

Preface

The distribution of organisms has fascinated scientists and naturalists since the times of Karl Linné (1707–1778), Alexander von Humboldt (1769–1859), Charles Darwin (1809–1882) and Alfred Wallace (1823–1913), who can be regarded as the founding fathers of biogeography. These brilliant scientists and their followers published thousands of studies on the distribution patterns of macroscopic organisms such as plants and animals and, to some extent, macroscopic fungi. Until the late 1990s, information about the distribution of microscopic information was extremely scant and the understanding was often biased due to the inability to distinguish biological species. The advent of molecular DNA-based identification in 1990s and development of high-throughput methods in late 2000s enabled, for the first time, to shed light on the ecology and biogeography of microorganisms. A vast majority of these studies concerned bacteria and other free-living microorganisms, either providing support or conflicting counterevidence to the hypothesis of Lourens Baas Becking (1895–1963) that ‘Everything is everywhere, but, the environment selects’). Because mycorrhizal symbiosis is essential for plant mineral nutrition and ecosystem nutrient cycling and the distribution of fungal symbionts is determined by the host plant, this fragmented knowledge motivated me to compile recent state-of-the-art information about the biogeographic aspects of fungi and their plant associations. This has been my topic of curriculum and field of research since 2001, which provided me a good position for such a challenge.

My initial idealistic view about the book was to cover all topics that are related to the biogeography of mycorrhiza, from definitions of the mycorrhizal groups and methods, to local processes such as assembly rules, dispersal mechanisms, means of reproduction and gene flow, to global patterns including climate effects, biogeography of representative groups, macroecology as well as global overviews and syntheses. Although a few renowned researchers declined to contribute, around 80% of the planned chapters were covered and a majority of these go beyond the state of the art in our current knowledge or provide completely novel insights into the biogeographic aspects of mycorrhizal plants and fungi. Hereby I also express my sincere gratitude to all expert reviewers (2–5 for each chapter), who readily

accepted the refereeing task and greatly helped to improve most chapters anonymously or non-anonymously.

The book is arranged so that it starts with overviews of methods and local processes, continues with regional and global-scale reviews and meta-analyses of specific groups and ends with more general syntheses in macroecology. Although all above-described chapters represent separate reviews, syntheses, extended case studies or a combination of these, many of the chapters synergistically add complementary or additive information to our overall knowledge. Chapter 1 provides an excellent overview of the most up-to-date methods in biogeography and phylogeography with several novel examples based on the poison-cap (*Amanita*) mushrooms. Chapters 2 and 3, respectively, review the current information about population ecology and dispersal mechanisms of ectomycorrhizal fungi and collectively indicate that the means of dispersal of fungi have a strong effect on the fungal population genetics, which has a major influence on population ecology, speciation and large-scale biogeographic patterns. Chapter 4 gives a novel synthesis about the mechanisms of coexistence among ectomycorrhizal symbionts on a fine scale, pointing to the particular importance of host plants. Chapter 5 reviews the mechanisms driving fungal diversity and composition of all mycorrhiza types from landscape to regional scale, indicating context-dependent latitudinal effects. These two chapters indicate that the main drivers of diversity and composition of EcM fungi differ greatly across the geographic scale, with increasing importance of host, edaphic, climatic and historical factors at larger scales. Chapter 6 is solely focused on ectomycorrhizal fungi, revealing several novel phylogenetic lineages and providing instructions for their high-throughput sequencing-based identification. Chapter 7 reviews the distribution of arbuscular mycorrhizal fungi and presents a novel global-scale niche analysis of the most common taxa in the context of species recognition. Chapters 8 and 9 provide timely reviews of the global distribution of orchid mycorrhiza and ericoid mycorrhiza, respectively, pointing to the gaps in knowledge and urgent research needs. Chapter 10 reviews the current state of knowledge about the ecology and biogeography of non-mycorrhizal root endophytes. The three latter chapters provide evidence that biogeographic patterns of ericoid mycorrhizal fungi, arbuscular mycorrhizal fungi and root endophytes have a lot in common in overall biogeographic patterns that, taken together, differ from ectomycorrhizal fungi as based on previous studies. Chapter 11 presents an overview of the global distribution of studies that determine mycorrhizal status and reviews recent knowledge about factors underlying the level of mycorrhizal colonization on a global scale. Chapter 12 strongly complements with Chap. 9 by providing an overview of the taxonomy, ecology and biogeography of the enigmatic basidiomycete genus *Tulasnella*, the main orchid root symbiont. Chapters 13, 14 and 15 focus on the biogeography, recognition of species and population ecology of the ectomycorrhizal fungi from the genus *Laccaria*, the asexual *Cenococcum geophilum* complex and the gourmet mushroom *Tricholoma matsutake*, respectively. Together with Chap. 1 and some recent overviews, these three chapters indicate that phylogenetic history and diversification patterns may strongly differ among ectomycorrhizal fungal groups that are potentially related to ecological

conditions, historical origin and reproductive biology. Chapter 16 describes the low mycobiont diversity and biogeography of a stress-tolerant tropical tree *Coccoloba uvifera* in the Caribbean basin and reveals several events of historical fungal host shifts from North American trees. Chapter 17 reviews the distribution of mycorrhizal types and alternative root nutritional strategies in Australia in a phylogenetic and historical perspective, pinpointing to multiple Australian plant groups that may exhibit hitherto overlooked mycorrhiza-like fungus–plant root associations. Chapter 18 presents a reanalysis of global diversity of ectomycorrhizal fungi from the perspective of dark diversity, species pool and community completeness, indicating the additional value of these alternative measures of diversity. Chapters 19 and 20 define the evolutionary lineages of ectomycorrhizal plant groups and illustrate their historical and present-day distribution patterns. Furthermore, Chap. 20 synthesizes the invasion potential of ectomycorrhizal plants considering probable global change scenarios. Finally, Chap. 21 provides a timely update about the principal definition and global distribution of mycorrhizal types and non-mycorrhizal plants in relation to habitat conditions and plant life form, with a strong additional focus on mycorrhiza misdiagnosis issues.

Taken together, this book provides a comprehensive overview of the distribution patterns of all mycorrhizal types, with individual contributions seeking to explain the underlying causes such as differences in dispersal mechanisms and phylogenetic and historical constraints. As major novelties, the book describes best practices and novel methods in biogeographic and phylogeographic studies (Chap. 1) and sets standards to the overall definition and interpretation of mycorrhizal symbiosis in plants (Chap. 21), including the novel treatment of ectomycorrhizal plant species in phylogenetically defined groups (Chap. 19), as well as revising this information for mycorrhizal fungi (Chap. 6).

The reviews and syntheses covered in this book open new perspectives in plant and fungal ecology and biogeography. Information about the mycorrhizal habit of plants enables construction of global distribution maps of mycorrhizal symbiosis when integrated with data about vegetation structure and density. Furthermore, knowledge about the distribution of mycorrhizal plants and fungi and their putative functional capacities allows modelling of soil processes in order to understand the role of mycorrhizal types in determining patterns of carbon and soil nutrient cycling from landscape to global scale and evaluating the shifts in these mycorrhiza-mediated processes under global change. The so far missing information about the driving forces of population dynamics, intraspecific and interspecific competition and community assembly rules would greatly improve our understanding of spatial and temporal turnover in fungal communities in the evolutionary perspective. Due to striking differences in ecophysiology and reproductive biology among fungi representing different mycorrhizal types, the evolutionary and biogeographic processes may differ greatly among these groups of fungi and urgently warrant further fundamental research.

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