



Syntrophic bacteria- and *Methanosarcina*-rich acclimatized microbiota with better carbohydrate metabolism enhances biomethanation of fractionated lignocellulosic biocomponents

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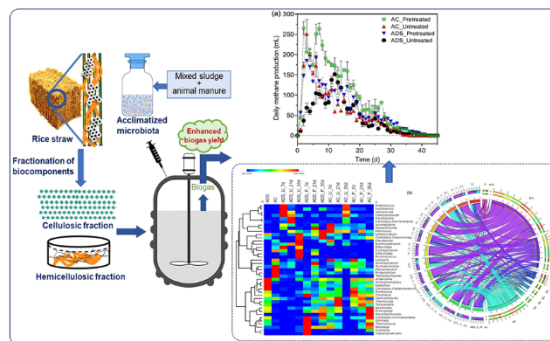
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HIGHLIGHTS

- Methane productivity of acclimatized (AC) and conventional sludge was compared.
- Fractionated lignocellulosic component enhanced (33.3%) biogas production by AC.
- Syntrophy between the syntrophic bacteria and *Methanosarcina* boosted methane yield.
- A high abundance of *Methanosarcina* points to acetoclastic methanogenesis.
- Carbohydrate, fatty acids, and methane metabolism were upregulated in AC digesters.

GRAPHICAL ABSTRACT



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ABSTRACT

An inadequate lignocellulosolytic capacity of a conventional anaerobic digester sludge (ADS) microbiota is the bottleneck for the maximal utilization of lignocellulose in anaerobic digestion. A well-constructed microbial consortium acclimatized to lignocellulose outperformed the ADS in terms of biogas productivity when fractionated biocomponents of rice straw were used to achieve a high methane bioconversion rate. A 33.3 % higher methane yield was obtained with the acclimatized consortium (AC) compared to that of ADS control. The dominant pair-wise link between Firmicutes (18.99–40.03 %), Bacteroidota (10.94–28.75 %), and archaeal Halobacteriota (3.59–20.57 %) phyla in the AC seed digesters indicated that the keystone members of these phyla were responsible for higher methane yield. A high abundance of syntrophic bacteria such as *Proteiniphilum* (1.22–5.19 %), *Fermentimonas* (0.71–5.31 %), *Syntrophomonas* (0.87–3.59 %), and their syntrophic partner *Methanosarcina* (4.26–18.80 %) maintained the digester stability and facilitated higher substrate-to-methane

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