

PhD Project Advertisement

Project title: Engineering myxobacterial super-predators to fight crop disease

Project No: FBS2022-65-Whitworth-ar

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Project description:

Background:

Plant pathogenic microbes (phytopathogens) cause huge economic losses and threaten food security globally. For example, *Ralstonia solanacearum* alone causes more than \$1 billion worth of potato crop losses each year in just the USA. To reduce pre-harvest wastage and increase food security, there is an urgent need to fight crop disease by targeting the removal of phytopathogens. Predatory bacteria such as myxobacteria have the potential to be used as biocontrol agents for this purpose, as they can prey upon phytopathogens, thereby reducing crop disease and promoting plant growth.

Myxobacteria are able to prey upon a broad range of prey microbes, including pathogenic bacteria and fungi. While all myxobacterial isolates have a broad prey range, occasional strains exhibit unusually effective predatory activity against specific prey. Such enhanced predatory activity does not correlate with strain phylogeny, which suggests that the genes responsible for enhanced predatory activity have been inherited horizontally rather than vertically.

This scenario is supported by genome sequencing, which shows that myxobacterial strains have small 'core genomes' – genes which every strain possesses. However, the majority of genes come from the 'accessory genome', which is largely unique to individual strains. Such variability between genomes can be exploited to identify the genes responsible for predation of specific prey. When predation genes have been identified, it is then possible to transplant them between strains, to generate 'super-predator' strains with increased predatory activity against particular prey, or with a broader activity against a range of prey. Super-predator strains would be advantageous for use as agricultural inoculants, as they would be better able to kill phytopathogens than environmental strains.

Hypothesis:

This studentship will test the hypothesis that transplantation of prey-specific predation genes can be used to alter the prey-range of myxobacterial predators, enhancing their ability to protect crops from disease and increasing crop yields.

Strategy:

To test this hypothesis, comparative genomics will be used to identify prey-specific predation genes in myxobacteria. Predation genes will be transplanted between strains to increase predatory activity against multiple pathogens. We will focus on novel genes and those which encode digestive enzymes/toxins rather than those which cause the production of antimicrobial compounds. We will also engineer super-predators to have reduced predatory activity against PGPRs (plant growth promoting rhizobacteria). The ability of the engineered 'super-predator' to protect crops from disease and to promote plant growth will then be assessed in planta.

Studentship Objectives:

Previously, we isolated >80 strains of *Corallococcus* spp., a genus of predatory myxobacteria. Around half of those strains have now been genome-sequenced, which showed that they are highly individual with large accessory genomes. Strains

also exhibited diverse patterns of predatory activity against a panel of prey microbes (including pathogenic bacteria and fungi), indicating the presence/absence of prey-specific predation gene in those strains.

Objective 1- Identification of predation genes.

The predatory activity of selected *Corallococcus* strains will be assayed against a prey panel of plant pathogenic fungi and bacterial PGPRs. Predator strains will be selected for further study based on their predatory activity, including good and bad predators of both types of prey. Any selected predators which have not been sequenced will then be genome sequenced and a GWAS (genome-wide association study) undertaken to identify predation genes whose presence/absence correlates with efficient predation of individual prey organisms.

Objective 2 – Transplantation of predation genes between strains.

Prey-specific predation genes from ‘donor strains’ will be cloned under the control of inducible promoters and introduced into ‘recipient strains’. Expression of transgenes will be assessed by qRT-PCR, and any impact on predatory activity against the panel of prey assayed. The intention would be to create ‘super-predators’, with enhanced predatory activity against key phytopathogens, and broader activity against a range of phytopathogens, but with minimal activity against PGPRs

Objective 3 – Crop protection using super-predators.

The ability of super-predators to reduce crop disease will be tested in planta against fungal pathogens of wheat, which is a priority crop. Disease will be measured in the presence/absence of pathogen, PGPRs and super-predators. Expression of key wheat stress response genes (e.g. defensin) will also be quantified by qRT-PCR as indicators of pathology.

Training opportunities:

This studentship lies at the interface between genetics, microbiology, plant biology and bioinformatics, and has been designed to gently introduce the student to an ever-expanding range of methods. The project team will provide full training in modern methods of genomic analysis, genetic engineering, microbiological techniques, gene expression measurements, plant pathology assays and bioinformatics/computational methods. Training will also be provided by the supervisors in the use of advanced computational infrastructures for genomic analyses, such as the high performance computing clusters available within IBERS, and via Supercomputing Wales. The applicability of these skills to problems across the life and medical sciences, make them ‘generically’ cross-disciplinary. The project includes funded research visits to Reading University during the PhD, attendance at summer school and funding to present research findings at national and international scientific conferences.

Student profile:

The project would be suitable for students with interests in cross-disciplinary research, involving fundamental and applied research in microbial genomics and molecular genetics. We are open to applicants from diverse backgrounds, including those with strong academic records in a biological, or otherwise relevant science, and with a clear interest in developing the expertise required to fulfil this exciting research program. The ability and motivation to learn new skills quickly would be highly advantageous as well as interests in scientific computing.

Funding particulars:

For up to date information on funding eligibility, studentship rates and part time registration, please visit the [FoodBioSystems website](#).