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
Outline

• Background
• Motivation
• Experimental Setup
• Results
• Insights
Background
Food Waste and Environmental Microbiomes
Background

Organic Waste

Conventional Anaerobic Digestion

Diagram:
- Organic Wastes
  - Sugars
  - Amino Acids
  - Fatty Acids
    - VFAs, ethanol, lactate
      - Acetate
        - \( \text{CH}_4, \text{CO}_2 \)
      - \( \text{H}_2, \text{CO}_2 \)

Processes:
- Hydrolysis
- Acidogenesis
- Acetogenesis
- Methanogenesis
Chain Elongation Process
Medium Chain Carboxylic Acids (MCCAs)

- Consist of 6 to 12 atoms of carbon

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
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.
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
Thank you!