

Medium Chain Carboxylic Acids Production from Food Waste

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Microorganisms have inhabited Earth for at least 3.5 billion years (Homann et al., 2018). Prior to the evolution of photosynthesis, microorganisms survived in strictly anaerobic (i.e., without oxygen) environments. In the absence of terminal electron acceptors, microorganisms rely on fermentation to recycle electrons internally. Microbial fermentations have supported humankind for hundreds of thousands of years. For several centuries, humans have also put microbes to work to convert organic wastes to beneficial products, specifically methane. As new scientific tools allow us to gain new insights into microbial fermentation pathways, we are finding new ways to use microbes to convert “wastes” to beneficial products. Considering the limited value of biogas and natural gas, it is important to revisit the anaerobic digestion process and study other important, and more valuable byproducts of the process, such as medium-chain carboxylic acids (MCCAs). MCCAs are monocarboxylic acids containing 6 to 12 atoms of carbon and have gained great attention as agricultural (and human) dietary supplements, especially as medium-chain triglycerides (MCTs) (Stamatopoulou et al., 2020). Additionally, they have been used for the production of personal care products, pharmaceuticals, dyes, and antimicrobials (Stamatopoulou et al., 2020). Recently, MCCAs have gained great attention and have been proposed as a precursor for liquid transportation fuels (Stamatopoulou et al., 2020). The production of medium chain carboxylates is a result of a biological process, called chain elongation, in which microorganisms convert short-chain volatile fatty acids (VFAs) into longer carbon chains (Angenent et al., 2016). Pure cultures and mixed microbial communities have been used, from several sources of inoculation, resulting in the formation of a variety of short and medium-chain carboxylic acids. Usually, pure cultures can provide more valuable information regarding the production of these valuable products, and several microorganisms have been isolated and identified recently (Scarborough et al., 2020). However, the drivers of microbial chain elongation remain elusive, limiting the ability to intelligently design and implement processes for MCCAs production. If humans are to expand our ability for recovering resources from organic wastes as MCCAs, additional understanding of the microbial processes involved in MCCAs production are needed.

Chain elongation is a biological anaerobic fermentation process in which microbiomes, elongate short chain carboxylic acids into MCCAs. Chain elongation is a relatively new term, used for the first time in the mid 2010's, however the use of fermentation to produce MCCAs has been studied for over 100 years (Scarborough et al., 2020; Stamatopoulou et al., 2020). For our study, a bioreactor with enriched for chain elongation microbial community was equipped, Jupiter 2 – from now on J2. J2 is supported by a control cabinet, with four peristaltic pumps, and a human-machine interface (HMI) to program and operate J2. The bioreactor is equipped with a water jacket, a pH and dissolved oxygen (DO) probe, an impeller and overhead mixer, and two thermometers to measure the temperature inside the vessel and in the water jacket. It also has four other ports to connect the influent supply, ports for buffer or acid for pH control, and a port for the effluent or for collecting samples. Finally, there is a chiller which circulates water that goes through the condenser to reduce evaporation. All of those are connected to the control cabinet which is connected to the HMI.

The bioreactor was operated for ten months to determine how several parameters can affect the MCCA production, prior to the current study. As a result, the microbial communities in the sugar-fed bioreactors were enriched for MCCAs production, as mentioned above. The goal of the current work is to determine how addition of real post-consumer FW impacts the enriched microbiome. FW originated from household sources was collected and, after preliminary processing, was supplied to a 2L bioreactor, under constant pH and temperature, 5.5 and 37°C respectively. The average influent chemical oxygen demand (COD) loading rate was 5.2 kg COD m³ d⁻¹, while the effluent was 4.8 kg COD m³ d⁻¹. During the entire study, the COD loading rates in the influent and the effluent were relatively constant (Figure 1). This is an indicator that most of the COD concentration in the influent was utilized by the microbial community for the production of high-value chemical.

The analysis of the collected samples for the MCCA production, showed that the most abundant carboxylic acid in the bioreactor was the butyric acid (C4), followed by the hexanoic/caproic acid (C6) and the acetic (C2) and octanoic/caprylic acid (C8). The average conversion rate of the butyric acid was 1.00 kg COD m³ d⁻¹, the hexanoic acid was 0.56 kg COD m³ d⁻¹, and the acetic and octanoic acid was 0.18 kg COD m³ d⁻¹ (Figure 2).

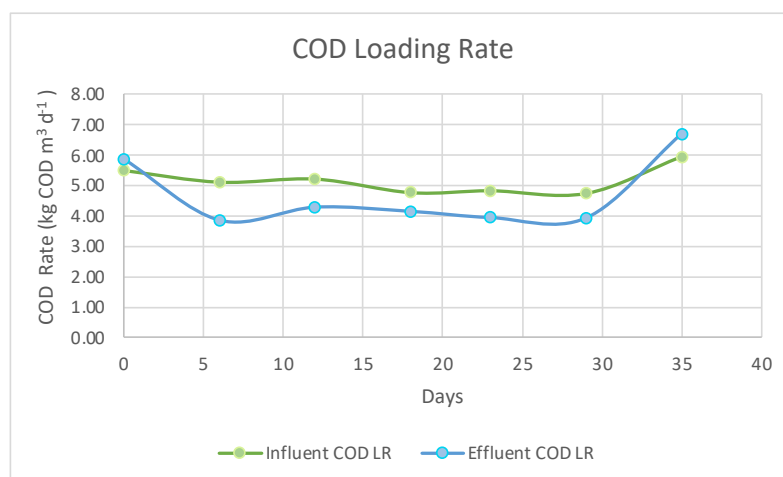


Figure 1: COD Loading Rate

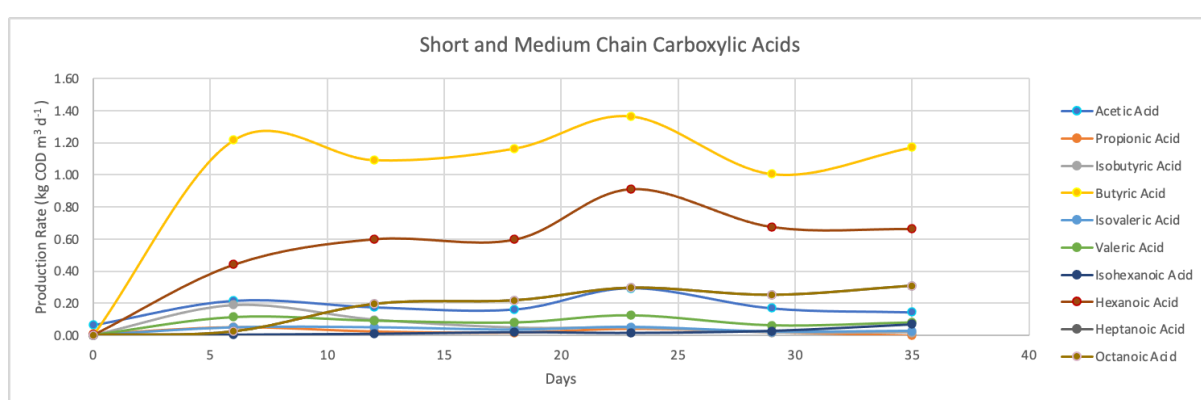


Figure 2: Short and Medium Chain Carboxylic Acids Production Rate

Samples were also collected for DNA and RNA sequencing. Analyses of the microbial community, using metagenomics and metatranscriptomics, are ongoing.

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