

Nitrobacter laanbroekii sp. nov.

Submitted by Nicol, Graeme

Species *Nitrobacter laanbroekii*

Etymology

[laan.broek'i.i] **N.L. gen. n.** *laanbroekii*, Named in honour of the Dutch microbiologist Hendrikus J. Laanbroek

Nomenclatural type

[INSDC Nucleotide: JBAMDA000000000.1](#)^{Ts}

Reference Strain

[Strain sc|0041992](#): NHB1

Description

Acidotolerant, chemolithoautotrophic nitrite-oxidizing bacterium. Cells are rod-shaped and possess typical *Nitrobacter* stacked intracytoplasmic membranes arranged as a polar cap of paired membranes. Oxidizes nitrite (NO₂⁻) stoichiometrically to nitrate (NO₃⁻). Acidotolerant, with growth occurring over a pH range of 3.5–7.5; the pH optimum is substrate-dependent, being pH 6.0 at an initial NO₂⁻ concentration of 500 µM but decreasing to pH 5.0 at lower NO₂⁻ concentrations (20–50 µM), with growth extending down to pH 3.5 at the lowest concentration. Growth occurs with initial NO₂⁻ concentrations up to 5 mM and is inhibited at ~10 mM. Growth occurs between 10°C and 30°C, with optimal growth at 25°C (maximum specific growth rate $\mu_{\max}$ of 1.17 d⁻¹ at 25°C and 0.5 mM NO₂⁻). Exhibits a relatively high affinity for nitrite, with an apparent half-saturation constant [K_m(app)] of 54 µM NO₂⁻ (at 25°C, pH 6), approximately one order of magnitude lower than *Nitrobacter hamburgensis* X14. Capable of forming nitrifying consortia with acidophilic and neutrophilic ammonia oxidizers, supporting their growth under acidic conditions through continuous removal of nitrite. Possesses a cyanase, enabling production of ammonium from cyanate and reciprocal cross-feeding with ammonia oxidizers. Genome comprises a 3.3 Mb chromosome and two plasmids (0.28 and 0.21 Mb), with an overall G+C content of 62.3 mol%. Encodes the nitrite oxidoreductase subunit genes *nxrA* (three copies), *nxB* (two copies), and *nxC*, accessory genes (*nrxX*, *nrxD*, cytochrome c class I), and nitrite/nitrate transporters. Possesses genes for dissimilatory sulphur oxidation (*soxXYZAB*), assimilatory nitrite reductase (*nirBD*), RuBisCO (Calvin cycle CO₂ fixation), PII-like regulatory proteins, four gene clusters encoding molybdopterin-containing carbon monoxide dehydrogenase (Mo-CODH, including *coxL/cutL*), formate dehydrogenase, the TorD chaperone, and molybdopterin cofactor biosynthesis genes. Lacks urea catabolic genes. Shares an average nucleotide identity (ANI) of 92.4% and average amino acid identity (AAI) of 86.5% with its closest validated relative, *N. hamburgensis* X14 (below the 95% ANI species threshold). Distributed widely in soils globally across a broad pH range; not restricted to narrow pH conditions. The reference strain is NHB1, originally isolated from pH 3.8 fertilized heathland soil (Hoorneboeg, Netherlands) under *Calluna vulgaris* and *Deschampsia flexuosa* vegetation. The genome sequence is available under NCBI BioProject accession number PRJNA1074292.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Hyphomicrobiales* » *Nitrobacteraceae* » *Nitrobacter* » *Nitrobacter laanbroekii*

References

Effective publication: Bachtsevani et al., 2026 [1]

Registry URL

<https://seqco.de/i:54967>

References

1. Bachtsevani et al. (2026). Acidotolerant soil nitrite oxidizer “ *Candidatus Nitrobacter laanbroekii*” NHB1 alleviates constraints on growth of acidophilic soil ammonia oxidizers. *ISME Communications*. [DOI:10.1093/ismeco/ycaf244](https://doi.org/10.1093/ismeco/ycaf244)

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:sq_furma** submitted by **Nicol, Graeme** and including 1 new name has been successfully validated.

Date of Priority: 2026-06-28 03:10 UTC

DOI: 10.57973/seqcode.r:sq_furma

