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2024_11_Civil_PL: Quantum Epigenetic Regulation of Micro-Aeration Microbiome for Methane Formation Control and Its Techno-Economic Implications Toward Achieving Net-Zero Carbon Emission

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Motivation: The urgency of addressing climate change, enhancing energy security, and mitigating environmental threats calls for a collective strategy to ensure a sustainable future. In the context of greenhouse gas (GHG) reduction, it's essential to consider the global warming potential (GWP) of various gases. Methane (CH4), for instance, has a GWP 28 times that of carbon dioxide (CO2) and a 100-year GWP of 36 times that of CO2. CH4 can serve as a valuable energy source, and by increasing its production and utilization while reducing emissions from sources like ruminant animals and the environment, we can offset the use of fossil fuels and decrease GHG emissions.

One intriguing yet often overlooked mechanism involves epigenomic modifications to manipulate microbial CH4 formation under micro-aeration conditions. For example, in the case of cows' rumination, micro-aeration-induced co-grinding and enzymatic degradation in the mouth enhance their rumination activities, leading to increased methane production. Preliminary experiments have demonstrated that micro-aeration can significantly boost lignocellulosic decomposition and methane yield. This enhanced methane yield is closely associated with microbial epigenetic modifications, including DNA methylation on N6-adenine and N4-cytosine (6mA and 4mC), which impact gene expression and regulation. Some studies have also reported high methane yield in micro-oxygen marine environments. Investigating this overlooked mechanism through physiological, meta-omics, and quantum simulation studies, and assessing its potential techno-economic impact, aligns with the 2019 revision of the UK Climate Change Act, which commits the UK to achieve Net-Zero emissions by 2050, as well as the UK's National Energy and Climate Plan (NECP) focusing on renewable energy development and GHG reduction.

Aim: The primary aim of this project is threefold:

1. To gain a comprehensive understanding of the microbial structure and epigenomic modifications (i.e., 6mA and 4mC) associated with micro-aeration conditions in methane yield when using cellulosic biomass.

2. To explore the regulation of these microbial processes using quantum information theory via a quantum computing platform.

3. To assess the techno-economic impact of these findings on the waste-to-energy biogas industry and the dairy product industry's ruminant animals.

Objectives (Obj) and Work Packages (WP):

Objective 1 (Obj1): Investigate microbial physiology under micro-aeration conditions.

Work Package 1 (WP1): Operate and study a micro-aerated cellulosic-fed digester.

Objective 2 (Obj2): Understand microbial epigenomics regulation under micro-aeration conditions.

Work Package 2 (WP2): Analyze sludge samples using hybrid long- and short-read 16S rRNA gene, meta-genomics, and -transcriptomics techniques, along with quantum simulation.

Objective 3 (Obj3): Evaluate the techno-economic impact on micro-aeration AD.

Work Package 3: Perform life cycle assessment

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