

Identifying beneficial plant-microbial interactions using multi-omic approaches

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Project Description: Microbes known as endophytes are usually bacteria or fungi, which live within specific plant tissues without causing disease. Many endophytes have been shown to boost plant growth and resilience. In the past, intensive breeding programs for food crops have been based around the use of chemical fertilizers and pesticides. They have ignored the interactions between the plant and its microbes, with the result that many beneficial microbial interactions have been modified or lost. Bioenergy crops such as Miscanthus, however, are largely undomesticated and so retain a unique and beneficial microbial community, representing a relatively untouched resource.

This PhD project will use bioinformatics, genomics and metabolomics to investigate the molecular and metabolic functioning of endophytes in bioenergy crops, thus providing new insights into plant-microbe interactions. Computational approaches will be central to this project. Current understanding of endophyte genomes and their metabolism is still relatively limited: for instance, a number of the isolated endophytes to be investigated in this project appear to be unique species, not yet represented in public DNA sequence databases. The challenge is to develop bioinformatics data analysis protocols that are tailored towards the unique issues associated with endophytes, including the need to reveal their metabolic inter-dependencies. Bacterial endophytes often have much reduced genomes in comparison to their free-living or pathogenic relatives. It is thought that the host provides a stable microenvironment that facilitates this process. Evolutionary adaption to an endophytic lifestyle results in relatively large quantities of genetic material being lost, leading to small, lean genomes with altered metabolic and signalling pathways. This project aims to better understand these changes. In particular, knowledge of the affected metabolic pathways will allow us to identify metabolic cross-talk between different endophytes and the plant, providing insights with broad application to agriculture.

The results of this project will ultimately contribute to the engineering of synthetic communities of microbes with beneficial properties that are able to act as probiotics to improve plant growth and drought tolerance. It is likely that the metabolic pathways and gene clusters identified will contribute towards synthetic biology applications, such as improving nitrogen-fixing in bacteria. In the longer term, the outputs will leverage existing symbiotic relationships between plants and microbes to design and engineer a range of useful interactions. In this way, biofuel crops can be further developed to grow on poor quality or damaged land, thus increasing the amount of agricultural land available for growing food. The results will also have transferable applications to agricultural crops.

Recent developments in high-throughput data intensive technologies like genomics and metabolomics are

revolutionizing the study of biological systems, including the whole agri-food system. Bioinformatics underpins and enables these technologies. It is a multidisciplinary data-intensive science that sits at the interface between the life sciences and the computational sciences. For the student this project offers a rare opportunity to be trained in a set of cutting-edge research skills that are highly in demand, and that provide excellent career prospects.

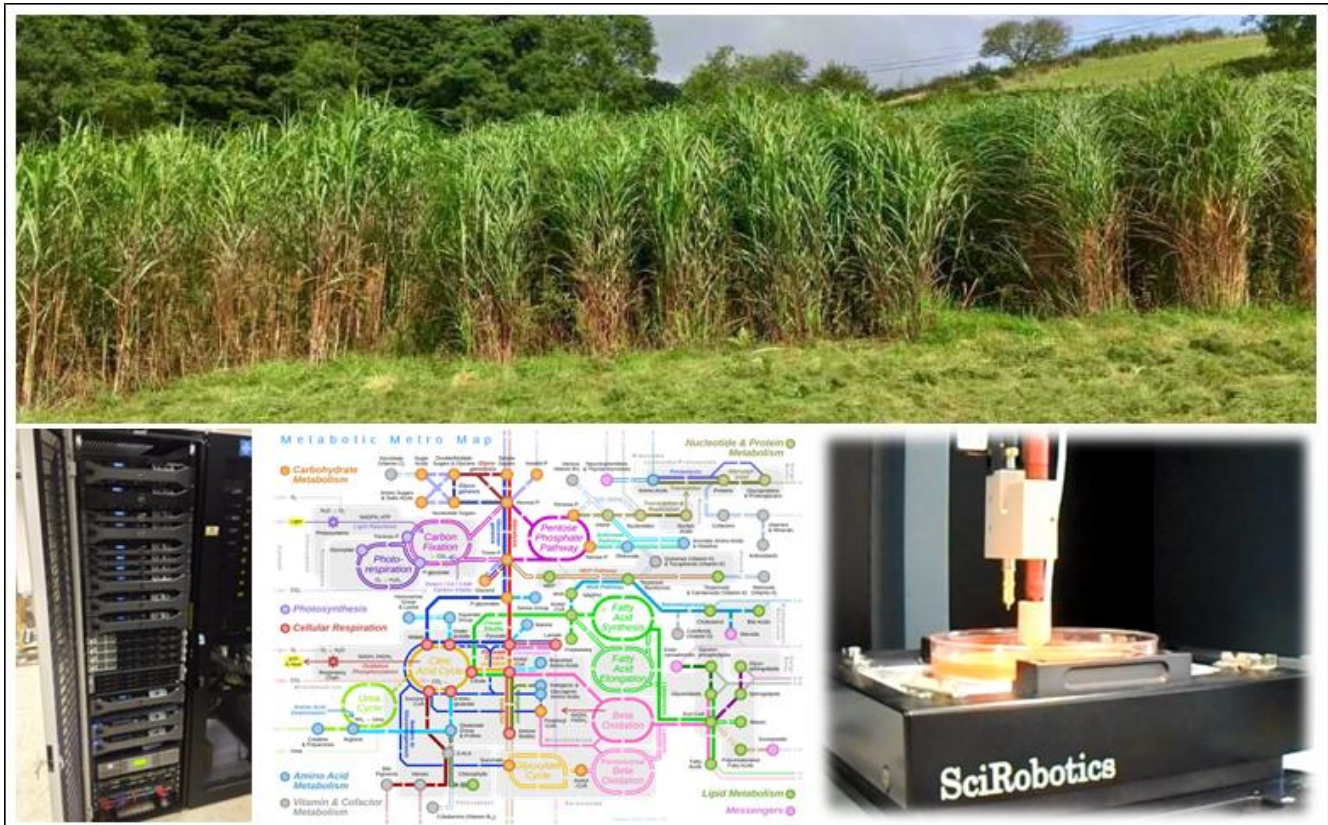


Figure 1: The project combines the use of high-throughput biological technologies with high performance computing to better understand metabolic interactions between energy grasses and entophytic microbes. The student will be provided with essential training in these advanced technologies.

References:

Understanding and engineering beneficial plant–microbe interactions: plant growth promotion in energy crops. Farrar, K., Bryant, D. & Cope-Selby, N., (2014), *Plant Biotechnology Journal*. 12, 9, p. 1193-1206