

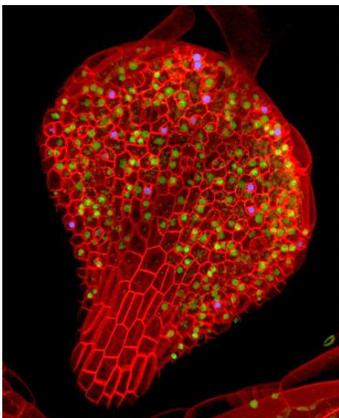
Dr. Dominique Bergmann

Associate Professor of Biology, Stanford University
Investigator, HHMI

Global and local scale transcriptional regulation of stomatal development



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Stomata are valve-like structures on the aerial surfaces of plants that mediate gas exchange between the plant and atmosphere. Work from several labs over the last decade has identified key regulators of cell fate, proliferation and polarity. Among the fate regulators are a set of bHLH transcription factors, SPEECHLESS (SPCH), MUTE, FAMA, ICE1/SCREAM and SCRM2 whose expression patterns and loss and gain of function phenotypes place them at key decision points in the lineage. These bHLHs are footholds from which we can begin to address broader questions about dynamic gene regulatory behaviors in developing tissues and mechanistic questions about how multiple inputs are integrated into specific fate decisions. For example, SPCH is required and sufficient for entry into the stomatal lineage and also for continued self-renewing divisions. SPCH is regulated at multiple levels—from gene expression to protein activity—and it can be used as an output to monitor the integration of information derived from developmental, hormonal and environmental signals. Likewise, FAMA can be used as a tool to understand how cell proliferation and terminal differentiation are regulated. On a larger scale, the bHLHs have been useful tools to capture the gene expression inventory of individual stomatal lineage cell types, and to monitor gene expression changes that correlate with transitions from one fate to another. Our next challenges are to integrate information from the “stomatal expression map” and from the signaling networks operating between stomatal lineage cells (and from more distant inputs) into predictive circuits of developmental and homeostatic behavior.

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