



# Using a large spatial database to explore relationships between fungal pathogens and their insect hosts

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## Introduction

This project relies on the USDA-ARS Collection of Entomopathogenic Fungal Cultures (ARSEF) database, begun as a research collection at the University of Maine in the early 1970s. ARSEF serves as a depot for entomopathogenic fungal specimens. The database contains nearly 8,000 fungal pathogen-insect host entries. Each entry includes taxonomy and geographic location. Here, we explore the dataset for macroecological patterns in host-pathogen relationships and major biases in the data.

## Objectives

- Identify patterns and biases in data by
  - Geography
  - Host taxonomy
  - Pathogen taxonomy
- Generate hypotheses about the distribution of generalists and specialists in dataset
- Visualize data

## Methods

### Data cleaning

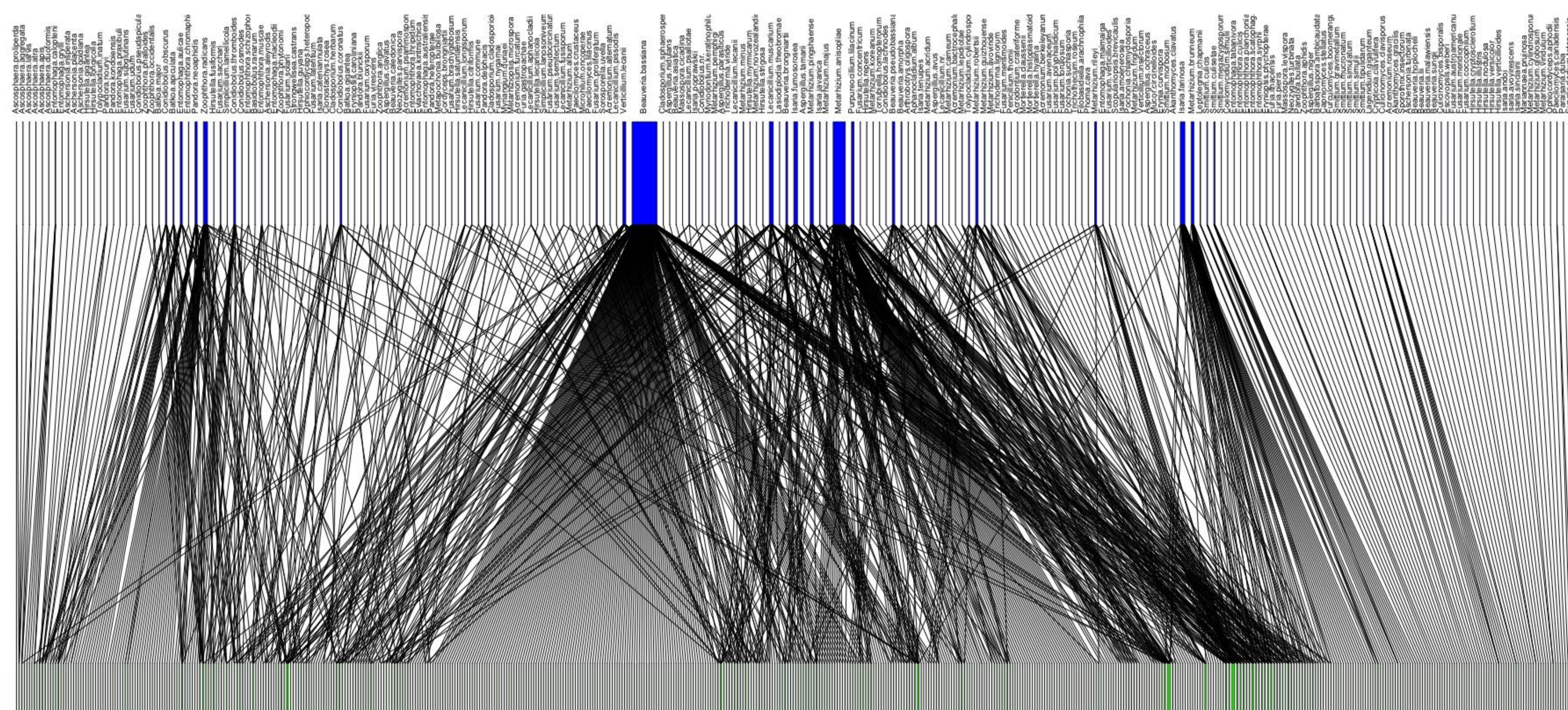
- We removed entries with hosts or pathogens not resolved to species.

### We summarized by insect order and fungal class

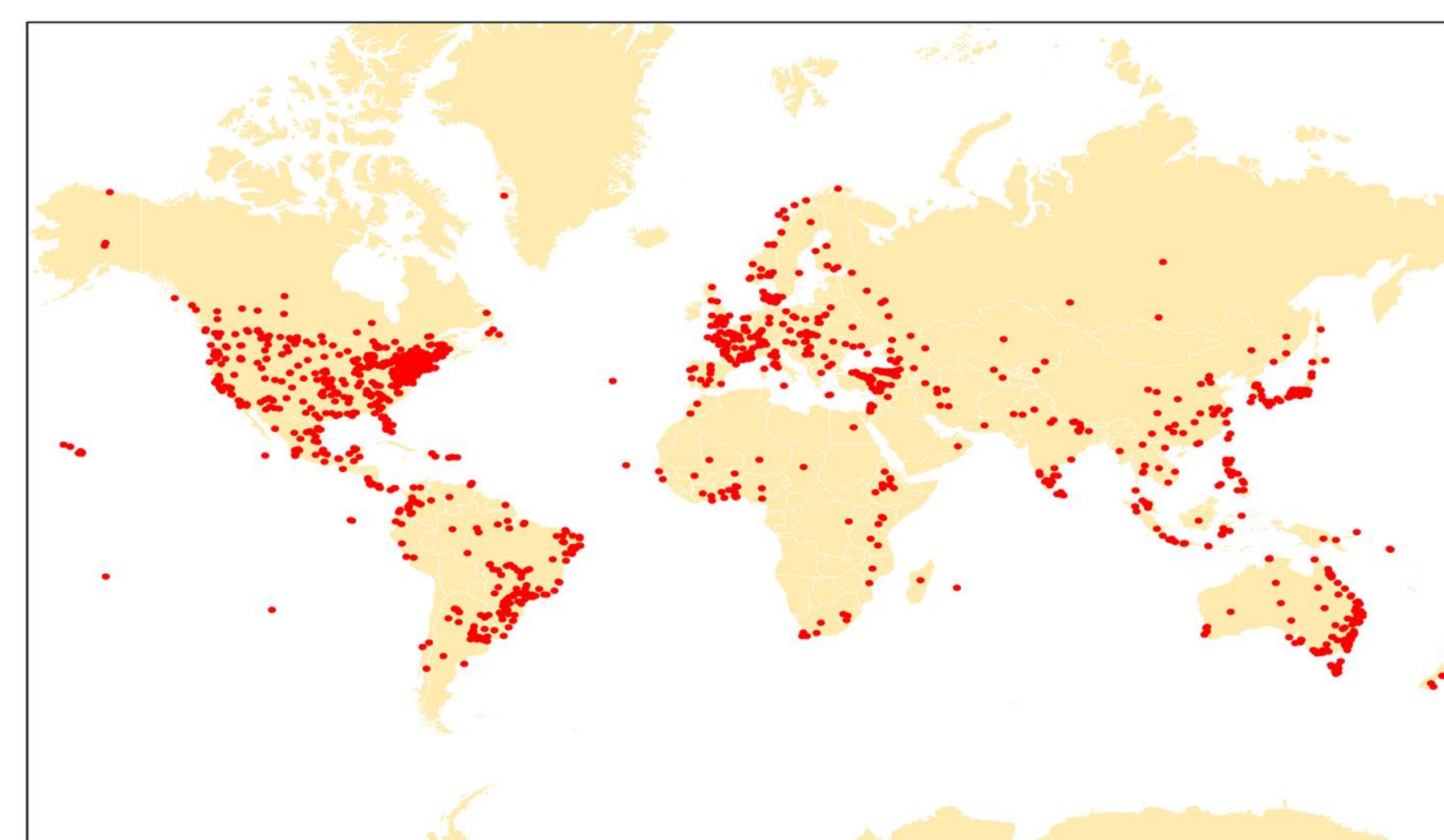
- Host-pathogen pairs
- Geographic locations
- Number of unique pathogens by host
- Number of unique hosts by pathogen

We constructed a bipartite network to visualize the entire set of interactions.

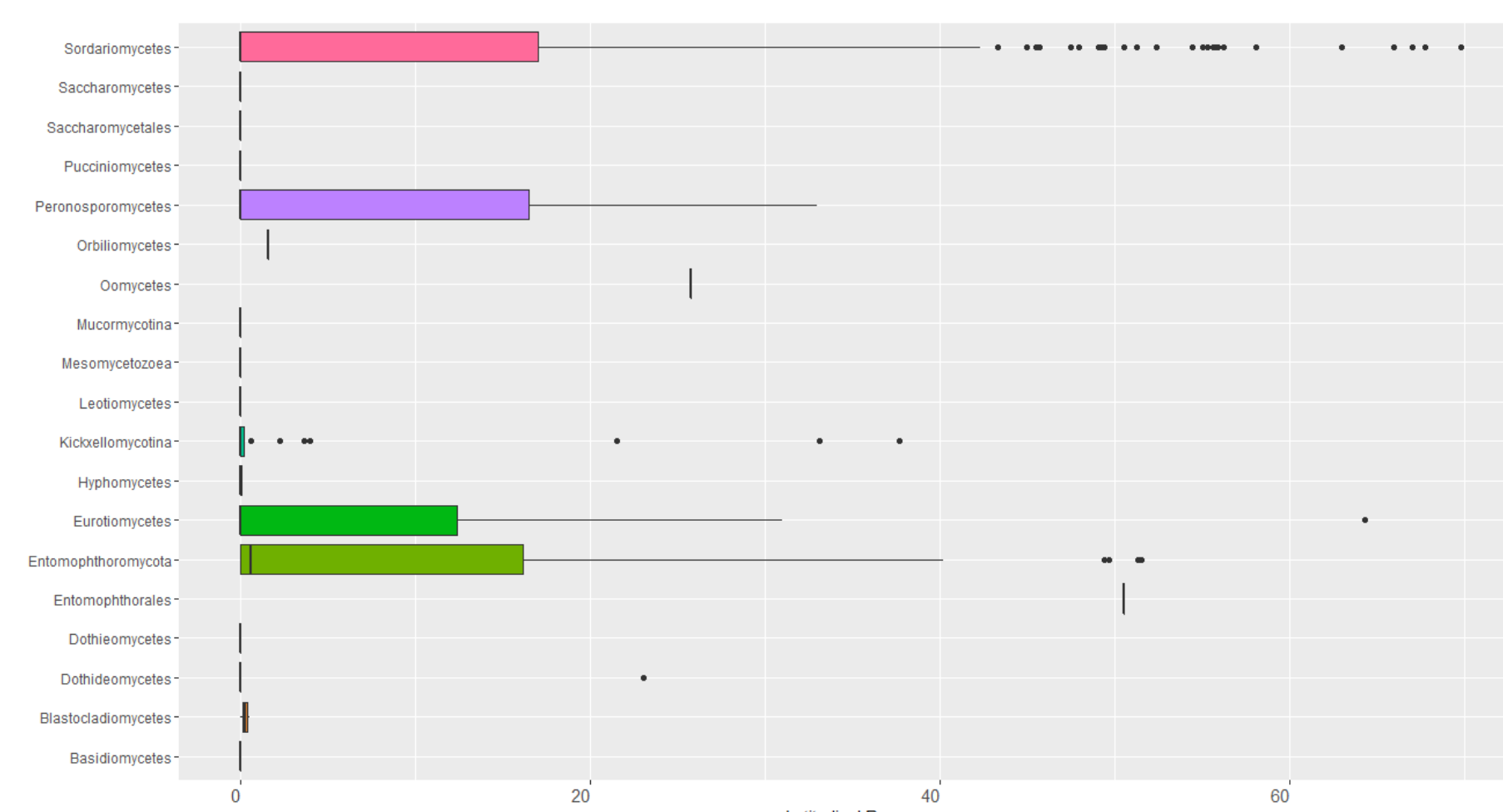
## Results



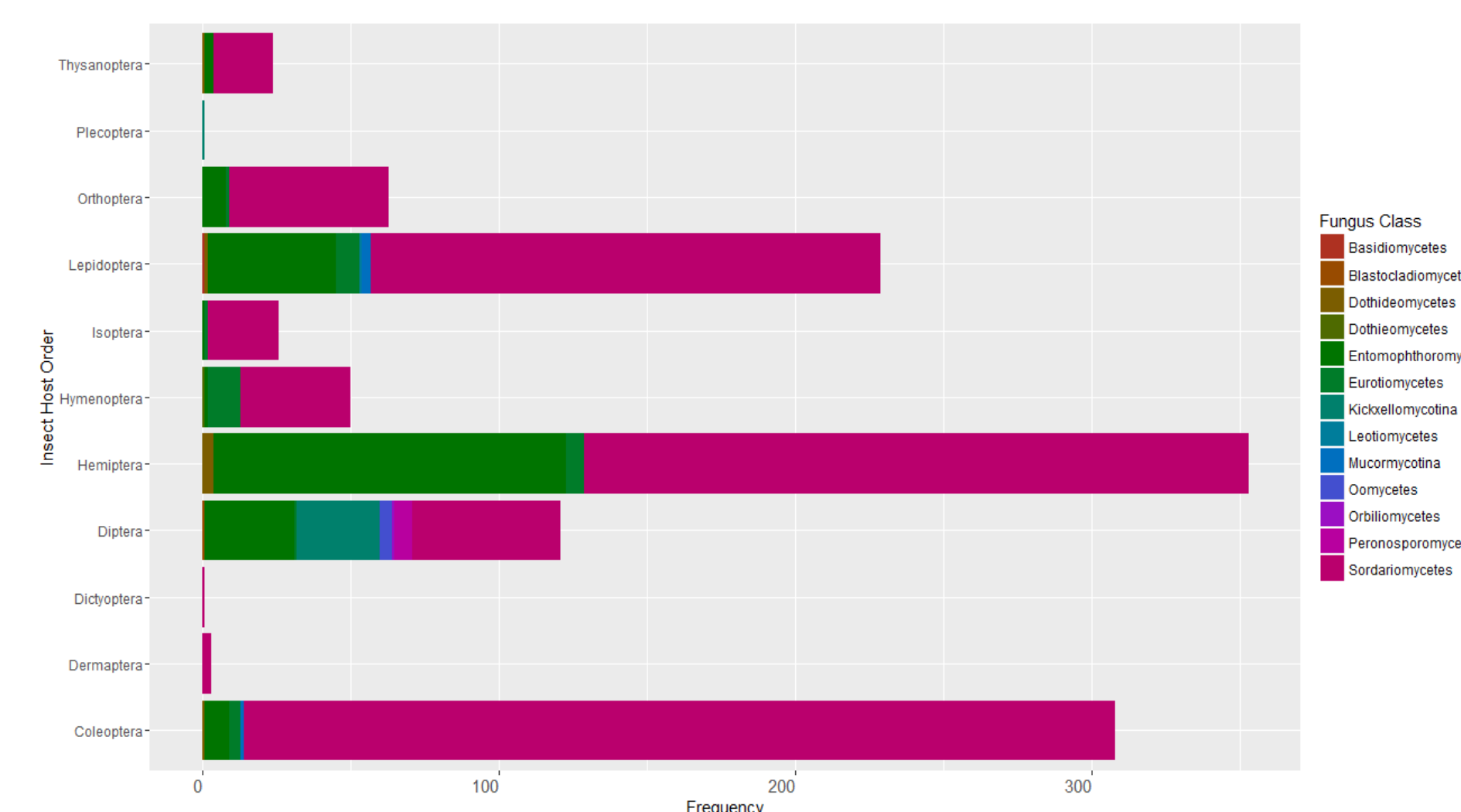
**Figure 1:** Bipartite network of pathogens (top) and hosts (bottom). Fungal species with many known hosts are represented by the blue areas on the graph. Hosts with many known pathogens are represented by the green areas.



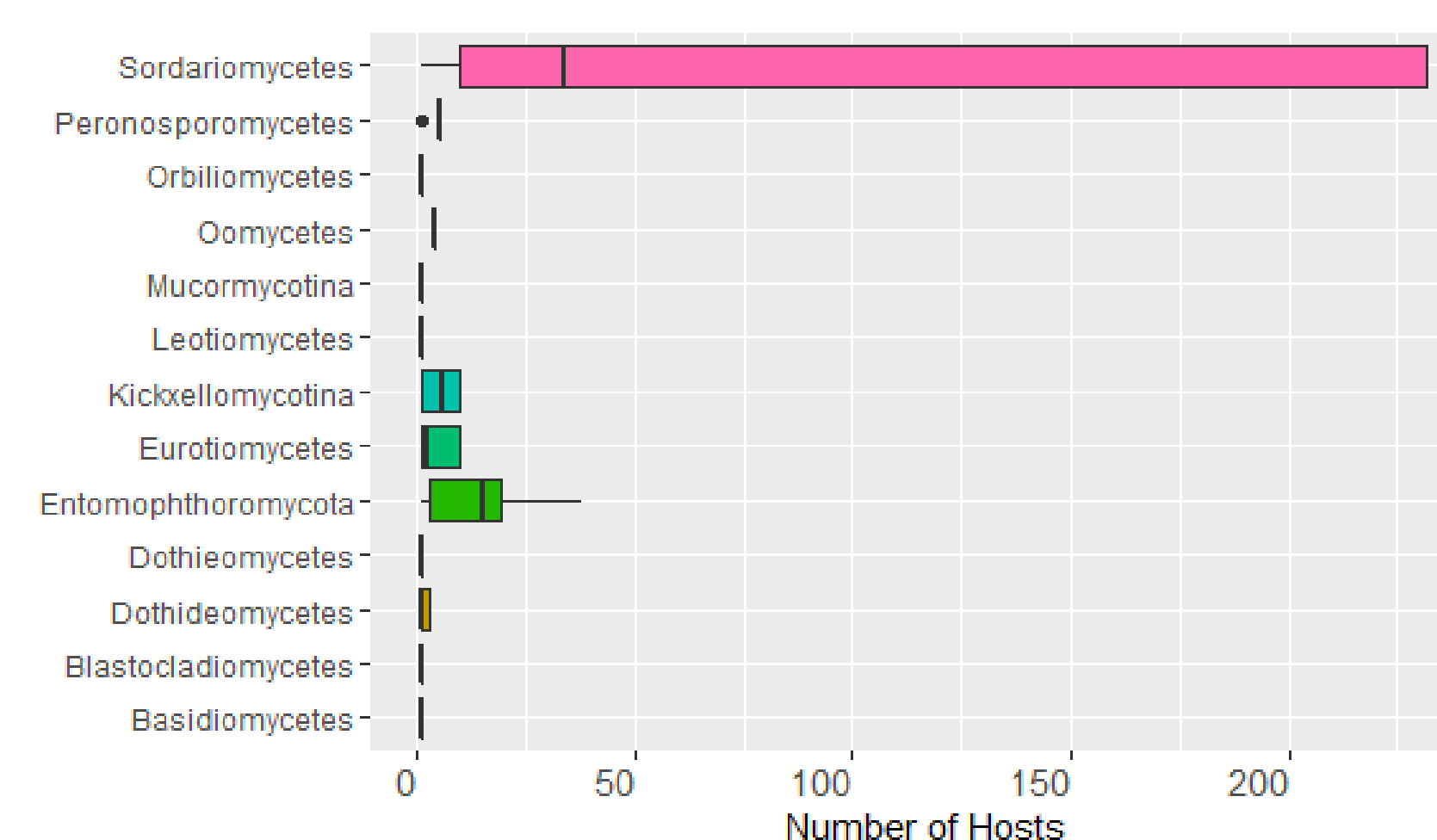
**Figure 2:** The global distribution of fungal entomopathogens from ARSEF



**Figure 4:** The distribution of latitudinal ranges by fungal class (0° to 60° represent tropical to temperate zones).



**Figure 3:** Frequency of infection of insect host orders by fungal classes.



**Figure 5:** Distribution of the number of insect hosts per species by fungal class.

## Discussion

### Findings:

- Several species of fungal pathogens such as *Beauveria bassiana*, *Metarhizium anisopliae*, *Isaria farinose*, and *Zoophthora radicans* dominate the database
- Most species in the database are known from only a single or several hosts
- While this pattern may reflect some degree of biology, *B. bassiana* and other biocontrol species are highly studied
- Although entomopathogenic fungus diversity is greatest in the tropics geographically, the data is clearly biased to the temperate zone where more labs equipped to identify fungi exist
- The data is also biased to a number of highly studied insect pests, such as the gypsy moth (*Lymantria dispar*) and emerald ash borer (*Agrilus planipennis*).
- Sordariomycetes* class includes both many host generalist species and geographically widespread species such as *B. bassiana*
- The beetles (*Coleoptera*), moths (*Lepidoptera*), ants, bees, and wasps (*Hymenoptera*), and true bugs (*Hemiptera*) are the most studied insect host orders due to their large number of species and pest species

### Future Explorations:

- Contrasting generalism at different taxonomic scales
- Contrasting the host range vs. geographic range size of fungal pathogens
- Determine studiedness of host and pathogen species using a search of the scientific literature to control for data biases in further analyses

## References

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