GDCB Special Seminar

Tuesday, June 28, 2022 — 4-5 p.m. **1330 Advanced Teaching and Research Building**

'Brassinosteroid gene regulatory networks at cellular resolution'

Abstract: Brassinosteroids (BRs) are a group of plant steroid hormones that regulate diverse processes such as cell division, cell elongation, and differentiation by controlling the activities of BES1 and BZR1 family transcription factors, which in turn mediate the expression of thousands of genes. The gene regulatory networks (GRNs) that control the diverse processes regulated by BRs are only partially understood, but likely involve additional context-specific regulatory factors. The Arabidopsis root is a tractable model to investigate these networks due to its simple organization and defined cell lineages. We recently constructed an integrated atlas of more than 110,000 cells using single-cell RNA-seq, which highlighted the continuous nature of development in the Arabidopsis root and provided new insights into cell identity acquisition (Shahan, Hsu, et al., 2022, https://doi.org/10.1016/j.devcel.2022.01.008). To further define spatiotemporal BR responses, we performed a time series single-cell RNA-seq experiment following BR treatment. Annotation enabled by our reference atlas allowed us to query BR-regulated gene expression among the majority of cell types and developmental stages of the root. We recovered known hotspots for BR signaling including the epidermis. Our data also indicate that BRs strongly influence gene expression in the cortex, especially in the elongation zone. Waddington-OT reconstruction of cortex trajectories showed that BRs trigger a shift from proliferation to elongation which is associated with increased expression of cell wall-related genes. Accordingly, loss of BR signaling in the cortex has little effect on meristem cell length but impairs cell expansion in the elongation zone. To discover regulators in the elongating cortex, we used CellOracle to infer GRN configurations across each cell type, developmental stage, and time point of our BR time series. Our GRNs and subsequent experimental analysis revealed two transcription factors that play a prominent role in cortex GRNs and affect BR-mediated cell elongation. Finally, we used scRNA-seq to define cell-type-specific changes in gene expression associated with reduced elongation in the cortex of our transcription factor mutants. When combined, these datasets represent more than 200,000 single-cell transcriptomes, providing a view of brassinosteroid-mediated gene expression at unprecedented resolution.

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