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Diverse life styles encoded in the genomes of eighteen *Dothideomycetes*

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The Dothideomycetes class of fungi includes many pathogens that infect a broad range of plant hosts. Here, we compare genome features of 18 different members of this class, including 6 necrotrophs, 9 (hemi)biotrophs and 3 saprotrophs, and discuss genome structure, evolution, and the diverse strategies of pathogenesis. The 18 genome sequences show dramatic variation in size due to variation in transposon expansions, but less variation in core gene content. During evolution, gene order in these genomes is changed mostly within boundaries of chromosomes by a series of inversions often surrounded by simple repeats. This is in contrast to major interchromosomal rearrangements observed in other groups of genomes. Several Dothideomycetes contain gene-poor and TE-rich putatively dispensable chromosomes of unknown function. In the current set of organisms, biotrophs and hemibiotrophs are mostly phylogenetically separated from necrotrophs and saprobes, which is also reflected in differences between gene sets represented in each group. The 18 Dothideomycetes offer a rich catalogue of genes involved in cellulose degradation, proteolysis, Cys-rich small secreted proteins and secondary metabolism, many of which are enriched in proximity of transposable elements, suggesting faster evolution because of both TE mobility and RIP effects.