Title: Identifying traits that underpin the genetic basis of drought tolerance in bioenergy poplar

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Project Goals: *Populus* serves as a promising biomass feedstock for a suite of industrial applications including biofuels conversion. Drought is one of the most important factors limiting cost-effective production of *Populus* biomass. The drought response in *Populus* is a complex trait requiring the regulation and coordinated interactions of many genes, and identification of genetic networks regulating drought response remains unaccomplished and is urgently needed to inform genetic improvement of *Populus* feedstocks for sustainable biomass production. The goal of this research is to determine the genetic basis of drought tolerance in bioenergy *Populus* enabling tree improvement and the wide-scale deployment of *Populus* for bioenergy in marginal and droughted environments. Fast growing feedstock crops are required for a future bioeconomy where plant-based biofuels, chemicals and biomass for Bioenergy with Carbon Capture and Storage (BECCS) will be utilized as part of a more sustainable, energy secure economy.

Methods: We will harness the natural genetic variation found in wild trees, adapted to different amounts of rainfall. Our main study population consists of 1,000 *P. trichocarpa* collected from a range of naturally droughted and wet environments, that already has a number of unique genomic and genetic resources for a tree species, that will be used here.

Drought tolerance, here defined as '*the maintenance of plant biomass production in the face of moderate and persistent drought stress*' is a highly complex trait and we will use high throughput phenotyping, including tower- and UAV-mounted multi-spectral proximal analysis to unravel how drought tolerance varies across this wide population.

Using the latest computational tools and the extensive sequence, re-sequence and RNASeq resources available and new ones to be developed, we will identify multiple genetic loci linked to traits and resolve them through hierarchical network analysis to the level of cis- and trans-acting eQTL.

We have identified a suite of traits of interest, from our own previous research, from the literature and from traits studied in other organisms including (i) **phenology traits**, that are related to seasonality and are unique in trees. We will focus on remotely-sense canopy greenness and function using tower-based mounted cameras (ii) **anatomical traits,** including stomatal density and index, leaf epidermal cell patterning and aspects of hydraulic functioning in wood. Some of these traits are highly heritable and may be of particular value to breeding and selection and (iii) **functional traits,** including water use efficiency (WUE), stomatal conductance and (iv) **performance traits** where we are quantifying the dynamics of tree biomass accumulation. For these traits, we will deploy UAV-based LiDAR and IR thermography.

Objectives:

(ii) To test the hypothesis that a suite of traits identified for drought tolerance in *P. nigra* can be measured in drought and control treatments in the wide germplasm collection of *P. trichocarpa*.

(iii) To use established and novel GWAS model approaches to identify gene loci linked to drought tolerance traits on interest in *P. trichocarpa*.

(iv) To undertake comparative analysis of GWAS results for drought tolerance traits in *P. nigra* and *P. trichocarpa.*

Impacts and benefits: This research will deliver new genotypes of *Populus* that are better suited and able to tolerate droughted environments, that are more likely in the future.

Publications
Taylor G., *et al* (2019). Sustainable bioenergy for climate mitigation: developing drought tolerant trees and grasses. Annals of Botany, 124: 513-520.

Muchero W. *e al* (2018). Association mapping, transcriptomics, and transient expression and transient expression identify candidate genes mediating plant-pathogen interactions in a tree. *Proc Natl Acad Sci USA* 115: 11573-11578.