

# Metabolite Production of *Thermoanaerobacterium saccharolyticum*

Gina Sternberg  
Chemical Engineering  
University of Minnesota

**Thesis:** This experiment was part of a larger project. A batch of a gene-deletion mutant strain of *Thermoanaerobacterium saccharolyticum* was grown in a bioreactor to test cell growth and production under certain conditions.

## Background

- Many microorganisms reproduce quickly, and as a result adapt to environmental conditions quickly
- In a bioreactor, cells (particularly those with recombinant DNA) are not in optimal conditions and will evolve. This limits how long a cell culture remains useful in a bioreactor
- **This experiment aims to study changes in metabolism of a *Thermoanaerobacterium saccharolyticum* culture over time**
  - *Thermoanaerobacterium saccharolyticum* is an anaerobic bacterium used for ethanol production from glucose and xylose.
  - In this experiment, a strain genetically modified with gene knockouts was grown using xylose as the carbon source.
- The experimental results will be compared to a computer model prediction to test its efficacy
  - An organism's overall metabolism can be described as a collection of basic reaction pathways
  - These pathways are called elementary modes, and analysis using them is called elementary mode analysis
  - Elementary mode analysis can be used to predict how a substance is metabolized by the organism
  - Quantitative analysis of probability of each of the pathways can be used to predict the most favorable pathways, and thus predict eventual evolution of the cells

## Experimental Methods

Growing the gene deletion mutant strain of *T. sacch* grown in bioreactor:

- **1 liter MTC media** with 20 g/L xylose carbon source
- **Nitrogen sparge** to keep anaerobic conditions
- At 24 hours, lag phase continued so 5% CO<sub>2</sub> gas was added at to the sparge to add carbonic acid
- CO<sub>2</sub> addition ended lag phase
- Bioreactor used base to maintain pH of 6.0 despite CO<sub>2</sub> in sparge and acid production by cells

Experimental samples analysis:

- **Samples taken at 4.5, 24.25, 29, 33.5, 47, 71.5, and 95 hours**, stored in cool environment to inhibit cell growth
- **HPLC identified major components (xylene, ethanol, lactic acid)** consumed or produced, measured concentrations with refractive index detector
- **Cell density measured** by spectrophotometer for optical density at ~260nm, which is linearly proportional to cell density

Figure 1

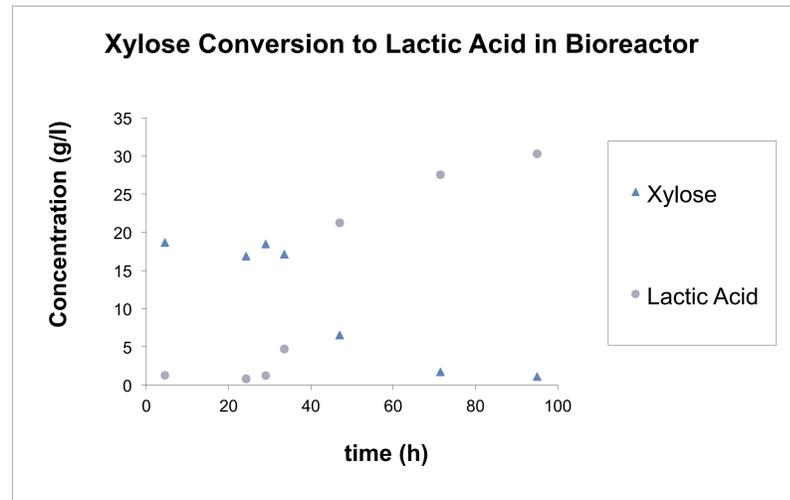
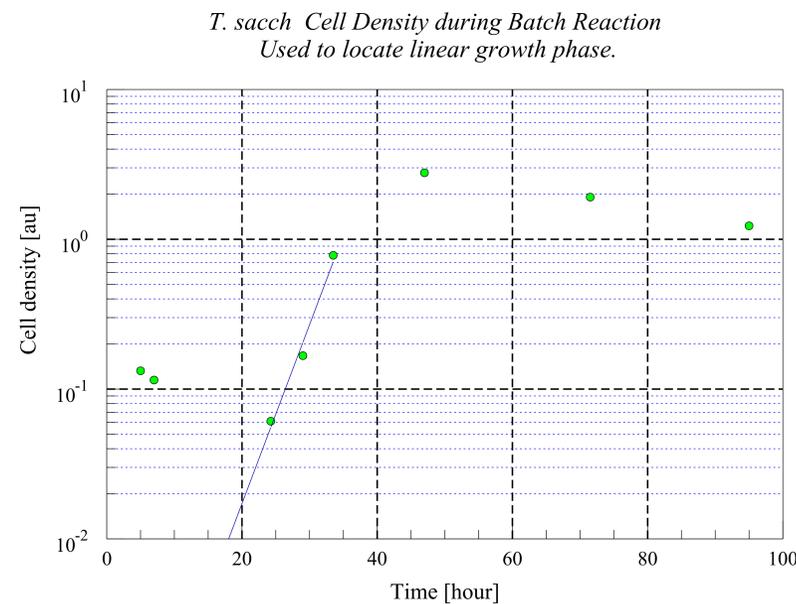


Figure 2



## Application

- **These experiments are the first step** in a bioreactor project
- The **goal of this experiment is to test and improve a model** based on elementary mode analysis to predict the evolution of cells in a bioreactor
- **Eventual goal of the project is to create an automated bioreactor** system to automatically take samples, with bioreactor used to continuously add feedstock and reduce cell density to encourage cell growth
  - Samples will be further analyzed for cell growth and media composition as generations of *T. sacch* adapt to the environment of the bioreactor
  - The experimental results can be compared to a computer model predicting the evolution of the cells' metabolism
  - The computer model provides quantitative analysis of metabolic pathways using elementary mode analysis
  - The cells are predicted to evolve to the most favorable metabolism, model predicts most favorable metabolism, so it should be able to predict evolution of the cells

## Conclusions

### Ethanol was expected major product

- Very low yield
- Maximum yield less than 0.18 g/L at 47 hours
- Concentration was below detection limit by 71.5 hours
- Possibly evaporated in sparge or consumed by cells

### Lactic acid was produced

- Yield higher than original xylose content
- Yield concentrations exceeded calibration curve, so final result is uncertain

### Bioreactor ran successfully

- MTC media and pH level provided environment conducive to cell growth
- Carbon dioxide in the sparge necessary for cell growth

## References

Unrean, P.; Srienc, F. Predicting the adaptive evolution of *Thermoanaerobacterium saccharolyticum*. *Journal of Biotechnology* [Online] **2012**, *158*, 259-266.

Unrean, P.; Srienc, F. Metabolic networks evolve towards states of maximum entropy production. *Metabolic Engineering* [Online] **2011**, *13*, 666-673.

Unrean, Pornkamol. (2010). Strain optimization through theoretical and experimental tools.. Retrieved from the University of Minnesota Digital Conservancy, <http://purl.umn.edu/101189>.