

Species *Pantoea varia*

Etymology

[va'ri.a] L. fem. adj. *varia*, varied, corresponding to the varying sources of isolation for members of this species

Nomenclatural type

[NCBI Assembly: GCF_900115075.1](#) ^{Ts}

Description

This species consists of the genomes of two strains: OV426, isolated during characterization of *Populus* root and rhizosphere microbial communities in Tennessee, USA, and AF015A5, isolated from an indoor dust sample in Oregon, USA (GCF_004798195.1). The two genomes have a pairwise ANI of approximately 97% and thus clearly belong to the same species. The genome of strain OV426 does not contain the enterobactin biosynthesis cluster, while it does contain the *pagI* genes encoding the autoinducer system (Sulja et al. 2022). This strain also contains a Hrp-2a T3SS, but its functionality has not been examined (Moretti et al. 2021). The nomenclatural type for the species is the genome of OV426^{Ts}, available under the NCBI assembly accession number GCF_900115075.1.

Classification

Bacteria » *Pseudomonadota* » *Gammaproteobacteria* » *Enterobacterales* » *Erwiniaceae* » *Pantoea* » *Pantoea varia*

References

Effective publication: Crosby et al., 2023 [1]

Registry URL

<https://seqco.de/i:31357>

References

1. Crosby et al. (2023). Genomic delineation and description of species and within-species lineages in the genus *Pantoea*. *Frontiers in Microbiology*. [DOI:10.3389/fmicb.2023.1254999](https://doi.org/10.3389/fmicb.2023.1254999)