

Map based cloning and characterisation of plant loci conferring resistance to a root infecting fungus

Supervisory team:

Rothamsted supervisor: Dr Kim Hammond-Kosack (Rothamsted Research) Academic supervisor: Dr Hans-Wilhelm Nützmann (University of Exeter) Dr Nida Ghori (Rothamsted Research), Dr Michael Deeks (University of Exeter), Dr Stephen Pearce (Rothamsted Research), Dr Wanxin Chen (Rothamsted Research), Dr Dan Smith (Rothamsted Research),

Collaborators: Dr Simon Griffiths (John Innes Centre)

Host institution: Rothamsted Research (Harpenden) Submit applications to this project to University of Exeter

Project description:

Ensuring global food security for the ever-growing global population is a major concern. Fungal pathogens destroy a substantial amount of all food and feed crops each year (~15%). Take-all (TA) is the most important threat to wheat root system health. This disease is caused by the fungus Gaeumannomyces tritici, which infects the roots and damages the vasculature tissue of the plants, thereby adversely affecting water and nutrient uptake. In high disease years, TA causes over 50% yield loss in the field and causes nitrate leaching from the soil into neighbouring watercourses as a result of the crop's reduced capacity to uptake soil nitrogen. Growers have few effective TA management strategies and there are no characterised sources of genetic resistance, so there is an urgent need to identify and deploy reliable, environmentally-friendly and durable sources of TA resistance. The best way forward is to find and exploit genetic sources of resistance to protect UK, European and global wheat crops from TA disease without compromising plant health and yield.

The student will use multiple bioinformatics approaches to predict and develop a high priority candidate gene list for the genomic regions associated with TA resistance identified from selected Watkins wheat lines from a Genome Wide Association Study (GWAS) analysis and the lines selected from a biparental mapping population analysis. Functional validation of these candidate genes will be done in the laboratory using transient virus induced gene silencing method (VIGS) and/or virus over-expression (VOX) in roots combined with root imaging and quantitative disease assessments. This new knowledge will permit the student and the advisory team to devise new TA control strategies.

This collaborative project is multidisciplinary with strong functional genomics, computational biology and bioimaging components. The student will spend time at Rothamsted Research (RRes) a world leading Agricultural Research Institute and the University of Exeter, a major international research intensive university with one of the largest bioscience departments in the country. The student will have access to world class research facilities and will receive outstanding interdisciplinary training from their advisory team. The student





will also receive training in how to give oral/poster presentations at laboratory meetings, workshops, attend national/international conferences, write scientific paper(s) for peer review and will take part in suitable public outreach events, for example The British Festival of Science and Cereals UK.

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.