PLANT BIOINFORMATICS

Applications

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BIOLOGICAL NETWORK RESOURCES

RIMAS

Regulatory Interaction Maps of Arabidopsis Seed Development

RIMAS is a web-based information portal and provides a comprehensive regularly updated overview of regulatory pathways and genetic interactions during Arabidopsis embryo and seed development.

MetaCrop

Metabolic pathway database for crop plant metabolism

MetaCrop is a database that summarizes diverse information about metabolic pathways in crop plants and allows automatic export of information for the creation of detailed metabolic models.

http://rimas.ipk-gatersleben.de

http://metacrop.ipk-gatersleben.de

NETWORK-BASED ANALYSIS OF EXPERIMENTAL DATA

Transcriptional control of Arabidopsis seed storage compound accumulation

LEC1/AFL-B3 transcription factors are involved in the regulation of several aspects of seed maturation, including the synthesis of storage compounds (seed storage proteins, LipoP) as well as the acquisition of dormancy and desiccation tolerance.

META-BIOLOGICAL MODELLING

Reconstruction of barley organ-specific stoichiometric models

Based on the pathway collection in the MetaCrop database, stoichiometric models have been generated for the barley leaf, stem and seed comprising between 335 and 355 biochemical and transport reactions each.

Multilevel metabolic modeling (MMM)

This approach integrates highly detailed, compartmentalized static metabolic models on the organ-scale (seed, leaf, stem) with a dynamic functional structural model (household model, HM) on the whole plant scale, resulting into a quasi-dynamic multi-organ model.

Analysis and visualization of source-sink interactions during barley seed development

In order to find efficient flux distributions across the whole plant metabolism, flux Balance Analysis (FBA) was applied to the quasi-dynamic, whole-plant model. This method enabled us to analyze the relations of source and sink organs during plant development, focusing on the seed developmental phase of barley. The model is capable of representing the sink-to-source shift of the barley stem in a quantitative and time-resolved manner and it provides evidence for significant contributions of the stem to seed filling.

References


