

# Demonstration of an In-Silico Approach for the Broad Screening of Carbohydrate Active EnZyme Capacities in Microbiome Bioreactors

## Background

- The deployment of microbial consortia in anaerobic fermentation systems to generate bioproducts promises significant advantages over single isolate systems but is difficult to optimize and control.
- Compared to available assays, systems biology approaches provide powerful molecular level information but are currently considered impractical for the higher throughput needs of screening and optimization.

## Approach

- To this end, we have designed and tested the potential of mass spectrometry-based targeted metaproteomics as a means of fast, sensitive, and extensive characterization of cellulolytic enzymatic capacities for anaerobic microbiome digestion systems.

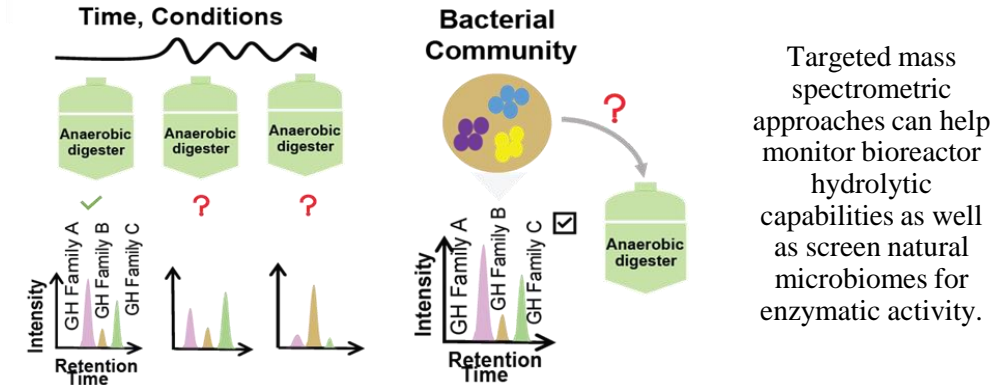
## Results

- A tractable unique set of peptides were identified that were sufficient to monitor the range of 5 key GH families in a constructed microbiome of 1401 genomes (representing a microbiome system that is likely more complex than most bioreactors).
- The unique peptides selected for groups of GHs were found to be sufficient for distinguishing enzyme specificity or microbial taxonomy.

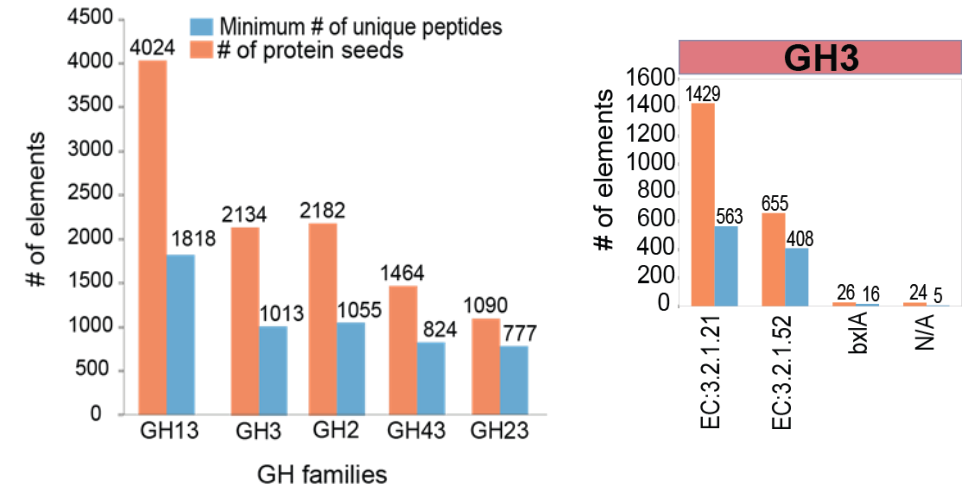
## Significance

- Targeted metaproteomics could be a valuable approach for estimating molecular level enzymatic capacities and responses of microbial communities to different substrates or conditions, which is a critical need in either building or utilizing constructed communities or defined cultures for bio-production.

Solis, Villalobos et al. *Biotechnol Biofuels* (2022) doi: 10.1186/s13068-022-02125-x



Targeted mass spectrometric approaches can help monitor bioreactor hydrolytic capabilities as well as screen natural microbiomes for enzymatic activity.



Even in a complex microbiome of 1401 microbes, a defined set of peptides can be used to monitor production of a GH family or other selected enzymatic activity.