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Comparative analysis of twelve
Dothideomycete plant pathogens

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Introduction
The Dothideomycetes are one of the largest and most diverse groups of fungi. Many are plant pathogens and pose a serious threat to agricultural crops grown for biofuel, food or feed. Most Dothideomycetes have only a single host and related Dothideomycete species can have very diverse host plants. Twelve Dothideomycete genomes have currently been sequenced by the Joint Genome Institute and other sequencing centers. They can be accessed via Mycosocm which has tools for comparative analysis.

Mycosocm. The web portal Mycosocm contains the genomes of all 12 sequenced Dothideomycetes, as well as 51 other fungal genomes sequenced by the JGI and other sequencing centers. Organism-specific and comparative tools are available to the user on http://jgi.doe.gov/mycosocm.

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Comparative transcriptomics. Microarray data is available for M. graminicola (pathogen of wheat, Kein et al. 2005 and 2007) and L. maculans (pathogen of oilseed rape plants, Roux et al. 2011). In both cases gene expression was analyzed during early and late stage of infection, allowing comparative analysis. There are 17 annotation terms that were over-represented in this group (p < 10^-3), meaning that they may be involved in the pathogenesis process.

Conclusions
• Genome size and repeat content vary widely in the twelve Dothideomycete genomes which are now available via Mycosocm.
• Many intra-chromosomal, but few inter-chromosomal rearrangements have taken place during Dothideomycete evolution.
• Several potentially dispensable chromosomes have been identified, similar to the ones in Mycosphaeraeae graminicola.
• Small Secreted Proteins (SSPs) are found in varying numbers across the Dothideomycetes.
• Many protein families unique to or over-represented in the Dothideomycetes have been identified.
• Comparative transcriptomics gives insight into conserved fungal responses during pathogenesis, leading to new targets to fight infections.

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