

Species *Pantoea communis*

Etymology

[com.mu'nis] L. fem. adj. *communis*, common or widespread, referring to the broad global distribution of members of this species

Nomenclatural type

[NCBI Assembly: GCF_011752685.1](#)^{TS}

Description

This species consists of seven genome-sequenced strains. The genomes are monophyletic with phylogenomic analyses. This clade shares an ancestor with the genomes of the GTDB species "*Pantoea rwandensis_B*". The minimal pairwise ANI among the seven genomes is as low as 97%. ANI between the seven genomes and the closest relative is approximately 94%, showing that the two clades represent two different, but closely related, species. Isolation sources include insects, like stink bugs (*Plautia stali*, *Sibaria englemani*, *Taurocerus* sp.), and an ant (*Atta laevigata*) fungus garden, as well as plants (*Garcinia morella*) and other environmental sources. Overall, this species shares plants and insects as isolation sources with many other *Pantoea* species, and no adaptation to any specific environment is evident.

Classification

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

References

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

Registry URL

<https://seqco.de/i:31366>

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