ascospores. These transcriptional changes coincided with changes in expression of genes encoding enzymes participating in chromatin organization, hinting at the occurrence of massive epigenetic regulation of gene expression during sexual reproduction.

Keyword: Ascospore; Epigenetic regulation; Plant disease; Sexual reproduction; Transcriptome

