Title
Maize *ETHYLENE INSENSITIVE3-LIKE* genes regulate plant architecture

Presenter
Josh Strable (NCSU)

Author list and affiliation
Alejandro Aragón-Raygoza[1], James Satterlee[2], Mary Galli[3], Erica Unger-Wallace[4], Charlie Beeler[4], Jeffrey Yen[2], Charlotte Fullbright[1], Erik Vollbrecht[4], Andrea Gallavotti[3], Josh Strable[1]

1. Department of Molecular and Structural Biochemistry, North Carolina State University
2. Plant Biology Section, Cornell University
3. Waksman Institute, Rutgers University
4. Department of Genetics, Development and Cell Biology, Iowa State University

Abstract
A key question in biology is how plants interpret internal and external factors to modulate growth. The hormone ethylene is a pivotal stress signal, and it plays a crucial role in plant development, where it acts largely to inhibit organ growth. Most of what is known about ethylene comes from studies in Arabidopsis. In contrast, our understanding of ethylene biology in C_4 cereal crops is markedly limited. Here, we characterize mutations in maize *ETHYLENE INSENSITIVE3(EIN3)-LIKE* genes that encode co-orthologs of the Arabidopsis EIN3/EIL1 transcriptional factors. By stacking independently derived mutations in *ZmEIL* genes, we uncovered novel leaf and internode phenotypes associated with mis-regulated growth. *Zmeil* mutants are sensitive to genetic background and environmental conditions. The mutants are insensitive to the ethylene precursor ACC. *Atein3-1* mutant seedlings that overexpress *ZmEIL* transgenes display the triple response when germinated in the presence of ACC, a phenotype indicative of restored ethylene sensitivity. We utilized single-cell transcriptomic analysis to identify cell-specific genetic signatures in *Zmeil* and normal shoots with and without ACC. Many previously characterized developmental regulators are mis-expressed in various cell clusters between the mutant and treatment conditions, compared with normal and mock treated, suggesting key roles for *ZmEIL* genes in coordinating the regulation of other developmental pathways in certain cell types. We leveraged DAP-seq to generate genome-wide *in vitro* ZmEIL:DNA interaction maps. Comparative analysis indicate a high degree of binding site overlap, suggesting transcriptional coordination for many genes. Overall, the findings reveal ethylene-related phenotypes in maize that are unlike those reported for *Atein3* mutants and indicate *ZmEIL* genes are central regulators of plant architecture. Taken together, this work provides novel insights into our understanding of ethylene signaling in maize.