SEMINAR SERIES
PLANT SCIENCES INSTITUTE

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Phenotype discovery from a maize seed and seedling phenomics pipeline

Predictive relationships between seed phenotypes and early seedling development is likely to benefit basic and applied plant biology research. A series of non-invasive methodologies were developed to phenotype individual maize kernels and early seedling root growth. More than 7000 seeds representing diverse maize inbred lines were phenotyped, including the Nested Association Mapping (NAM) population parents, the Wisconsin Diversity Panel, the B73xNC350 RIL population, and classic kernel composition mutants. Each individual kernel was weighed, subjected to near infrared reflectance (NIR) spectroscopy, machine vision 3D shape analysis, and then germinated to quantify primary root growth rate and gravitropism with automated image analysis. Position on the cob was tracked for NAM parental lines enabling the discovery of a novel trait that interrelates kernel shape, composition, and local seed set on the ear. Statistical modeling revealed that kernel NIR spectra had significant relationships to root growth and gravitropic responses. At different times during the three hour gravitropism time course, kernel weight, density, and oil correlated with root tip angle. Partial Least Squares regression of the NIR spectrum to seedling growth characteristics is sufficient to enrich kernels into general classes of root growth responses. This work demonstrates how a longitudinal phenotype pipeline can generate results that support the discovery of predictive relationships between traits.

Date: Wednesday, November 11, 2015
Time: 4:10 pm- 5:00 pm
Room: 1414 Molecular Biology

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