Project Title | Global diversity and ecosystem functions of a newly discovered plant-microbe symbiosis
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Host University | University of Warwick
Theme | Organisms & Ecosystems
Supervisory team | Professor Gary Bending, University of Warwick, gary.bending@warwick.ac.uk
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Project Highlights

- We have discovered a previously unknown plant-microbial symbiosis with global distribution
- You will unravel the diversity of the fungal symbionts involved, the factors which control their distribution, and determine its potential contribution to ecosystem processes through genome analysis
- The project will provide training in a wide range of modern molecular ecological analyses in combination with bioinformatic analyses

Overview

Arbuscular mycorrhizas (AM) are the most widespread symbiosis between higher plants and fungi, and have major impacts on ecosystem processes, including biogeochemical cycling and the diversity and productivity of plant communities. Fungi forming AM have been assumed to comprise the phylum Glomeromycota. However, we have shown that fungi which form the distinctive ‘fine root endophyte’ (FRE) AM morphotype are actually members of the phylum Mucoromycota, which diverged from the Glomeromycota over 700 million years ago, before the colonization of land by plants. Although we know that FRE are globally distributed, and can be abundant within ecosystems, we know almost nothing about the diversity, ecology or ecosystem function of the fungi involved. However, evidence suggests that FREs and Glomeromycota have different interactions with the environment and may be functionally distinct. In this project you will investigate the diversity and composition of FRE across UK and Australian habitats and plant families, and determine the key environmental and soil factors which determine assembly of FRE communities. FREs are not culturable and cannot be grown in pure culture. In order to understand the ecological function of FREs, you will assemble genomes of FREs from environmental metagenomes. The assembled genomes will be used to investigate the presence of traits associated with key biogeochemical cycling processes, so that the ecological significance of FRE can be established.

Methodology

We will use soil DNA from the Countryside Survey to investigate landscape diversity and distribution of FRE. Countryside survey is a regular audit of the UK countryside covering all common UK habitats, including grasslands, arable fields, heaths and woodlands. Over 1000 samples are available. This
work will be supplemented with samples from Australian ecosystems to enable a global picture of FRE diversity and distribution to be established. Data from this study will be used to select specific sites for more detailed analysis of FRE distribution, such as seasonal variation and plant species preferences for FRE. Sites with contrasting communities of FRE will be selected for metagenome sequencing, and bioinformatic approaches will be used to reconstruct genomes of FRE, to enable analysis of the potential contribution of FRE to soil biogeochemical processes.

Training and skills
Training will be provided in a wide range of molecular techniques (DNA extraction, PCR, sequencing), ecological analysis methods (multivariate analysis and network analysis), metagenome sequencing and bioinformatics.

CENTA students are required to complete 50 days training throughout their PhD including a 10 day placement. In the first year, students will be trained as a single cohort on environmental science, research methods and core skills. Throughout the PhD, training will progress from core skills sets to master classes specific to CENTA research themes.

Partners and collaboration (including CASE)
The student will have a training placement at Centre for Ecology and Hydrology in Bangor, examining the diversity and distribution of FREs and Glomeromycotan fungi in large national scale sequencing datasets.

There will be opportunities for a research placement at the University of Western Australia, Perth (dependent on funding) for field work to collect samples from Australian habitats.

Possible timeline
Year 1: Analysis of FRE diversity and community assembly in UK habitats using next generation sequence analysis. Community diversity, composition, and associations between Glomeromycotan and FRE Mucoromycotan fungi, will be determined.

Year 2: Targeted sampling of UK and Australian habitats to investigate seasonal dynamics and plant species preferences for FRE

Year 3: Metagenome sequencing of environmental samples and reconstruction of FRE genomes

Further reading

Further details
Please add project/institutional contact details including a link to the application website if applicable

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How to apply
Information and links at the following webpage:
https://warwick.ac.uk/fac/sci/lifesci/study/pgr/apply