

Application Call 2024 - Project 5

For the love of spice -

plant secondary metabolites and recruitment of bacterial metabolic networks

Supervisors:

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Background:

Recruitment of bacteria to plant organs like leaves is important for plant development, health and survival. Understanding these processes is likely to be important for developing tools for more sustainable agriculture. Plant secondary metabolites are highly diverse, but many of them have convergent functions in immunity across plant species. Surprisingly, some of these metabolites also seem to have functions in recruitment of non-pathogenic plant-associated bacteria. Metabolism of these complex chemicals by bacteria seems to profit from the cooperative effort of multiple species, ultimately resulting in recruitment of specific metabolic networks. How bacteria work together to process these important chemicals, the breadth of this activity, as well as the implications for plant health are still unknown.

Project description:

In this project, you will work in a dynamic, international team to study how and why bacterial metabolic networks take shape during metabolism of plant secondary metabolites as well as implications for plant health. To do so, you will need to employ microbial ecological, molecular biological and biochemical techniques to study what types of inter-species interactions arise and the ecological effects that follow. Methods can include metagenomic community profiling, synthetic community building and manipulation, and genetic manipulation of both hosts and bacteria.

Candidate profile:

- A dedicated team player who enjoys creatively doing science and adapting 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/or plant science
- Skillful in experimental design and analytical methods.

• A good knowledge of statistical approaches and using programming for data analysis (for example, R and sequencing data analysis) is advantageous.

Reading:

Unger et al. (2023) <u>Beyond defense: Glucosinolate structural diversity shapes</u> <u>recruitment of a metabolic network of leaf-associated bacteria.</u> **Available on:** *bioRxiv* doi: https://doi.org/10.1101/2023.12.04.567830