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Author
Sanow, Stefan, PhD

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High-throughput machine-learning quantification of plant cellular barriers across species and microbial treatments

Stefan Sanow[1], Yifei Gu[2], Tamera Taylor[1], Dustin Hadley[2], Randy Carney[2], Siobhan Brady[1]*

[1]Department of Plant Biology and Genome Center, University of California, Davis, CA, USA

[2]Department of Biomedical Engineering, University of California, Davis, CA, USA

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***Abstract*:**

Plant cellular barriers such as lignin, suberin, and aerenchyma are central to plant defense, yet their quantitative analysis remains labor-intensive and poorly reproducible across experiments. This limitation restricts rigorous comparisons across genotypes, treatments, and species. Here, I present a high-throughput machine-learning–based image analysis pipeline that enables automated, quantitative assessment of multiple cellular barriers from microscopy data.

Using sorghum as a model system, and extending the approach to rice and millet, the pipeline simultaneously extracts quantitative features describing endodermal lignification, suberization, and aerenchyma formation across tissues, genotypes, and microbial treatments. Application of this framework reveals barrier-specific responses to beneficial microbes that are difficult to resolve reproducibly using conventional manual quantification approaches. These quantitative phenotypes provide a foundation for testing how microbe-induced modulation of host barriers relates to resistance against parasitic plants such as *Striga*, as well as broader pathogen interactions.

Overall, this work establishes a reproducible and transferable platform for integrating cellular barrier phenotypes into plant defense studies. By enabling scalable, quantitative analysis of structural traits, the approach supports more rigorous experimental design and comparative analyses relevant to crop resilience and sustainable disease management.

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***Contact Information for Presenting Author**: ssanow@ucdavis.edu*