

<b>Project Title</b>	Global diversity and ecosystem functions of plant-microbe symbioses
<b>University (where student will register)</b>	University of Warwick
<b>Which institution will the student be based at?</b>	As above
<b>Theme (Max. 2 selections)</b>	<a href="#">Climate &amp; Environmental Sustainability</a> <input checked="" type="checkbox"/> <a href="#">Organisms &amp; Ecosystems</a> <input checked="" type="checkbox"/> <a href="#">Dynamic Earth</a> <input type="checkbox"/>
<b>Key words</b>	Biodiversity, metagenomics, ecosystem functions, rhizosphere, soil
<b>Supervisory team (including institution &amp; email address)</b>	<p><b>PI:</b> Professor Gary Bending, University of Warwick gary.bending@warwick.ac.uk</p> <p><b>Co-I:</b> Prof Chris Quince, Earlham Institute, Norwich, UK C.Quince@warwick.ac.uk</p> <p>Dr Rob Griffiths, Centre for Ecology and Hydrology, Bangor, UK rig@ceh.ac.uk</p> <p>Dr Megan Ryan, University of Western Australia, Australia <a href="mailto:megan.ryan@uwa.edu.au">megan.ryan@uwa.edu.au</a></p> <p>Dr Ryan Mushinski, University of Warwick, UK</p>

### Project Highlights:

- We have discovered a previously unknown and abundant plant- mycorrhizal symbiosis with global distribution
- You will unravel the diversity of the fungal symbionts involved, the factors which control their distribution, and determine their 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 terrestrial ecosystem processes, including biogeochemical cycling and the diversity and productivity of plant communities. Fungi which form 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 globally, and key environmental factors determining their abundance and distribution. In order to understand the ecological function of FREs, you will assemble genomes of FREs from environmental metagenomes. The assembled genomes will used to

investigate the presence of traits associated with key biogeochemical cycling processes, so that the ecological significance of FRE can be established.

#### **Methodology:**

Initial analysis of existing DNA databases will be used to investigate diversity and distribution of FRE and Glomeromycota across habitats and the ecological drivers of their distribution. Existing field sites in use in parallel projects will be used for more detailed analysis of FRE distribution, such as seasonal variation, plant species preferences and responses to land use and management. Metagenome sequencing 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.

Students will be awarded CENTA2 Training Credits (CTCs) for participation in CENTA2-provided and 'free choice' external training. One CTC equates to 1/2 day session and students must accrue 100 CTCs across the three years of their PhD.

#### **Partners and collaboration (including CASE):**

The student will have an opportunity for a training placement at Centre for Ecology and Hydrology in Bangor, examining the diversity and distribution of FRE and Glomeromycotan mycorrhizal 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 investigate FRE in Australian habitats and to examine impacts of the FRE symbiosis on plant growth and nutrient uptake.

#### **COVID-19 Resilience of the Project:**

The project will comprise a mix of experimental and field work and desk based data mining from existing environmental sequence datasets. During any lockdown periods the data mining components of the project will become the focus of the programme.

#### **Possible timeline:**

**Year 1:** FRE community diversity, composition, and associations between Glomeromycotan and FRE arbuscular mycorrhizas.

**Year 2:** Ecological interactions and drivers of FRE diversity using targeted field sites

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

**Further reading:**

Orchard, S., Hilton, S., Bending, G.D., Dickie, I.A., Standish, R.J., Gleeson, D., Jeffery, R.P., Powell, J.R., Walker, C., Bass, D., Monk, J., Simonin, A., Ryan, M.H. A. (2016) Fine endophytes (*Glomus tenue*) phylogenetically align with Mucoromycotina, not Glomeromycota. *New Phytologist* **213**, 481-486.

Orchard, S., Standish, R.J., Dickie, I.A., Walker, C., Moot, D, Ryan, M.H. (2017) Fine root endophytes under scrutiny: a review of the literature on arbuscule-producing fungi recently suggested to belong to the Mucoromycotina. *Mycorrhiza* **27**, 619-638.

**Contact:**

Professor Gary Bending  
School of Life Sciences  
University of Warwick  
CV4 7AL  
02476575057  
[gary.bending@warwick.ac.uk](mailto:gary.bending@warwick.ac.uk)