

**Title:**

Exploring the influence of substrate and pH on microbial community dynamics in anaerobic digestion

**Authors:**

Lisa Jourdain<sup>1</sup>, Pierre Rossi<sup>2</sup>, Wenyu Gu<sup>1</sup>

**Institution(s):**

1- Laboratory of Microbial Physiology and Resource Biorecovery (MICROBE), ENAC, IIE, École Polytechnique Fédérale de Lausanne (EPFL), Ecublens, Switzerland 2- Central Environmental Molecular Biology Laboratory (CEMBL), ENAC, IIE, École Polytechnique Fédérale de Lausanne (EPFL), Ecublens, Switzerland

**Abstract (300 words maximum): :**

The anaerobic food chain describes the sequential degradation and utilization of biopolymers by a community of microorganisms in the absence of dioxygen. The anaerobic digestion (AD) process utilizes such microbial degradation networks to reduce organic waste volume while producing biogas as a renewable energy source. More recent interest has developed in applying AD to produce fatty acids as useful precursors for repurposing organic wastes. Previous research has characterized the different trophic layers and microbial metabolic groups carrying out digestion and identified key biological and operational factors affecting AD dynamics. However, it is still challenging to design a stable process that continuously produces targeted fatty acids with high productivity and purity by finely tuning the AD microbiota. As an initial step towards understanding the interactions of different factors and the dynamic feedback between microbial activity and the environment, we carried out enrichment experiments of microbiota taken from three different AD reactors with varying feedstock, operational conditions, and geographical locations. Minimal media containing glucose, cellobiose, or no carbon substrates (as negative controls) at three different pH levels (5.5, 6.5, and 7.5) were used. The production of metabolites (short-chain fatty acids, H<sub>2</sub>, CO<sub>2</sub>, and CH<sub>4</sub>) was monitored. Despite the different inocula, we observed the enrichment community converging functionally depending on substrate and pH conditions. Through multidimensional analysis of metabolites and 16S sequencing results, we will evaluate the relevance of substrate and pH in selecting community function.