# From Ocean to Octane

## Using Transcriptomics for Biofuel Engineering

Microalgae and cyanobacteria may be a significant source of renewable energy. The combination of their minimal nutrient requirements, easily manipulated genetics and highly efficient photosynthetic abilities to harvest and convert solar energy into biofuels makes them a promising resource for biofuel production. Transcriptomics can be used to optimize biofuel production in these hosts.

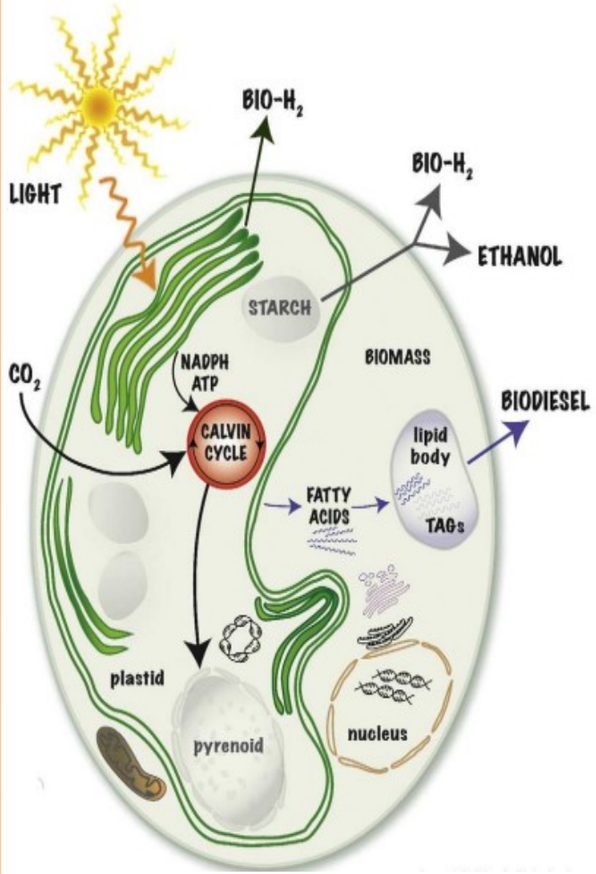


**Figure 1** Biofuel-producing metabolic pathways in algae (Beer et al. 2009)

## Why Use Transcriptomics?

High concentrations of biofuel products, such as butanol and ethanol, negatively impacts cellular growth and metabolic processes, resulting in reduced production of biofuel. Anfelt et al. (2013) explain that trancriptomics can be used to identify the transcriptome response of a cell to varying concentrations of biofuels and this information can be used to engineer more biofuel-tolerant strains of hosts. With transcriptome sequencing, they identified specific genes that were upregulated and downregulated in response to butanol exposure. Using this information, they selectively engineered cells to overexpress genes which produce proteins that are known to improve butanol tolerance and cell viability.

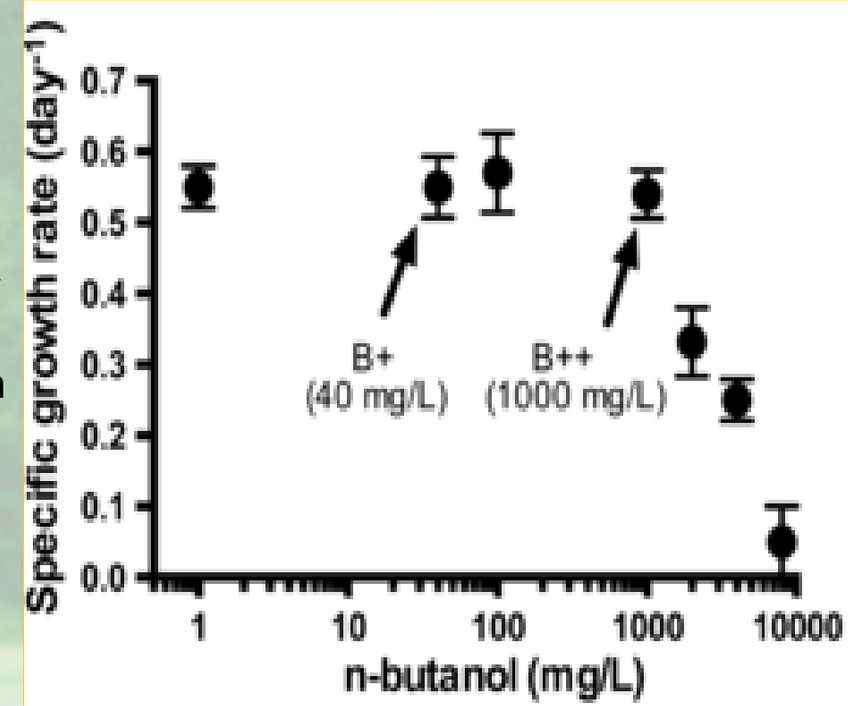


**Figure 2** Cyanobacterial growth rates decrease with increasing n-butanol concentrations (Anfelt et al. 2013)

## Looking Towards the Future

Biofuel engineering will continue to advance as sequencing technology improves. Novel and comparative transcriptomics will improve cellular engineering and optimize biofuel production.


References

Dienst et al. 2014 Biotech. for Biofuels ● Beer et al. 2009 Cur. Opin. in Biotech. 20:264-71 ● Anfelt et al. 2013 Appl. Environ. Microbiol. (79)23:7419-27