

Basidiomycete Genomics

Genomes and post-genomic tools have an impact on every field of biology, and this is particularly true for the field of basidiomycete research. While these fungi have a long history of research, several factors have caused a slower progress in understanding specific biological features when compared to the research in ascomycete fungi. One reason for this is that no basidiomycete fungus has a research community as large as for the various 'model' ascomycetes, such as several *Aspergillus nidulans*, *A. niger*, *Aspergillus fumigatus*, *Aspergillus oryzae*, *Neurospora crassa*, *Trichoderma reesei* or *Penicillium chrysogenum*. In addition, genetic modification has been challenging in many basidiomycete fungi, especially in wood decaying white rot and brown rot species.

A significant moment in basidiomycete research was the publication of the *Phanerochaete chrysosporium* (Martinez, Larrondo et al. 2004) and *Ustilago maydis* (Kämper, Kahmann et al. 2006) genomes, as this provided a wealth of information on the molecular basis of many biological processes. It also revealed both similarities with and differences to ascomycete fungi, for which several genomes were already available at the time.

During the past 10 years, basidiomycete genomics has developed exponentially. While initially the genomes of individual species were sequenced (e.g. (Eastwood, Floudas et al. 2011) (Morin, Kohler et al. 2012) (Ohm, de Jong et al. 2010)), sequencing has more recently switched to increasingly large sets of species enabling detailed comparative studies (e.g. (Duplessis, Cuomo et al. 2011) (Floudas, Binder et al. 2012) (Binder, Justo et al. 2013) (Kohler, Kuo et al. 2015)), not only at the genomic but also at the transcriptomic and proteomic level. One result of this is that our understanding of basidiomycete biology has advanced significantly on many topics. Another important outcome has been that these large genome projects have brought the community together in consortia unprecedented before the genomic era.

These developments were the reason for us to suggest a special issue in FGB on Basidiomycete Genomics, to showcase some of the advances that have been made over the last two decades. The issue covers a range of topics, such as mating, plant pathogenicity and commercial cultivation of mushrooms, as well as a range of life styles, such as white and brown rot, and rusts. We would like to thank all authors for contributing their studies, and Nancy Keller and the staff at Elsevier for their support in preparing this issue.

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