Multi-organ genome-scale metabolic modeling of tomato plant

Leo Gerlin, Antoine Escourrou, Ludovic Cottret, Stephane Genin, Caroline Baroukh

Multi-organ genome-scale metabolic modeling of tomato plant

Leo Gerlin[1], Antoine Escourrou[2], Ludovic Cottret[1], Stephane Genin[1] and Caroline Baroukh[1], (1)LIPME, Université de Toulouse, INRAE, CNRS, Castanet-Tolosan, France,

Abstract Text:
Plant growth relies on a division of physiological roles between organs: assimilation of soil nutrients and water is performed by root while synthesis of organic carbon from CO_2 is performed by photosynthetic tissues. The plant saps allow exchanges between the two organs: ascending xylem sap transmits root products and nutrients extracted from the soil to the aerial parts of the plant while descending phloem sap gives organic carbon to the roots. Representing each organ and their respective role is thus important to accurately predict the effect of external (ex: nutrition) or internal (ex: mutations) perturbations on the physiology of the plant. We developed a multi-organ genome-scale metabolic model of tomato plant (*Solanum lycopersicum*). The model combines networks of leaf, stem and root. Exchanges are performed by xylem and phloem sap. Our model was intensively calibrated with experiments we performed at various scales, gathering physiological data (growth, transpiration) and metabolomics (biomass composition, xylem sap chemistry). This model allowed us to explore the metabolic flux distribution in different organs and to study for the first time the organic composition of sap fluxes. Physiological properties of the organs (growth rates, ratios) allowed to predict key properties of xylem sap, such as the predominance of glutamine, suggesting that these properties are majorly driven by plant physiology. We also used our model to predict plant responses to different perturbations. First, we examined the effects of nitrogen nutrition on growth, and then the impact on metabolic fluxes of reduced mitochondrial citrate synthase activity in a transgenic tomato line. In both cases, the predictions were consistent with experimental studies, showing that our model is accurate and thus a useful tool to decipher how internal or external perturbations impact the whole plant.

Session Selection:
Multi-scale Modeling
Submitter's E-mail Address:
leo.gerlin@inrae.fr
Preferred Presentation Format:
Oral Only
First Presenting Author
Presenting Author