

## Describing the prevalence of antimicrobial resistance in UK deer populations

**Main supervisor:** [Dr Tristan Cogan: Tristan.Cogan@bristol.ac.uk](mailto:Tristan.Cogan@bristol.ac.uk)

**Second supervisor:** [Dr Aiden Foster: aiden.foster@bristol.ac.uk](mailto:aiden.foster@bristol.ac.uk)

**Proposed start date:** 1<sup>st</sup> July 2021 (flexible)

**Length:** 6 weeks

**Project description:** Venison from wild deer has been implicated in the outbreak of several diseases over the past decade. This highlights the lack of knowledge around the public health risk of both venison consumption and human interaction with wild or captive deer. Antimicrobial resistance (AMR) genes are commonly carried by livestock and could be a public health concern if passed onto humans through contaminated meat, like the outbreaks mentioned previously. Evidence from other countries has also shown an association between the carriage of AMR genes in wild deer and their proximity to livestock or areas applied with manure and human waste. Wild deer could be a potential reservoir for AMR genes that can be passed to livestock and while there is no evidence for this currently, it has been demonstrated that wild deer harbouring nematodes with anthelmintic resistance can transmit these to livestock.

A previous MRes study (not yet published) researched the prevalence of several enteric pathogens in wild, farmed, park and zoo deer from across the UK. Using faecal DNA samples from this study, we hope to take this work further and identify the prevalence of antimicrobial resistance genes carried by these bacteria in UK deer using multiple PCR assays for resistance genes. Prevalence data for wild deer can then be analysed to identify if resistance is correlated with proximity to livestock (using data from the OH-STAR project, University of Bristol).

We hope that this can further our understanding of the risk that deer may pose to livestock and public health.

In terms of COVID mitigation strategies, the samples are already collected, so no mitigation is needed as long as lab access continues. If lab access isn't possible the student will carry out a desk based analysis of the MRes data on pathogen carriage in wild deer and develop a multivariate model to identify factors that predispose animals.

## Environmental and evolutionary cues regulating isoprene emission by plants in human-modified tropical landscapes

**Main supervisor:** [Dr Tommaso Jucker: t.jucker@bristol.ac.uk](mailto:t.jucker@bristol.ac.uk)

**Proposed start date:** 7<sup>th</sup> June 2021 (flexible)

**Length:** 6 weeks

**Project description:** Isoprene is one of the largest indirect contributors to climate change that most people have never heard of. It is a volatile organic compound emitted by plants in response to heat stress (Taylor et al. 2018), which then interacts with other gasses in the atmosphere to increase the production of both ozone and methane. Most of the world's isoprene is emitted from tropical landscapes, where it is believed to play an important role in mitigating the effects of high temperatures on photosynthesis. However, not all tropical plants emit isoprene – with a relatively small number of species emitting a lot while many others emit none at all. This project will attempt to understand why isoprene emission varies so dramatically among different plant species. It will test the hypothesis that plants which contribute disproportionately to isoprene emissions are also those that dominate landscapes dedicated to agricultural production. These human-modified tropical landscapes are several degrees warmer than their natural counterparts (Jucker et al. 2018), potentially giving isoprene-emitting species a competitive edge by allowing them to maintain high rates of photosynthesis under hotter conditions. If true, this would represent a large and thus far overlooked source of anthropogenic greenhouse gas emissions. To test this hypothesis this project will leverage leaf isoprene emission measurements taken from >100 tropical plant species across a land-use intensity gradient in Malaysian Borneo.

This is a desk-based project based entirely on existing data. As such, the project is at very low risk from Covid-19 disruptions, and if necessary could be conducted without requiring in-person access to the University.

### References:

Taylor et al. (2018) *New Phytologist*, 220, 435-446

Jucker et al. (2018) *Global Change Biology*, 24, 5243-5258

## Expression, purification and characterization of modular protein complexes

**Main supervisor:** [Dr Fabio Parmeggiani: fabio.parmeggiani@bristol.ac.uk](mailto:fabio.parmeggiani@bristol.ac.uk)

**Proposed start date:** 5<sup>th</sup> July 2021 (flexible)

**Length:** 6 weeks

**Project description:** One of the goals of protein engineering is to be able to precisely design three-dimensional structures that can host specific functionalities, resulting in, for example, spatially arranged enzymes, organized display of signalling molecules or nanomaterials with defined structures. We use computational approaches developed in our group<sup>1,2</sup> and repeating units<sup>3</sup> as modular structural building blocks to design protein architectures instead of redesigning proteins from scratch each time, improving speed and reliability, and reducing time and costs.

To produce large structures, we can separately expressed and purified proteins that, when combined, self-assemble into multimeric complexes. The modular nature of our designs allows us to minimize the need to design novel protein-protein interfaces and to use the same modules in different contexts producing a broad range of architectures by simply changing the components.

**Aims and objectives.** In this project, the student will explore self-assembling complexes as viable method to produce custom modular designs.

The student will assemble target complexes using available genes in the lab containing compatible interfaces. Single proteins will be expressed in *E. coli* and purified by Immobilized Metal Affinity Chromatography and size exclusion chromatography (SEC). Proteins will be characterized by circular dichroism and dynamic light scattering (DLS). The affinity between pairs of interacting proteins will be determined by isothermal titration calorimetry. Complexes will be characterized by shift in SEC and DLS upon assembly, monitoring also stepwise addition of the components.

If access to the laboratory will need to be restricted, the project will focus instead on the computational design of new interfaces and new modular architectures.

References :

- (1) Yeh et al. <https://doi.org/10.1016/j.jsb.2017.09.001>
- (2) Yeh et al. <https://doi.org/10.3389/fbioe.2020.568318>
- (3) Brunette et al. <https://doi.org/10.1038/nature16162>

## Investigating regional diversity in plant root adhesion

**Main supervisor:** [Prof. Claire Grierson: claire.grierson@bristol.ac.uk](mailto:claire.grierson@bristol.ac.uk)

**Second supervisor:** Dr Emily R Larson: [emily.larson@gmail.com](mailto:emily.larson@gmail.com)

**Proposed start date:** 15<sup>th</sup> June 2021 (flexible start date)

**Length:** 6 weeks

**Project description:** Environmental conditions that increase soil erosion have drastic effects both on the loss of pristine landscapes and crop fields. The interactions between plant roots and their environment are required for plant development/success because the roots are the main site for nutrient and water uptake. These interactions also help roots anchor themselves into their surroundings, which in turn, secures the soil and reduces erosion caused by wind and rain. How plant roots modify these interactions to support their growth and respond to changes in their environment is largely unknown.

To understand how root-soil interactions are shaped by regional differences in soil composition, you will participate in two experiments:

1. Use a novel centrifuge-based assay to quantify the adhesive strength of roots of different *Arabidopsis* ecotypes collected from around the world.
2. The *Arabidopsis* ecotypes with adhesion phenotypes will be used in flood erosion simulations to correlate root adhesion with soil erosion resistance.

These results will be used to build hypotheses about how root physiology responds to and is modified by soil properties.

If COVID mitigation is required, the student can partake in the data analysis and interpretation of the results collected in the lab by other, more senior lab members. The student will learn to organise and evaluate raw data, and then use these data to run statistical tests and models to present and interpret root-substrate adhesion between the different *Arabidopsis* ecotypes. This work will include becoming proficient in R, ImageJ, and additional software commonly used in research. It will also be an opportunity to practice critical thinking and problem solving required for data interpretation.

## Mothers matter: examining the dynamics and consequences of maternal care in an unusual insect system

**Main supervisor:** [Dr Sinead English: sinead.english@bristol.ac.uk](mailto:sinead.english@bristol.ac.uk)

**Proposed start date:** 1<sup>st</sup> July 2021 (flexible)

**Length:** 6 weeks (flexible)

**Project description:** In many organisms, the amount and quality of parental care has lasting consequences for offspring behaviour, physiology and survival. Much of this research has focused on avian or mammalian models, yet insect systems provide show a remarkable diversity of parental care and are highly amenable to laboratory studies. This project will focus on maternal behaviour in an exciting, novel system to study parental care in insects: the viviparous cockroach, *Diploptera punctata*, which is well studied as a model for juvenile hormone synthesis. In this species, females give birth to live young and provide them with milk-like substance in utero. They are highly gregarious and continue to associate with mothers after birth, yet very little is known about the extent and nature of maternal care during early development.

The aim of this project will be to investigate whether offspring developing in the presence of their mothers have higher survival and fewer antagonistic social interactions than those who develop without a mother. The student will use video analyses to characterise maternal behaviour, the first such study of its kind in these cockroaches. The student can also ask whether male and female offspring respond differently to maternal interactions, and removal of care might have different effects depending on the number of siblings present. The student will gain experience in insect husbandry, morphological and behavioural analysis. The results from this study will provide important baseline data for future work on the transgenerational effects of maternal nutrition or stress on offspring fitness in this system.

**Covid-19 contingency:** If laboratory access is restricted, videos of the experimental set-up will be recorded by the project supervisor and the student will have the opportunity to score behaviour remotely. The student will still be an active member of the research group with lab meetings due to be held remotely during this period.

