

# Genome-Wide Transcriptional Regulation in *Saccharomyces cerevisiae* in Response to Carbon Dioxide

## Background/Objective

Sugar metabolism by *Saccharomyces cerevisiae* produces ample amounts of CO<sub>2</sub>, which is highly soluble in fermentation media and so might affect yeast metabolism. To elucidate the overlooked effects of CO<sub>2</sub> on yeast metabolism, we studied the transcriptional regulatory networks (TRNs) of *S. cerevisiae* grown on glucose under CO<sub>2</sub> conditions as compared to N<sub>2</sub> and O<sub>2</sub> limited conditions.

## Approach

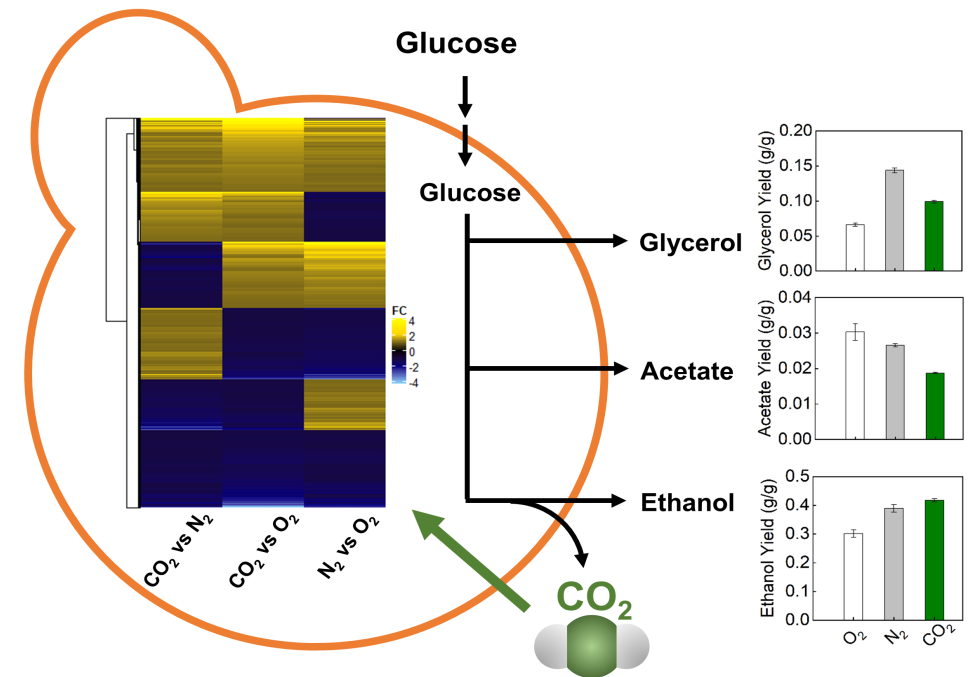
- Conducted glucose fermentation by *S. cerevisiae* in tightly sealed vials with a headspace gas of high CO<sub>2</sub>, high N<sub>2</sub>, or limited O<sub>2</sub>, respectively.
- Performed transcriptional analysis of *S. cerevisiae* under different gas conditions to screen for genes that regulate fermentation and other metabolic pathways under CO<sub>2</sub> conditions.

## Results

- Discovered that the MAPK signaling pathway plays a role in CO<sub>2</sub> sensing in yeast with distinctively up-regulated genes in signal receptors and transcriptional factors.
- Discovered that CO<sub>2</sub> also orchestrates carbohydrate synthesis, heme synthesis, membrane and cell wall metabolism, and respiration in yeast.
- Glycerol yield decreased under CO<sub>2</sub> conditions due to decreased mRNA levels of the enzymes in the glycerol synthesis pathway.

## Significance/Impacts

This study highlights the potential of CO<sub>2</sub> to modulate cellular metabolism and decrease the byproduct effect of glycerol production.



CO<sub>2</sub> affected glycerol, acetate and ethanol yield during glucose fermentation and induced genome-wide transcriptional regulation in *S. cerevisiae*.