Climate Adaptation in *P. trichocarpa*: Key Loci Identified for Stomata and Leaf Traits

Background/Objective

- Drought poses significant challenges to bioenergy crops such as *Populus trichocarpa*. Understanding the genetic and physiological basis of adaptation is crucial for breeding more resilient varieties. Large-scale drought experiments with diverse genotypes are necessary for identifying loci useful for genomic breeding but have been lacking in bioenergy trees.

Approach

- This study leveraged the largest drought experiment conducted to date in *P. trichocarpa*. We evaluated over 1000 genotypes under drought and control conditions, measuring a suite of leaf and stomatal traits. Genome-wide association studies (GWAS), climate association analyses, and RNA-seq were used to identify adaptive loci, and climate models were applied to predict shifts in adaptive allele frequencies.

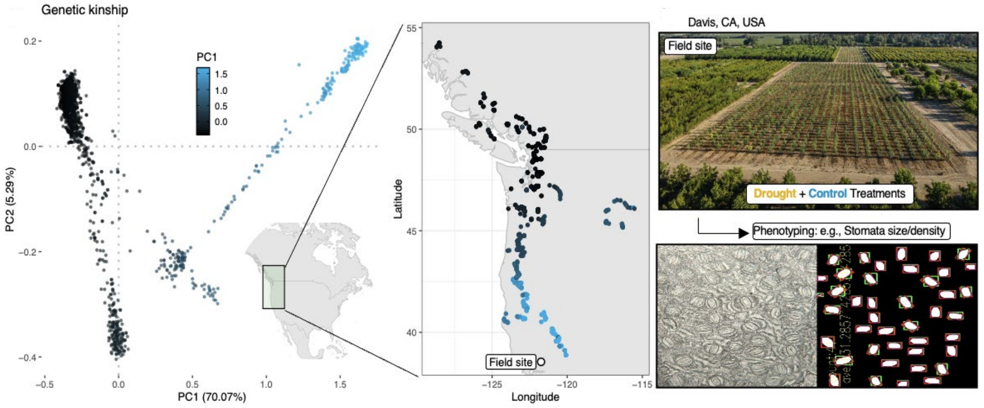
Results

- Drought had major effects on tree physiology but varying effects across genotypes. Generally, water stress reduced growth but increased water-use efficiency and genotypes from drier climates had smaller, denser stomata, consistent with adaptive differences in water use strategies. A major-effect locus on Chromosome 10 containing a tandem array of KCS (3-ketoacyl-CoA synthase) genes explained variation in stomatal size, and modeling suggests that increasingly arid environments will favor these alleles for smaller stomata.

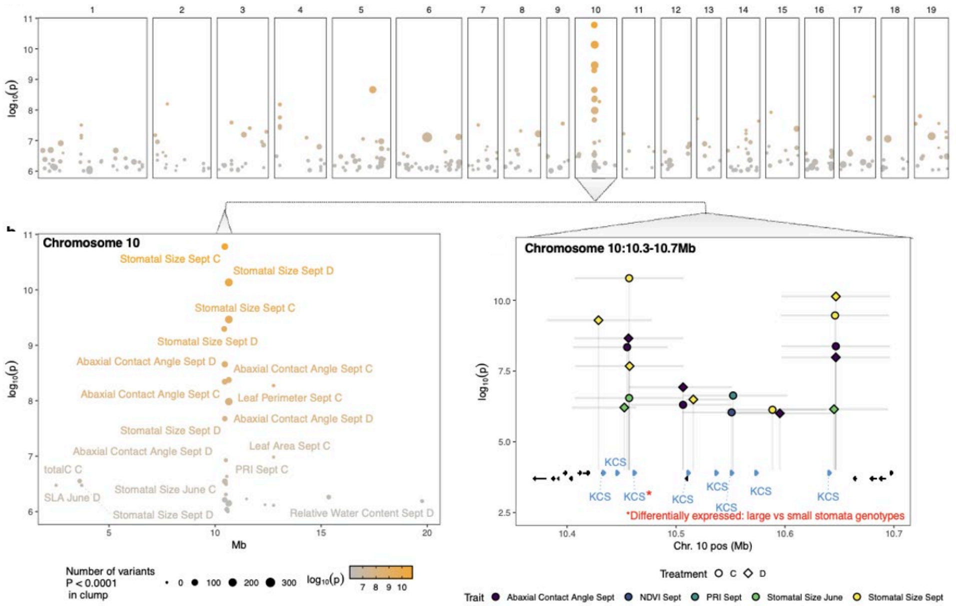
Significance/Impacts

- This research characterized plant physiological response to drought and defined the adaptive importance of genetic variation. It identified key drought-adaptive traits, most notably a major genetic locus controlling stomatal size, which can be used to accelerate breeding via marker-assisted selection in the future. These insights can help guide stress-resilient breeding for sustainable bioenergy production.

Klein, et al. *New Phytologist* (2025) In press



***Populus trichocarpa p*opulation and experimental overview.**



GWAS identified a Chromosome 10 region linked to stomatal size, highlighting KCS genes.