

Multi-tissue Genome-scale Metabolic (GSM) Model of *Populus trichocarpa* Identifies Overexpression Targets for Improving Drought Tolerance

Background

- *Populus trichocarpa* (also called black cottonwood, or poplar) is a promising bioenergy crop because it is a fast-growing woody plant able to grow in marginal lands such as those that are drought prone, thereby reducing competition for arable land. However, metabolic phenotypes of drought resilience are poorly understood and existing methods to examine them are time-intensive.

Approach

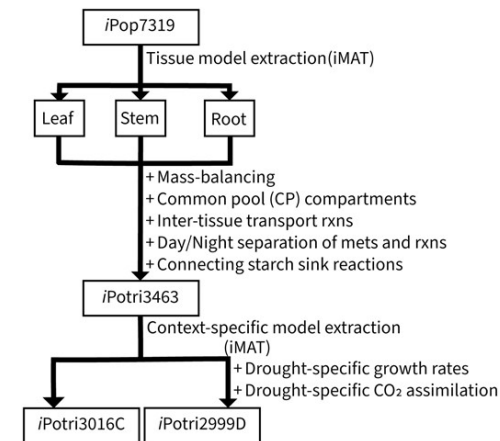
- Using tissue-level transcriptomics datasets and a previously published generic poplar GSM model (*iPop7319*), tissue-specific GSM models were extracted, curated, and combined in a mathematical framework to create a multi-tissue diurnal GSM model of poplar. Using condition-specific transcriptomics data, *iPotri3463* was further differentiated into drought (*iPotri2999D*) and control (*iPotri3016C*) models. These models were subjected to knockdown analysis by reducing the flux of reactions which increased under drought conditions.

Results

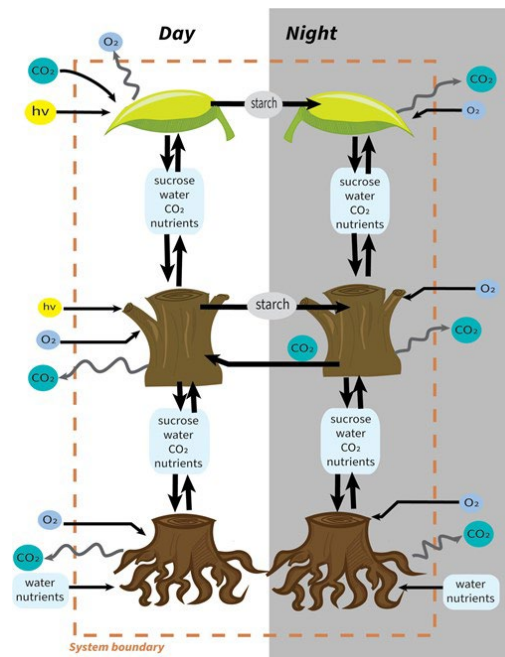
- We reconstructed the first poplar-specific whole-plant GSM model, the second such model for a woody plant.
- Constraints on carbon assimilation, gene expression (through GSM differentiation), and growth recreated highly differentiated drought and control conditions. The drought model shows increased GABA production (including a unique pathway) and the violaxanthine cycling, as validated in drought-stressed plants.
- The knockdown analysis correctly recapitulated previously-known overexpression targets for improving drought tolerance (e.g., glutamine synthase and farnesyl diphosphate synthase) and uncovered new promising targets (e.g., ferulate-5-hydroxylase).

Significance

- Given the long generation time for plants, particularly woody plants, *in silico* computational modeling is a comparatively rapid method of finding and characterizing promising interventions that boost drought tolerance.



Poplar model reconstruction workflow for integrating transcriptomics to generate tissue and condition specific models.



Conceptual illustration of the model structure for the multi-tissue diurnal poplar models. Day and night components are highlighted alongside uptakes of light and carbon dioxide, as well as transports between tissues of fluid and micronutrient flows.

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