

187. Abiotic Stress Networks Converging on FT2 to Control Growth in Populus

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Project Goals:

Woody feedstock plants such as *Populus* show substantial natural variation in growth responses to various environmental conditions; however, the complex, multi-genic nature of these traits slows breeding for optimal biomass production in specific climates and on marginal lands. The identification of FT2 as an integrator of multiple abiotic signals in *Populus* (Hsu et al. 2011) provides a focal point for discovering and integrating transcriptional, protein-DNA interaction (PDI) and protein-protein interaction (PPI) networks controlling growth in response to environmental conditions. This project is focusing on two abiotic conditions that are key determinants of growth—daylength and nitrogen (N) availability. Our overarching hypothesis is that uncovering convergent and divergent regulatory networks that control responses to these two abiotic stresses will advance genetic improvement for adaptation to one or a combination of abiotic environmental conditions. To elucidate these networks, transcriptomic responses to daylength and N availability will be studied in multiple tissue/organs of *Populus trichocarpa* Nisqually-1. These responses will be studied in time series experiments that encompasses both cessation and resumption of shoot growth. The effects of the daylength and nutrient regimes on RNA abundance will be quantified by RNA-Seq. Three types of libraries will be prepared from each sample: total RNA, small RNA, and degradome. This data will serve as the basis for identification of differentially regulated genes and global gene regulatory network construction. A second aim is to identify targeted PPI and PDI networks using yeast-two-hybrid (Y2H) and Y1H to both validate and extend the regulatory networks reconstructed from the transcriptome experiments. This aim will initially focus on identifying networks both upstream and downstream of FT2. Understanding the mechanisms that determine periods of growth and quiescence will identify specific control points that can be manipulated to maximize growth in different environments. Based on the network development, a few genes will be selected for functional analysis in transgenic poplar to validate their utility for enhancing plant growth and yield under different environmental conditions.

References

1. Hsu CY, Adams J, Kim H, No K, Ma C, Strauss SH, Drnevich J, Vandervelde L, Ellis JD, Rice M, Wickett N, Gunter LE, Tuskan GA, Brunner AM, Page GP, Barakat A, Carlson JE, dePamphilis C, Luthe DS, Yuceer C (2011) FLOWERING LOCUS T duplication coordinates reproductive and vegetative growth in perennial poplar. *Proc Natl Acad Sci USA* 108:10756-10761.

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