

Understanding of entire plant metabolism in response to environmental stresses via genome-scale mathematical model

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Abstract:

Drought and high temperature stresses affect plant metabolism, limit plant growth and development, and cause a major threat to agricultural production worldwide. In order to generate a plant which can tolerate those stresses and grow under unfavourable conditions, a number of researches, especially through plant breeding and metabolic engineering, have been conducted. Great advancement has been made to identify major regulatory mechanisms at a transcript level. However, precise relationships among metabolites at a metabolic level are yet unclear. In this study we integrated mathematical approaches to model the entire metabolism of Arabidopsis. The transcriptome data taken from public databases were combined into the model to estimate flux distribution in the metabolic network and simulate changes of metabolic fluxes in response to drought and high temperature stresses. In the presentation, we will predict changes in metabolite levels in the entire metabolism and discuss characteristics of metabolic pathways which are significantly influenced by these stresses. This information will be valuable for designing an alternatively optimal biosynthesis for metabolic engineering to generate stress tolerant plants in the future.

Keywords: Arabidopsis, environmental stress, mathematical modelling, metabolomics, plant metabolism, transcriptomics