Application Call 2025 - Project 7

Plant secondary metabolites and the barley microbiome

Supervisors:

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Background:

Recruitment of bacteria to plant organs, such as leaves, is important for plant development, health, and survival. Understanding these processes can help develop new tools for sustainable agriculture. Specialized plant metabolites have important functions in defense against pathogens and herbivores in many plant species. Surprisingly, some of these metabolites also seem to function in the recruitment of nonpathogenic plant-associated bacteria. Metabolism of these complex chemicals by bacteria seems to result from the cooperative efforts of multiple species, ultimately resulting in the recruitment of specific metabolic networks. How bacteria work together to process these important chemicals, the breadth of this activity, and the implications for plant health remain largely unknown.

Project description:

> “There were three pests into the east,
> Three pests both great and high,
> And they hae sworn a solemn oath
> John Barleycorn should die.”
> *Modern interpretation of the folk song John Barleycorn (must die)*

Barley is an important crop plant, and an emerging model system for understanding plant microbiome interactions in grasses. Gramine is a secondary metabolite that is produced, stored and secreted in large amounts by some barley accessions. This metabolite is thought to play important roles in protection against devastating pests, which, as the old folk song suggests, would take advantage of barley. As a nitrogen-containing indolic compound, gramine is also a potentially valuable resource for components of the barley microbiome that can tolerate it. However, the mechanism through which this important metabolite interacts with the microbiome remains unknown. In this project, you will work on a dynamic, international team to study how and why bacterial metabolic networks are shaped by gramine in barley. To do so, microbial ecological, molecular biological, and biochemical techniques are needed to understand how microbiomes interact with gramine, including the interspecies interactions that arise and the ecological effects that follow. Methods include metagenomic community profiling, synthetic community building and manipulation, metabolomics, and genetic manipulation of both hosts and bacteria.

Candidate profile:

- A dedicated team player who enjoys creative science and adapts to new techniques.
- An MSc (or equivalent), ideally in natural sciences (Microbiology, Biochemistry, Genetics) or a related field
- Excellent background in microbial ecology, microbiology, biochemistry, and plant science.
- Demonstrated experience with experimental design and analytical methods.
- A good knowledge of statistical approaches and the use of programming for data analysis (for example, R and sequencing data analysis) is advantageous.

Further Reading:

Dias et al. (2024) Biosynthesis of the allelopathic alkaloid gramine in barley by a cryptic oxidative rearrangement. ***Science.*** doi: https://doi.org/10.1126/science.adk6112

Unger et al. (2024) Beyond defense: Glucosinolate structural diversity shapes recruitment of a metabolic network of leaf-associated bacteria. ***Nature Communications*** doi: https://doi.org/10.1038/s41467-024-52679-7