

Going Green: reprogramming roots into shoots using TCP transcription factors

Supervisory team:

Main supervisor: Dr Simon Scofield (Cardiff University)

Second supervisor: Dr Tamara Lechon (Cardiff University)

Collaborators: Dr Walter Dewitte (Cardiff University), Prof Jim Murray (Cardiff University)

Host institution: Cardiff University

Project description:

As cells differentiate, their capacity to switch fate becomes progressively limited, which poses a problem for repairing tissues and organs. Unlike other multicellular organisms, plants are known for their developmental plasticity. For example, shoot cuttings can regenerate root systems and vice versa. During regeneration, plant cells have the unique capability to change their identity by reprogramming their fate, a key mechanism in their ability to regenerate organs and tissues. Cell fate reprogramming requires changes in gene expression, which in turn requires changes in chromatin accessibility so that different genes can be accessed by the transcription machinery. Crucially, some transcription factors called pioneer factors can bind inaccessible chromatin and change its conformation so that other factors can access the DNA to initiate transcription, changing gene expression and causing cell reprogramming to a different fate. Ectopic overexpression of a plant transcription factor, TCP4, drives the conversion of Arabidopsis roots into shoot/stem-like organs, indicating that TCP4 has a central role in plant cell reprogramming. TCP4 regulates the expression of several chromatin remodellers, which suggests that TCP4 has a broader role in controlling the chromatin landscape and might be a novel plant pioneer factor.

To understand how TCP4 reprogrammes root cells, a combination of next generation sequencing techniques, bioinformatics, and live cell imaging in inducible TCP4 lines will be used to obtain a comprehensive picture of the TCP4-induced switch in cell fate. Chromatin maps from different timepoints of the root-to-shoot conversion process will be obtained through the use of chromatin particle spectrum analysis (CPSA) and chromatin immunoprecipitation (ChIP-seq). These maps will be compared to global changes in gene expression (RNA-seq) induced by TCP4 at the same timepoints to identify regions of the chromatin that may have been made accessible by TCP4 to initiate gene expression. The conversion of roots into shoots will also be monitored using fluorescent labels that allow us to recognise cell identity by confocal microscopy. This will help us understand the mechanisms that allow TCP4 to reprogramme roots and will contribute to establishing general principles of plant cell reprogramming.

This project is an exciting opportunity to learn multidisciplinary skills and techniques with wide applications. The project will lead to new insights in regulation of transcription and pioneering activity in plants and could lead to developing more efficient methods of plant propagation for sterile species, from a wider range of tissues, and provide new strategies for improving agricultural traits and food security.

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.