

Genomics of non-model fungi: opportunities and challenges

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ABSTRACT:

With the advent of high-throughput DNA sequencing and bioinformatic analyses, there is a substantial growth of generated fungal genomes not only for genetic models but also many other non-model species. For the latter case, genomics can be utilized as a tool to understand fungal evolution through adequate taxon sampling from a lineage of interest. In addition, comparative genomics of multiple species can determine if knowledge from a model organism can be applied for a broader context. In this presentation, I will illustrate cases how genomic sampling of non-model species can be a powerful tool for fungal biology research using smut fungi as the system. Smut fungi (Ustilaginomycotina) are a group of pathogenic fungi that primarily infect cereal crops. The corn smut fungus *Ustilago maydis* serves as a renowned model organism for studying genetic recombination, fungal dimorphism and plant-microbe interactions. However, in terms of biodiversity, Ustilaginomycotina is one of the most overlooked lineages in the fungal tree of life. I will first discuss taxonomy and systematics of smut fungi through the lens of phylogenetics, phylogenomics and comparative genomics. The second part will focus on multispecies comparative studies to understand fungal dimorphism, a phenomenon by which a fungus can grow both as a unicellular yeast form and as a multicellular hyphal form. I will conclude by briefly talking about my studies in other group of fungi, as well as discussing challenges I encountered when conducting genomic studies in non-model fungi.

KEYWORDS:

Biodiversity; Smut fungi; Fungal dimorphism; Comparative analyses; Evolutionary biology