

Characteristics and mechanisms of mass transfer differentiation during high solids anaerobic digestion of food waste

Lili Li^{1*}, Kun Wang¹, Qingwei Gao¹, Qingliang Zhao^{1*}

¹State Key Laboratory of Urban Water Resource and Environment, School of Environment, Harbin Institute of Technology, Harbin 150090, China

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Presenting author email: lill199504@163.com

Exponential population growth, economic development, and rapid urbanization are the key contributors to a considerable rise in food waste (FW) generation (Zamri et al., 2021). Converting waste to energy is a well-known method of valuable bioenergy, and an effective method of waste management in practice (Fang et al., 2020). Anaerobic digestion (AD), as a vital technology of circular bio-economy, has received substantial attention due to its ability to simultaneously reduce energy consumption and increase energy recovery (Angelidaki et al., 2018). High-solids anaerobic co-digestion (HS-AD) of FW is a promising alternative to conventional AD as it can further improve the economics by reducing the overall size of the digestion system, transportation costs and energy consumption for heating (Cheng et al., 2020). However, HS-AD of FW is always accompanied by difficult mass transfer due to its complex rheological properties (i.e., viscosity), the water content and water distribution (Abbassi-Guendouz et al., 2012; Garcia-Bernet et al., 2011). Factors such as differences in the substrate nature and limitations of the reactor construction can lead to the dead zones within the HS-AD system, resulting in mass transfer differentiation. The mass transfer (diffusion and convection) characteristics of the HS-AD system under complex rheological properties and the microbial metabolic mechanisms under the differences in mass transfer still remain unclear. Therefore, mass diffusion characteristics and mass transfer differences of digestate were analyzed, and microbial metabolism mechanisms were elucidated in the dominant regions of different mass transfer types in the HS-AD system.

Here, semi-continuous anaerobic digestion experiments were carried out in a vertical anaerobic digestion reactor with temperature control ($37\pm 1^\circ\text{C}$) in an outer water bath jacket (Fig. 1). The reactor was operated at a steady OLR of $5 \text{ kgVS}\cdot\text{m}^{-3}\cdot\text{d}^{-1}$ with a HRT of about 45 d for a total of 3 HRTs. Daily biogas production and methane content were recorded during the experimental run, and the efficacy of the HS-AD system was evaluated by testing pH, ammonia, SCOD, and VFAs every 2-3 d. A computational fluid dynamics (CFD) model was applied to analyze the hydrodynamics of different anaerobic digesters, and to determine the distribution of dead and mixing zones. Microbial community characterization of digestate in different regions using high-throughput sequencing.



Fig.1 Diagram of (a) digester; (b) meshing of the physical model

Experimental results showed that the percentage of dead zones in the reactor with velocities below $0.001 \text{ m}\cdot\text{s}^{-1}$ in the steady state phase of operation was 4.5%, mainly at the bottom of the reactor cone (Fig. 2a). Velocity distribution is the most commonly used metric to describe whether mixing is homogeneous or not, but it is not a good metric by itself to describe whether mixing is homogeneous or not because it ignores the effect of diffusive mass transfer. Dimensionless Peclet (Pe) numbers help to explicitly quantify convection-diffusion mass transfer. The Pe number distribution is similar to the velocity distribution, i.e., the dead zone is dominated by diffusive mass transfer, while the mixing region is dominated by convective mass transfer (Fig. 2b).

There were differences in the microbial community structure between the mixing zone and the dead zone. Bacteroidetes and Firmicutes were the dominant bacterial phyla in the mixing area, while the dominant bacterial phylum in the dead zone was Chloroflexi (Fig. 3a). The dominant archaeal genus in the mixing area was *Methanosarcina* with a relative abundance of 45.19%, while *Methanothrix* was the dominant archaeal genus in the dead zone with an average relative abundance of 28.51% (Fig. 3a). Both the mixing zone and the dead zone increased methane production from the acetic acid pathway, but agitated mixing induced different dominant acetic acid-producing strains (Fig. 3c, 3d), and *Methanosarcina* and *Methanothrix* served as potential microbial markers for identifying the dead zone.

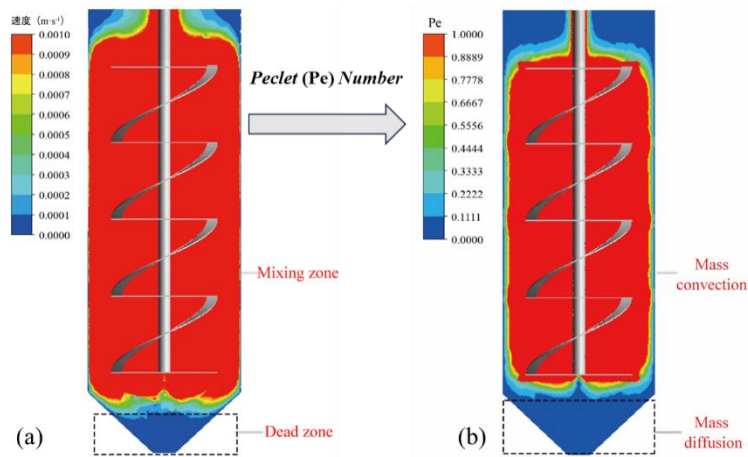


Fig.2 Regional velocity field distribution (a) and Pe number distribution (b) of the HS-AD system

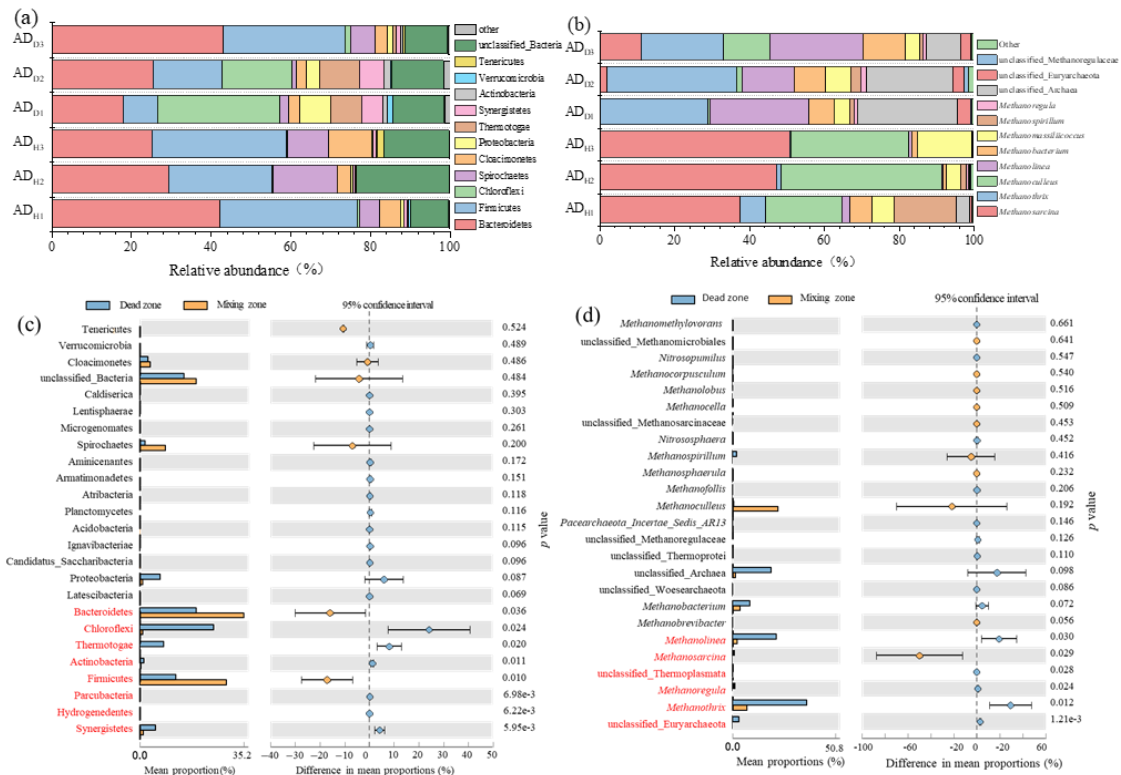


Fig.3 Changes in relative abundance at the level of major bacterial phyla (a) at the level of major archaeal genera (b); analysis of variability at the level of bacterial community phyla (c) and major archaeal genera (d) under different regions of the HS-AD system

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