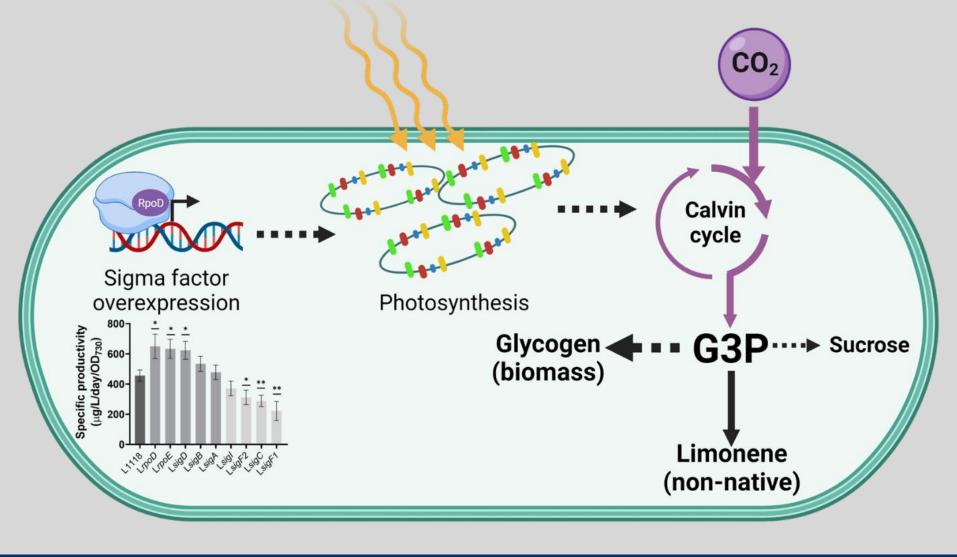


Thermodynamics contributes to high terpene productivity in cyanobacteria Shrameeta Shinde¹, Sonali Singapuri¹, Zhenxiong Jiang¹, Bin Long², Danielle Wilcox¹, Cami Klatt¹, Joshua S. Yuan², and <u>Xin Wang¹</u> ¹ Department of Microbiology, Miami University, Oxford, OH 45056 ² Synthetic and Systems Biology Innovation Hub, Department of Plant Pathology and Microbiology, Texas A&M University, College Station, TX 77843

Background

The terpene family is highly diverse with more than 50,000 unique chemical structures. Terpenes are condensed from two C5 precursor isomers, isopentenyl pyrophosphate (IPP) and dimethylallyl pyrophosphate (DMAPP). Limonene, a C10 monoterpene, has been tested to use as a drop-in fuel additive for combustion engines and as the substitute for aviation fuels. kerosene Photosynthesis-driven CO₂ conversion to terpenes is particularly attractive for biofuel applications due to its low carbon footprint but is challenged with low productivities. We hypothesize that the low terpene yield in phototrophs is constrained by thermodynamics due to CO_2 delivery to cells.



Methods

Cyanobacteria growth. Cyanobacteria were grown at 30 °C under 50 μ mol/m²/s and varied intensity of cool white LED illumination in the Multi-Cultivator MC 1000-OD (Photon Systems Instruments, Czech Republic).

Limonene measurement. Limonene was collected using an absorbent trap containing HayeSep porous polymers (Sigma, USA) attached to the outlet of individual 1-L Roux bottles. Every day, limonene was eluted from the trap with 1 mL hexane supplemented with 10 µg/mL cedrene (Sigma, USA) as the internal standard. The eluted sample was analyzed by GC-MS in a Thermo Trace 1300 ISQ quadrupole (QD) (Thermo Fisher Scientific, USA) system.

Synthetic Oxygen evolution measurement. performance was measured using the Clark-type oxygen electrode (Qubit systems, Ontario, CN). The final oxygen evolution rate calculated was corrected with the dark respiration rate and normalized to chlorophyll content.

Shotgun proteomics. Comparative proteomics was conducted through LC-MS/MS on the Thermo LTQ Orbitrap XL by operating under the data-dependent mode. Normalized spectral abundance (NSAF) was used to compare the protein change between wild type and the engineered (L*rpoD*) cells.

