Transcriptional landscaping in plant stem cells: from chromatin to gene regulatory networks

Supervisory team:
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Project description:

All terrestrial life ultimately depends on plant meristems – small groups of undifferentiated cells that produce all major plant organs such as leaves and flowers. In the shoot apical meristem (SAM) of higher plants such as Arabidopsis, gene regulatory networks (GRNs) control cell growth, fate and identity to balance the formation of new organs, such as leaves and flowers, with maintenance of meristem integrity, ensuring the sustainable supply of pluripotent cells necessary for growth. Transcription factors, particularly the homeodomain protein SHOOT MERISTEMLESS (STM), play critical roles in SAM function through regulation of target gene expression. However, the components and structure of the STM GRN are not fully understood.

This project aims to develop a comprehensive understanding of the STM gene regulatory network in the SAM. STM encodes a Knotted1-like TALE homeodomain transcription factor that is expressed only in the meristem. Loss of STM function leads to failure to develop or maintain the meristem, while STM overexpression inhibits leaf cell differentiation and promotes the de novo formation of ectopic shoot meristems. These dramatic phenotypic changes suggest a central role for STM in the GRN(s) that regulate meristem development and function.

To understand how STM operates and how its role is integrated with the wider meristem GRNs, a multi-layered transcriptional landscaping approach will be undertaken. First, putative STM target genes will be identified using inducible STM overexpression and RNAi (gene silencing) followed by genome-wide RNA-seq analysis. In order to determine which of these STM-responsive genes are directly regulated by STM, global chromatin immunoprecipitation (ChIP-seq) will be performed to identify genomic regions to which STM is bound. Since STM also affects the chromatin structure to control the differentiation status of cells, chromatin particle spectrum analysis (CPSA) will be used to analyse the chromatin structure in the genomic regions bound by STM, placing the putative STM binding sites within the wider landscape of nucleosomes and other DNA-bound factors. Bayesian network analysis will then be used to infer GRN structure and relationships among the STM target genes.

This project is exciting opportunity to train under the supervision of two established experts in meristem biology, and to learn multidisciplinary skills and techniques including molecular genetics, plant cell and tissue culture, bioinformatics and developmental biology. The project will lead to new insights into networks controlling meristem development and could lead to novel strategies for the manipulation of plant growth, architecture and yield.