Species *Sphingomonas phytovorans*

Etymology

[phy.to.vo'rans.] **Gr. neut. n.** *phyton*, plant; **L. pres. part.** *vorans*, devouring, destroying; **N.L. fem. part. adj.** *phytovorans*, plant-devouring

Nomenclatural type

INSDC Nucleotide: CP119314.1 [Ts]

Description

A species established on the basis of MiGA taxonomic novelty analyses, AAI, dDDH, 16S rRNA gene phylogenetic reconstruction and the type material is the genome MAG_3606. Genomic metrics include ANI (80.99), AAI (80.97) and dDDH d4 (22.2). The MAG was reconstructed from lignocellulolytic bacterial consortium and encoded for 95 CAZymes, 29 of them involved in lignocellulose degradation. In addition, putative genes for PET and PUR hydrolisis were found within the MAG.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Sphingomonadales* » *Sphingomonadaceae* » *Sphingomonas* » *Sphingomonas phytovorans*

References

Effective publication: Díaz-García et al., 2024 [1]

Registry URL

https://seqco.de/i:24103

References

1. Díaz-García et al. (2024). Andean soil-derived lignocellulolytic bacterial consortium as a source of novel taxa and putative plastic-active enzymes. *Systematic and Applied Microbiology.* DOI:10.1016/j.syapm.2023.126485