Reconstruction of the Genome-scale Metabolic Model of *Picochlorum renovo* Euihyun Kim, Sophia Alonso, Cristal Zuniga, Karsten Zengler UC San Diego Department of Bioengineering **JACOBS SCHOOL OF ENGINEERING** University of California, San Diego

Bioengineering

Objective

Picochlorum renovo has shown to be a fast-growing species that is resistant to heat and high salinity, making it a prime candidate for a future source of bioproducts at industrial scale. Our objective is to create a metabolic model of *P*. renovo in order to contribute to the current scientific understanding of *P. renovo*.

Background

Microalgae are unicellular plants with the ability to perform photosynthesis and produce algal biomass¹. Algae store energy as lipids and triglycerides, which can then be extracted to be used for production of biofuel, food, and other products we rely on² in an environmentally friendly and sustainable way. *Picochlorum renovo* has shown to be a fast-growing species that is resistant to heat and high salinity, making it a prime candidate for a future source of bioproducts at industrial scale. The manual curation of a metabolic model of *P. renovo* would allow further understanding of this microalga at metabolic level with information on the systematic biology of metabolism and biochemical transformations.



Figure 1. Graph depicting growth of Picochlorum renovo against other microalgal species in simulated outdoor conditions³.



References

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[3] L. R. Dahlin, A. T. Gerritsen, C. A. Henard, et al., Development of a high-productivity, halophilic, thermotolerant microalga Picochlorum 388. (2019) Biol. Commun. renovo. https://www.nature.com/articles/s42003-019-0620-2.

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D-Glu 2,4-D 9-HO

Table 2. Seven metabolites from one of the NREL datasets, sorted by Metabolite ID, BIGG ID, or KEGG ID. Sorted 100 most abundant from both datasets.

odel.rxnNames	Model.equation	Model.grRules (update)	
ate transport via diffusion	glyclt[e] <=> glyclt[c]	contigs00000797	
ne transport via diffusion	gua[e] <=> gua[c]	contigs00002852	
ransport, extracellular	h2o[e] <=> h2o[c]	contigs00004901	

datasets from NREL.

	Matabalita ID in		
Name	PicreModel	BIGG ID	KEGG
Tunic	Therewieder	DIGGID	REGO
eic acid	InIc[c]		
ctic acid	lac-L[h]		
Z,8Z,11Z)-icosatrienoyl]-sn-glycero-3-phosphoethanolamine		pear_hs	
ophan	trp-L[c]		
ucono-delta-lactone	gal14l-L[c]		
Dichlorotoluene			https://www.ger
TrE			N/A

Since P. renovo is an aspiring source of sustainable fuel and energy and capable of consuming CO2 and other greenhouse gases, the mass production of *P. renovo* is a vital solution for globally replacing the fossil fuels and implementing biofuels. The completed metabolic model of P. renovo accurately depicts the interactions of P. renovo with environment and other microorganisms. The analysis of these interactions will precisely provide the systems biology of *P. renovo* as well as genomic organization and metabolism. As a result of the curated metabolic model of *P. renovo* with illustrations of its systems biology, the efficient growth mechanism in response to different environmental factors and other microbes can be designed. Therefore, systematic and scientific design in methods of planting the P. renovo outdoors for mass production ultimately promote biofuels sustainable and energy.



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Discussion

Conclusion

• The creation of the metabolic model of *P*. renovo will contribute to the scientific understanding of its genomic organization and metabolism.

• The model was created through the refinement of an initial metabolic model and converted into a computational model.

• The completed metabolic model of P. renovo is used to examine different metabolic capabilities and induce biological hypotheses.

• The next step would be to use the model for insight, and to refine if necessary.

Acknowledgement