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Conference Abstract

When Fungal Blind Spots Spill Over: How Knowledge Gaps Undermine Invasion Science and Conservation

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Abstract

Knowledge gaps in fungal biodiversity constrain both conservation efforts and progress in invasion science. Fungi and fungus-like organisms represent an increasingly recognised but still underrepresented component of biological invasions, with the potential to strongly affect native biota, ecosystem functioning, and human livelihoods. Non-native pathogens may encounter naïve hosts, potentially causing significant declines in native species and altering communities. Examples include ash dieback in Europe, myrtle rust in the Southern Hemisphere, and chytridiomycosis impacting amphibians worldwide. Co-introduced ectomycorrhizal fungi can facilitate plant invasions, as shown for pines in the Southern Hemisphere, while saprobes influence decomposition processes and nutrient cycling. Yet the broader consequences of fungal invasions for native fungal communities and the ecosystem functions and services they underpin remain largely unexplored.

Invasion science has historically focused on plants and vertebrates, and although fungi are increasingly receiving attention, major knowledge shortfalls in species diversity, geographic distributions, and host associations continue to limit progress. Non-native species checklists are strongly biased towards plant pathogens. Ectomycorrhizal fungi, which—due to their close host associations—are expected to follow similar introduction

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pathways, are much less well represented. A global quantification of non-native plant pathogen–host associations shows that over half of all recorded associations in non-native ranges involve novel associations with native plants or co-xenic associations with non-native plants that do not co-occur in the pathogen's native range. Strikingly, over 40% of records cannot be confidently classified due to insufficient information on pathogen biogeography, also highlighting gaps in knowledge of hosts in native ranges. These limitations may bias estimates of host breadth and host shifts, weaken risk assessments, and propagate into conservation decisions that rely on robust distributional and interaction data.

These examples highlight how incomplete knowledge of fungal diversity and distribution constrains both conservation and the capacity to anticipate and manage biological invasions of fungi. Addressing these gaps through coordinated monitoring, adherence to best practices and standards, and the development of interoperable, curated datasets linking occurrence data, host associations, and biogeographic metadata will improve the ability to detect, understand, and mitigate fungal invasions. Ultimately, a holistic perspective on fungal biodiversity recognises that conservation and invasion science are mutually dependent: progress in one domain depends on progress in the other.

Keywords

knowledge gaps - fungal invasions - host association - co-introduction - spillover - Oomycota - Eumycota - native range

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Conflicts of interest

The authors have declared that no competing interests exist.