

Project Title	Circadian rhythms in plant-microbe-soil interactions
University (where student will register)	University of Warwick
Theme (Max. 2 selections)	Climate & Environmental Sustainability <input checked="" type="checkbox"/> Organisms & Ecosystems <input checked="" type="checkbox"/> Dynamic Earth <input type="checkbox"/>
Key words	Circadian, plant-microbe interactions, biogeochemistry, biodiversity
Supervisory team (including institution & email address)	<p>PI: Professor Gary Bending, University of Warwick gary.bending@warwick.ac.uk</p> <p>Co-I Professor isabelle Carre, University of Warwick isabelle.carre@warwick.ac.uk</p> <p>Co-I Dr Ryan Mushinski, University of Warwick Ryan.mushinski@warwick.ac.uk</p> <p>Co-I: Prof Davey Jones, Bangor University d.jones@bangor.ac.uk</p>

Project Highlights:

- Circadian clocks represent adaptations to the rhythmic nature of our environment because they allow organisms to adjust their physiology ahead of predictable daily changes in light and temperature conditions linked to the rotation of the earth
- The soil proximal to plant roots, termed the rhizosphere, is a zone of particularly intense microbial activity. These microbial communities are key determinants of plant health and are dominant drivers of carbon, nitrogen and phosphorus biogeochemical cycling processes in terrestrial ecosystems
- We have shown that rhizosphere microbiota exhibit diurnal cycles of abundance, linked to functioning of the plant circadian clock. You will use a range of cutting edge molecular and biogeochemical approaches to investigate the significance of rhizosphere microbial circadian rhythmicity for the cycling and bioavailability of nutrients, and its significance for plant health.

Overview: *Maximum 350 words*

Plants live in close association with complex communities of microbes which together constitute their 'microbiome'. The microbiome interacts with the plant in numerous ways; some microbes are beneficial and promote plant growth, while others are pathogens which reduce crop yields. Understanding and harnessing interactions within the microbiome has enormous importance for devising net zero carbon emission sustainable agricultural systems while ensuring food and energy security, and mitigating the threats posed by climate change and land degradation.

Research at Warwick has demonstrated that a variety of factors control the composition of microbial communities which inhabit the root zone, including plant genotype and

developmental stage, local environment, and geographical distance. However recently we have shown that there are microbial **diurnal** cycles in the root zone, involving rhythmic changes in transcriptional activity in diverse groups of bacteria and fungi.

In this project you will derive detailed understanding of diurnal root metatranscriptome dynamics (ie plant and microbial transcriptomes) and investigate the links between plant and microbial gene expression. You will investigate the extent to which diurnal dynamics of microbial community activity and function, particularly nutrient cycling processes, are linked to diurnal cycles of carbon flow to the root zone and changes in plant gene expression associated with the plant circadian clock.

Methodology: *Maximum 150 words*

You will use a variety of experimental resources, including plant mutants with altered circadian clock genes. These will be used together with amplicon, metagenome and metatranscriptome sequencing, and quantitative PCR to profile the structure, abundance and functional characteristics of the microbiome, and key microbial groups with specialized functional traits. Metabolomic analysis of the root zone will also be conducted, and the relationship between diurnal rhythmicity of microbial communities and the cycling and bioavailability of nutrients within the root zone will be determined using biogeochemical approaches.

Training and skills: *Maximum 100 words – excluding CENTA training information*

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 range of chemical analyses as appropriate (e.g. C and N biogeochemistry, metabolomics), molecular techniques (DNA extraction, PCR, sequencing), metagenome and metatranscriptomic 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)	

Respiratory and Contact Infection Resilience of the Project: *Maximum 100 words:*

The project will comprise a mix of field work, laboratory work and desk based bioinformatic analysis. During any lockdown periods, bioinformatic components of the project will become the focus of the programme.

Possible timeline:

Year 1: Investigate diurnal rhythmicity of rhizosphere microbiome biodiversity

Year 2: Characterise diurnal rhythmicity of rhizosphere biogeochemistry, focussing on the nitrogen or phosphorus cycle

Year 3: Determine diurnal rhythmicity of key microbial functional signatures related to nitrogen or phosphorus cycling

Further reading:

Berendsen RL *et al.* (2012) The rhizosphere microbiome and plant health. *Trends in Plant Science* 17, 478-486.

Ingle, R., Stoker, C., Stone, W., Adams, N., Smith, R., & Grant, M. *et al.* (2015). Jasmonate signalling drives time-of-day differences in susceptibility of Arabidopsis to the fungal pathogen *Botrytis cinerea*. *The Plant Journal* 84, 937-948.

Hilton, S., Picot, E., Schreiter, S., Bass, D., Norman, K., Oliver, A., Moore, J.D., Mauchline, T.H., Mills, P.R., Teakle, G.R., Clark, I.M., Hirsch, P.R., van der Gast, D.J., Bending, G.D. (2021) Identification of microbial signatures linked to oilseed rape yield decline at the landscape scale. *Microbiome* 9, 1-15.

McKay Fletcher, D., Shaw, R., Sánchez-Rodríguez, A., Daly, K., van Veelen, A., Jones, D., Roose, T. (2019). Quantifying citrate-enhanced phosphate root uptake using microdialysis. *Plant And Soil* 461, 69-89.

Lidbury, I.D.E.A., Borsetto, C., Murphy, A.R.J., Bottrill, A., Jones, A.M.E., Bending, G.D. *et al.* (2021) Niche-adaptation in plant-associated Bacteroidetes favours specialization in organic phosphorus mineralization. *ISME J* 15, 1040-1050.

Further details:

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Information and links at the following webpage:

<https://warwick.ac.uk/fac/sci/lifesci/study/pgr/apply>