Species *Defluviibacillus avedoerensis*^{Ts}

Etymology

[a.ve.doe.ren'sis] **N.L. masc. adj.** *avedoerensis*, of the city Avedoere from which the MAG is retrieved from

Nomenclatural type

NCBI Assembly: GCA_016703665.1 ^{Ts}

Description

Rod shaped bacteria (2.1± 0.4 x 0.6±0.1 µm) abundant in activated sludge globally.
Based on genome-wide gene annotaion it has the potential for full glycolysis, pentose phosphate pathway, citric acid cycle and glyoxylate pathway. It furthermore showed potential for transportation of polar amino acids and branched amino acids.
Presence of *narGHI* genes showed potential to reduce nitrate along with potential for further conversion via *norB* . It also had the potential to reduce nitrite to nitric oxide via nitrite reductase, *nirS.*
Defluviibacillus avedoerensis had predicted all genes of the three pathways (polyP, glycogen and PHA) associated with Pao metabolism.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Defluviibacillus* » *Defluviibacillus avedoerensis*^{Ts}

References

Effective publication: Petersen et al., 2025 [1]

Registry URL

https://seqco.de/i:44098

References

1. Petersen et al. (2025). Diversity and physiology of abundant Rhodoferax species in global wastewater treatment systems. *Systematic and Applied Microbiology*. DOI:10.1016/j.syapm.2024.126574