2023 International Congress on Invertebrate Pathology and Microbial Control & 55th Annual Meeting of the Society for

55th Annual Meeting of the Society for Invertebrate Pathology



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Program and Abstracts









targeting agricultural pests, housing over 14,000 fungi and protistan microorganisms isolated from insects, spiders, nematodes, mites, and other invertebrates. Optimizing use of these organisms for biocontrol requires selection of strains with suitable host specificity (i.e., small non-target effects on other insects) that are not toxic to humans and other wildlife. Associated metadata on pathogen hostassociations, substrate, and collection location can guide initial selection of appropriate strains for development, but the predictive value of this information for biocontrol efficacy is limited. A better understanding of the genetic basis of biocontrol phenotypes and a phylogenomic framework for predicting them is required. This understanding can also support genetic modifications of fungal strains, offering new avenues to enhance biocontrol, including improved virulence, host-specificity, and survival in field settings. Entomopathogenic fungi continue to garner intense research and applied interest across multiple sectors, with increasing information generated annually on their efficacy, chemical repertoires, and genetic content. In particular, the genomes of entomopathogenic fungi are now routinely assembled without centralization of these impactful resources. We are developing a pipeline for synthesizing publicly available genomic, genetic, and biochemical resources for ARSEF isolates and developing best practices for the generation and sharing of biological control phenotypic data. This synthesis will provide a broad foundation for evaluating potential uses of entomopathogenic fungi in this growing collection. We envision these resources will enable researchers to more efficiently identify genetic factors underlying key biocontrol phenotypes, expedite the selection of successful biocontrol agents, and facilitate genetic manipulations to improve effectiveness.

POSTER SESSION. Wednesday, 13:30 - 15:30 PF-2

Large prevalence of Batkoa sp. (Entomophthorales) in Stomoxys populations in Reunion Island

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In Reunion Island and throughout the world, cattle farms are heavily affected by outbreaks of *Stomoxys* stable flies, which have a very serious impact on the health and economic situation of these farms. In 1981, a first observation mentioned a fungus infecting stable flies in Reunion. The objectives of this study were 1) to precise the distribution of the fungus in the island's cattle farms, 2) to characterize the fungus morphologically and molecularly and 3) to carry out pathogenicity tests by experimental transmission. A field survey carried out in 2021, revealed the presence of infected stable flies in all environments and altitudes of the island. More than 80 % of the farms were positive, revealing that this fungus is responsible for an island-wide infection, potentially regulating *Stomoxys* populations. Moreover, up to twenty *Stomoxys* speciments could be found stuck to a single leaf. The fungus was also observed on other flies species (*Calliphora* sp., *Lucilia* sp.).

In the laboratory, this fungus could be grown on different solid and liquid culture media. Morphological observations revealed an *Entomophthorales* producing round conidia with a papilla, simple conidiophores and rhizoids. Taxonomic classification based on

morphological characteristics led to *Batkoa apiculata*. Molecular analysis, while confirming that the fungus belongs to the genus *Batkoa* (Humber, 1989), revealed that the most related strains are not associated with any described species or clustered with species not yet accepted such as *B. australiensis*. The ability of the fungus to infect adult of *Stomoxys niger niger* and *Stomoxys calcitrans* was demonstrated using a conidia shower from infected *Stomoxys*. To our knowledge, this is the first *Batkoa* disease described in natural populations of *Stomoxys*, remarkable for its intensity and durability. Further studies are needed to determine its potential as a biological control agent against stable flies in Réunion and elsewhere.

POSTER SESSION. Wednesday, 13:30 - 15:30 PF-3

Isolation and genome sequencing of an Ophiocordycipitaceae mutualist from an Entomophaga-infected leafhopper

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Entomopathogenic fungi are defined by their ability to penetrate and kill insects. However, some of these entomopathogenic fungi are also capable of developing mutualistic partnerships with plants and insects in their native environment. There have been numerous examples, particularly in sap-feeding insects, where mutualistic bacterial symbionts have been supplanted by "yeast-like symbionts" (YLS). These fungal symbionts are characterized by blastosporelike budding, occupation of discrete host tissues and vertical transmission. YLS development mirrors hypocrealean pathogen development in insect hemolymph, and YLS are most often identified as members of the family Ophiocordycipitaceae. A leafhopper (Draeculacephala spp.) epizootic caused by an Entomophaga sp. was observed in Ohio in 2021 on iNaturalist, and we investigated this pathogen. During this investigation, stained cross-sections of the host body revealed these leaf hoppers were co-infected with a YLS interspersed among Entomophaga sp. hyphal bodies. Entomophthoralean fungi are fastidious, requiring complex medium for isolation and culturing. During unsuccessful attempts to culture the Entomophaga sp., the YLS was isolated in Grace's insect medium as blastospores. This fungus was identified as a novel YLS in the Ophiocordycipitaceae, and demonstrated reduced and slow hyphal growth on complex solid medium, typically used for culturing entomophthoralean fungi. A 34-Mb draft genome was assembled using Illumina NextSeq, resulting in a BUSCO completeness assessment of 97.7% using the ascomycota odb10 dataset. Phylogenetic and genome wide comparisons with other members of the Ophiocordycipitaceae confirm the placement of our fungus among this diverse family of parasitic and mutualistic fungi. Many questions remain regarding how fungi navigate this perpendicular shift in transmission, but it is clear that these symbiotic replacements are recurrent and recent. This genome and our comparative analysis will provide insight into this evolutionary transition, which represents one outcome of in insecta microbial conflict.