Genome-based systemic approach for microalgal biofuel production

Choul-Gyun Lee
Marine Bioenergy Research Center, Department of Marine Science & Biological Engineering,
Inha University, Incheon 402-751;
e-mail: leecg@inha.ac.kr

Key words: Microalgae, OMICs, in silico *model*

Introduction. Eukaryotic microalgae are attracting a lot of attention due to their potential for sustainable production of biofuel precursors such as lipids, starches, alcohols and hydrogen gas. In addition, they can convert solar energy into biomass using carbon dioxide by photosynthesis. Recently various attempts in biological fields have been made to produce microalgal biofuel. Especially since genome database of *Chlamydomonas reinhardtii* was published in 2007, high throughput omics data of eukaryotic microalgae have been accumulating at a rapid rate. Among omics data, genomics and transcriptomics researches are developing rapidly by development of NGS technologies. Over 30 whole genome sequencing of eukaryotic microalgae were in progress or completed in the JGI (Joint Genome Institute) and transcriptome of *Dunaliella tertiolecta*[1] and *Nannochloropsis gaditana*[2] was characterized by NGS (next generation sequencing). With accumulation of these enormous data, macroscopic view of cellular network has been required requisitely. To date as the one of research tools to gather and analyze huge information, systems biology is worth of remark. Through the use of systems biology, molecular and cellular phenomena of eukaryotic microalgae could be modeled using integrated and interacting network of genes, transcripts, proteins and biochemical reactions under stressful conditions.
To enhance lipid productivity from microalgae, *in silico* model of eukaryotic microalgae was reconstructed based on OMICS data. It can make us fully understand the lipid accumulation mechanism within eukaryotic microalgae.

Methods. We selected the target eukaryotic microalgae by their physiological behavior, genome size and habitant. Cells were grown photoautotrophically at 50 $\mu E/m^2/s$ in three fold f/2 medium with 2% CO_2. Transcriptome, proteome and metabolome were analyzed by RNA sequencing, LC-MS/MS and GC-MS respectively. Metabolic reconstruction was performed by SimPheny™.

Results. Chlorophyta, Rhodophyta and Eustigmatophyta were selected as target eukaryotic microalgae. Fatty acid contents and carbohydrate contents were observed to be differentially regulated in microalgae under nitrogen depleted condition (Fig.1). To characterize fatty acid accumulation mechanism, genome data was used as a frame work for metabolic reconstruction. Transcriptome (Fig.2), proteome (Fig.3) and metabolome analysis of the cells were performed and integrated to reconstruct cellular network in eukaryotic microalgae.

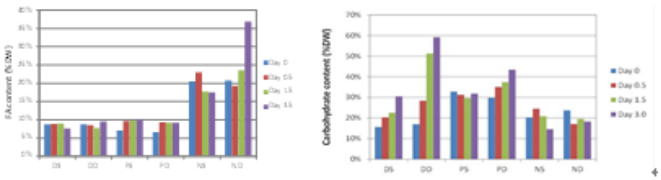

Fig. 1 Physiological changes of eukaryotic microalgae under stressful condition

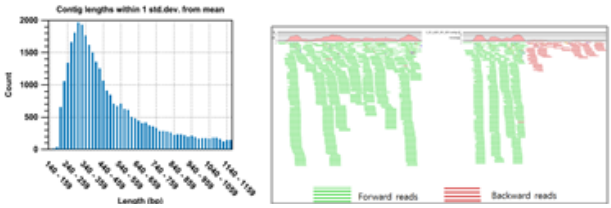

Fig. 2 Transcriptome analysis of eukaryotic microalgae

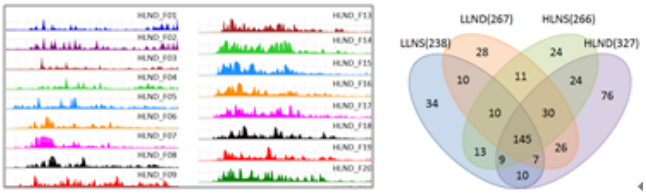

Fig. 3 Proteome analysis of eukaryotic microalgae

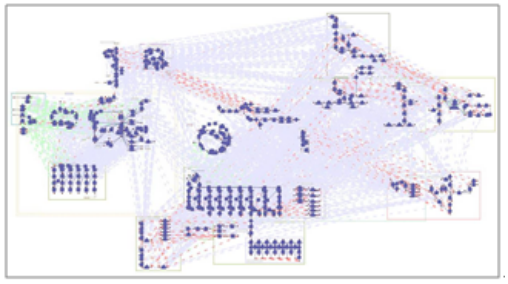

Fig. 4 Metabolic mapping of eukaryotic microalgae

Conclusions. This *in silico* analysis integrated multi-omics data could become the driving force for exploiting metabolic and regulatory mechanisms to improve microalgal cells as a biofuel producer.

Acknowledgements. This research was supported by Marine Bioenergy Center funded by Ministry of Land, Transport and Maritime Affairs of Korean Government and by a National Research Foundation grant funded by the Ministry of Education, Science and Technology, Korea.

References.

1. Rismani-Yazdi, H., B. Z. Haznedaroglu, K. Bibby, and J. Peccia (2011) *BMC Genomics*. 12: 148.
2. Radakovits, R., R. E. Jinkerson, S. I. Fuerstenberg, H. Tae, R. E. Settlage, J. L. Boore, and M. C. Posewitz (2012) *Nat. Commun*. 3.