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Characterization and variation of microbial community structure during the anaerobic treatment of *N*, *N*-dimethylformamide-containing wastewater by UASB with artificially mixed consortium

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## **ACCEPTED MANUSCRIPT**

<sup>1</sup> Characterization and variation of microbial community structure during the anaerobic treatment of N, N-dimethylformamide-containing wastewater by UASB with artificially mixed consortium

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ABSTRACT: A lab-scale UASB was operated successfully to anaerobically treat wastewater containing approximately 2000 mg L<sup>-1</sup> *N*, *N*-dimethylformamide (DMF) by artificially mixing anaerobic granular sludge with DMF-degrading activated sludge. DMF was effectively degraded by the UASB under a low OLR of 1.63 ~ 4.22 g COD L<sup>-1</sup> d<sup>-1</sup>, with over 96% DMF removal efficiency and a high methane production rate. However, the DMF-degrading ability gradually weakened along with increases in the OLR. The analysis of the microbial community structure by high-throughput sequencing revealed a decline in the abundance of the facultatively anaerobic DMF-hydrolyzing bacteria originating from activated sludge with increasing OLR, further deteriorating the methanogenic degradation of DMF. When the OLR was lowered again, the slow growth of those facultative anaerobes recovered, and slight improvements in the removal were noted. Methylotrophic methanogens utilized the intermediate products from the hydrolysis of DMF, which kept increasing in abundance throughout the entire experimental period.

**Keywords:** *N*, *N*-dimethylformamide, artificially mixed consortium, facultative anaerobes, hydrolysis, methylotrophic methanogens

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