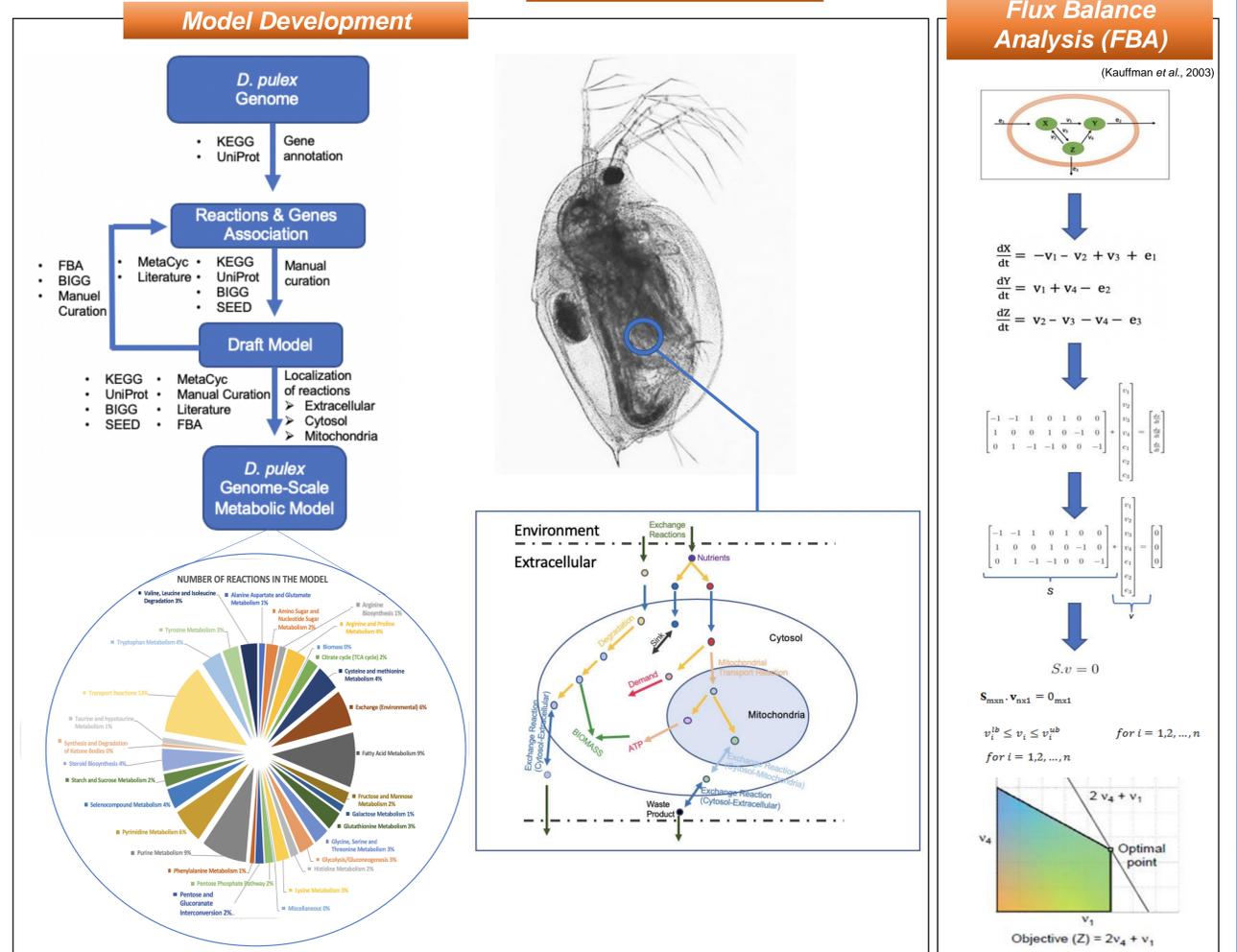


Summary

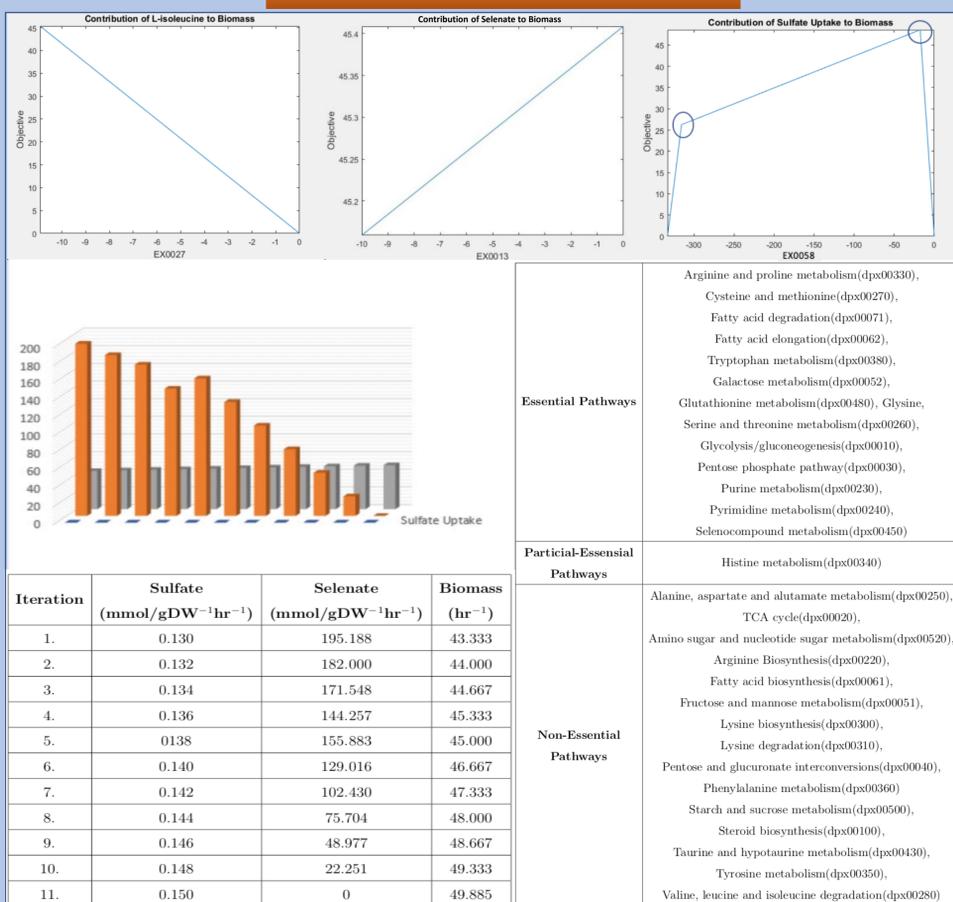
Background Aspects

- ❖ Water fleas are an outstanding part of the food chain. *D. pulex* is one of the important water flea and a keystone of the freshwater due to being very sensitive to poisoning and environmental changes. Therefore, they are mainly used in measuring and observing the effects of the ecological changes. By Colbourne *et al.*, the whole genome was published in 2011.
- ❖ Annotated-genome sequences are integrated with the models which are called Genome-Scale Metabolic Models (GSMM) and they became a platform for the analysis of high-throughput omics data.
- ❖ The main idea of this study is the reconstruction of the genome-scale metabolic model of an ecological organism *D. pulex* by utilizing the computational systems biology approaches.
- ❖ The recent model consists of
 - ❖ 1051 Reactions
 - ❖ 774 Metabolites
 - ❖ 697 Genes
- ❖ It is known that L-isoleucine is extracted from *D. pulex* and has a positive impact on growth of the organism. Also, selenium contamination is toxic to the ecosystem. It is known that the sulfate uptake can be reduced selenate or selenium concentration (Ogle and Knight, 1996).

Methods



Results



Discussions

- ❖ In this study, *D. pulex* genome-scale metabolic model was reconstructed.
- ❖ Flux prediction analysis was performed by FBA with COBRA Toolbox (Becker *et al.*, 2007).
- ❖ The pathways were categorized into three groups;
 - Essential pathways
 - Partial essential pathways
 - Non-essential pathways
- ❖ It is obtained that concentrations of L-isoleucine and the biomass are mutually linked to each other as assumed.
- ❖ Highest selenate accumulation was detected when the sulfate uptake was close to zero.
- ❖ *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

- Becker, S. A., Feist, A. M., Mo, M. L., Hannum, G., Palsson, B. Ø., & Herrgard, M. J. (2007). Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. *Nature protocols*, 2(3), 727-738.
- Colbourne, J. K., Pfrender, M. E., Gilbert, D., Thomas, W. K., Tucker, A., Oakley, T. H., ... & Bauer, D. J. (2011). The ecoresponsive genome of *Daphnia pulex*. *Science*, 331(6017), 555-561.
- Kauffman, K. J., Prakash, P., & Edwards, J. S. (2003). Advances in flux balance analysis. *Current opinion in biotechnology*, 14(5), 491-496.
- Ogle, R. S., & Knight, A. W. (1996). Selenium bioaccumulation in aquatic ecosystems: 1. Effects of sulfate on the uptake and toxicity of selenate in *Daphnia magna*. *Archives of Environmental Contamination and Toxicology*, 30(2), 274-279.