# Exploiting the chemical genomics of Pseudomonas spp. for natural product antifungals effective against fungal pathogens of wheat.

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***Submit applications to this project to University of Bath***

**Project description:**
Wheat is an important staple crop within global food production systems. It is the most widely cultivated cereal in the world, with more than 220 million hectares planted annually, and the consumption of wheat accounting for around 20% of total calories consumed globally. With an increasing global population, a major challenge facing humanity is how agricultural systems will be able to rapidly increase food production, in line with increasing demand. Fungal pathogens are a major contributor to the wheat 'yield gap', the difference between the potential yield of crops and the actual yield harvested, with current estimates suggesting wheat yield losses of around 21.5% exist due to pathogens and pests.

Zymoseptoria tritici as well as Aspergillus and Fusarium species, are causes of major fungal diseases of wheat, causing threats to food security either by direct yield loss or through food contamination with mycotoxins, with 5-10% of wheat containing Aspergillus or Fusarium mycotoxins above safe limits. Resistance to all known classes of fungicides has arisen over the last 30 years, and new chemical control strategies are urgently needed. Environmental bacterial isolates could potentially be an untapped source of naturally derived antifungal compounds effective against these pathogens. Pseudomonas bacteria have shown great promise as a source of novel antifungal secondary metabolites, with a proven ability to antagonise many fungal plant pathogens, both in vitro and in planta, through the production of secondary metabolites.

The biosynthesis of secondary metabolites from localised clusters of genes, referred to as biosynthetic gene clusters (BGCs) can be predicted from bacterial genome assemblies using software such as antiSMASH, utilising hidden Markov models (HMM) rule-based detection. Combined with analytical chemistry approaches of the interactions between Pseudomonas and fungal pathogens, predictive bioinformatics of secondary metabolites offers the opportunity to prioritise candidate BGCs for further characterisation, through site-directed mutagenesis. Mutants will be generated in genes predicted to encode core biosynthetic functions within BGC candidates, and the effect on the fungal antagonism phenotype and chemical profile of agar extracts examined. This PhD project will combine microbiology, bioinformatics and analytical chemistry to explore the interactions between Pseudomonas bacteria and economically important fungal pathogens of wheat. Using these approaches as part of a bio-prospecting pipeline to identify novel bacterial secondary metabolites implicated in fungal antagonism could ultimately lead to future crop protection products, that are urgently needed to retain control of these pathogens in wheat fields.

**Our aim as the SWBio DTP is to support students from a range of backgrounds and circumstances. Where needed, we will work with you to take into consideration reasonable project adaptations (for example to support caring responsibilities, disabilities, other significant personal circumstances) as well as flexible working and part-time study requests, to enable greater access to a PhD. All our supervisors support us with this aim, so please feel comfortable in discussing further with the listed PhD project supervisor to see what is feasible.**