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Animal-associated fungi: Editorial

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ABSTRACT

Of 1882 fungal species described in 2019, only 3.5% were animal-associated. This percentage is representative of the poor understanding we have of this group of fungi, which are ephemeral, sometimes inconspicuous, and difficult to access, while often requiring specialized methods for their study. Following a two-session symposium on animal-associated fungi during the 2019 Annual Meeting of the Mycological Society of America, this special issue presents the work of 61 researchers in 16 countries. Twelve articles cover animal-associated fungi among Ascomycota, Basidiomycota, and Neocallimastigomycota—describing 29 new species, presenting new evolutionary hypotheses, and unearthing new ecological data.

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Approximately 138 000 species of fungi have been formally described (Kirk 2019), but many taxonomic groups remain poorly understood. In their overview of fungal biodiversity, Mueller and Schmitt (2007) compared the number of described species with that of estimated species for major groups of fungi; for insect-associated species, the authors revealed that a meager 1.5% were described. Of 1882 newly described fungal species in 2019, only 3.5% were associated with animals and included 48 species of Sordariomycetes, 14 Laboulbeniomycetes, three Kickxellomycetes, and one Saccharomycetes (Cheek et al. 2020). Because of their ephemeral lifestyle and sometimes inconspicuous nature, it comes as no surprise that global fungal diversity estimates and higher-taxonomy phylogenetic studies often neglect animal-associated fungi. These fungi are notoriously difficult to access and often require special methods for microscopy, culturing (when possible), and DNA-based molecular techniques. Increasing knowledge of interactions between animals and fungi helps mycologists understand how fungi contribute to ecosystem function.

This issue honors the wonderful improvements that have been made over the last few years in the study of animal-associated fungi. The use of molecular phylogenetics has immensely shaped the direction of the field; whereas alpha-taxonomy reigned the field up to a few years ago, a polyphasic approach has largely taken over, and the generation of the first genome-scale data will provide yet another toolbox to answering many questions in studying interactions of parasitic fungi and their animal hosts. The inspiration for this issue comes from a symposium held at the 2019 Annual Meeting of the

Mycological Society of America in Minneapolis, Minnesota. Researchers reflecting different stages of career (graduate students, postdocs, researchers, and tenure-track faculty) and diversity (male, female, Latino, white, and first-generation college students) presented their work during two sessions: (i) Functional Insights into Fungal Symbionts of Insects and (ii) Exploring Diversity and Biology of Animal-Associated Fungi. The culmination of the enthusiasm expressed by organizers, presenters, and attendees is this special issue, which comprises 12 articles by 61 authors at 40 different institutions and affiliations in 16 countries.

The issue starts with a contribution by Blackwell et al. (2020) who disentangle the taxonomic confusions that have long surrounded the arthropod-associated Laboulbeniomycetes. The authors discuss premolecular and DNA-based evolutionary hypotheses and present a new phylogenetic reconstruction of the class, which now includes three orders and two informally named clades. Macias et al. (2020) then employ molecular phylogenetic data and morphology to investigate whether *Massospora*—a genus of obligate, sexually transmitted pathogens of many cicada species—is monophyletic and to delimit species boundaries. The next article, by Elliott et al. (2020b), explores animal-fungus interactions from another angle, with a focus on mycophagy. By studying fecal samples of the Australian-endemic Hastings River mouse (*Pseudomys oralis*), the authors present new insights into the diet of this species and link its role as a disperser of ectomycorrhizal fungi to the health of ecosystems. Using DNA barcoding, phylogenetic analyses, and morphology,

Koch et al. (2020) investigate species richness and reveal two undescribed taxa of rhizomorph-forming species of Marasmiineae that are used by birds in nest construction in the Neo- and Afrotropics. In the next article, Mayers et al. (2020) characterize the mycangial fungal mutualists of members of the ambrosia beetle tribe Xyloterini (Curculionidae, Scolytinae) and describe a new genus and four new species.

The following two articles focus on *Ophiocordyceps*, a genus of approximately 240 described species that attack ants worldwide, including “zombie-ant fungi” with the capacity to manipulate the behavior of their hosts. Following fieldwork in Ghana and Brazil, Araújo et al. (2020) apply molecular phylogenetic, ecological, and morphological data to delimit species within *Ophiocordyceps* subgenus *Neocordyceps*. Next, based on the placement of *Desmidiospora myrmecophila* among isolates of *Ophiocordyceps* spp. in a four-locus dataset of Ophiocordycipitaceae, Saltamachia and Araújo (2020) propose a new synonym for this species, *Ophiocordyceps desmidiospora*, following the One Fungus One Name (1F1N) principle (Hawksworth et al. 2011).

The next couple of articles combine morphological data with molecular phylogenetic studies in describing new species for science. Gutierrez et al. (2020) describe a new species of *Herpomyces* from Argentina parasitic on *Periplaneta fuliginosa*, the smokybrown cockroach. *Herpomyces spegazzinii* is named to honor the legacy of Dr. Carlos Luis Spegazzini, whose contributions to the knowledge of South American Laboulbeniales are unmatched. Liu et al. (2020) not only describe and illustrate a new species of *Gloeandromyces* (Laboulbeniales) from *Mastoptera guimaraesi* bat flies in Ecuador and Panama but also discuss the use of secondary barcodes in Laboulbeniomycetes taxonomy. Elliott et al. (2020a) describe a new truffle species (*Hysterangium bonobo*) fed on by bonobos in the rainforests of the Democratic Republic of the Congo. Hanafy et al. (2020) propose eight species in seven newly described genera of Neocallimastigomycota (*Agriosomyces*, *Aklioshbomyces*, *Capellomyces*, *Ghazallomyces*, *Joblinomyces*, *Khoyollomyces*, and *Tahromyces*), isolated from fecal samples of herbivores in the United States, Wales, and India. Finally, Jankowiak et al. (2020) present the results of their fungal surveys of bark beetles, cerambycid beetles, and weevils associated with conifers in Norway, Poland, and Russia, uncovering seven undescribed species and two common, previously described species of *Graphilbum* (Sordariomycetes, Ophiostomatales).

In all, eight new genera and 29 new species are introduced in this issue. Of those, eight species belong to the phylum Neocallimastigomycota, 16 to class

Sordariomycetes, two to class Laboulbeniomycetes (Ascomycota), and three to class Agaricomycetes (Basidiomycota). Despite these contributions, the diversity of animal-associated fungi remains largely uncharacterized, as we are only beginning to scratch the surface of these complex systems. Similarly, ambrosia beetle fungal symbionts and members of the Neocallimastigomycota are still vastly overlooked despite much progress over the past decade. The studies presented in this special issue provide a glimpse of the biodiversity and complexity of fungal communities associated with animals by using an array of techniques, tools, and sequence data. It is our hope that with this issue we are able to share our passion for these most enigmatic fungi and encourage a new generation of mycologists to continue studying them.

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