Rewiring root regulators for fine-tuning the legume-rhizobial symbiosis

Project Reference: TRG-SAI-KS

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BBSRC DTP main strategic theme: Bioscience for sustainable agriculture and food

BBSRC DTP secondary strategic theme: Understanding the rules of life

Project outline:

Legumes grow specialized root nodules to host beneficial nitrogen-fixing bacteria. These provide the plant with ammonia and form the basis of sustainable farming. Symbiotic nodules are functionally and morphologically distinct from lateral roots as they can accommodate nitrogen-fixing bacteria intracellularly.

Like lateral roots, symbiotic root nodules initiate from inner tissue layers. We previously showed that the initiation of lateral roots and nodules converges at a common developmental program. We now need to know what additional nodule-specific programs are required to differentiate symbiotic root nodules from lateral roots.

Repression of root identity has emerged as one of the key aspects by which nodule organ identity genes such as the LIGHT SENSITIVE SHORT HYPOCOTYL (LSH) transcription factors promote the development of functional nodule primordia that can support bacterial colonisation. LSHs repress root meristem regulators, and loss-of-function mutations in their genes cause nodule-to-lateral root conversions. The initiation and development of nodules relies heavily on both the function and repression of conserved root morphogenesis pathways and cellular processes, thus posing a fascinating contradiction that requires investigation for future translational opportunities. In this project, the student will test the hypothesis that differences in the spatial and temporal expression and function of root developmental regulators contribute to morphological and functional divergence between lateral roots and nodules.

For this work, the student will make use of the well-established LSH gain- and loss-of-function backgrounds and perform functional analyses on root meristem regulators previously identified to be repressed by LSHs. The regulators include members of the PLETHORA and UPBEAT families and members of the EPIDERMAL PATTERNING FACTOR-LIKE peptide family which are functionally linked to the fine-tuning of auxin-cytokinin crosstalk and to reactive oxygen signalling. In the Arabidopsis root, these regulatory components have been shown to determine the rates and planes of cell division, the rate of cell expansion and the transition from proliferation to differentiation. In legumes, we have observed that differences in these cellular processes underpin the divergence between lateral roots and nodules, but the roles and causal links of these root meristem regulators remain unclear.

In order to dissect how these regulators are expressed and functioning in the legume root context, the student will use a combination of molecular functional genetics and genetic and chemical perturbation and rescue experiments. EPFL peptide studies will be performed in collaboration with the Chater group, RBG Kew. Functional analyses will be facilitated by quantitative deep tissue imaging of reporter lines for gene expression and protein localisation and marker lines for cell division, cell geometry and bacterial infection. The quantitative data generated by the student will serve as the foundation for mathematical modelling which will be performed in collaboration with research groups at SLCU.

Overall, this project will provide mechanistic insights into how differences in cell division and expansion at early stages of development result in organs as different in form and function as the lateral root and the symbiotic root nodule. By understanding these mechanisms, we can translate these findings into improved rooting functions and rhizobial symbioses for more sustainable agriculture.