Medium Chain Carboxylic Acids Production from Food Waste

Panagiota Stamatopoulou*, Matthew Scarborough
*PhD Candidate

Department of Civil and Environmental Engineering
University of Vermont

10th ICSSWM
June 22nd, 2023

THE UNIVERSITY OF VERMONT
CIVIL & ENVIRONMENTAL
ENGINEERING

Outline

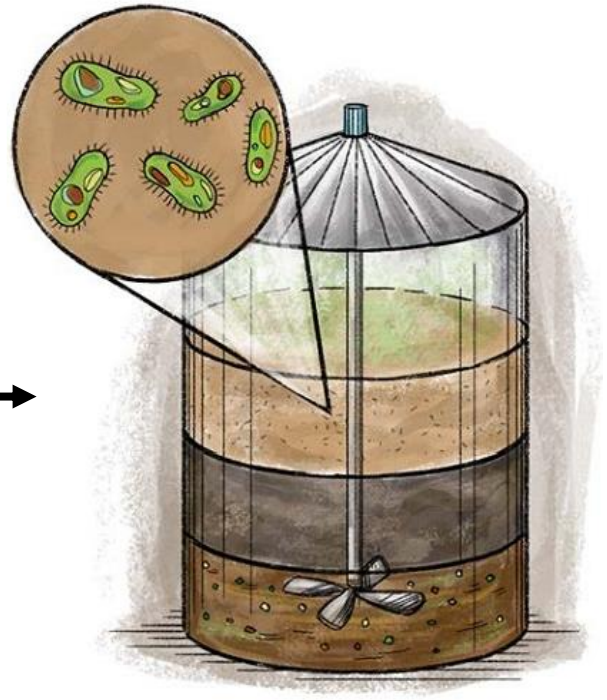
- Background
- Motivation
- Experimental Setup
- Results
- Insights

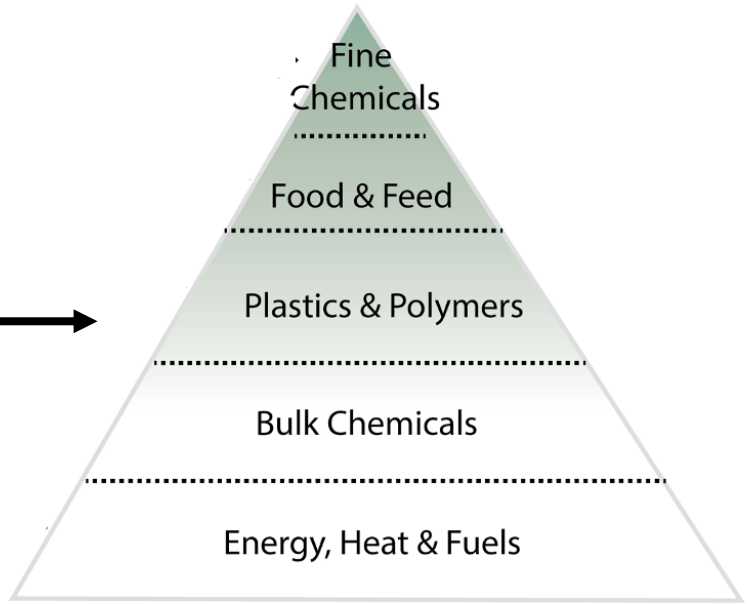
Background

Food Waste and Environmental Microbiomes

Background

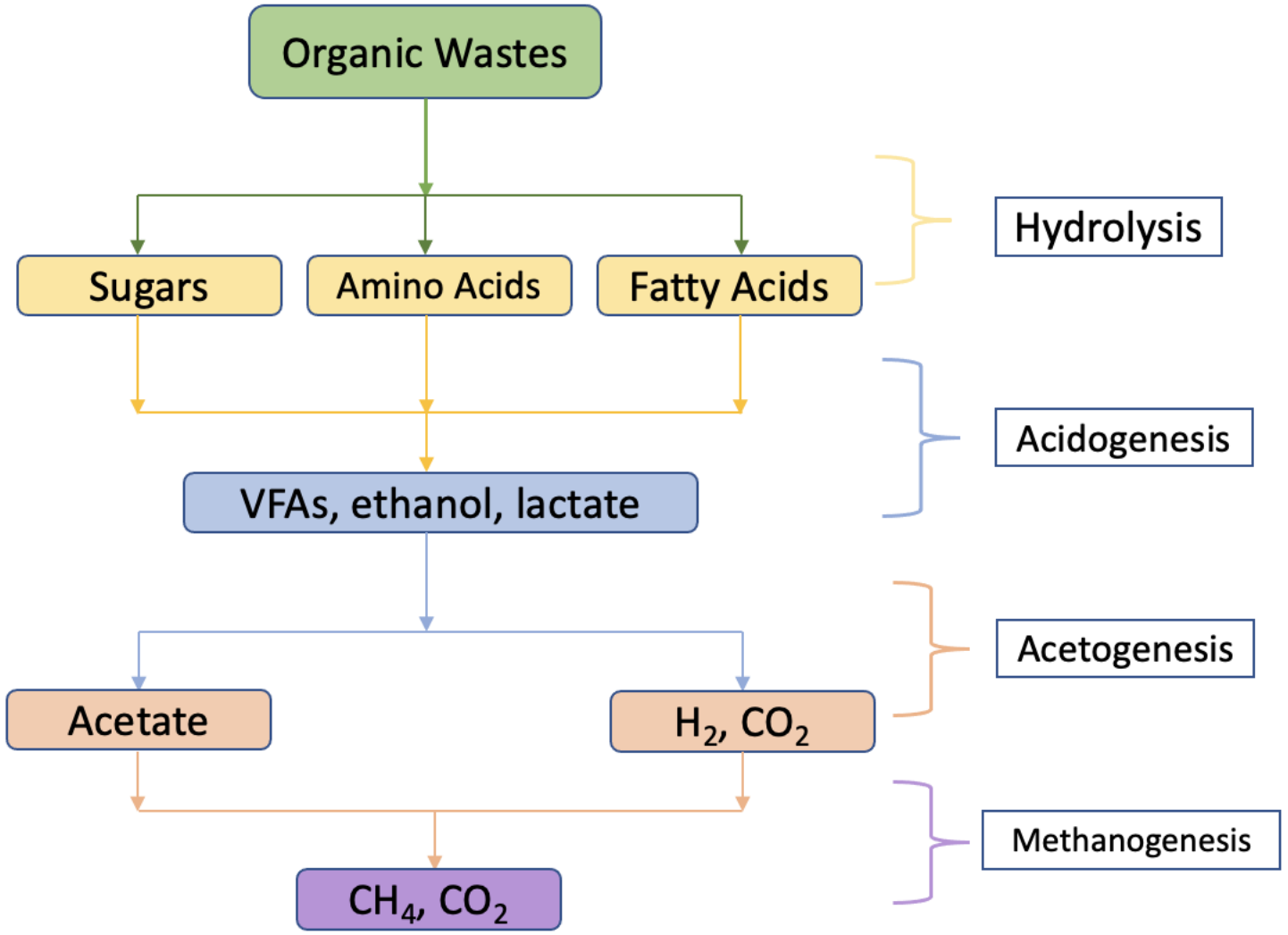
Organic Waste



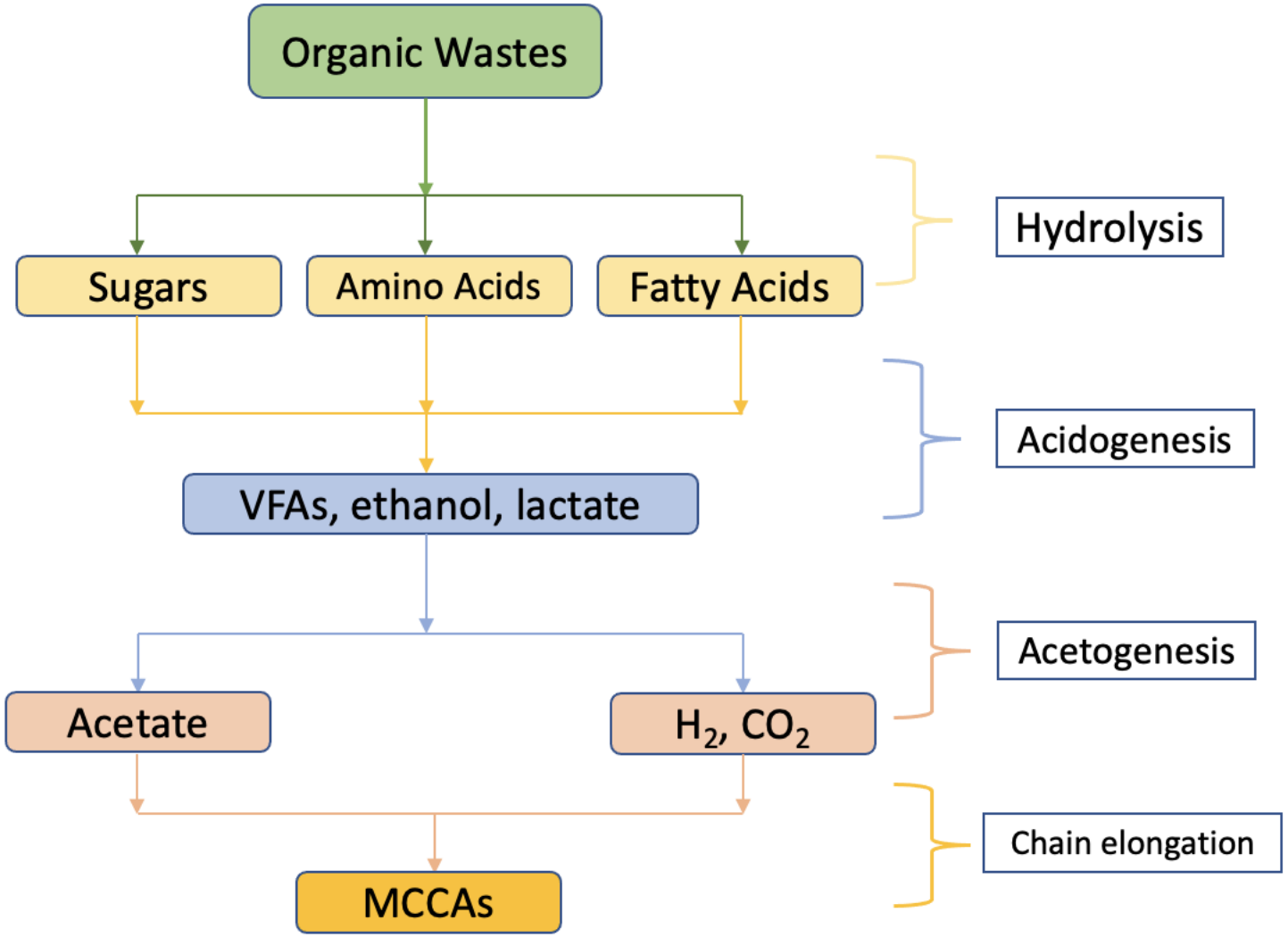


Scarborough, M, et. al. 2021. Current Opinion in Microbiology

Conventional Anaerobic Digestion

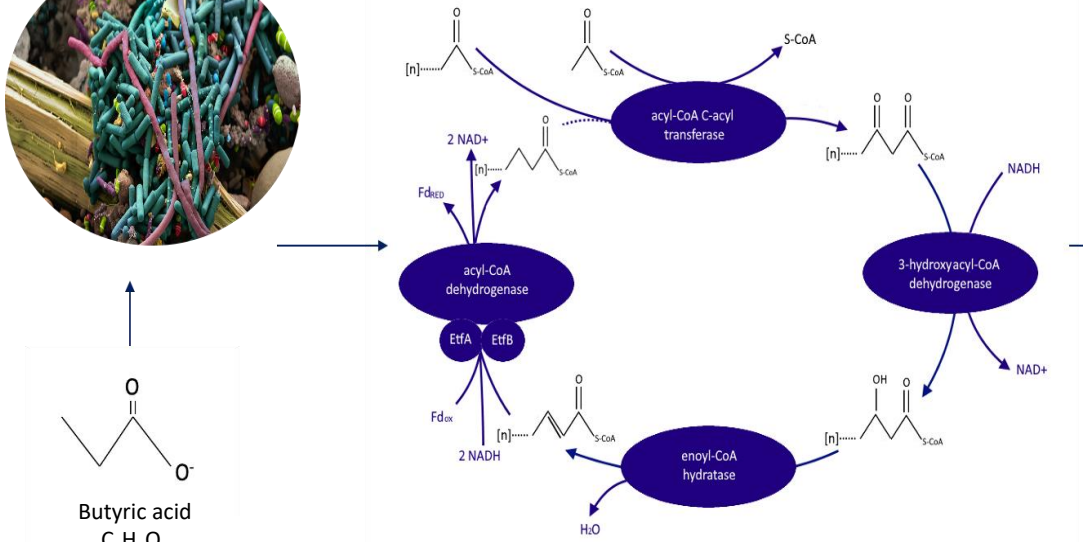


Chain Elongation Process



Medium Chain Carboxylic Acids (MCCAs)

- Consist of 6 to 12 atoms of carbon



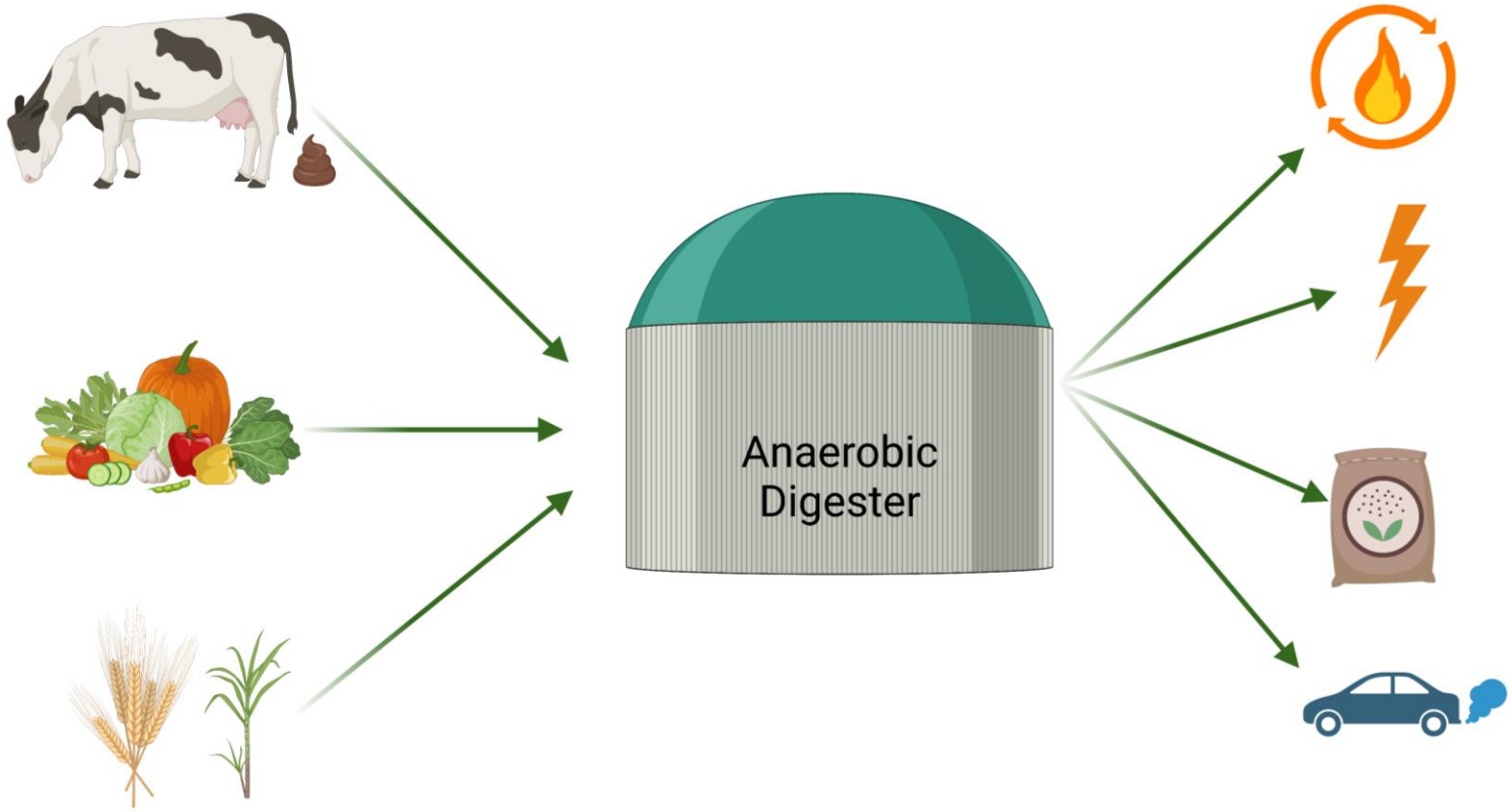
Hexanoic (Caproic) acid
$C_6H_{12}O_2$

Butyric acid
$C_4H_7O_2$

- Dietary-nutritional supplements, especially as medium-chain triglycerides (MCTs),
- Production of personal care products, pharmaceuticals, dyes, and antimicrobials,
- Production of liquid transportation fuels has gain great attention and is in progress.

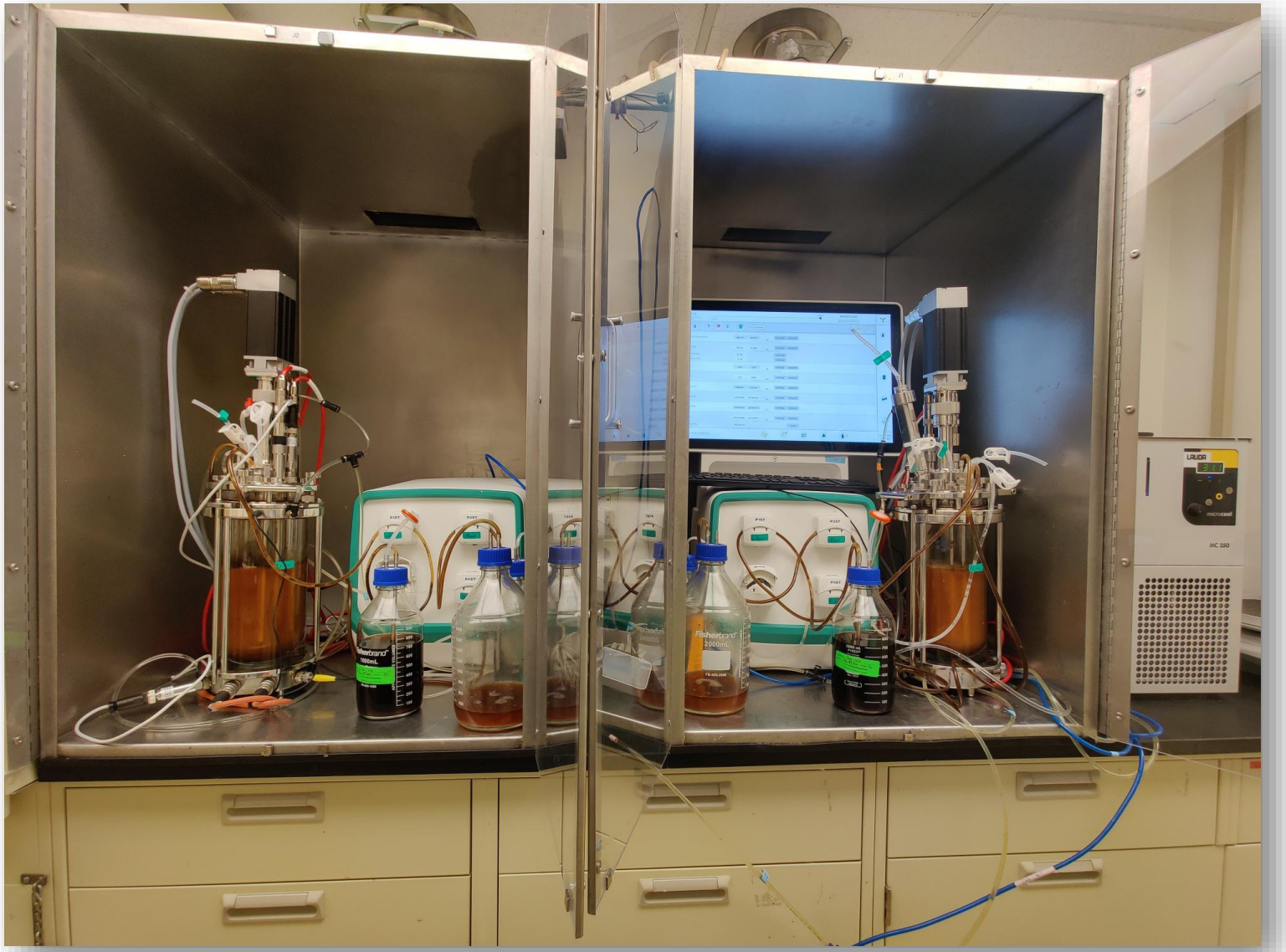
Motivation

Motivation



Experimental Setup and Methods

Experimental Setup



Experimental Setup

Operating Parameters:

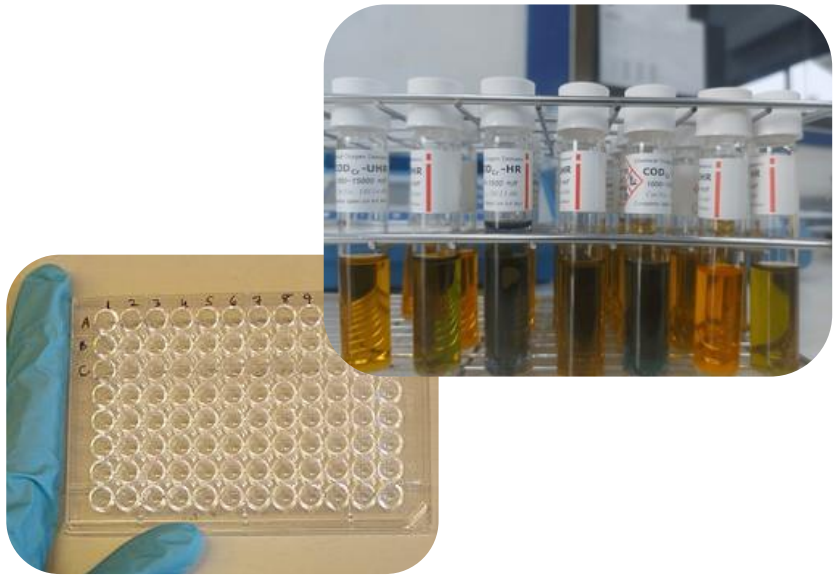
- Enriched biomass with chain elongators
- Non-sterile feedstock: real food waste
- HRT: 6 days
- pH: 5.5
- Temperature: 37°C

- No external electron donor

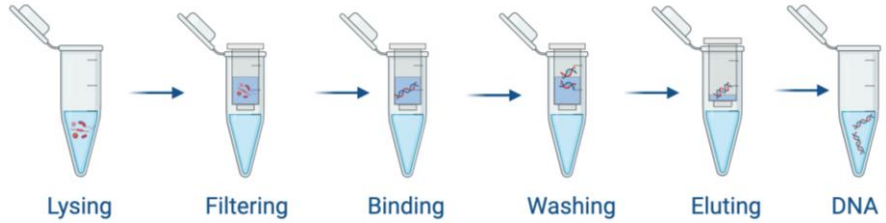
Methods

Analyzing Samples:

- sCOD
- NH_4-N
- Proteins
- Fats
- Carbohydrates

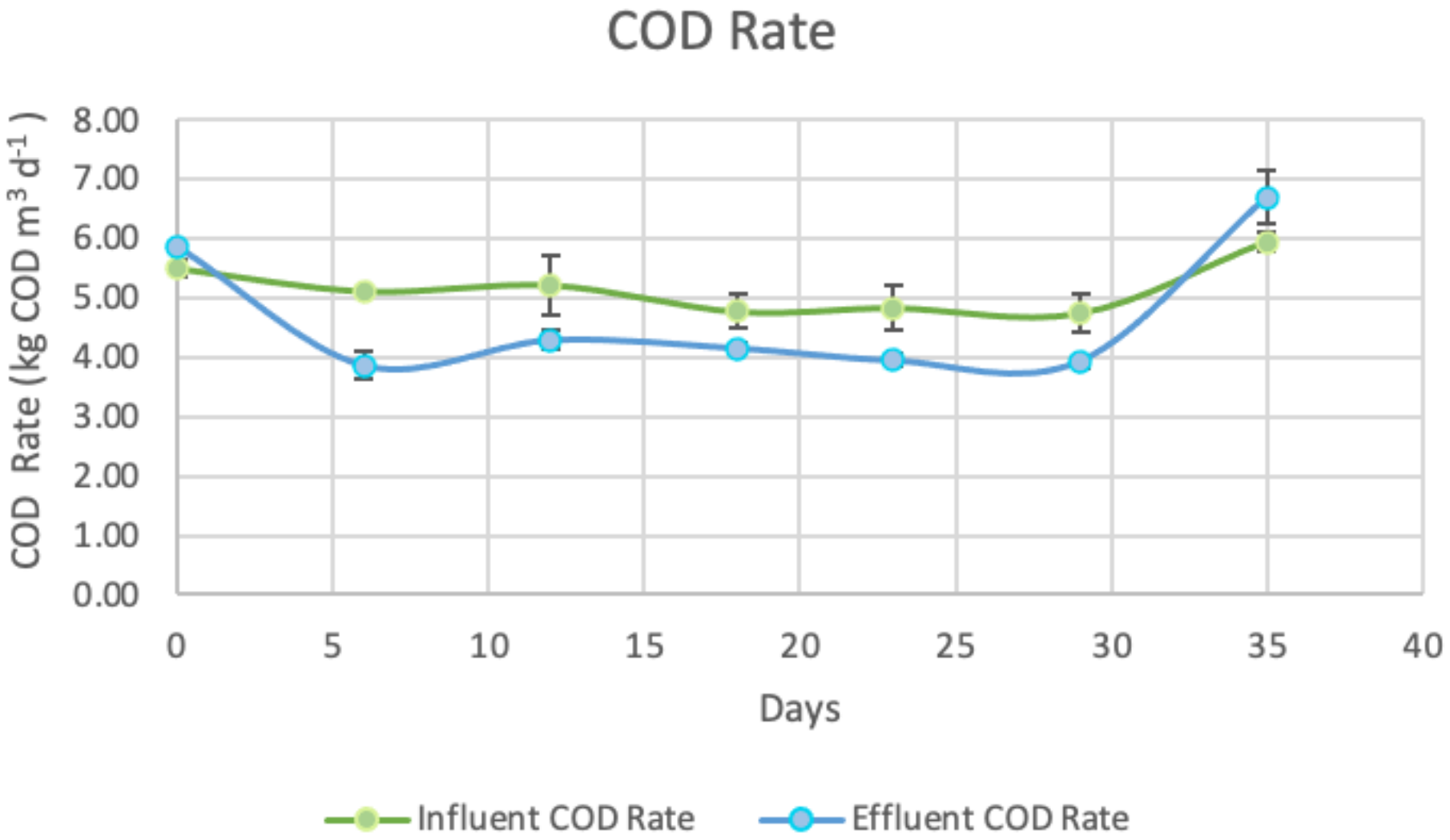


- Headspace Gas
- Short and Medium Chain Fatty Acids
- Metagenomic and Metatranscriptomic analysis

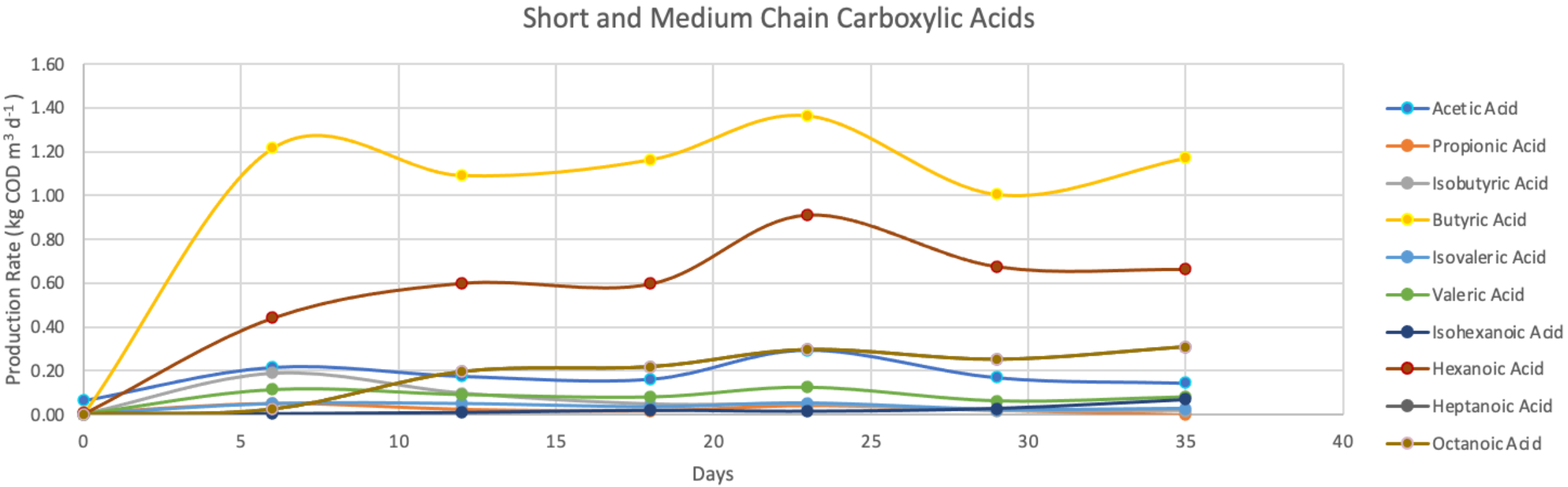


Results

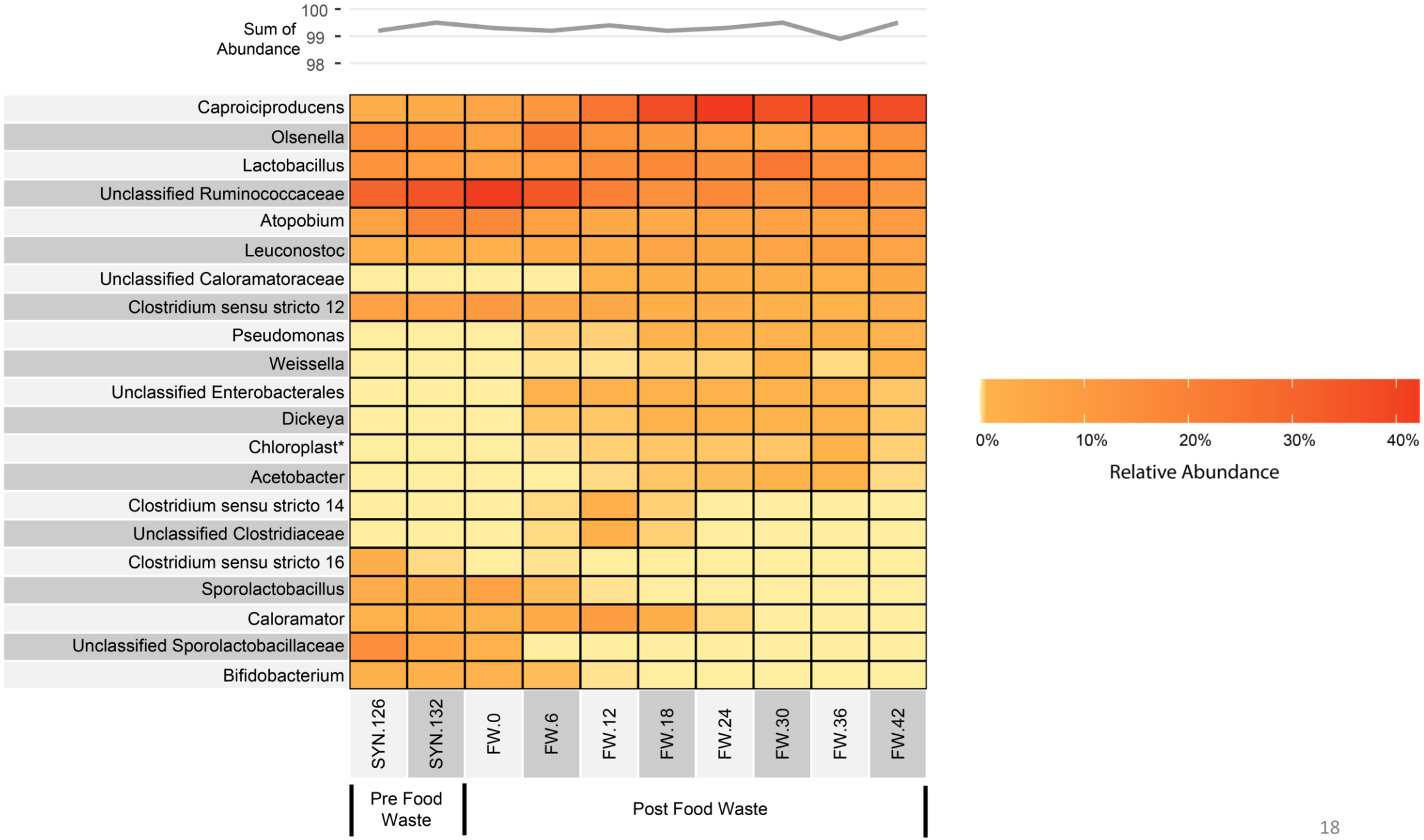
Results



Influent and effluent COD rate was relatively constant. This is common in the chain elongation process.



- Acetic acid – precursor for reverse β-oxidation - is low.
- Butyric acid – one cycle of reverse β-oxidation – is the most abundant carboxylic acid.
- Hexanoic acid – second cycle of reverse β-oxidation – the second most abundant carboxylic acid and the most abundant MCCA.


100
99
98
Sum of Abundance
Caproiciproducens
Olsenella
Lactobacillus
Unclassified Ruminococcaceae
Atopobium
Leuconostoc
Unclassified Caloramatoraceae
Clostridium sensu stricto 12
Pseudomonas
Weissella
Unclassified Enterobacterales
Dickeya
Chloroplast*
Acetobacter
Clostridium sensu stricto 14
Unclassified Clostridiaceae
Clostridium sensu stricto 16
Sporolactobacillus
Caloramator
Unclassified Sporolactobacillaceae
Bifidobacterium
SYN.126
SYN.132
FW.0
FW.6
FW.12
FW.18
FW.24
FW.30
FW.36
FW.42
Pre Food Waste
Post Food Waste
0%
10%
20%
30%
40%
Relative Abundance

Insights

Insights

- 46% of COD in food waste was fermented to VFAs or MCCAs
- 17% of COD in food waste was converted to MCCAs
- Microbial community changed after adding food waste
  - A relatively simple microbial community emerged
  - 10 genera accounted for > 90% of reads
  - Relative abundance of Caproicproducens increased
  - Relative abundance of an Unclassified Ruminococcaceae decreased
  - New simple fermenting bacteria arose

NEXT STEPS:

- Metagenomic and metatranscriptomic analyses

Acknowledgments

THE UNIVERSITY OF VERMONT
CIVIL & ENVIRONMENTAL
ENGINEERING

NASA

UVM FOOD SYSTEMS RESEARCH CENTER

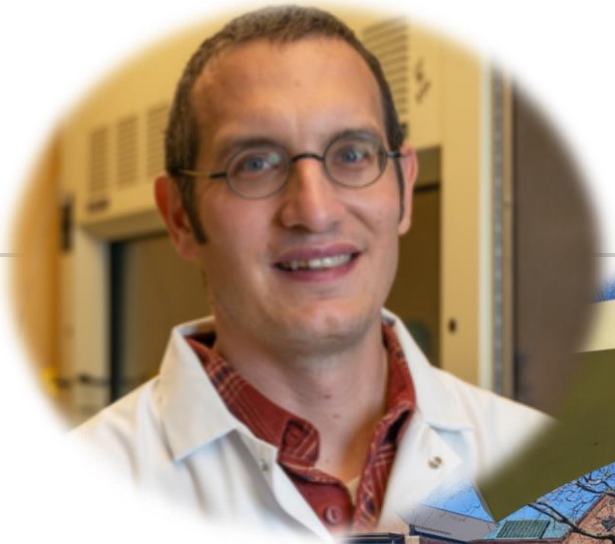
USDA ARS

NASA
Vermont Space Grant Consortium

THE GERONDELIS FOUNDATION

SWANA
SOLID WASTE ASSOCIATION OF NORTH AMERICA
NNE SWANA

EMERG
at the University of Vermont



Thank you!