Effects of perturbing polyamine metabolism on development and stress responses in Arabidopsis thaliana

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Project description:

There is an urgent need to understand plant development and responses to stresses to maximise crop production and ensure food security, especially in the face of climate changes. Plant hormones play key roles in regulating flowering, seed development and responses of plants to both environmental stresses and pathogens. Polyamines are essential metabolites that have some roles that resemble plant hormones, but their exact role in plant development is unknown. Polyamine homeostasis is maintained by a balance of biosynthesis and breakdown as well as interconversion amongst different polyamines. Copper amine oxidases (CuAOs) form a family of related enzymes that catabolise polyamines and have a role in plant stress responses and in plant development. Polyamine levels also seem to affect other plant hormones such as gibberellic acids (GAs) – key regulators of plant growth and reproduction. Initial data indicate that down-regulation of multiple CuAOs results in changes to flowering time, plant architecture and seed production. Using CuAO mutants generated through artificial micro RNAs, CRISPR/Cas9 and T-DNA insertions in the model plant Arabidopsis thaliana, the project will investigate the effects of mutating single or multiple CuAO genes in Arabidopsis at a phenotypic and cellular level.

A major goal is to gain a better understanding of how polyamines and GAs interact. This will be explored through biochemical analyses of GA and polyamine content in different organs of mutants compared to wild type and through transcriptomic analysis of mutants to identify target genes.

The project will therefore provide training in three key areas leaving space for the student to develop their own interests: (1) plasmid vector construction including CRISPR constructs, and plant transformation (2) biochemical analysis of metabolites and plant hormones (3) Analysis of development and stress responses in transgenic lines through sterile culture, microscopy, transcriptomics and metabolomics (4) statistical analysis of big data sets.