

Project Title	Global diversity and ecosystem functions of plant-microbe symbioses
University (where student will register)	University of Warwick
Which institution will the student be based at?	As above
Theme (Max. 2 selections)	Climate & Environmental Sustainability <input checked="" type="checkbox"/> Organisms & Ecosystems <input checked="" type="checkbox"/> Dynamic Earth <input type="checkbox"/>
Key words	Symbiosis, Microbiome, biodiversity, metagenomics, mycorrhizas
Please explain how the project fits within the NERC remit	The project fits NERC science areas of ecology, biodiversity and systematics, environmental microbiology and environmental genomics
Supervisory team (including institution & email address)	PI: Professor Gary Bending, School of Life Sciences, University of Warwick, gary.bending@warwick.ac.uk Co-I: Dr Ryan Mushinski, School of Life Sciences, University of Warwick, rymush@iu.edu Prof Chris Quince, Earlham Institute, UK Christopher.Quince@earlham.ac.uk Dr Megan Ryan, University of Western Australia, Australia megan.ryan@uwa.edu.au

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 (including 1 high quality image or figure):

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 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:

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. This could include collaboration with the global crop microbiome project which is investigating the microbiomes of the world’s major crops using a global dataset. Existing field sites in use in parallel projects will be used for more detailed analysis of FRE biodiversity and 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:

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.

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

Partners and collaboration (including CASE):

Name of L1/L2 Partner (where applicable)	
Name of CASE partner (where applicable – project proposal must be accompanied by a letter of support from the CASE partner)	

Further information on partners and collaboration (including CASE):

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.

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:

Albornoz, F. E., Ryan, M. H., Bending, G. D., Hilton, S., Dickie, I. A., Gleeson, D. B, Standish, R. J. (2021). Agricultural land-use favours mucoromycotinian, but not glomeromycotinian, arbuscular mycorrhizal fungi across ten biomes. *New Phytologist*, 233, 1369-1382.

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.

Albornoz, F.E., Orchard, S., Standish, R.J., Dickie, I.A., Bending, G.D. et al. (2021) Evidence for niche differentiation in the environmental responses of co-occurring mucormycotinian fine root endophytes and glomeromycotinian arbuscular mycorrhizal fungi. *Microbial Ecology* **81**, 864-873.

Further details:

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