Goldschmidt 2021 Abstract
https://doi.org/10.7185/gold2021.6574

Jiasongfangiella alkanivorans gen. nov., sp. nov., a novel bacterium with degradation of alkanes isolated from the sediment of the Mariana Trench

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It was reported that a bundant n-alkanes were observed in sinking particles at 2000, 4000, and 6000 m seawater of the Mariana Trench. However, the active hydrocabonclastic microorganisms in trench sediment are largely unknown. A Gram-staining-negative, facultative anaerobic, long-rod shaped with flagellum bacterium designated strain C2-1, was isolated from the sediment at the depth of 3000 m in the Mariana Trench. Based on GTDB taxonomy, strain C2-1 is considered to represent the uncultured genus "UBA2009", most closely related to the genus *Thalassolituus* and *Oliebacter*. The complete genome of strain C2-1 is 4.39 Mb with 53.1% G+C content and encodes 3,842 genes, including one *n*-alkane hydroxylase *alkB and* several genes involved in carbohydrate utilization. Physiological experiments confirmed under both normal and *in situ* hydrostatic pressure (30 Mpa), strain C2-1 could utilize straight-chain *n*-alkanes (C16-C18) as sole carbon source that was detected from our *in situ* samples, for which the name *Jiasongfangiella alkanivorans* is proposed. Environmentally,18 metagenome-assembled genomes (MAGs) of "*Jiasongfangiella" were* retrieved from public available datasets sampled from seawater and underground water, indicating wide distribution and various ecotypes of this genus. Compared to 16 genomes from 6 most closely related genus, strain C2-1 and most of those MAGs occupy genus-specific nitrate reductase *narGHI*, which might contribute to the adaption of low oxygen environment in deep marine sediments. Taken together, strain C2-1 representing as a novel facultative *n*-alkane degrader provides a good model to investigate organic *carbon* degradation in the deep-sea ecosystems, which may facilitate a deeper understanding of microbial environmental adaptability and better utilization for bioremediation purposes in the future.