

Microbiome dynamics and pathogen spread in pollinator species networks

Supervisory team:

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Project description:

Insect pollinators are crucial for agricultural sustainability, but the health and abundance of pollinators is in decline. It is increasingly clear that gut-associated microbial communities play a vital role in pollinator health, determining resistance to pathogens and shaping host nutrition. Previous work on pollinator microbiomes has tended to focus on single species, so that we lack a comprehensive understanding of how biological interactions among species shape microbiome structure and function. Understanding the complex relationships among pollinators, their microbiomes and the environment is also essential for understanding transmission routes of key parasites and pathogens that impact pollinator health.

The project will use an interdisciplinary approach, integrating molecular estimates of pollinator microbiotas with ecological network data on species interactions. This will yield valuable insights into how heterogeneity in the frequency of intra- and interspecific interactions drives variation in microbiomes and subsequent pollinator health and resistance to pathogens.

Project Aims

The balance between aims will depend partly on the student's developing interests

(1) Quantify the importance of pollinator phylogeny, and the degree of plant specialization, for predicting the microbiomes of pollinator taxa

Using a meta-analytic approach, we will use published sequencing data from a broad range of wild pollinators to understand the impact of host phylogeny on microbiome composition. We will also annotate the phylogeny with ecological trait data including degree of host plant specialisation to test the prediction that more generalist species have more diverse gut microbiota.

(2) Determine the relative importance of host plant specialisation and direct interactions on flowers in influencing microbiome composition and dynamics

This will be a novel investigation of how fine-scale variation in pollinator behaviour and space use influences gut microbiota dynamics. It will involve intensive field surveys of pollinators to build species interaction networks and use of these networks to predict microbiome structure derived from 16S rRNA sequencing. We will test the prediction that co-foraging pollinators have more similar gut bacterial communities, independent of host phylogeny.

(3) Use metagenomic data to build putative transmission networks to understand the potential routes of pathogen spread

Sharing of microbial strains is a powerful tool to detect the combined effects of direct and indirect interactions as conduits of potential pathogen spread. The student will generate microbial strain-sharing data using metagenomics and produce putative transmission networks. These will be compared with the direct interaction network in [2] to investigate the relative importance of direct versus indirect routes of transmission.

Our aim as the SWBio DTP is to support students from a range of backgrounds and circumstances. Where needed, we will work with you to take into consideration reasonable project adaptations (for example to support caring responsibilities, disabilities, other significant personal circumstances) as well as flexible working and part-time study requests, to enable greater access to a PhD. All our supervisors support us with this aim, so please feel comfortable in discussing further with the listed PhD project supervisor to see what is feasible.