The Role of Winter-Biased Genes in Biomass Productivity of Hybrid Poplar

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Renewable biomass is a promising source of bioenergy that can help to reduce reliance on fossil fuels. Biomass accumulation is a year-round process for perennial trees that contribute a significant amount of material to the bioenergy industry. However, the molecular processes behind wood growth tend to only be studied in summer and greenhouse conditions. Investigating winter protection in trees is crucial for understanding and enhancing year-round wood productivity, especially with impending climate changes. We performed seasonal sampling of xylem tissues from poplar trees for RNA sequencing to identify genes and their genome duplicates that are preferentially expressed in different seasons. Genes with winter-biased expression are involved in a wide range of metabolic processes, including carbohydrate metabolism. Carbohydrates stabilize cellular membranes and proteins in stressful conditions to provide protection across the plant, and carbohydrate storage reserves fuel spring regrowth before photosynthesis resumes. Candidate genes involved in carbohydrate processes were identified, prioritizing those with winter-biased expression between paralogs. We designed gRNAs to target individual or duplicated genes for CRISPR-Cas9 knock-out in *Populus tremula* × *alba* INRX 717-1B4. Transgenic trees have already been generated and will be utilized in a series of experiments aimed at exploring the effects of the gene mutations on carbohydrate metabolism and poplar growth phenology during seasonal transitions. This study takes a step towards understanding the molecular basis of winter protection in trees. The results could be used to develop new strategies for improving the cold hardiness of trees, which could lead to increased wood productivity and a more sustainable source of renewable bioenergy.