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Publication Date
2013-03-12
Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen *Dothideomycetes*

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March 2013

The work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under Contract No. DE-AC02-05CH11231
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Introduction

The class of *Dothideomycetes* is one of the largest and most diverse groups of fungi. Many are plant pathogens and pose a serious threat to agricultural crops that are grown for biofuel, food, or feed. Most *Dothideomycetes* have only a single host plant, and related species can have very diverse hosts. Eighteen genomes of *Dothideomycetes* have currently been sequenced by the Joint Genome Institute and other sequencing centers. Here we describe the results of comparative analyses of the fungi in this group.

Effector genes involved in infection

Lifestyles are largely phylogenetically separated. This is also reflected in the gene classes that are potentially involved in plant pathogenesis (effec tors). Necrotrophs and saprotrophs generally have more effector genes than (hemi)biotrophs.

Whole-genome DNA comparison

From macro synteny to mesosynteny. Closely related species show a pattern of nearly perfect macro synteny (A). This pattern degrades in comparisons with progressively distantly related species (B-D). The syntenic regions become short and spread across scaffold pairs. This phenomenon is most predominant among *Dothideomycetes*. It has previously been called mesosynteny (Hane et al. 2011). Here we show that mesosynteny appears to be due to intra-chromosomal inversions. Very few inter-chromosomal rearrangements take place. Interestingly, simple repeats (i.e., low-complexity DNA) are over-represented near inversion breakpoints (data not shown).

Dispensable chromosomes

Several *Dothideomycetes* have (putatively) dispensable chromosomes. Eight of the 21 chromosomes of *Mycosphaerella graminicola* are dispensable (i.e. not necessary for survival). Those dispensable chromosomes are smaller, less gene-dense and more repeat-rich than the core chromosomes. Proteins encoded by genes on these chromosomes less frequently contain a Pfam domain. Their function is unknown (Gooden et al. 2011). Scaffolds with similar characteristics are also present in five other *Dothideomycetes*: *Mycosphaerella*, *Cochliobolus heterostrophus*, *Setosphaeria turcica*, *Leptosphaeria maculans*, and *Stagonospora nodorum*.

Conclusions

- The genomes of 18 *Dothideomycetes* (of which 15 are plant pathogens) are currently sequenced and available via MycoCosm.
- Necrotrophs and saprotrophs generally have more effector genes than (hemi)biotrophs.
- Some classes of effector genes are over-represented near Transposable Elements, where they are subjected to Repeat Induced Point mutations (RIP).
- This may speed up their evolution.
- During *Dothideomycete* evolution many intra-chromosomal inversions, but few inter-chromosomal rearrangements have taken place. This process may keep dispensable chromosomes intact.
- Comparative transcription data gives insight into conserved fungal responses during pathogenesis, leading to new targets to fight infections.

References


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