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Thursday, September 26, 9:00-9:45 a.m.

Image-based phenotyping technologies for understanding root development: From genome to phenome

Roots are morphologically complex networks that provide the foundation for plant health and productivity. Understanding the genetics underlying their growth and development has been slowed both by complex root-environment interactions and a lack of imaging technologies that provide comprehensive and spatially accurate data sets at high-throughput. We will present the development of a semi-automated, digital 3D root phenotyping pipeline for crop plants grown in a homogenous gellan-gum environment, and its use to map regions of the rice genome controlling root architecture, including five large-effect multivariate quantitative trait loci. Additionally, this flexible root analysis method is being used to investigate the architectural basis of enhanced nitrogen uptake in maize, a dampened growth inhibition response in maize lines recurrently selected for grain yield at high planting density, and for time series analyses of growth response to nutrient availability.

As with all currently available root phenotyping technologies, this method is not adaptable to all root phenotyping experiments. We will discuss tradeoffs of several current root architecture analysis methods, and their pairing with the biological question of interest. For example, observing root-microbial interactions using a transparent soil system, using X-ray CT and PET imaging technologies to conduct high-resolution functional studies in soils, and parameter estimation in 2D versus 3D images. Ultimately each technology adds to the root phenotyping toolbox, and the best method is that which best addresses the question.