

## The Potential Hidden Within Sorghum Diversity Populations

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In this talk, we will explore the power of new genomics and phenotyping resources to unravel the complex genetic architecture underlying multiple traits of interest in sorghum. The foundation of this research lies in the sorghum association panel, a population assembled over fifteen years ago to represent global sorghum genetic and phenotyping diversity. To date the sorghum association panel has been phenotyped for over 200 traits across diverse environments. Generating a new and high-density genetic marker dataset containing more than 40 million SNPs enabled the identification of novel significant associations from previously collected field experiment phenotypes. Using image analysis based phenotyping, we successfully mapped the locations of genes, including the cloned genes *tan1* and *y1*, responsible for regulating variation in the production of specialized metabolites within sorghum grain. A novel high throughput assay for testing the impact of grain samples on the human gut microbiome in vitro established a link between the composition of human gut microbiomes and the consumption of sorghum varieties, mediated by the abundance of metabolites within the sorghum grain. The relationship between sorghum genetic variation and the abundance of bacterial taxa associated with human health was validated via a QTL mapping study. Our study demonstrates the potential to link specific alleles in crop genetics to human health via the food-gut-health axis as well as how new genomic and phenotyping resources can extract fresh insights from existing sorghum field studies.

### References:

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