

Characterization of genotypic and environmental influences on *Zea mays* cuticle deposition

Travis Hattery — Ph.D. Defense Seminar (virtual)

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Major: Molecular, Cellular and Developmental Biology
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Abstract: The cuticle is a multi-layer polymer comprised of esterified derivatives of very long-chain fatty acids, which is infused with and coated by non-polar and amphipathic cuticular lipids, also known as cuticular waxes or extracellular surface lipids. These cuticular components are synthesized by epidermal cells and accumulate on most aerial tissues of plants, collectively serving as a moisture retention mechanism and also forming a protective barrier against both biotic and abiotic stresses. However, the underlying genetic control of synthesis, transport, and localization of cuticular components is not fully understood. To thoroughly dissect the regulatory and synthetic pathways responsible for cuticle composition, as well as the role the cuticle plays in environmental protection, this work harnesses the vast genetic and phenotypic diversity available in maize (*Zea mays* L.).

Silk cuticular wax profiling of 468 genetically diverse inbred lines of the Wisconsin Diversity Panel grown in 3-environments revealed that genotype, environment, and their interaction (GxE) explained up to 76%, 59%, 31% of cuticular wax variation, respectively. Importantly, specific weather parameters (i.e., solar radiation and precipitation) acting at specific times in plant development were identified as putative modulators of cuticular wax composition. Because genotype explains the greatest proportion of the observed variance in cuticular wax composition, the underlying genetic control of cuticular wax metabolite traits was probed via a genome-wide association study. These metabolite traits associated with a mixture of regulatory mechanisms at the transcriptional, co-transcriptional, translational, and post-translational levels. Also associated are protein-coding genes associated with enzymatic functions and cuticular wax transport mechanisms.

Collectively, this work builds the foundation for diverse functional hypotheses regarding targeted stress-response studies and may be utilized in coordination with community genome, transcriptome, and proteome resources to further elaborate the complex regulatory mechanisms surrounding cuticle deposition.

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