Species *Polynucleobacter hoetzingerianus*

Etymology
[hoet.zin.ge.ri.a'nus] **N.L. masc. adj.** *hoetzingerianus*, named after the Austrian scientist Mattias Hoetzinger, who characterized several species of the genus Polynucleobacter

Nomenclatural type
NCBI Assembly: GCA_965234555.1 [Ts]

Reference Strain
Strain sc|0038960: RE-M21

Description
Type strain is *Polynucleobacter hoetzingeranus* RE-M21 (GCA_965234555.1), isolated from 0.5 m depth from the Římov Reservoir, Czechia (date: 2019-08-05), *via* high-throughput dilution to extinction cultivation. RE-M21 has a genome size of 1.8 Mbp with a genomic GC content of 46.6%, contains 3 rRNA genes and 40 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). No genes for flagellar assembly and chemotaxis were annotated. Pathways for cyanate degradation, thiosulfate oxidation (Sox pathway), glycolate oxidation and the biosynthesis of all amino acids except for aspartate were predicted. Further, pathways for thiamine, riboflavin, NAD, pantothenate, coenzyme A, biotin, THF, ubiquinone, and heme biosynthesis were identified. The closest cultivated relative is *Polynucleobacter sp.* MWH-UH24A (GCF_018687475.1), with an average amino acid identity of 82.7% and average nucleotide identity of 74.9%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Polynucleobacter; s__Polynucleobacter sp027486235.

Classification
Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Polynucleobacter* » *Polynucleobacter hoetzingerianus*

References
Effective publication: Salcher et al., 2025 [1]

Registry URL
https://seqco.de/i:48717

References

1. Salcher et al. (2025). Bringing the uncultivated microbial majority of freshwater ecosystems into culture. *Nature Communications*. DOI:10.1038/s41467-025-63266-9