

Understanding the epigenetic basis for variability in stress responses in plants

Supervisory team:

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Host institution: Cardiff University

Project description:

Extreme weather events associated with climate change are causing increased crop losses year-on-year. As sessile organisms, plants have to respond to abiotic stresses such as heat, drought, and high salinity by modifying their growth and metabolism. These responses require coordinated changes in gene expression across the plant that are regulated by conserved signalling pathways. Although these pathways are genetically encoded, responses can vary from plant to plant and even cell to cell. Little is known about what causes cell to cell variation, but such variation will affect the overall efficiency of the response and hinder our ability to engineer crops that perform consistently. This project will use cutting-edge microscopy and bioinformatic techniques to produce a map of epigenetic changes at single cell resolution that can be used to identify gene targets that will improve the consistency and efficiency of stress responses in crops.

Gene expression requires transcriptional complexes to access and bind specific DNA sequences. Although every cell contains a full copy of the genome, differences in DNA packaging mean that not all genes are equally accessible. Recent advances in single cell techniques, including high resolution 3D imaging of the nucleus and single cell sequencing approaches have identified changes in DNA organisation and accessibility that may explain why specialised cell types respond differently to the same signals. However, less is known about how DNA accessibility varies between cells of the same type. We therefore need to investigate how asynchronous cellular processes such as the cell cycle, which are known to cause major re-organisation of DNA, impact and modify sensitivity to stress. This project is part of a programme of ongoing systems biology research at Cardiff University to improve crop resilience to abiotic stress. You will use the model species *Arabidopsis* to understand how stress responses vary from cell to cell and to investigate the epigenetic causes of this variation. You will gain highly desirable practical skills in designing, preparing and analysing single cell sequencing datasets; performing high-resolution confocal microscopy and image analysis; and using niche plant physiology and data handling skills to develop stress response assays. The ultimate goal is to use these data to identify candidate genes that could be used to engineer improved crops.

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.