Actinotalea subterranea sp. nov.

Submitted by Grouzdev, Denis

Species *Actinotalea subterranea*

Etymology

[sub.ter.ra.ne'a] **L. fem. adj.** *subterranea*, subterranean, referring to the site of isolation

Nomenclatural type

NCBI Assembly: GCA_008364845.1 ^{Ts}

Reference Strain

Strain scl0039752: HO-Ch2 (= VKM Ac-2850 = KCTC 49656)

Description

Description is based on two strains. Cells are Gram-stain-positive rods, motile at the early stage of incubation. Colonies formed after 5 days incubation on R2A medium at 28 °C are yellow, smooth, circular, convex, and non-transparent, with entire edges. Grows on PCA, nutrient agar, R2A, and LB media. Growth of the type strain occurs in the presence of 0–4% (*w*/*v*) NaCl (optimum, 1–2% NaCl), at pH 6.0–8.8 (optimum, pH 8.0–8.3) and at 10–40 °C (optimum, 28 °C). Growth of the reference strain occurs at 15–40 °C, 0–6% (*w*/*v*) NaCl and pH 6.2–8.5 with optimal conditions at 22–28 °C, 2–4% (*w*/*v*) NaCl and pH 6.6–7.5. Catalase-positive and oxidase-negative. Cells are positive for the following enzyme activities: esterase (C4), N-acetyl-β-glucosaminidase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, β-glucuronidase, naphthol-AS-BI-phosphohydrolase, leucine arylamidase, esterase lipase (C8), lipase (C14), valine arylamidase, acid phosphatase, and cystine arylamidase, but negative for trypsin, α-chymotrypsin, alkaline phosphatase, α-mannosidase, urease, and α-fucosidase. Does not produce indole or H2S, but NH3 is produced from peptone. Negative for the methyl red test and Voges–Proskauer reaction. Reduces nitrate to nitrite in a medium with acetate, but does not reduce nitrate to N2. Chemoorganoheterotrophic, facultatively anaerobic. In aerobic conditions utilizes peptone, yeast extract, acetate, and pyruvate; acid is produced from aesculin (Fe citrate), L-arabinose, arbutin, D-cellobiose, D-fructose, D-galactose, D-glucose, glycogen, D-mannose, salicin, D-sucrose, D-xylose, D-maltose, D-mannitol, starch, D-trehalose, D-turanose, and N-acetylglucosamine, but not from D-adonitol, amygdalin, D-arabinose, D-arabite, L-arabite, dulcitol, erythritol, D-fucose, L-fucose, inositol, inulin, D-lactose, D-lyxose, methyl-βD-xylopyranoside, methyl-αD-mannopyranoside, methyl-αD-glucopyranoside, D-melibiose, D-melicitose, gluconate K, 2-ketogluconate K, 5-ketogluconate K, D-ribose, L-rhamnose, D-sorbitol, L-sorbose, D-tagatose, xylitol, and L-xylose. In API 20E tests, positive for fermentation/oxidation of glucose, sucrose, and arabinose; and negative for arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, L-tryptophan deaminase, gelatinase, citrate utilization, indole production, and fermentation/oxidation of inositol, sorbitol, and rhamnose. Acetic, propionic, iso-butyric, and iso-valeric acids and CO2 are the major products of anaerobic glucose fermentation. Hydrogen is not produced. Sensitive to ampicillin (10 μg), chloramphenicol (30 μg), penicillin (10 μg), ciprofloxacin (5 μg), and erythromycin (15 μg), but resistant to gentamicin (10 μg) and kanamycin (30 μg). The peptidoglycan type is A4β, containing L-Orn (Lys)-D-Ser-D-Glu. The major cell-wall sugar is rhamnose; galactose, mannose, and glucose are also present. Major fatty acids (>5%) are *anteiso*-C15:0, C14:0, C16:0, and C15:0. The major menaquinone is MK-9(H4). The major polar lipids are diphosphatidylglycerol, unidentified glycolipids, and phosphoglycolipids.
The type strain is HO-Ch2T, isolated from the methanogenic enrichment obtained from a petroleum reservoir (Nurlat, Russia). The DNA G + C content of the genome of the type strain HO-Ch2T is 73.4% and the genome size is 4.0 Mb. The EMBL/GenBank accession numbers for the 16S rRNA gene sequence and genome sequence of strain HO-Ch2T are MT225794 and GCA_008364845.1, respectively.

Classification

Bacteria » *Actinomycetota* » *Actinomycetes* » *Micrococcales* » *Cellulomonadaceae* » *Actinotalea* » *Actinotalea subterranea*

References

Effective publication: Semenova et al., 2022 [2]

Registry URL

https://seqco.de/i:39440

References

1. Semenova et al. (2022). Correction: Semenova et al. Physiological and Genomic Characterization of Actinotalea subterranea sp. nov. from Oil-Degrading Methanogenic Enrichment and Reclassification of the Family Actinotaleaceae. Microorganisms 2022, 10, 378. *Microorganisms*. DOI:10.3390/microorganisms10050862
2. Semenova et al. (2022). Physiological and Genomic Characterization of Actinotalea subterranea sp. nov. from Oil-Degrading Methanogenic Enrichment and Reclassification of the Family Actinotaleaceae. *Microorganisms*. DOI:10.3390/microorganisms10020378

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:bk0hdqw0** submitted by **Grouzdev, Denis** and including 1 new name has been successfully validated.

Date of Priority: 2025-06-15 12:11 UTC
DOI: 10.57973/seqcode.r:bk0hdqw0