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Insights into adaptations to a near-obligate nematode endoparasitic lifestyle from the finished genome of *Drechmeria coniospora*

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Although annual crop losses due to plant-parasitic nematodes are estimated at a staggering $157 billion worldwide, options for nematode pest management are very limited due to environmental safety concerns. This situation demands further research to discover effective and environmentally responsible alternatives to replace legislatively withdrawn nematicides. Biological control agents, such as nematophagous fungi, may be part of the answer when applied in the context of integrated pest management systems. Thus, understanding the mechanisms governing the interactions between nematophagous fungi and their nematode prey, and biocontrol strategies based on these interactions are key issues for crop protection. Nematophagous fungi employ three distinct predatory strategies: nematode trapping, parasitism of females and eggs, and endoparasitism. While endoparasites play key roles in controlling nematode populations in nature, their application for integrated pest management is hindered by the limited understanding of their biology. We present a comparative analysis of a high quality finished genome assembly of *Drechmeria coniospora*, a model endoparasitic nematophagous fungus, integrated with a transcriptomic study. Adaptation of *D. coniospora* to its almost completely obligate endoparasitic lifestyle led to the simplification of many orthologous gene families involved in the saprophytic trophic mode, while maintaining orthologs of most known fungal pathogen-host interaction proteins, stress response circuits and putative effectors of the small secreted protein type. The need to adhere to and penetrate the host cuticle led to a selective radiation of surface proteins and hydrolytic enzymes. Although the endoparasite has a simplified secondary metabolome, it produces a novel peptaibiotic family that shows antibacterial, antifungal and nematicidal activities. Our analyses emphasize the basic malleability of the *D. coniospora* genome: loss of genes advantageous for the saprophytic lifestyle; modulation of elements that its cohort species utilize for entomopathogenesis; and expansion of protein families necessary for the nematode endoparasitic lifestyle.

Biography

Yuquan Xu has completed his PhD from China Agricultural University and Post-doctoral studies from the University of Arizona and University of California, San Diego. His research focuses on combinatorial biosynthesis of fungal polyketides. He has published more than 23 papers in reputed journals.

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