

RECONSTRUCTION AND ANALYSIS OF GENOME-SCALE METABOLIC MODEL OF *DAPHNIA PULEX*

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Daphnia pulex is the keystone organism of the environmental studies in aquatic ecosystems. The study on *D. pulex* genome was first published in February 2011 and contributed to numerous scientific researches [?]. The developments in the experimental and computational methods have led to state-of-art technologies including *D. pulex* genome analysis, which provides a basis for genome-scale metabolic modeling and systems biology. The reconstructed metabolic model uses gene, protein and reaction associations, which are obtained from the gene annotation process [?]. Since the experimental studies take so long and demand a high effort, our genome-scale metabolic model provides new information as a guide to experimental studies. In this study, all collected data such as reactions, genes, and enzymes are taken from KEGG and UniProt databases and lumped into the model to predict the flux rates [?, ?, ?]. The metabolic model of *D. pulex* consists of 1051 reactions, 774 metabolites, and 697 genes. The current model can be used for elaborative understanding of cellular mechanisms and the effect of perturbations on *D. pulex* metabolism against environmental toxicants. *D. pulex* can be regarded as a model organism and hence the reconstructed genome-scale network can be further improved for context-specific investigation in the light of applied mathematics.

References

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