

Neomicrothrix subdominans sp. nov.

Submitted by Nielsen, Per Halkjær

Species *Neomicrothrix subdominans*

Etymology

[sub.do'mi.nans.] **L. prep.** *sub*, below; **L. pres. part.** *dominans*, dominant; **N.L. fem. part. adj.** *subdominans*, indicating the abundance of this organism often below the dominant species *Neomicrothrix parvicella*

Nomenclatural type

[NCBI Assembly: GCA_016719385.1](#) ^{Ts}

Description

Filamentous bacteria commonly found in municipal activated sludge WWTPs. The species was defined based on phylogenomic and 16S rRNA-based phylogenetic analysis. The filaments are $1.0 \pm 0.2 \mu\text{m}$ wide and $98 \pm 19 \mu\text{m}$ long. It is a heterotroph and has a potential to reduce nitrate to nitrite. Based on metabolic potential they could consume long chain fatty acids and can accumulate and store lipids under both aerobic and anaerobic conditions. *In situ* analysis showed that they are able to store poly-P, but not cycle it.

Classification

Bacteria » *Actinomycetota* » *Acidimicrobia* » *Acidimicrobiales* » “*Neomicrotrichaceae*” » *Neomicrothrix* » *Neomicrothrix subdominans*

References

Effective publication: Nierychlo et al., 2021 [1]
Corrigendum: Oren, 2022 [2] (from “*Microthrix subdominans*”)

Registry URL

<https://seqco.de/i:609>

References

1. Nierychlo et al. (2021). Low Global Diversity of *Candidatus Microthrix*, a Troublesome Filamentous Organism in Full-Scale WWTPs. *Frontiers in Microbiology*. [DOI:10.3389/fmicb.2021.690251](#)
2. Oren (2022). *Candidatus List No. 4: Lists of names of prokaryotic *Candidatus* taxa*. *International Journal of Systematic and Evolutionary Microbiology*. [DOI:10.1099/ijsem.0.005545](#)

Register List Certificate of Validation

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List **seqco.de/r:eg6x77q2** submitted by **Nielsen, Per Halkjær** and including 1 new name has been successfully validated.

Date of Priority: 2026-01-29 10:06 UTC
DOI: 10.57973/seqcode.r:eg6x77q2

