

Nitrobacter laanbroekii sp. nov.

Submitted by Graeme, Nicol

Table 1: Complete list of names proposed in the current register list.

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Nitrobacter laanbroekii</i>	[laan.broek'i.i] N.L. gen. n. <i>laanbroekii</i> , Named in honour of the Dutch microbiologist Hendrikus J. Laanbroek	Acidotolerant, chemolithoautotrophic nitrite-oxidizing bacterium. Cells are rod-shaped and possess typical <i>Nitrobacter</i> stacked intracytoplasmic membranes arranged as a polar cap of paired membranes. Oxidizes nitrite (NO ₂ ⁻) stoichiometrically to nitrate (NO ₃ ⁻). 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 NO ₂ ⁻ concentration of 500 µM but decreasing to pH 5.0 at lower NO ₂ ⁻ concentrations (20–50 µM), with growth extending down to pH 3.5 at the lowest concentration. Growth occurs with initial NO ₂ ⁻ 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 µ _{max} of 1.17 d ⁻¹ at 25°C and 0.5 mM NO ₂ ⁻). Exhibits a relatively high affinity for nitrite, with an apparent half-saturation constant [Km(app)] of 54 µM NO ₂ ⁻ (at 25°C, pH 6), approximately one order of magnitude lower than <i>Nitrobacter hamburgensis</i> 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 <i>nxrA</i> (three copies), <i>nxrB</i> (two copies), and <i>nxC</i> , accessory genes (<i>nxrX</i> , <i>nxD</i> , cytochrome c class I), and nitrite/nitrate transporters. Possesses genes for dissimilatory sulphur oxidation (<i>soxXYZAB</i>), assimilatory nitrite reductase (<i>nirBD</i>), RuBisCO (Calvin cycle CO ₂ fixation), PII-like regulatory proteins, four gene clusters encoding molybdopterin-containing carbon monoxide dehydrogenase (Mo-CODH, including <i>coxL/cutL</i>), 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, <i>N. hamburgensis</i> 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	<i>Nitrobacter</i>	INSDC Nucleotide: JBAMDA000000000.1 Ts	seqco.de/i:54967

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		NHB1, originally isolated from pH 3.8 fertilized heathland soil (Hoorneboeg, Netherlands) <i>Deschampsia vulgaris</i> and <i>Deschampsia flexuosa</i> vegetation. The genome sequence is available under NCBI BioProject accession number PRJNA1074292.			