Advancing fungal dispersal ecology through traits and data harmonization
Short Title: Fungal dispersal traits
Project Leaders: Bala Chaudhary Co-Leaders: Cameron Egan, Kabir Peay

Project Summary: Dispersal is a key mechanism driving the geographic distributions of species on Earth, but dispersal theory and methods are based primarily on macroorganisms with microbial dispersal paradigms emerging only recently. In fungi, numerous traits related to dispersal (e.g. spore traits, fruiting body traits, dispersal syndromes) are likely linked to fungal biogeographic patterns, but these hypotheses remain largely untested. We aim to harmonize fungal dispersal trait data with DNA sequence-based taxon occurrence data to test trait-based predictions regarding the dispersal capabilities of fungi across spatial scales. We will also assess the potential for fungal dispersal to buffer against range shifts predicted with global climate change. This work will contribute to our understanding of global fungal biodiversity and ecosystem function, as well as aid in predicting plant and human fungal disease outbreaks. Finally, we will integrate fungal dispersal models with global climate change predictions to assess the potential for fungal range shifts in a changing world.

Public Summary: Fungi have captured the imagination of the public for their pivotal roles in ecosystems, the parts they play in world foods and culture, and their curious impacts to human health and well-being. But why do we see certain fungi in certain locations? How did they get there and what are the ways that fungi move from place to place? This working group studies the relatively uncharted discipline of fungal dispersal ecology. Combining global datasets, we aim to better understand how beneficial and pathogenic fungi disperse at a variety of spatial scales.

Introduction: Why fungal dispersal?

Dispersal is a fundamental ecological process driving the abundance and distribution of organisms at local scales and contributing to biogeographic patterns at global scales (Nathan et al. 2008). Dispersal also influences metapopulation dynamics, gene flow, and as a result, micro- and macroevolutionary processes (Saastamoinen et al. 2018). However, dispersal ecology and its theoretical underpinnings are largely based on animal and plant model systems, with extensions to microbial ecology developing only in recent years. In the case of microbes, when working to disentangle the relative effects of niche-based and neutral processes on the assembly of ecological communities, "dispersal" has been used synonymously with "neutral" as it is assumed that "everything is everywhere" (Martiny et al. 2006, Peay et al. 2010, Lowe and McPeek 2014). For microbes in particular, environmental filtering has been overemphasized relative to our understanding of how much dispersal impacts the observed structure of communities. Increasingly, research indicates that, for certain microbes like fungi, dispersal is an incredibly important functional trait axis and dispersal traits can be very predictive of where species occur (Norros et al. 2014, Golan and Pringle 2017, Lagomarsino Oneto et al. 2020). Still, we lack a generalized sense of how dispersal shapes global scale patterns of fungal biogeography or local community ecology, which has ramifications for fungal biodiversity and ecosystem function (Driscoll et al. 2014).

Between 3 and 13 million species of fungi exist on Earth, with numerous vital roles in ecosystems from decomposers to mutualists, parasites to predators (Kendrick 1992). Fungi are also central players in social-ecological systems, important for the maintenance of ecosystem functions and services, agroecosystems and global food security, and linked to human health (Chaudhary et al.

2022a). Fungal pathogens affect crop yield and global trade, with emerging plant diseases (e.g., banana wilt) having profound effects on global food security that disproportionately impact developing nations (Fones et al. 2020). Regarding human health, research indicates that climate change will expand the incidence certain fungal diseases like Valley Fever (i.e. *Coccidioides*) (Gorris et al. 2019) which disproportionately affects prison inmates and migrant workers in the southwestern U.S. (Cat et al. 2017). Improving our predictive understanding of fungal dispersal is key to understanding whether human intervention is required to control disease outbreaks and restore healthy fungal communities. Finally, models integrating fungal movement with global change are needed to enhance our ability to predict fungal range shifts in a changing world.

Scientists have been studying fungal dispersal for over a century, but methodological and systems advances (Figure at right from Chaudhary et al. 2022), have improved our ability to examine previously cryptic taxa and address questions at greater spatial and temporal scales. Work that combines trait-based computational analytics, eDNA observations, and biophysical modeling (from the disparate disciplinary worlds of ecology, agriculture, and epidemiology) has the potential to contribute to frontiers in fungal dispersal research.
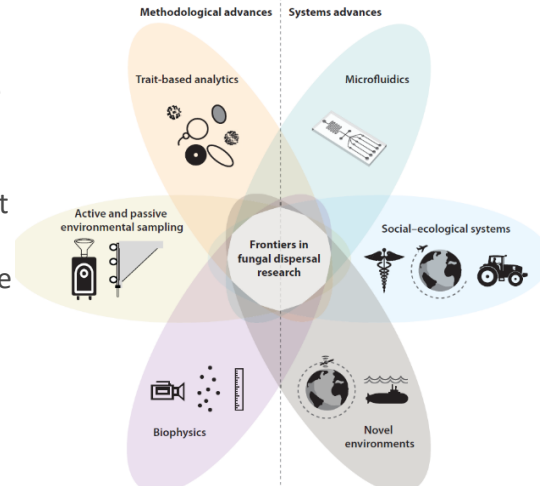
Previous research has combined fungal traits data with DNA sequence-based species occurrence data to make inferences about dispersal, but efforts are often limited with respect to geographic extent, fungal taxa, or number of traits (Norros et al. 2015, Chaudhary et al. 2020). The geographic extent of over 26,000 fungal taxa was negatively correlated with spore size, but other dispersal traits were not analyzed (Aguilar-Trigueros et al. 2023). Other traits that could inform fungal dispersal predictions include spore surface ornamentation, fruiting body type, growth rate, or dispersal syndrome (e.g. wind dispersed, animal dispersed). Certain traits that support environmental persistence (e.g. spore wall thickness, melanin content) also likely to influence dispersal capabilities (Golan et al. 2023).

A **critical knowledge gap** exists in our understanding of fungal dispersal because global data on dispersal-related traits are limited. Thus far, spore size is the main trait that is utilized to make predictions regarding fungal dispersal despite many other fungal dispersal traits existing in disparate data locations. Furthermore, ecologists, crop pathologists, and epidemiologists study fungal dispersal separately creating unrelated datasets. If harmonized, fungal dispersal trait data could be vastly expanded and predictions regarding dispersal capabilities based on dispersal mechanisms or biophysics could be tested with global sequence-based occurrence data.

PROJECT GOALS
The overarching goal of this project is to harmonize DNA sequence-based taxon occurrence data with dispersal trait data to test trait-based predictions regarding the dispersal capabilities of fungi across spatial scales. We will also assess the potential for fungal dispersal to buffer against range shifts predicted with global climate change. We will address three key research questions with the following project goals:
1) **What are fungal dispersal traits?**

Goal 1: Synthesize data to create FUNDISP, a new fungal trait database aimed at boosting fungal trait data relevant to dispersal. Based on expert knowledge and generalizations with respect to phylogeny, habitat, and fungal functional group, we will synthesize data on spore traits, (e.g. surface ornamentation, wall thickness, melanization), fruiting body traits (e.g. type, location), and dispersal syndrome (e.g. wind dispersed, animal dispersed).

2) **Which fungal traits are the most related to species geographic range extent and the best indicators of fungal dispersal across spatial scales?**

Goal 2: Using FUNDISP, link fungal dispersal traits to global DNA-based species occurrence data to examine the relationship between traits and geographic extent. FUNDISP will also be used to inform numerical simulations of atmospheric transport that incorporate meteorological data to follow the trajectory of spores in the atmosphere.

3) **Can fungal dispersal buffer against range shifts predicted with global climate change?**

Goal 3: Using a climate envelope approach, employ Threshold Indicator Taxa ANalysis (Baker and King 2010) and spatial-temporal-environmental model fitting to project fungal range shifts expected with climate change. Knowledge regarding fungal dispersal will aid in determining the feasibility of climate-related migration for different groups of fungi.

PROPOSED ACTIVITIES

The project will begin with a virtual **kickoff meeting** among project leaders to develop a project management plan, begin organizing participants, and recruit early career researcher (ECR) participants (see DEI section). The project leaders will organize a **data strategy meeting** with dataset owners/curators and other interested working group participants to begin harmonizing fungal trait and sequence-based occurrence data; to facilitate more in-person interactions but save costs, this hybrid data strategy meeting will be held immediately before the International Mycological Association meeting in August 2023.

At **Meeting #1** (in-person), all participants will collaboratively finalize the harmonization of fungal dispersal trait data creating FUNDISP from different data sources (see attached data table). We will also unite harmonized global soil data from Aguilar-Trigueros et al. 2023 with NEON soil fungal data and aerial sampling efforts such as the Global Spore Sampling Project (Ovaskainen et al. 2020) and SPORELIFE (Finnish Meteorological Institute). Computing resources at ESIIL (and data scientist support) will enable 1) the rapid concatenation of large DNA sequence-based biogeographic datasets and 2) the use of FUNDISP to create numerical simulations of fungal dispersal in the atmosphere given specific meteorological conditions. By the end of this meeting we expect to have completed Goal 1 and conducted preliminary analyses for Goal 2.

Meeting #2 will be virtual, but participants will still be asked to block out time for full group meetings and subgroup breakout sessions via Zoom. The purpose of this meeting is to finalize analyses for Goal 2 and collaboratively craft a manuscript (Product #2) on how dispersal traits are related to fungal geographic range extent. In this meeting we will also begin planning for climate envelope analyses (Goal #3) to be conducted at ESIIL during Meeting #3.

At **Meeting #3**, we will harmonize sequence-based occurrence data with climate change prediction data, specifically regarding precipitation changes, temperature changes (daytime and nighttime), and air turbulence changes. These climate variables affect the liberation of spores from sporocarps, the formation of above and belowground sporocarps, as well as long distance spore dispersal in the

air (Roper et al. 2010). Computing resources at ESIIL will enable climate envelope predictions for fungi (and fungal traits) and we aim to have analyses completed and a manuscript drafted (Product #3) by the completion of this meeting.

PROPOSED TIMETABLE	Time Period	Participants
Kickoff Planning Meeting (virtual)	Spring 2024	Project leaders
Data Strategy Meeting (hybrid)	Summer 2024	Project leaders & data leads
Meeting 1 (in person)	Fall 2024	All participants
Meeting 2 (virtual)	Winter 2025	All participants
Meeting 3 (in person)	Spring 2025	All participants
Subgroup meetings as needed (virtual)	Fall/winter 2025	Subgroup Participants
Mentor-mentee meetings	Quarterly	All participants

OUTCOMES
Product #1 – FUNDISP, a new synthesis database and code to enable trait-based analysis of fungal dispersal. FUNDISP will be deposited at a vetted data repository (e.g. Dryad) and we will publish a data descriptor in a peer-reviewed journal (e.g *Scientific Data*) to facilitate its use.
Product #2 – Manuscript: Is dispersal capability predicted by traits related to geographic range extent?
Product #3 – Manuscript: Can fungal dispersal overcome shifting climate envelopes?
Training – Three ECRs will receive training in synthesis research and collaboration skills.

Open Data Statement - Project leaders are committed to contributing to a scientific culture of open data. We will oversee the sharing and long-term archiving of FAIR-compliant datasets and code workflows (Wilkinson et al. 2016). The project leaders and numerous participants are open data stewards with experience publishing data, data descriptors, and code (Chaudhary et al. 2016).

ADVANCING DEI
The rapidly growing discipline referred to as "the science of team science" demonstrates with considerable evidence that the most effective, high-functioning, collaborative teams have members that are diverse with respect to identity, discipline, and career stage *and* possess interpersonal skills that promote social sensitivity and emotional engagement (Cheruvelil et al. 2014). We have carefully crafted a skilled working group that is excited about the science, has a shared vision, and is diverse with respect to multiple dimensions of professional and personal identity:
- Disciplinary diversity: As described above, researchers who study fungal dispersal often focus on specific taxonomic and functional groups or use specific methodological approaches. To bridge fungal functional groups, we have invited researchers who work in ecology, agriculture, and epidemiology, as well as researchers who work across fungal taxonomic groups. We also were intentional to include researchers who use different approaches; several group members use mathematical modeling and biophysics, while others use large-scale eDNA sampling campaigns, and still others use trait-based computational analytics.
- Diverse identities: Our proposed list of participants includes 12 fungal dispersal ecology experts who represent a diverse array of researchers across multiple identity dimensions. The project leader self-identifies as a woman of color and the majority of proposed

participants are women. We would have liked to include more participants from outside of the U.S., but, due to budget limitations, this would have resulted in a smaller working group with lower disciplinary diversity.

- Diverse career stages: Participation in synthesis working groups enhances scientific career success and can promote retention and advancement for ECRs (Hampton and Parker 2011, Biancani et al. 2018). ECRs contribute to working group success as they often possess cutting-edge computational methods for data synthesis. Our proposed working group is diverse with respect to career stage, comprising 4 early career Assistant Professors (including 1 Teaching Assistant Professor and 1 Research Fellow), 4 mid-career Associate Professors, and 4 full Professors. We have included 3 funded spots for ECRs (either advanced PhD students or postdoctoral researchers) and will put out an open call to encourage participation from trainees outside of existing networks. PI Chaudhary has used the open call technique previously, which contributed to high trainee engagement and working group success (Chaudhary et al. 2022b).

In addition to working group composition, we will employ group policies and structures that support social sensitivity and emotional engagement, an important characteristic of effective and high-functioning collaborations (Cheruvelil et al. 2014). Accountability mechanisms can be used to encourage ethical research conduct and professional peer engagement. First, Project Leaders will lead the collaborative development of a robust **authorship policy**, guided by a full group discussion around credit and transparency (Kiermer 2023). Next, we will discuss **collaboration norms** (Youtie and Bozeman 2014) and create a working group **code of conduct**, which will outline mechanisms for conflict resolution (Cheruvelil et al. 2014). Finally, to promote inclusion across career stages, all working group members will be paired in **1-on-1 mentor-mentee matches**, creating a mini mentoring program (i.e. "buddy system") to ensure inclusion in intellectual endeavors of the working group. PI Chaudhary recently ran a similar mentor-mentee match as part of a working group, which substantially helped ECRs engage and take on leadership roles in subgroup projects.

Rationale for ESIIL support and opportunities for ESIIL collaborations

To our knowledge, there has never been an ecological or evolutionary synthesis working group funded to address questions specific to microbial, let alone fungal, dispersal. Previous working groups on patterns in microbial biodiversity (Martiny et al. 2006) and fungal functional ecology (Zanne et al. 2019) were supported by the National Center for Ecological Analysis and Synthesis, but their contributions to fungal dispersal were largely conceptual and theoretical. We are finally at the point in the science where global data on species occurrences exists and where theory regarding fungal dispersal traits has advanced. Much of the eDNA data will be in raw sequence form, which will require ESIIL's advanced computing capabilities to enable an efficient bioinformatics pipeline; merging trait-based spore dispersal modeling with climate envelope models will also require substantial computing power.

As much as possible, we would like to take advantage of ESIIL staff for data analytical support throughout the project. Although we do not anticipate needing long-term database storage, we would like to make considerable use of the ESIIL Discovery environment, cloud storage during the duration of the project, and assistance from ESIIL Data Science staff with coding, data wrangling, and statistical model fitting. We look forward to participating in future Innovation Summits or Hackathons and integrating our work into future ESIIL activities.

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