

Spatiotemporal Transcriptomics of *Populus* Growth in Response to Daylength and Nutrient Availability

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Project Goals: The overall goal of this project is to elucidate the regulatory networks that govern transitions between growth and quiescence in response to two abiotic conditions – daylength and nutrient availability. Studying these two abiotic signals will enable identification of commonalities and differences among different environmental signaling networks that converge on the *Populus* central shoot growth regulator FT2.

In woody plants, a variety of unfavorable abiotic conditions ultimately induce shoot apical and cambial growth cessation and terminal budset, a quiescent state that has classically been defined as ecodormancy. If the limiting factor is supplied, trees will rapidly resume shoot growth. We conducted experimental treatments in which daylength and nutrient availability were reduced to induce quiescence and then increased to resume growth. These experiments lasted several weeks with sampling of relevant tissues (shoot apex/bud, leaf, root, and vascular cambium) at 11 time points. While bud set and dormancy induction in response to short days is well-studied, and proceeded as expected, less is known about the dynamics of nutrient-mediated growth cessation. We found that under nutrient deficiency, the active shoot apex transitioned more rapidly to the final budset stage, but quiescence of the cambial meristem was delayed. Moreover, these plants quickly resumed growth with subsequent fertilization. mRNA libraries were prepared from each of three biological replicates of the shoot apex, leaf and root samples/time points, resulting in 234 libraries sequenced on an Illumina HiSeq 2500 instrument, and we are currently in the process of mapping and calculating transcript abundance metrics for these data. Laser capture microdissection is being used to isolate the cambial zone at phenotypically distinct time points for mRNA libraries. In parallel, we are preparing small RNA and degradome libraries for a subset of the samples, which will provide an additional layer of transcriptional regulatory information. These data will collectively be used to develop transcriptional networks that describe spatially and temporally explicit regulatory relationships for both daylength and nutrient-mediated quiescence. Functional relationships among key network regulators will be further characterized through transgenic manipulation.

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