Development and use of novel gene technologies to increase biomass yield in the woody perennial Populus spec. (PopMass) Project C - Modification of tree architecture

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Poplar (*Populus sp*.) is grown on short rotation plantations as a biomass resource for sustainable energy. Wood quality is highly influenced by tree architecture, with less branched plants being favorable in terms of quality. In contrast, high branch numbers are beneficial during the establishment phase of short rotation plantations since additional leaf area of branches contributes to carbon fixation. Moreover, early canopy closure and the resulting suppression of weed growth is an important trait for fast growing trees on short rotation plantations.
The aim of this project is to modify branching in poplar to improve wood quality and yield.
Shoot architecture (branching) is regulated by the recently identified strigolactones. This class of plant hormones controls expression of the transcription factor BRC1 which suppresses bud outgrowth. We use gene knockdowns through expression of amiRNAs to modify tree architecture by targeting biosynthesis and signaling of strigolactones. Twelve independent transgenic poplar lines with a down-regulation of the strigolactone biosynthesis gene *MAX4* were obtained. All lines exhibit a hyperbranching phenotype. Grafting experiments and biometric parameters like internode length point to a decreased strigolactone biosynthesis in the *max4* knock down lines. Wood biomass production varies considerably between these lines. Lines with increased branching and biomass production will be selected to identify poplar lines with improved performance.
Isolation of an axillary bud specific promoter to enable tissue specific expression of genes for manipulation of bud outgrowth control is a second goal in our project. The *Arabidopsis BRANCHED1* promoter was characterized in poplar but showed unspecific activity. A putative poplar ortholog of *BRANCHED1* was identified. This gene is exclusively expressed in axillary buds and the promoter of this gene will be analyzed in promoter-reporter lines.