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 Mycocosm which has tools for comparative analysis.

Mycosphaerella graminicola

Mycosphaerella graminicola

Lepotosphaeria maculans

Mycosphaerella fijiensis

Dispersable chromosomes. *M. graminicola* has experimentally been shown to have chromosomes that are dispensable (not necessary for survival). These chromosomes have lower GC content, higher repeat content, lower gene density and a lower percentage of proteins with a PFAM domain. As an example, chromosome 14 is shown. Similar chromosomes (or scaffolds) have been computationally identified in other Dothideomycetes. Examples are shown here. Their dispensability will have to be confirmed in the lab.

**Comparative transcriptomics.** Microarray data is available for *M. graminicola* (pathogen of wheat; Keen et al. 2005 and 2007) and *L. maculans* (pathogen of oil seed rape plants; Rouzel 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 < 10⁻⁴), 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 Mycocosm.
- Many intra-chromosomal, but few inter-chromosomal rearrangements have occurred during evolution. This observation is called ‘mesosynteny’ and is observed in all 12 Dothideomycetes. The mechanism behind it is unknown.
- A large part of the Dothideomycete protein families (as determined by MCL clustering) has been implicated in fungus-plant interactions in several cases, for example during pathogenesis or ectomycorrhizal symbiosis. Within the Dothideomycetes there are large differences in numbers of PFAMs. The definition of SSP that was used here is < 200 amino acids, presence of a secretion signal and absence of a transmembrane domain.

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