

PREFACE



FUNGAL-PLANT INTERACTIONS: A NEVER ENDING STORY OF FRIENDS AND FOES

The fungi are a very large and highly diverse group of microorganisms. They have successfully exploited many different habitats to obtain preformed organic compounds as nutrients as they are heterotrophic for carbon. Amongst these habitats, plants are rich sources of carbon and other nutrients that are, to no one's surprise, host to diverse fungal communities both above and below the ground. Arbuscular mycorrhizal fungi are likely to have accompanied the ancestral plants that emigrated from water to land 400 hundred million years ago. Many of their descendant contemporary fungi are adapted to take advantage of the nutrient niches afforded to them by the huge diversity of plants all over the earth. As saprophytes, they break down and decompose every parts of plants through the release of a large set of efficient degradative enzymes. Solubilized compounds are then absorbed and used for growth and development. Many fungi interact with plants, providing supplies of vital nutrients, such as nitrogen and phosphorus, which increased improve plant health and promote plant growth. Others use the resources of living plants directly for their own needs causing damage, disease, and even the death of those plants. Through most of history, people have feared fungi. Despite crop protection chemicals, available disease-resistant crop varieties, and novel cultural practices, an estimated 15% of global crop production is lost to pre-harvest plant disease. A prerequisite for learning how fungi interact with plants to promote their growth or cause damage is to have their complete blueprint, specifically the genome sequence that reveals the gene repertoire and the genes expressed during the interaction. In this volume, we address some of the genomic insights gained into the biology of world's most important groups of fungi interacting with plants and update the state of knowledge of the genomics of major fungal-plant interactions.

The first two chapters (Kohler & Tisserant, 2014; Kuo, Bushnell, & Grigoriev, 2014) provide up-to-date overviews of the next-generation sequencing techniques and bioinformatic tools deployed for studying fungal genomes and transcriptome—paving the way towards the 1000 fungal genomes. Chapter 3 reviews how genomics enables a glimpse into the

putative role of transposable elements in the evolution and environmental adaptation of plant-interacting fungi (Grandaubert, Balesdent, & Rouxel, 2014).

The following chapters are dedicated to case studies of the genomics of devastating plant fungal pathogens. In Chapter 4, Hacquard (2014) describes how comparative genomics of powdery mildews was used to highlight the impact of the reproductive mode and the evolutionary history of these plant parasites on the evolution of obligate biotrophy. As shown in Chapter 5, comparative analysis of the genomes of smut fungi, as well as transcriptome profiling approaches, allowed the identification of regulatory elements controlling pathogenic development as well as of secreted effector genes with important functions in plant interaction (Doehleman, Schirawski, & Kämper, 2014). In Chapter 6, Duplessis, Bakkeren, and Hamelin (2014) provide an overview of the current knowledge on rust genomics and highlight how next-generation sequencing techniques are moving this field forward, providing new avenues in the understanding of fungal biotrophy.

Symbiotic fungi are the focus of four chapters. The evolutionary history and genomes of the ectomycorrhizal truffles are deciphered by Payen, Murat, and Bonito (2014) in Chapter 7. In Chapter 8, Hess and Pringle (2014) describe the natural histories and the genomes of *Amanita* species. The long-awaited genome of the model arbuscular mycorrhizal fungus *Rhizophagus irregularis* is the focus of Malbreil, Tisserant, Martin, and Roux's (2014). In Chapter 10, Schardl et al. (2014) provide a wide-ranging coverage of members of the Clavicipitaceae in Chapter 11 and delve deeply into evolutionary scenarios relating to the origins of ergot alkaloids synthesis.

Chapter 11 (Lundell, Mäkelä, de Vries, & Hilden, 2014) and Chapter 12 (Lind, Stenlid, & Olson, 2014) are devoted to wood-decaying and litter-decomposing fungi. They describe the formidable complexity of the wood-decay-related machineries in Basidiomycota and their key role in carbon cycling in terrestrial ecosystems.

In the final chapter, Stukenbrock (2014) demonstrates how the history of species and the underlying genetics associated with the establishment of reproductive isolation can be unravelled by using large-scale comparative genomics.

I am especially indebted and grateful to these authors for the high quality of their contributions. Thanks to their effort, we have produced the most complete and up-to-date treatment of the genomics of plant-fungal interactions. This book should provide guidance for future research.

I hope that this book will serve as a primary research reference for researchers and research managers working in the expanding field of

mycology, fungal genomics, as well as plant–microbe interactions. It should provide a useful resource for experienced as well as new researchers and students.

ACKNOWLEDGEMENT

F. M. M.'s research group is part of the Laboratory of Excellence ARBRE (ANR-11-LABX-0002-01).

FRANCIS M. MARTIN

Institut National de la Recherche Agronomique (INRA),
UMR 1136 INRA/Lorraine University,
Interactions Arbres/Micro-organismes,
Centre de Nancy, Champenoux,
France

REFERENCES

- Doehleman, G., Schirawski, J., & Kämper, J. (2014). Functional genomics of smut fungi—From genome sequencing to protein function. *Advances in Botanical Research*, 70, 143–172.
- Duplessis, S., Bakkeren, G., & Hamelin, R. (2014). Advancing knowledge on biology of rust fungi through genomics. *Advances in Botanical Research*, 70, 173–209.
- Grandaubert, J., Balesdent, M. H., & Rouxel, T. (2014). Evolutionary and adaptive role of transposable elements in fungal genomes. *Advances in Botanical Research*, 70, 79–107.
- Hacquard, S. (2014). The genomics of powdery mildew fungi: Past achievements, present status and future prospects. *Advances in Botanical Research*, 70, 109–142.
- Hess, J., & Pringle, A. (2014). The natural histories of species and their genomes: Asymbiotic and ectomycorrhizal *Amanita* fungi. *Advances in Botanical Research*, 70, 235–257.
- Kohler, A., & Tisserant, E. (2014). Exploring the transcriptome of mycorrhizal interactions. *Advances in Botanical Research*, 70, 53–78.
- Kuo, A., Bushnell, B., & Grigoriev, I. (2014). Fungal genomics: Sequencing and annotation. *Advances in Botanical Research*, 70, 1–52.
- Lind, M., Stenlid, J., & Olson, A. (2014). *Heterobasidion annosum* s.l. genomics. *Advances in Botanical Research*, 70, 371–396.
- Lundell, T., Mäkelä, M., de Vries, R., & Hilden, K. (2014). Genomics, life-styles and future prospects of wood-decaying and litter-decomposing Basidiomycota. *Advances in Botanical Research*, 70, 329–370.
- Malbreil, M., Tisserant, E., Martin, F., & Roux, C. (2014). Genomics of arbuscular mycorrhizal fungi: Out of the shadows. *Advances in Botanical Research*, 70, 259–290.
- Payen, T., Murat, C., & Bonito, G. (2014). Truffle phylogenomics: New insights into truffle evolution and truffle life cycle. *Advances in Botanical Research*, 70, 211–234.
- Schardl, C. L., Young, C. A., Moore, N., Krom, N., Dupont, P. Y., Pan, J., et al. (2014). Genomes of plant-associated Clavicipitaceae. *Advances in Botanical Research*, 70, 291–327.
- Stukenbrock, E. (2014). Speciation genomics of fungal plant pathogens. *Advances in Botanical Research*, 70, 397–423.