



# **PhD Project Advertisement**

**Project title:** Smart control of crop diseases: how can we best combine fungicides and plant resistance genes? **Project No:** FBS2023-69-Mikaberidze-ra

**Lead supervisor:** Dr. Alexey Mikaberidze, University of Reading (UoR); School of Agriculture, Policy and Development; Crop Science Department

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# **Co-supervisors:**

Dr. Martin Swain, Aberystwyth University (AU), Institute of Biological, Environmental & Rural Sciences (IBERS); Dr. Lindsay Todman, University of Reading; School of Agriculture, Policy and Development; Centre for Agri-Environmental Research;

Dr. Ricardo Kanitz, Syngenta (Switzerland); Crop Protection Research & Development, Global Product Biology

# **Project description:**

The project will investigate the interaction between the fungal pathogen *Zymoseptoria tritici (Zt)* and its host plant wheat. *Zt* causes septoria tritici blotch (STB), the most damaging disease of wheat in Europe and one of the largest constraints on wheat production globally. The disease is especially serious in the UK because of conducive climatic conditions. It is becoming increasingly difficult to control STB, because *Zt* is capable of rapidly evolving resistance to fungicides and adapting to disease-resistant wheat varieties and environmental conditions. It is recognized that no single control measure is durable in the face of the pathogen's notorious adaptive capacity, hence the two key control methods – fungicides and disease resistance genes in wheat – need to be combined in a manner that optimizes not only control efficacy in the short term, but also their sustainability in the longer term. This interdisciplinary project will make a major contribution to this goal using a powerful combination of large-scale field experimentation with novel high-throughput phenotyping techniques, bioinformatic analyses, state-of-the-art machine learning and mathematical modelling approaches.

In the first phase, a field experiment will be conducted during two consecutive years to investigate the STB epidemic development in a large number of different wheat genotypes. The amount of disease will be measured using both the conventional visual assessments and novel digital phenotyping approaches, and the daily weather data will be recorded. The data on epidemic development will be linked to genomic data already available for the wheat population under study, and in this way you are likely to identify new genetic bases of STB resistance in wheat. In the second phase, powerful machine learning techniques will be used to combine the three types of data (disease measurements, weather data and wheat genomic data) and construct a model predicting the seasonal STB epidemic development. Finally, in the third phase of the project, the outcomes of the two previous phases will be incorporated into a modelling framework (epidemiological/evolutionary model) that describes how the pathogen population changes over time in its interaction with the host population of wheat plants. The model will incorporate the effect of two control measures: fungicides and STB resistance genes in wheat. This will allow you to optimize choices of fungicide treatment programmes and diseaseresistant wheat cultivars that maximize net benefit of growers over a short term of a single growing season. You will then be able to compare the outcomes with the predicted net benefit over a longer term of a number of consecutive growing seasons, taking into account disease levels, weather variables and wheat genomes. The outcomes will establish the scientific basis for the software product that growers can use to guide their choices regarding fungicide applications and wheat cultivars.













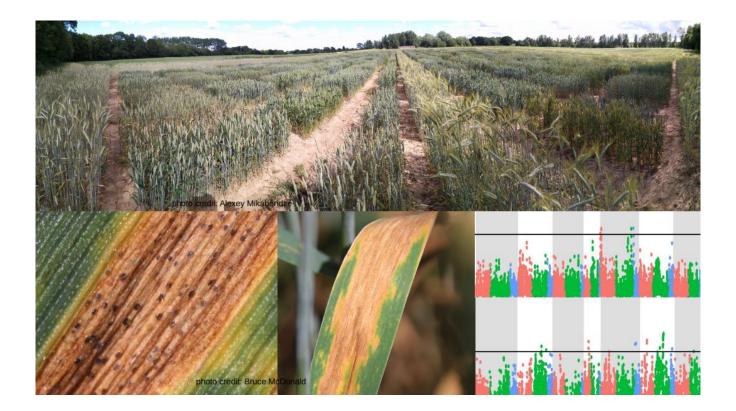


Figure 1: Upper panel: wheat MAGIC population grown at the Sonning field site of the University of Reading; lower panel left and middle: symptoms of septoria tritici blotch (STB) on wheat leaves; lower panel right: Manhattan plot, a typical outcome of the quantitative trait loci mapping identifying regions in the wheat genome associated with a particular STB resistance phenotype.

#### **Training opportunities:**

The student will acquire inter-disciplinary skills in designing and conducting large-scale field experiments with crop pathogens, acquiring large datasets with the help of novel digital phenotyping approaches, use machine learning and mathematical modelling to extract knowledge from data. The student will receive extensive training by the supervisory team in computer programming to handle large and complex data sets and conduct mathematical and computational modelling using Linux, Python and R. The student will have access to advanced computational infrastructures, such as the high-performance computing clusters available at Aberystwyth, and via Supercomputing Wales, and receive appropriate training in their usage. The student will be embedded within the extensive international collaborative network of the supervisory team that includes plant pathologists, genomics experts, modellers and practice-oriented researchers, enabling the student to make use of these diverse sets of expertise. A three-month placement with Syngenta will provide the student with the industry's perspective on the project's outcomes, expanding the range of possible employment options after the completion of the project. The unique combination of empirical, mathematical and computational skills as well as a valuable professional network developed in the course of the project will increase the student's chances to find a high-profile job in academia, governmental agencies or industry.

The project is a CASE studentship partly funded by Syngenta Crop Protection (Switzerland). This will provide the student with the opportunity of a three-month placement with Syngenta towards the end of the project.

## **Student profile:**

This studentship is available only to individuals who are eligible for UK fees status. The project would suit an ambitious student interested in combining experimentation in the field with mathematical and computational modelling of agrifood biosystems. The ideal candidate would have:

- A degree (minimum BSc 2.1) in a either a quantitative discipline (such as physics, mathematics or computer science), biology or agricultural/environmental sciences
- A strong interest in biology applied to agriculture
- A strong interest in mathematical/computational modelling of biological processes
- A desire to link the models with real-world field experiments and spend equal proportions of time doing experimental research and modelling/computational research
- The ability and motivation to quickly learn new skills
- Programming skills

Please note that experience in mathematical modelling or bioinformatics are important, but not essential, as extensive training will be offered in both. We encourage applications from diverse backgrounds.

# Stipend (Salary):

FoodBioSystems DTP students receive an annual tax free stipend (salary) that is paid in instalments throughout the year. For 22/23 this is £17,668 and this will increase slightly each year at rate set by UKRI.

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

## **Equality Diversity and Inclusion:**

The FoodBioSystems DTP is committed to equality, diversity and inclusion (EDI), to building a doctoral researcher(DR) and staff body that reflects the diversity of society, and to encourage applications from under-represented and disadvantaged groups. Our actions to promote diversity and inclusion are detailed on the <u>FoodBioSystems DTP website</u>.

In accordance with UKRI guidelines, our studentships are offered on a part time basis in addition to full time registration. The minimum registration is 50% FT and the studentship end date will be extended to reflect the part-time registration.

#### **References:**

**Mikaberidze, A.** & McDonald, B.A., 2020 A tradeoff between tolerance and resistance to a major fungal pathogen in elite wheat cultivars. *New Phytologist*, 226: 879-890, doi:10.1111/nph.16418;

bioRxiv pre-print: https://doi.org/10.1101/354357.

Karisto, P., Hund, A., Yu, K., Anderegg, J., Walter, A., Mascher, F., McDonald, B.A., & **Mikaberidze, A.**, 2018 Ranking quantitative resistance to Septoria tritici blotch in elite wheat cultivars using automated image analysis, *Phytopathology*, *108*, *568–581*.

**Mikaberidze, A.**, Mundt, Ch. & Bonhoeffer, S., 2016 Invasiveness of plant pathogens depends on the spatial scale of host distribution, *Ecological Applications*, 26, 1238–1248, E-print arXiv:1410.0587.