Unveiling the Stomatal Development Trajectory in Barley via Single-Cell Transcriptomics

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13 March, 2026

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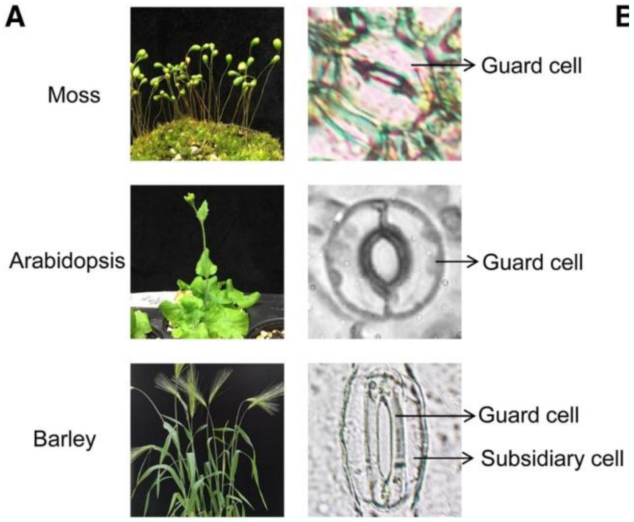
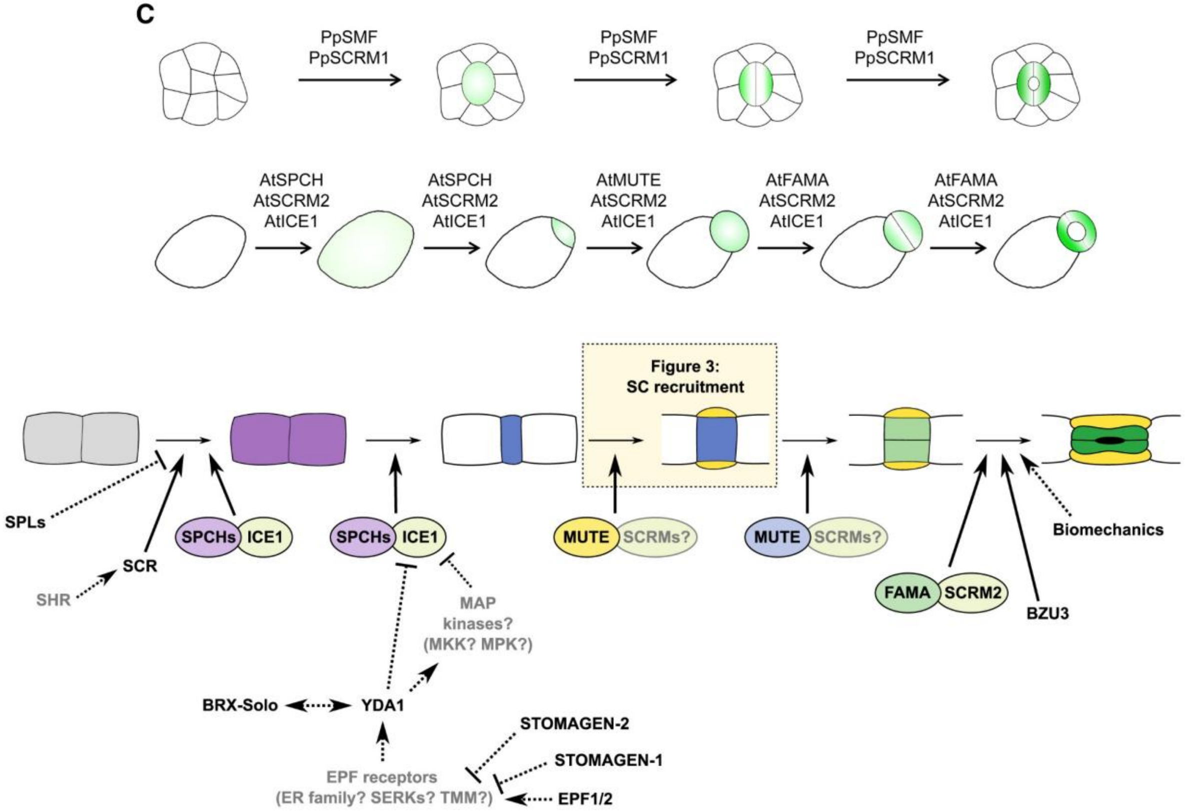
Background



Stomata in most land plants are formed by two kidney-shaped guard cells, while stomata of grass species are formed by two dumbbell-shaped guard cells (GC) flanked by two subsidiary cells (SC).

In *Arabidopsis*, AtSPCH is required to establish stomatal lineage and drive asymmetric division, and AtMUTE helps to produce guard mother cells (GMCs), followed by production of mature guard cells with AtFAMA.



(Cai *et al.*, 2017; Berg and Raissig, 2025)

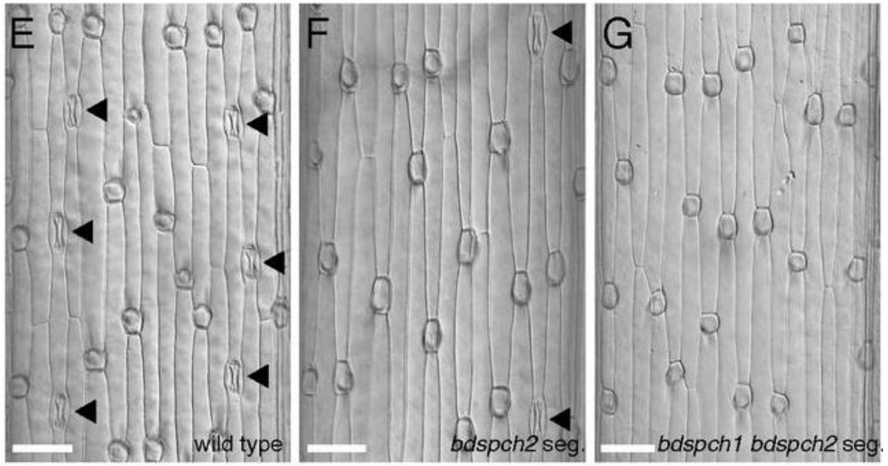
Background

SPCH

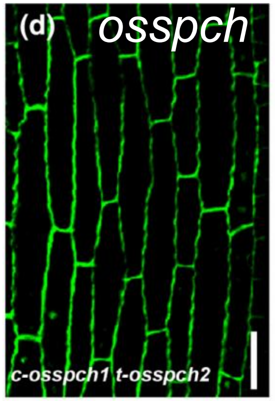
MUTE

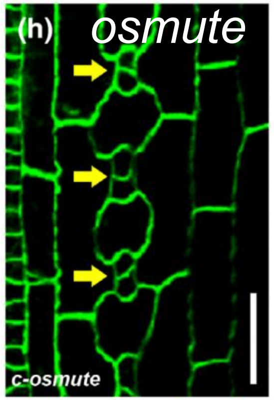
FAMA

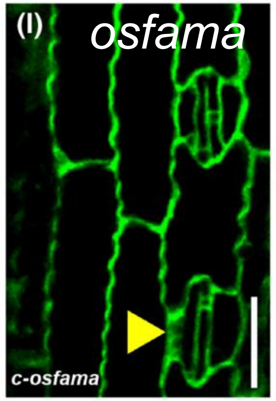
bdspch



bdmute

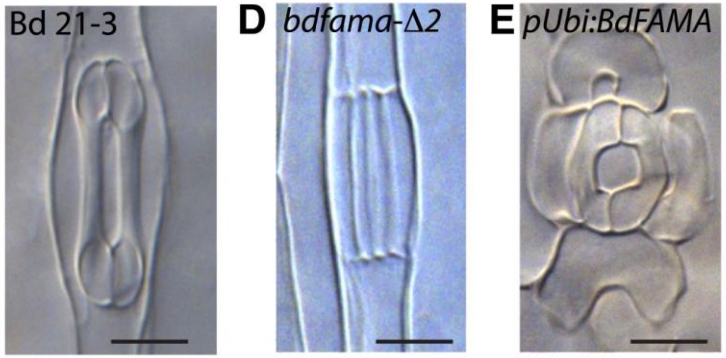




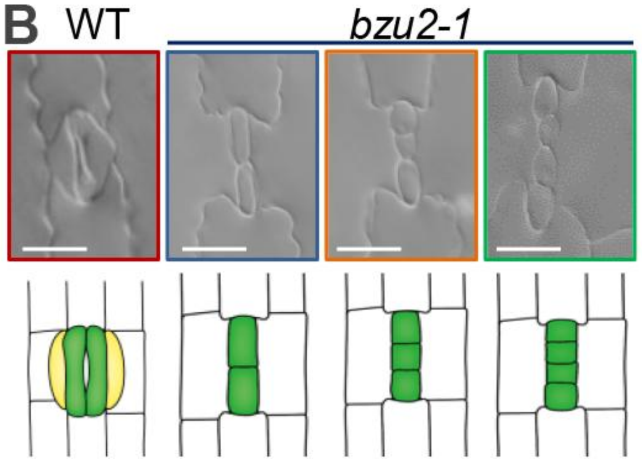


Various mutants reveal distinct stomatal phenotypes, highlighting both conserved and divergent roles across species.

bdfama



zmmute

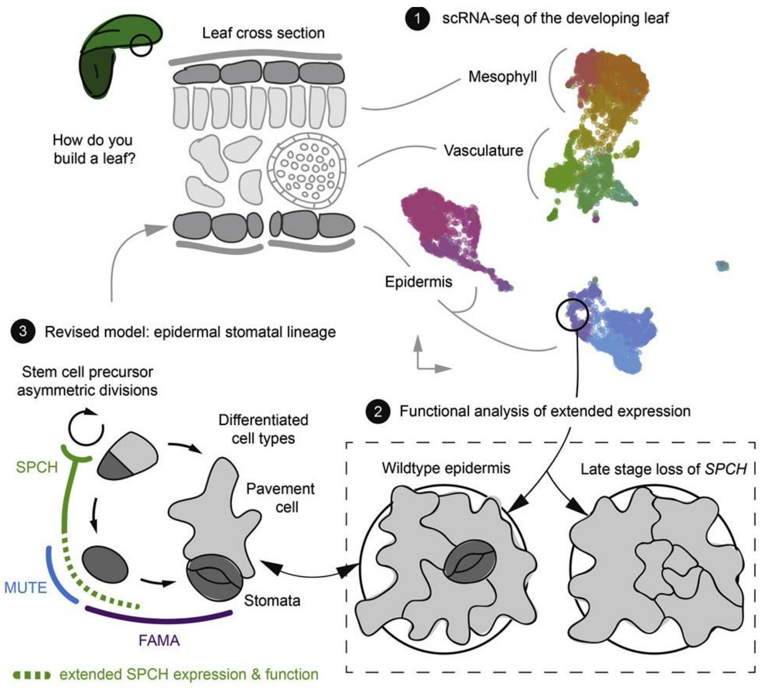


(Raissig *et al.*, 2016, 2017; Wang *et al.*, 2019; Wu *et al.*, 2019; McKown *et al.*, 2023)

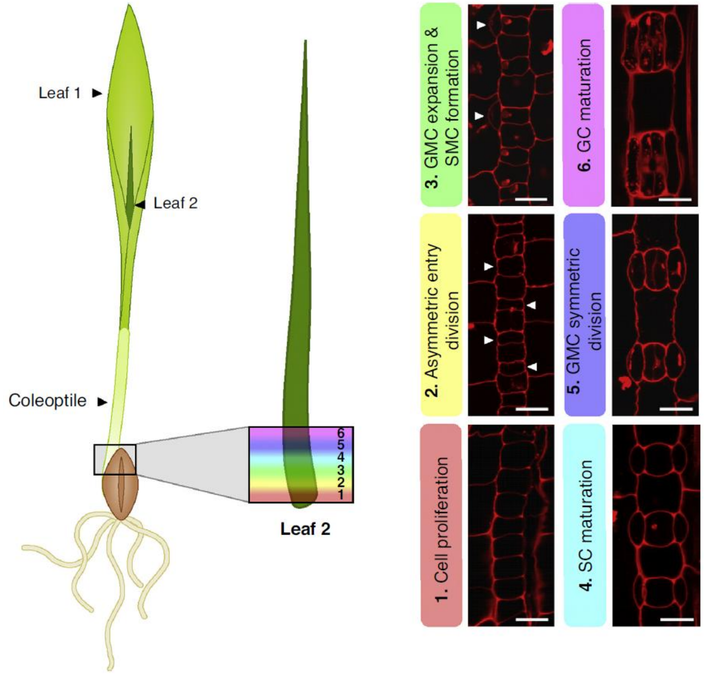
Background

Single-cell transcriptomics has emerged as a powerful tool, driving remarkable progress in our understanding of cell lineage trajectories across a wide range of plant and animal systems.

- ➢ How does stomatal development occur in barley?
- ➢ What roles do bHLH transcription factors SPCH, MUTE and FAMA play in this process?



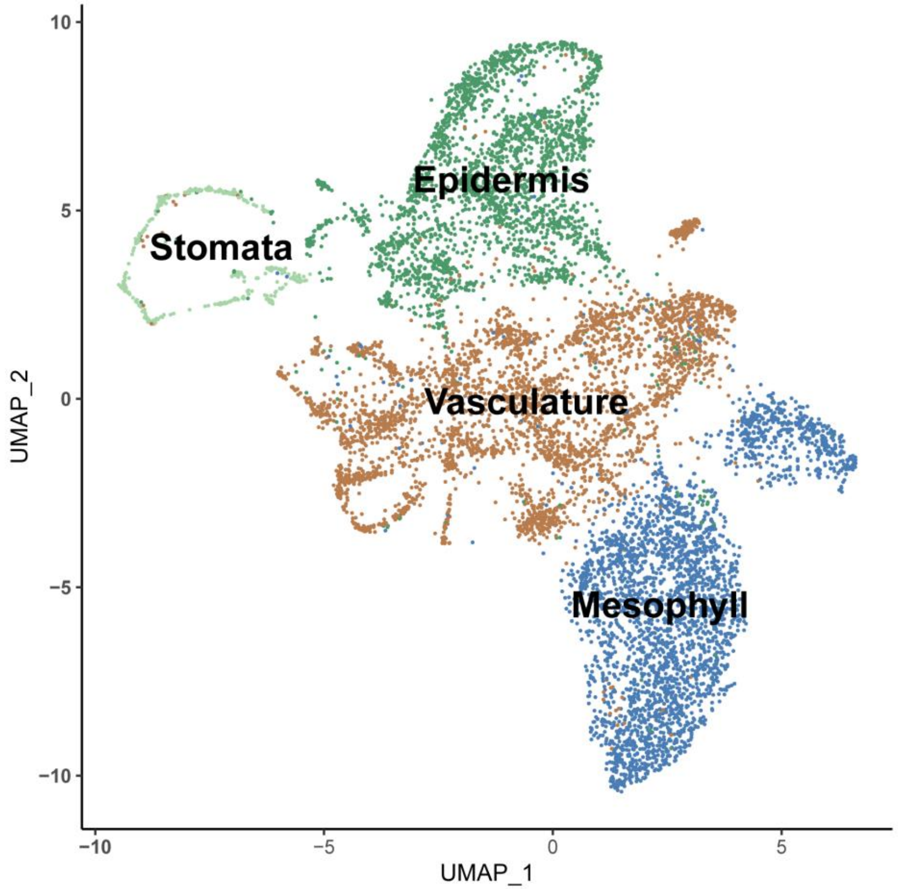
(Lopez-Anido *et al.*, 2021)

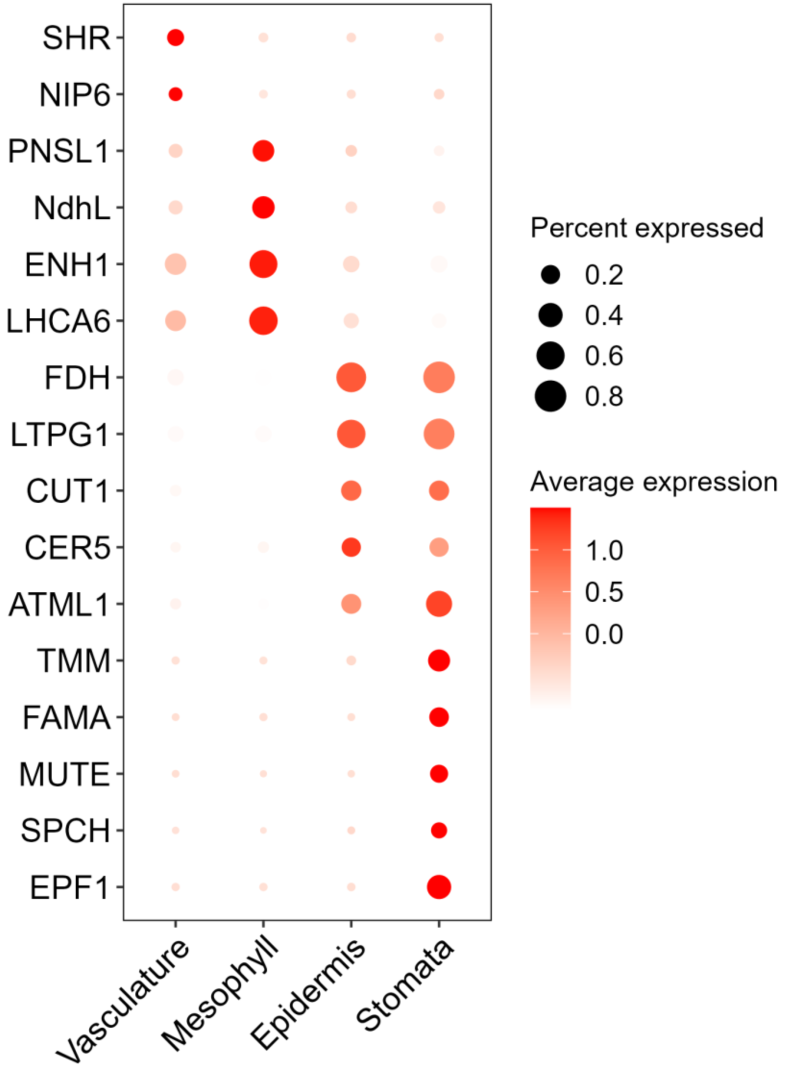


leaf base

(Hepworth *et al.*, 2018)

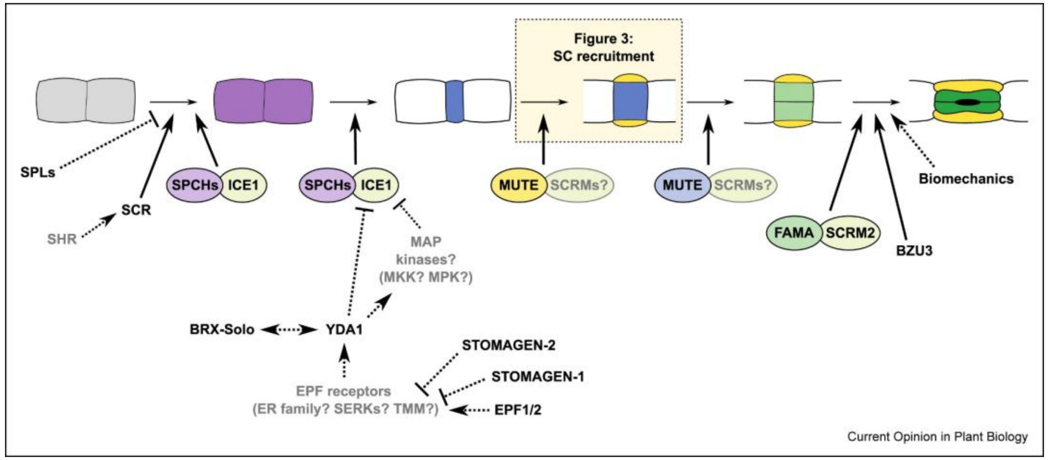
A single-cell transcriptomic atlas of leaf base





- The data revealed five clusters, which were annotated into four primary cell types.
- Notably, the stomata cluster displayed a distinctive ring-like structure in UMAP.

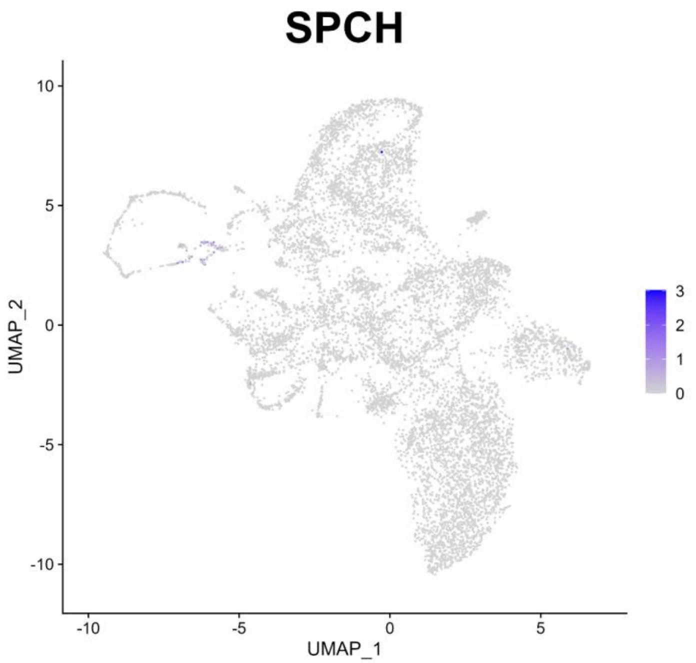
A single-cell transcriptomic atlas of leaf base

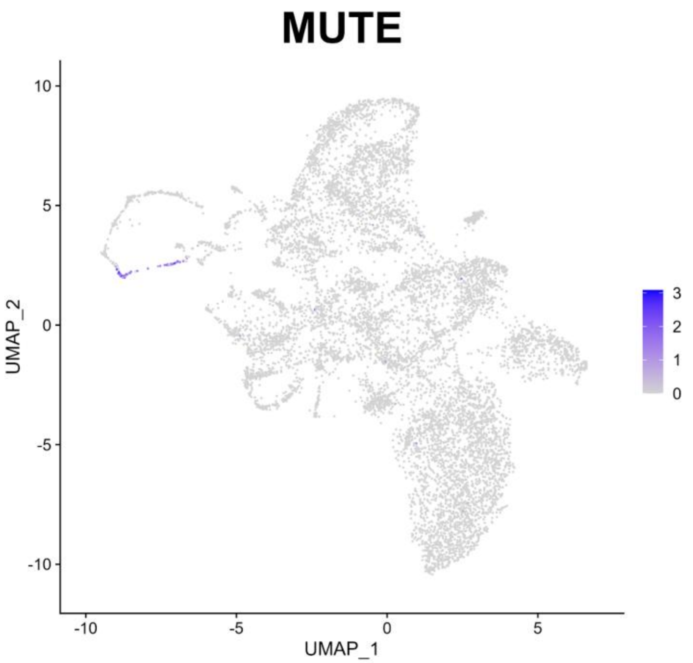


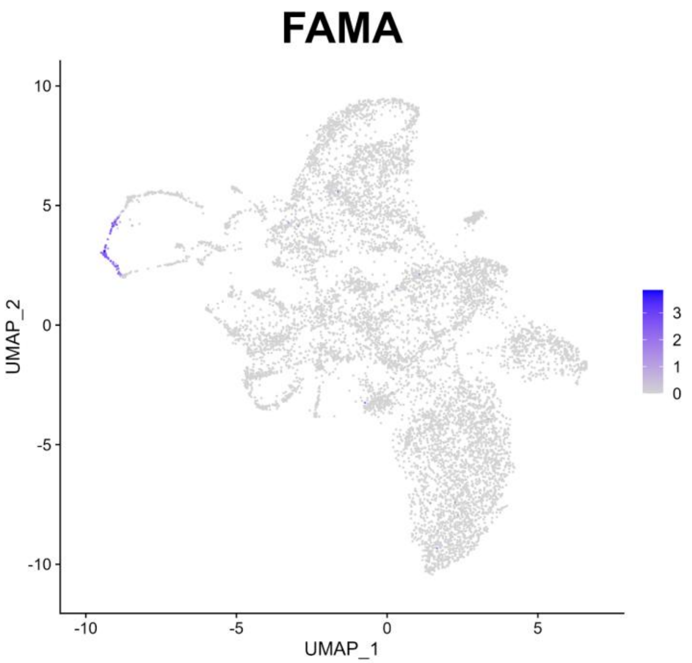
Current Opinion in Plant Biology

Sequentially activated.

Partial temporal overlap.

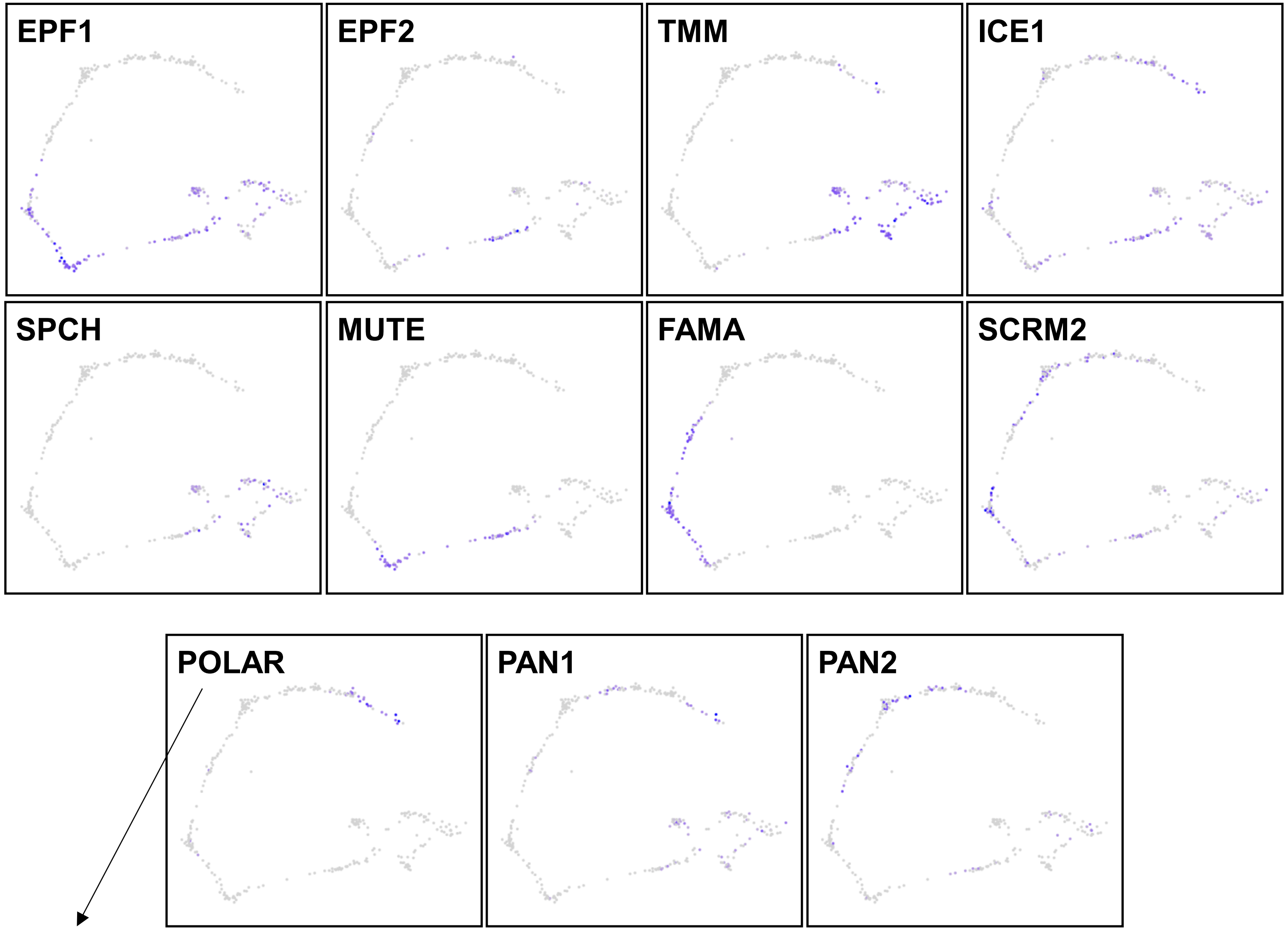




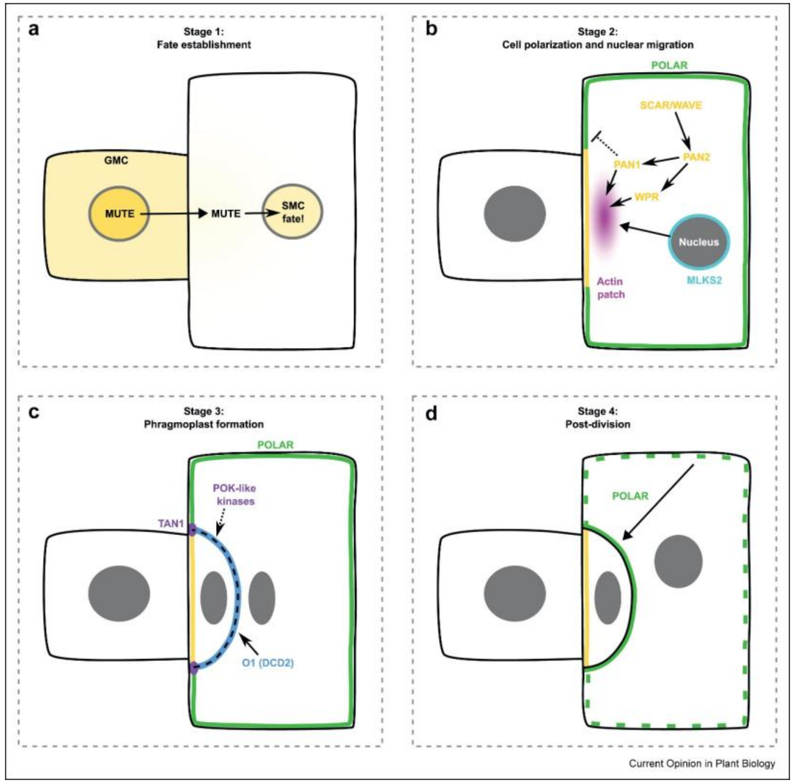


A single-cell transcriptomic atlas of leaf base

stage-specific expression



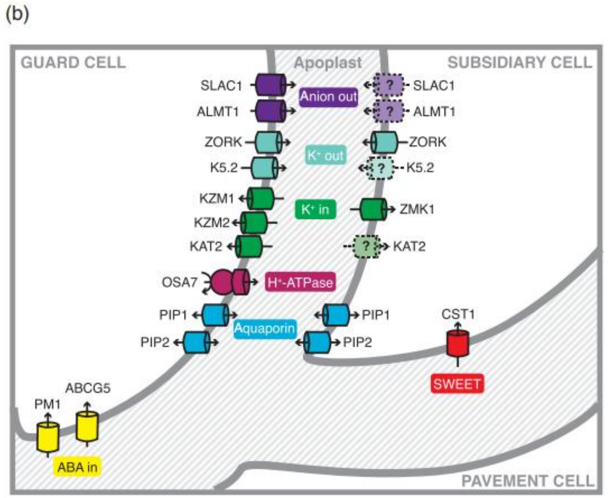
Interestingly, *ICE1* and *SCRM2* did not exhibit clear stage-specific expression patterns.



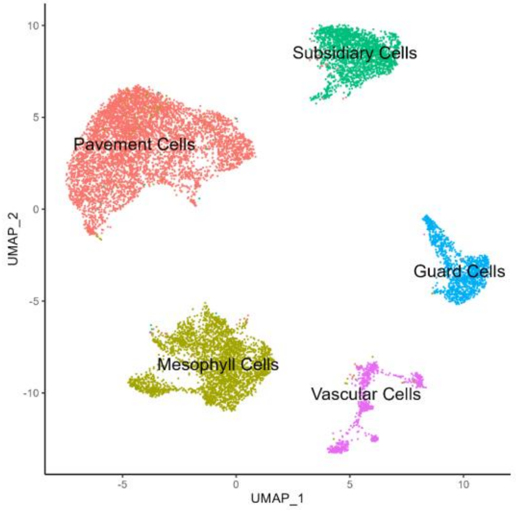
(Berg and Raissig, 2025)

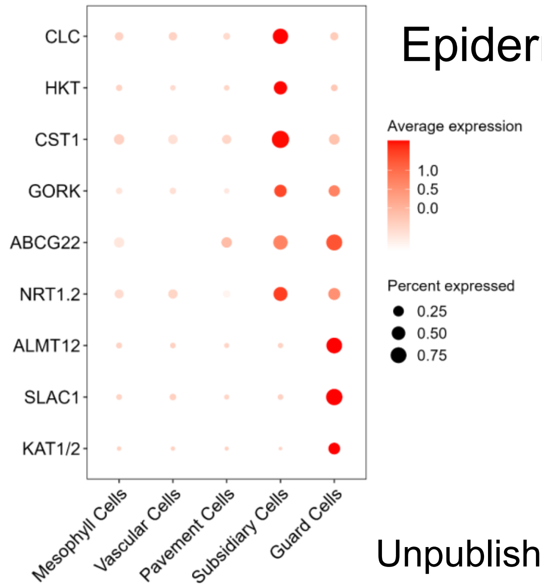
To establish polarity in SMCs.

A single-cell transcriptomic atlas of leaf base



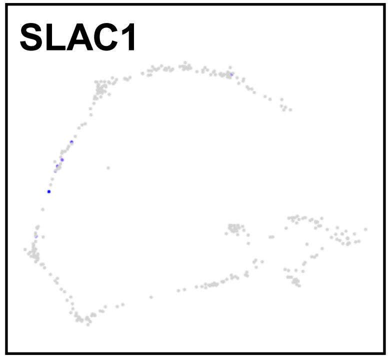
(Chater *et al.*, 2017)

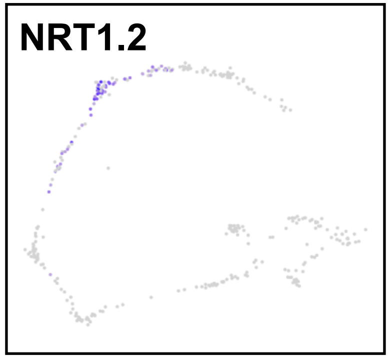


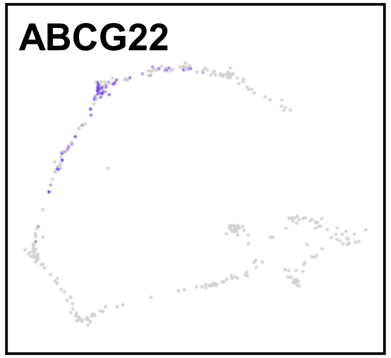


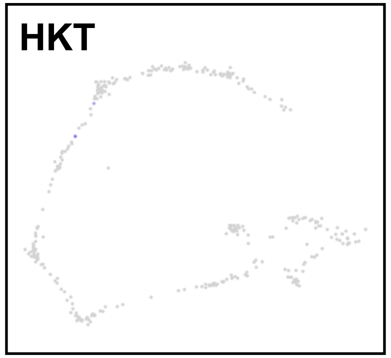
Epidermis

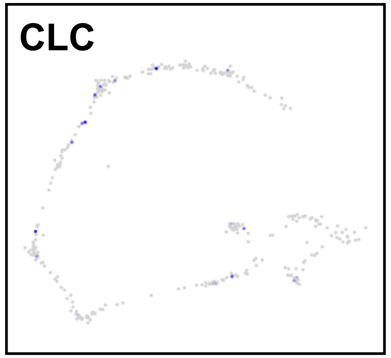
Unpublished data







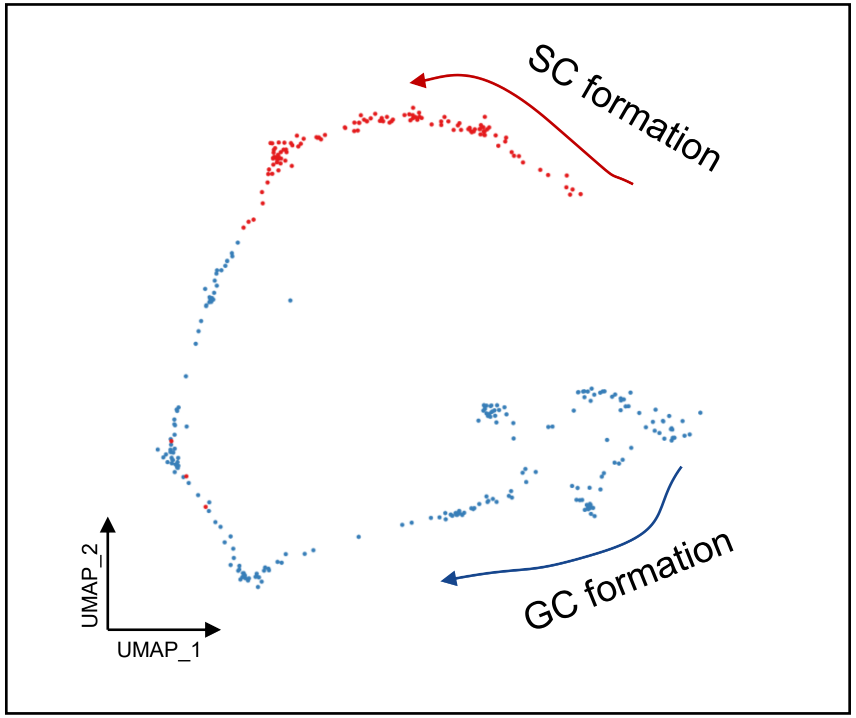




ALMT12, *KAT1/2*, *GORK* and *CST1* were not expressed in leaf base.

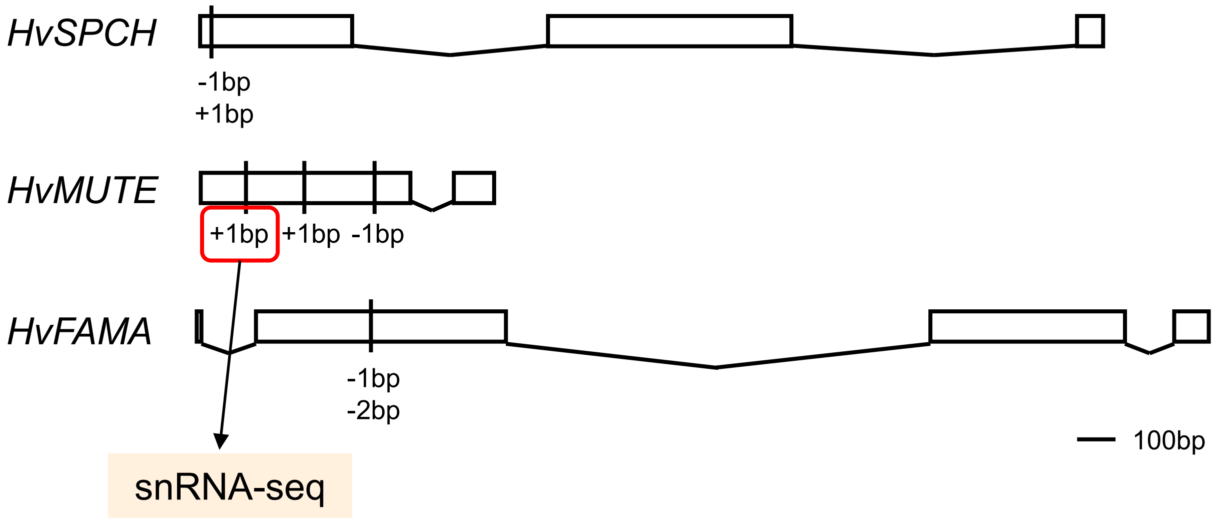
Young GC and SC are found in the leaf base, rather than mature ones.

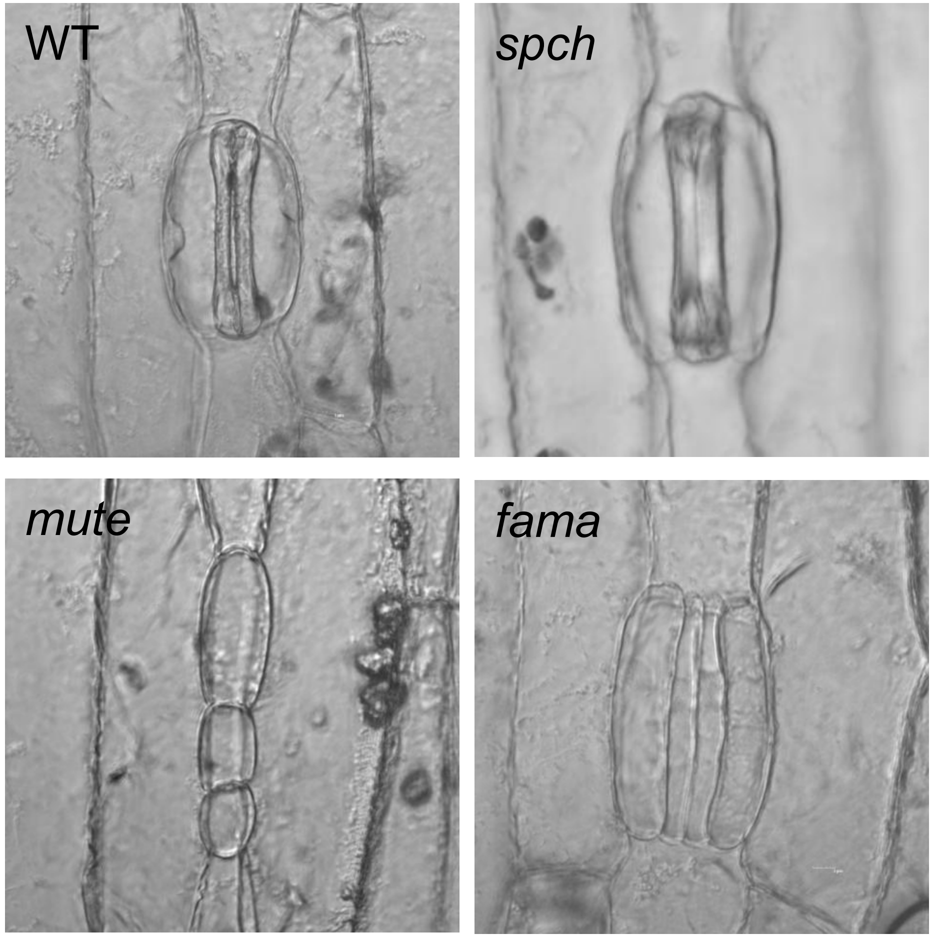
A single-cell transcriptomic atlas of leaf base



Blue indicates the developmental trajectory of GC, and red indicates that of SC.

Stomatal phenotype of *spch, mute,* and *fama* mutants

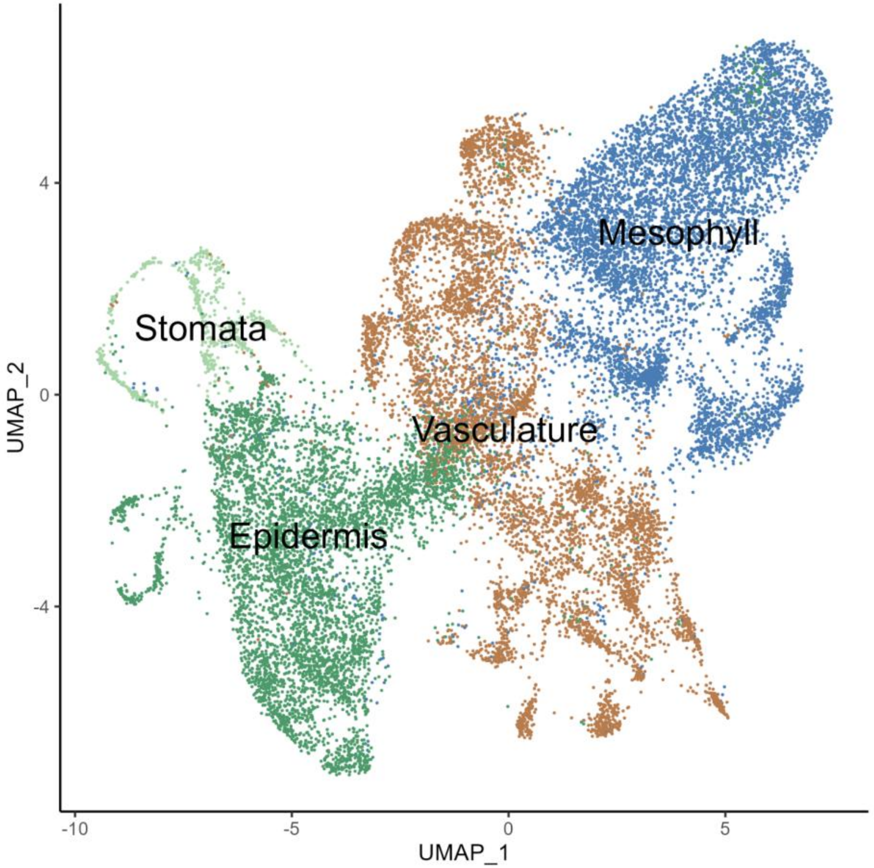


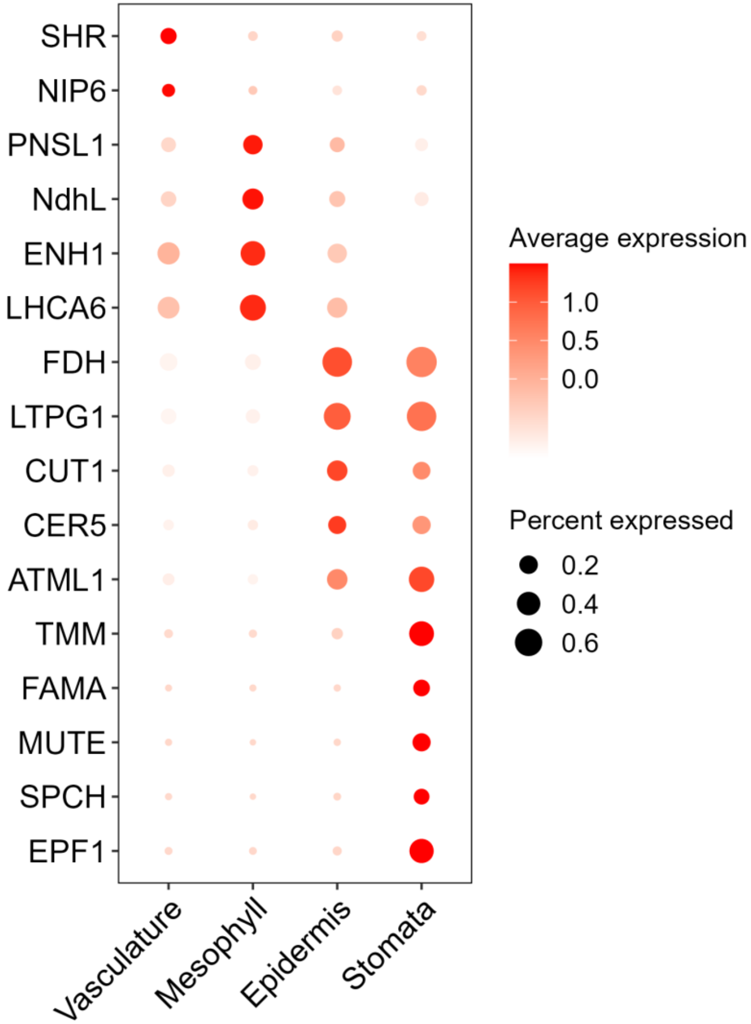


- Loss of HvSPCH did not significantly alter stomatal morphology. In contrast, *hvmute* and *hvfama* mutants exhibited severe stomatal defects.
- Homozygous mutants of *MUTE* and *FAMA* are lethal at the seedling stage.

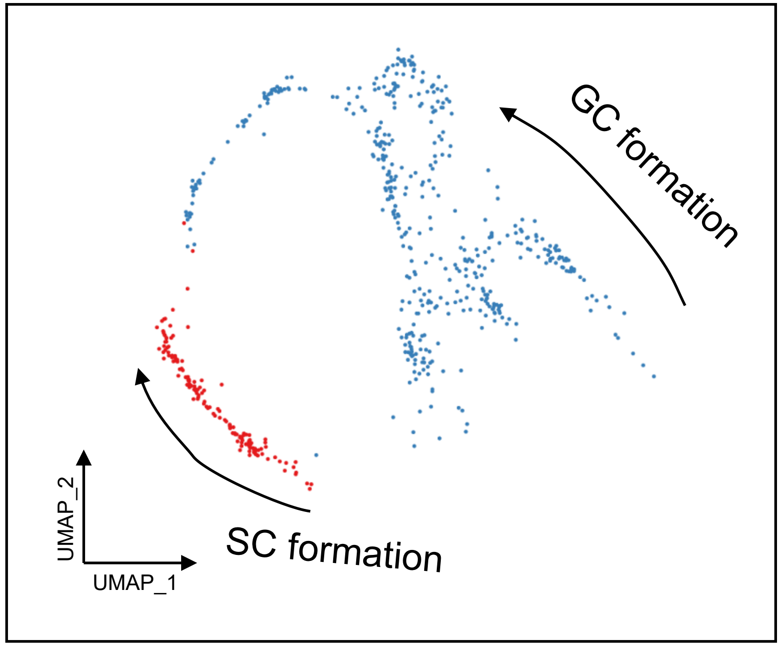
Integrating WT and *mute* transcriptomes to define the function of MUTE

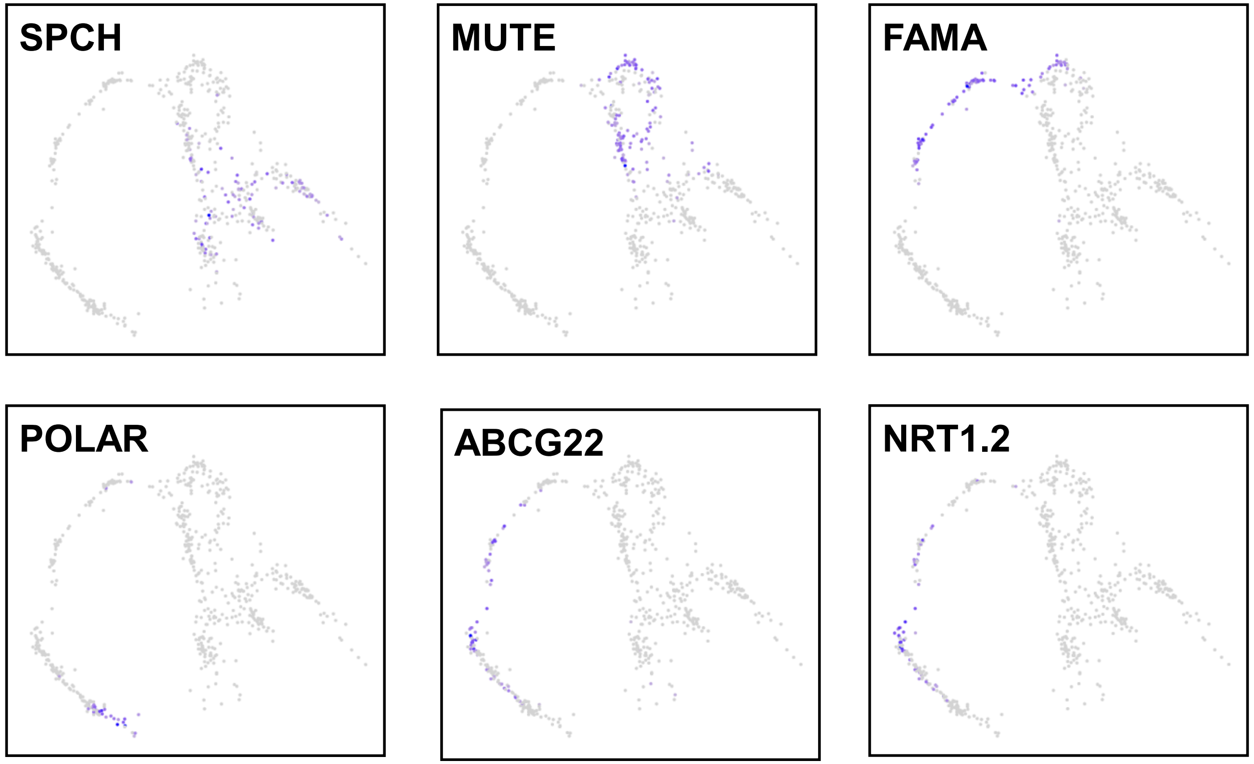
The snRNA-seq data of wild-type (WT) and *hvmute*.



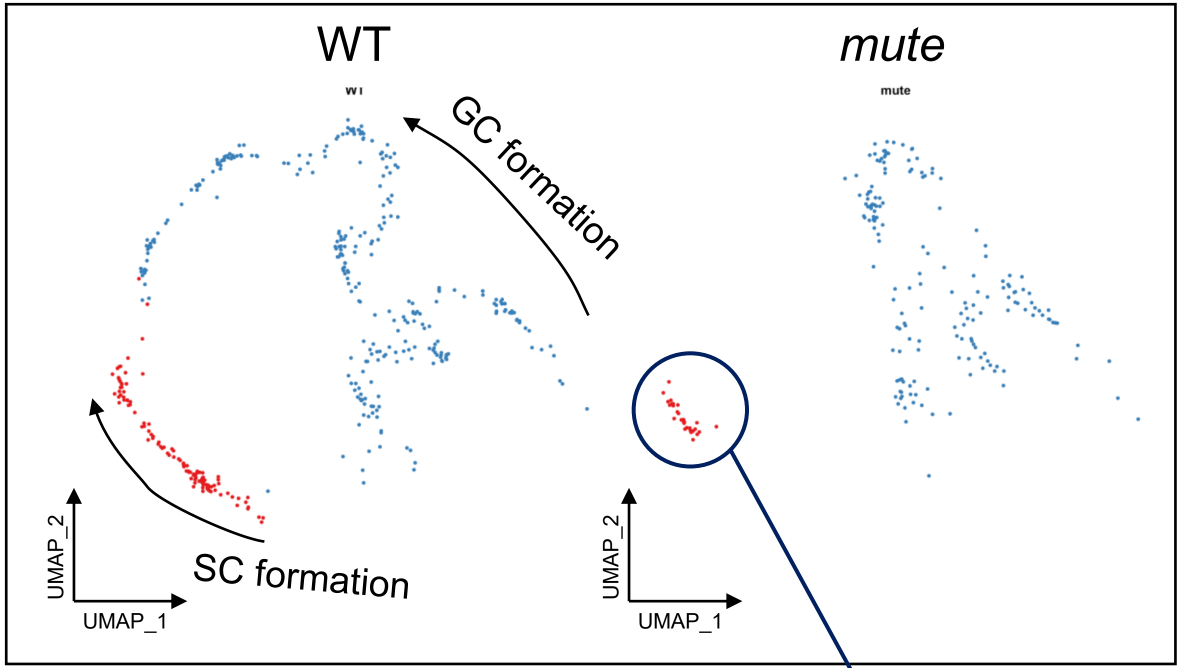


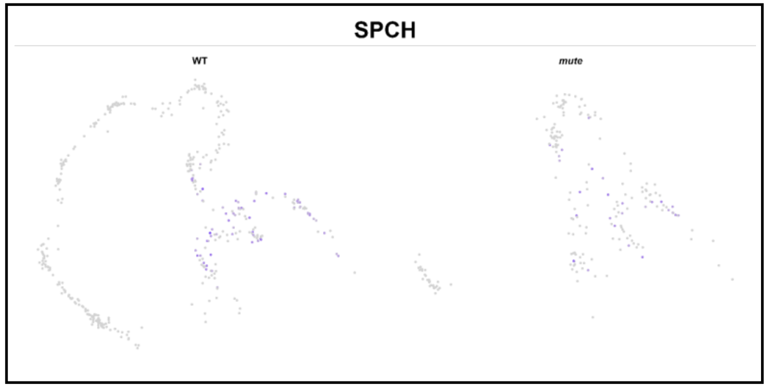
Integrating WT and *mute* transcriptomes to define the function of MUTE

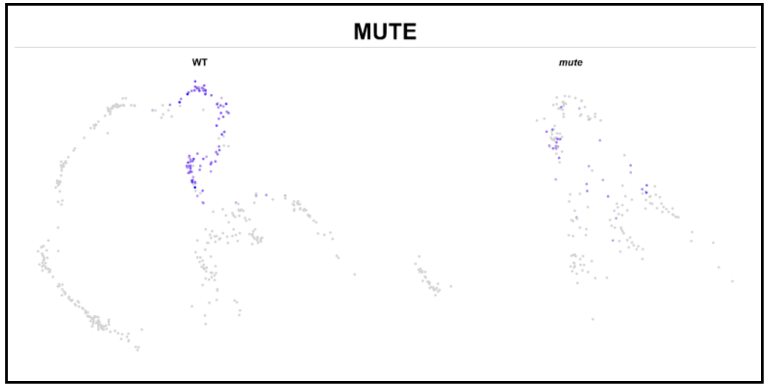


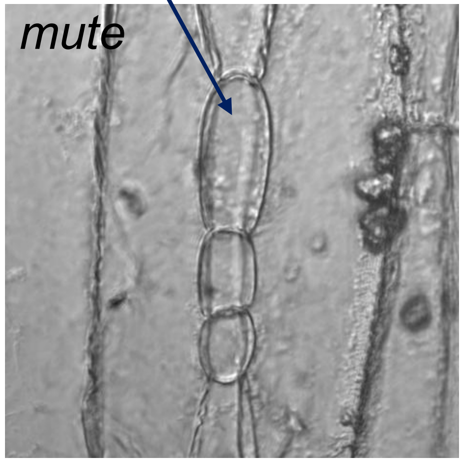


Integrating WT and *mute* transcriptomes to define the function of MUTE

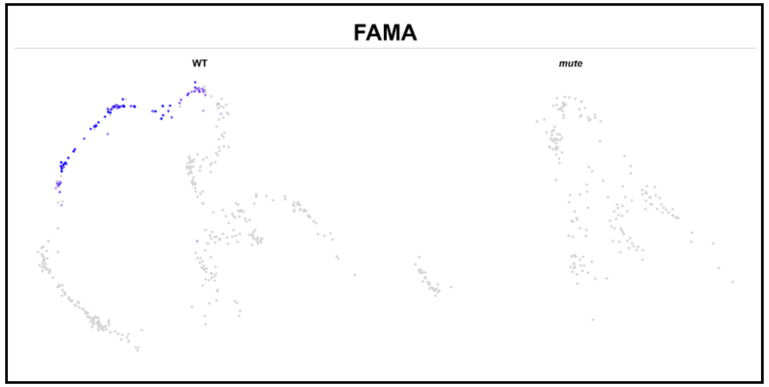




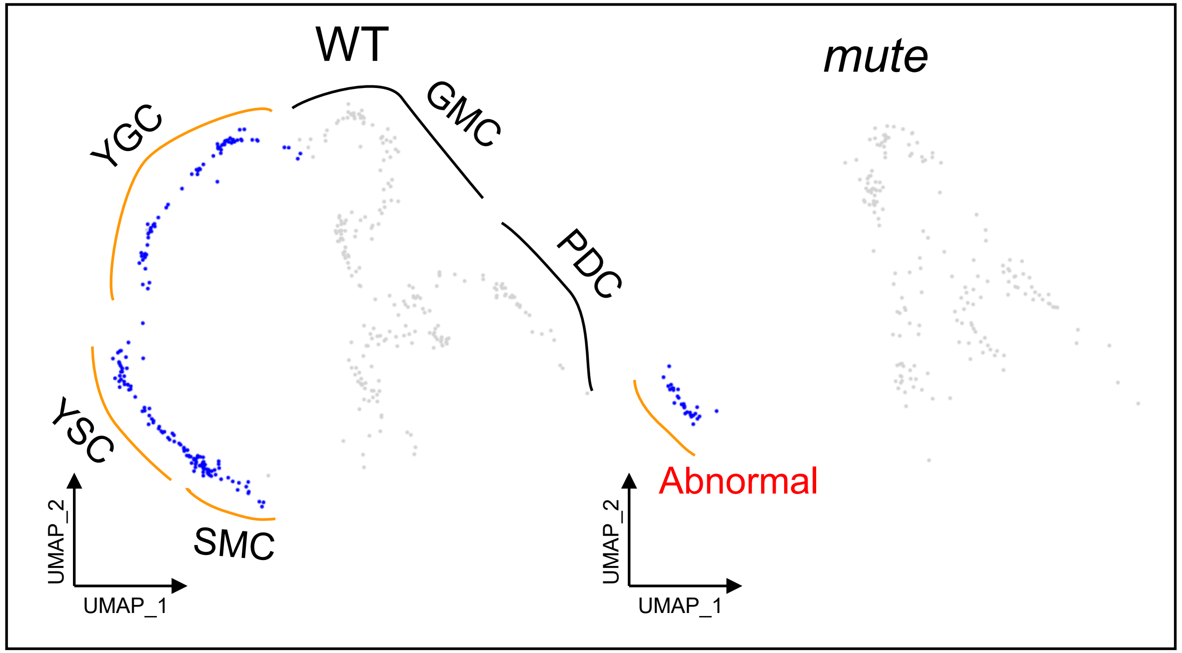


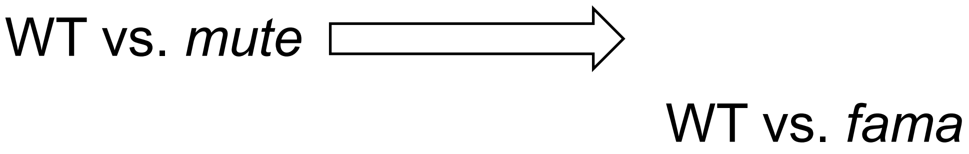


Specific cell populations are missing in the *mute* mutant.



Integrating WT and *mute* transcriptomes to define the function of MUTE



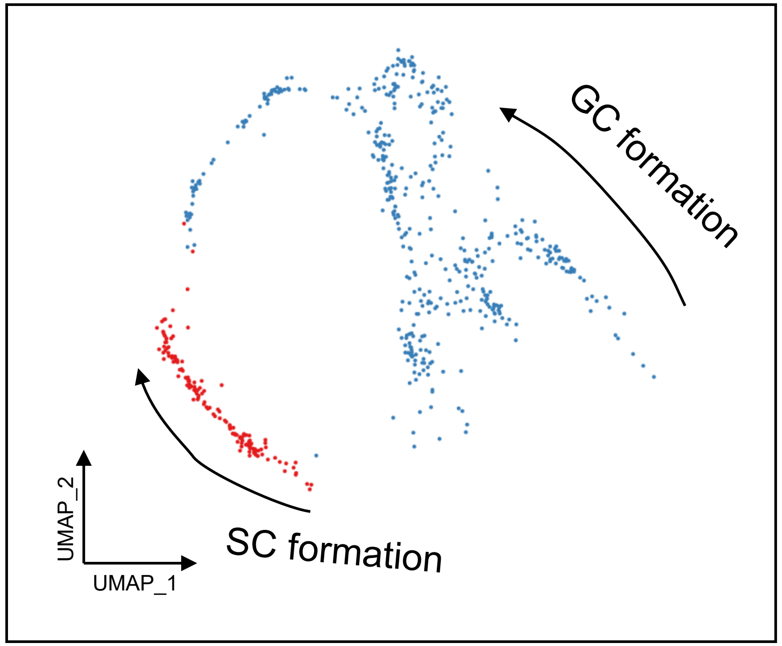

WT vs. *mute*

WT vs. *spch*

WT vs. *fama*

Currently, our analysis remains preliminary. Further integration of snRNA-seq data from *hvspch* and *hvfama* mutants was the next step to map the regulatory hierarchy among SPCH, MUTE, and FAMA.

Perspective



◆ Mapped the stomatal developmental landscape in barley at single-cell resolution.

◆ Revealed an asynchronous "ring-like" trajectory coupling guard cell and subsidiary cell fates.

☐ To demonstrate the essential and specialized roles of HvSPCH， HvMUTE and HvFAMA in cereal stomatal innovation.

Acknowledgements


Prof. Guoping Zhang


Prof. Shengguan Cai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Thank you for listening!

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