

Dr. John Vogel

Thursday, September 26, 4:00 p.m.

Phenomic analysis of natural and induced variation in *Brachypodium distachyon*

Brachypodium distachyon is a small annual grass that serves as a model for the grasses due in part to its compact stature, rapid generation time and simple growth requirements. These attributes also make *B. distachyon* an attractive subject for phenomic analysis. We are collaborating with the CSIRO High Resolution Plant Phenomics Centre in Canberra, Australia to examine natural and induced phenotypic variation in two *B. distachyon* collections. The first collection consists of 150 diverse natural accessions. In this collection we observed considerable variation in the phenotypes examined including 3-fold differences in photosynthetic rate, 5-fold differences in growth rate, 10-fold differences in biomass and dramatic differences in root architecture. The second collection examined consists of 600 homozygous T-DNA lines selected from our growing T-DNA collection (we currently have >20,000 T-DNA lines, <http://brachypodium.pw.usda.gov>). These lines were phenotyped using visible, fluorescence and infrared imaging in order to identify lines for more detailed genetic characterization. Along these lines, we have demonstrated co-segregation of specific phenotypes with T-DNA insertions for two mutants and have begun complementation tests to definitively demonstrate that the loss of function of the tagged gene is responsible for the observed phenotypes.