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Use of genome-scale metabolic models for plant metabolism

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Genome-scale metabolic models (GSMM) have been extensively applied for a wide variety of organisms. However, for plants genome-scale modeling is still in its infancy. It has been successfully developed for Arabidopsis in the last few years. In this study we appraise the existing GSMM for Arabidopsis by computing biomass accumulation using flux balance analysis (FBA) and attempt to outline potential applications for horticultural crops in the future. The predicted growth rates for the Poolman et al. (2009) and Dal'Molin et al. (2010) model were quite similar, despite different carbon sources were provided (glucose and sucrose, 100 mmol/g*h DW). The exchange fluxes for respiration in nonphotosynthetic cells confirmed that plants prefer NH₃ in the process of nitrogen assimilation. When carbohydrates were used as substrate for respiration the Respiratory quotient (RQ) of Poolman's model approached 1, which is consistent with experimental data. For the Dal'Molin's model the RQ is less than 1. H₂S is utilized in the Dal'Molin model as sulfur source, whereas sulfate (SO₄²⁻) is consumed in the Poolman's model. The Poolman's model seems to reflect biological reality more closely than the Dal'Molin model. This could be due to the subcellular compartmentation included in the Dal'Molin model, adding subcellular compartmentation of reactions was done manually. In conclusion, to apply constraints-based reconstruction and analysis (COBRA) methods, including FBA, to plant metabolism requires careful analysis and possibly curation of existing GSMM's.