

## Species *Sphingomonas phytovorans*

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### 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](#)<sup>Ts</sup>

### 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 hydrolysis 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