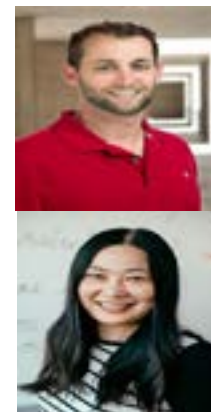


Epigenetics and Epigenomics

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Recently developed Open Tools and Resources for Arabidopsis Researchers

Socrates – open-source software for analysis of single cell ATAC-seq data
 (<https://github.com/plantformatics/Socrates>)

Recent or Future activities of Subcommittee members

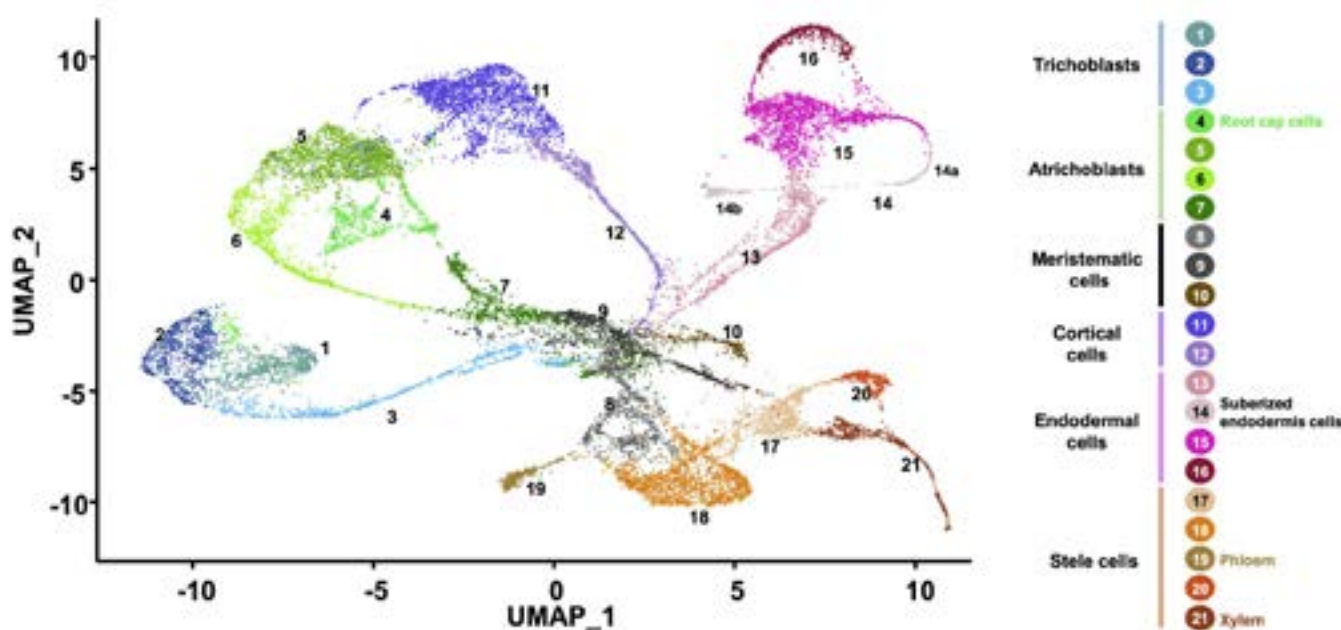
2021: Cold Spring Harbor-Asia Conference: Integrative Epigenetics in Plants, Awaji, Japan December, 2021

Selected Publications

Single-cell epigenome profiling (ATAC-seq studies):

- Farmer *et al* (2021) Single-nucleus RNA and ATAC sequencing reveals the impact of chromatin accessibility on gene expression in Arabidopsis roots at the single-cell level. *Molecular Plant* [https://www.cell.com/molecular-plant/fulltext/S1674-2052\(21\)00001-0](https://www.cell.com/molecular-plant/fulltext/S1674-2052(21)00001-0)

This study demonstrates the use of single cell RNA and chromatin accessibility to map molecular phenotypes at a single cell resolution. Epigenetic reproduction and memory



Functional annotation of the Arabidopsis root cell-types

(A) Assignment of Arabidopsis root cell types based on the characterization of the expression profile of cell-type and cell-death marker genes.

- Borg *et al* (2020) Targeted reprogramming of H3K27me3 resets epigenetic memory in plant paternal chromatin. *Nature Cell Biology* <https://www.nature.com/articles/s41556-020-0515-y.pdf?origin=ppub>

This paper reveals multi-layered epigenetic mechanisms in reprogramming the paternal epigenomes for faithful propagation and reproduction. Epigenetics and cell fate decisions/reprogramming

- Jin *et al* (2021) LEAFY is a pioneer transcription factor and licenses cell reprogramming to floral fate. *Nature Communications* <https://www.nature.com/articles/s41467-020-20883-w>

This research highlights the role of LEAFY as a pioneer transcription factor important for cell fate transitions. Genomic editing of intronic enhancers

- Meng *et al* (2021) Genomic editing of intronic enhancers unveils their role in fine-tuning tissue-specific gene expression in *Arabidopsis thaliana*. *The Plant Cell* <https://academic.oup.com/plcell/advance-article/doi/10.1093/plcell/koab093/6187954>

This study highlights the presence of important cis-regulatory elements in introns and validates their function using genome editing and reporter assays. Epigenetics and environmental interactions/adaptation

- Jiang J *et* (2021) UVR8 interacts with de novo DNA methyltransferase and suppresses DNA methylation in *Arabidopsis*. *Nature Plants* <https://www.nature.com/articles/s41477-020-00843-4>

This study uncovered a functional and mechanistic connection between a UV light signaling pathway and DNA methylation and highlights a potential role of DNA methylation in UV adaptation.

Planning for Fourth Decadal Roadmap

We need to identify all epigenetic regulatory elements (*cis* and *trans*) in all cell types and genotypes under both normal and various stress conditions in *A. thaliana*.