

Title: Identification of gene regulatory networks downstream of auxin and ethylene driving root hair development

Gene regulatory networks underlying plant development controlled by phytohormones are complicated. Much research is aimed at understanding how these hormones operate in isolation, either through exogenous application of a single hormone or mutation of key pathway players that operate downstream. In reality, gene regulatory networks driving development are more complicated and interwoven, and the research focused at understanding hormonal crosstalk is underdeveloped. My research is aimed at elucidating the gene regulatory networks that are downstream of both auxin and ethylene to drive root hair development. To reveal the genes that are transcriptionally activated or repressed by both hormones in hair cells and non-hair cells, I will employ the INTACT (isolating nuclei tagged in specific cell types) method. This system works by expressing a nuclear targeting fusion protein (NTF), which consists of a biotin ligase recognition peptide conjugated to the WPP domain of Arabidopsis RAN GTPASE ACTIVATING PROTEIN 1 and a green fluorescent protein under the control of a hair cell-specific promoter (*ADF8p*) or a non-hair cell-specific promoter (*GL2p*). The NTF is co-expressed with a biotin ligase under the control of a constitutive promoter. The result is cell type-specific biotinylated nuclei that can be pulled down with streptavidin-coated magnetic beads, as streptavidin binds to biotin. I will use this method to isolate nuclei from hair cells and non-hair cells in Arabidopsis plants treated with the immediate ethylene precursor 1-aminocyclopropane-1-carboxylic acid (ACC) or the auxin indole-3-acetic acid (IAA) to reveal the genes that have altered expression in response to these hormones. The non-hair cell line will act as a control to determine the genes that are specifically responsible for hair cell development, as both hair cells and non-hair cells form the root epidermis and are thus expected to share much of the same transcriptional machinery.