

## **Integrated Omics Analyses of a Populus Pedigree for Crop Improvement**

**Chongle Pan (PI), Jingui Chen (Co-PI), Wellington Muchero**

**Oak Ridge National Laboratory**

**Abstract:** Populus is a DOE flagship plant for biofuel biomass production. Improving Populus as a feedstock crop is a major focus of DOE Bioenergy Research Centers (BRCs) and many academic laboratories. Here, we aim to determine structural and local variations in the genomes of Populus trichocarpa and Populus deltoides using PacBio/Illumina sequencing and understand the molecular ramifications of these polymorphisms in the function of fine roots, stem xylem tissues and leaves using transcriptomics, proteomics and metabolomics. The proposed research will focus on 7 selected Populus genotypes from a pseudo-backcross population. We will reconstruct haploid-resolved genomes for five genotypes in the pedigree, including the two P. trichocarpa genotypes, the two P. deltoides genotypes, and the F1 hybrid genotype, using PacBio/Illumina hybrid sequencing. . If successful, we will create the first full-haploid resolution for individual diploid genomes and the first high-quality reference genome for P. deltoides. More importantly, the results will allow us to perform a series of comparative genomics analysis. We will also measure the transcriptomes, proteomes and metabolomes in the fine roots, stem xylem tissues and leaves of greenhouse-grown triplicate trees of the 7 genotypes. Because of the resolved haploid genomes in these genotypes, we will be able to further resolve the expression levels of the two alleles of many genes in the three tissues. The perfectly matched individual genome/transcriptome/proteome/metabolome results across three major plant tissue types will greatly improve the functional annotation of the P. deltoides and P. trichocarpa genomes, including gene model construction, metabolic pathway reconstruction and regulatory network inference. The findings from this study will be used by researchers in DOE BRCs and general scientific community. An improved reference genome for P. trichocarpa and a new reference genome for P. deltoides will allow better analysis of results across many experiments on these plants. The genomic variations identified between different genotypes will provide new understandings of Populus evolution and allow better usage of natural populations of Populus for eQTL, GWAS and breeding.