Chelativorans multitrophicus gen. nov., sp. nov. and Chelativorans oligotrophicus sp. nov., aerobic EDTA-degrading bacteria

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Two previously isolated strains (DSM 9103T and LPM-4T) able to grow with EDTA (facultatively and obligately, respectively) as the source of carbon, nitrogen and energy were investigated in order to clarify their taxonomic positions. The strains were strictly aerobic, Gram-negative, asporogenous and non-motile rods that required biotin for growth. Reproduction occurred by binary fission. The strains were mesophilic and neutrophilic. Their major fatty acids were summed feature 7 (consisting of C₁₈:₁ω₇c, C₁₈:₁ω₉t and/or C₁₈:₁ω₁₂t) and C₁₉:₀ cyclo ω₈c. The polyamine pattern revealed homospermidine as a major polyamine. Predominant polar lipids were phosphatidylcholine, phosphatidylglycerol, phosphatidylethanolamine, phosphatidyl(dimethylethanolamine, phosphatidylmonomethylethanolamine and diphasosphatidylglycerol. Mesorhizobium–specific ornithine lipid was absent. The predominant isoprenoid quinone was Q₁₀. The DNA G+C values were 60.8 and 63.1 mol% (Tₘ) for strains LPM-4T and DSM 9103T, respectively. The level of 16S rRNA gene sequence similarity between these EDTA-utilizers was 99.3 % while the DNA–DNA hybridization value was only 37 %. Both strains were phylogenetically related to members of the genera Aminobacter and Mesorhizobium (95–97 % sequence similarity). However, DNA–DNA hybridization values between the novel EDTA-degrading strains and Aminobacter aminovorans DSM 7048T and Mesorhizobium loti DSM 2626T were low (10–11 %). Based on their genomic and phenotypic properties, the new alphaproteobacterial strains are assigned to a novel genus, Chelativorans gen. nov., with the names Chelativorans multitrophicus sp. nov. (type strain DSM 9103T=VKM B-2394T) and Chelativorans oligotrophicus sp. nov. (type strain LPM-4T=VKM B-2395T=DSM 19276T).

EDTA is a chelating agent from the group of aminopoly-carboxylic acids that are able to form stable, water-soluble complexes with many metal ions. At present, the amount of EDTA utilized worldwide amounts to some 103 000 tonnes per year. It is used in many diverse fields including the photographic and galvanic industries, in textile and paper manufacturing, for decontamination of nuclear power installations, as a component of industrial cleaners, as an additive in cosmetics and food products, in gas scrubbing for the removal of hydrogen sulfide from waste gases and in agricultural applications to improve the uptake of micronutrients to correct trace metal deficiencies in plants (Potthoff-Karl et al., 1996; Weilenmann et al., 2004). The predominantly water-based use of EDTA and the recalcitrance of EDTA to biodegradation have resulted in high concentrations of this agent in surface waters. The extensive environmental EDTA pollution that has been observed in

Abbreviations: APL, aminophospholipid; DPG, diphosphatidylglycerol; PC, phosphatidylcholine; PDE, phosphatidyl(dimethylethanolamine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PHB, poly-β-hydroxybutyrate; PL, phospholipids; PME, phosphatidylinositol; ethanolamine.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains DSM 9103T and LPM-4T are EF457243 and EF457242, respectively.

The TLC for the polar lipid analysis and four additional phylogenetic trees are available with the online version of this paper. A comparison of the major fatty acid contents of the novel strains and those of related genera is presented as a supplementary table.
recent years has become a cause for concern, in particular because of its possible contribution to the mobilization of heavy and toxic metal ions deposited in sediments and soils and also due to the contamination of drinking water (Sillanpää, 1997; Bucheli-Witschel & Egli, 2001). In order to develop appropriate biotechnological processes to deal with EDTA pollution, the isolation and detailed characterization of micro-organisms able to mineralize EDTA is required.

So far, only a few EDTA-degrading alphaproteobacterial strains have been isolated as pure cultures, i.e. *Agrobacterium radiobacter* sp. ATCC 55002 (Lauff et al., 1990; Palumbo et al., 1994), subsequently reclassified as *Rhizobium radiobacter* (Young et al., 2001), and the Gram-negative strains BNC1 (=DSM 6780; Nörtemann, 1992), DSM 9103T (Weilenmann et al., 2004), LPM-4T (Chistyakova et al., 2005) and ANP11 (Nörtemann, 2005). The four latter strains have several features in common, for example growth with EDTA and no growth with iron-complexed EDTA. The present study focused on the taxonomic description and identification of strains DSM 9103T and LPM-4T.

Strains DSM 9103T and LPM-4T were grown on a mineral medium, 'E', containing (l−1): 1.0 g Na4EDTA; 1.0 g MgSO4.7H2O; 0.26 g KH2PO4; 0.4 g CaCl2·2H2O and 4 g NaHPO4·12H2O at pH 7.0. Medium E was supplemented with 2 ml Widdel’s trace element solution (Pfennig et al., 1981) and 1 ml vitamin solution (Egli et al., 1988) per litre.

Physiological tests were performed according to Gerhardt et al. (1994). Utilization of a wide range of growth substrates was determined after the strains had been cultivated on mineral medium E for 2 weeks with EDTA replaced by 1% (NH4)2SO4 and various carbon compounds (more than 60 were tested). The ability of the strains to undergo autotrophic growth on H2 + CO2 + O2 or under CH4 + O2 was tested as previously described by Doronina et al. (2000). Carbohydrates, organic acids and amino acids were added at concentrations of 0.05–0.3% (w/v), while alcohols were added at concentrations of 0.2–0.5% (v/v). The novel bacterial strains were stored in liquid mineral medium E for 1 month, on agar slants at 4°C for 2 weeks or in a freeze-dried state with a protectant (skimmed milk) for over a year.

Cell morphology was examined using batch cultures grown for 24 h on medium E for both strains and on medium supplemented with fumarate and ammonium chloride (0.5 g l−1) for strain DSM 9103T. An aliquot of cell suspension was mounted on a Formvar-coated copper grid and stained with 0.2% (w/v) phosphotungstic acid (pH 7.2). For thin sectioning, cells were collected by centrifugation and pre-fixed with 1.5% (v/v) glutaraldehyde in 0.05 M cacodylate buffer (pH 7.2) and washed three times with 1% (w/v) OsO4 in 0.05 M cacodylate buffer (pH 7.2) for 3 h at 20°C. After dehydration in a series of alcohols, cells were embedded in Spurr epoxy resin and sectioned with a microtome (2128 Ultratome; LKB). Ultrathin sections were mounted on copper grids and double-stained with uranyl acetate and lead citrate (Fig. 1). Negatively stained preparations and thin sections were viewed with a transmission electron microscope (JEM-100B; JEOL) at operating voltages of 60 kV and 80 kV, respectively. Cells of the novel isolates were Gram-negative, non-motile, asporogenous rods that were 0.5–1.0 × 0.7–2.0 μm in size. Cells of both strains multiplied by binary fission. When grown on medium E agar, colonies of both strains were white and 0.1–0.3 mm in diameter after 7 days incubation at 30°C. The metabolic features of the EDTA-degrading strains have been described previously (Witschel et al., 1997; Doronina et al., 2006).

Sensitivity to antibiotics was examined by placing Difco discs on cells spread on agar plates. The discs contained the following antibiotics (μg): gentamicin (10), neomycin (30), streptomycin (10), ampicillin (10), nalidixic acid (30), lincomycin (2), oxacillin (10), neomycin (30) and novobiocin (5). The effect of antibiotics on cell growth was assessed after 2 weeks.

The poly-β-hydroxybutyrate (PHB) content in the cell biomass was determined by reverse-phase HPLC (Korotkova et al., 1997).

Fatty acids were extracted from cells in the exponential growth phase [medium containing 1 g l−1 EDTA and trypticase soy broth supplemented with 1.5% (w/v) agar]. A 200 μl aliquot of a 5.4 M solution of anhydrous HCl in methanol was added to 30 mg dry biomass and the mixture was heated at 70°C for 2 h. The methyl esters of fatty acids and aldehyde derivatives were measured by GC.

**Fig. 1.** Electron micrographs of ultrathin sections of EDTA-grown cells of strain LPM-4T (a) and strain DSM 9103T (b) showing electron-dense polyphosphate inclusions. Bars, 0.5 μm.
obtained were extracted twice with 100 μl hexane. The extract was dried and silylated in 20 μl N,O-bis(trimethylsilyl)trifluoroacetamide for 15 min at 65°C. A 1 μl sample of the reaction mixture was analysed with a GC-MS system (model HP-5985B; Hewlett Packard) equipped with a capillary column (25 × 0.25 mm) consisting of fused quartz containing an Ultra-1 non-polar methylsilicone phase. The temperature program was run from 150°C (2 min isotherm) to 250°C at 5°C min⁻¹ and then from 250 to 300°C at 10°C min⁻¹. Data processing was carried out with a computer (HP-1000; Hewlett Packard) by using the standard programs of the GC-MS system (Hewlett Packard) as described by Doronina et al. (2003). The fatty acid profile of strain DSM 9103ᵀ was composed of summed feature 7 (C₁₈:₁₋₇, C₁₈:₁₋₉t and/or C₁₈:₁₋₁₂B, 67.63%) and C₁₉:₀ cyclo ω8c (23.05%). Strain LPM-₄ᵀ had rather similar profile containing summed feature 7 (67.31%) and C₁₉:₀ cyclo ω8c (20.72%) (see Supplementary Table S1 in IJSEM Online). Species of the genera Aminobacter, Pseudaminobacter and Mesorhizobium also contain summed feature 7, summed feature 4 (C₁₆:₁₋₇c and/or C₁₅:₀ iso 2-OH) and C₁₆:₀ iso and C₁₆:₀ fatty acids. The hydroxy fatty acid C₁₂:₀ 3-OH is also present in species of the genus Aminobacter. Fatty acids C₁₇:₁₋₀₈c and C₂₀:₁₋₀₉t were not detected in strains DSM 9103ᵀ and LPM-₄ᵀ. The absence of fatty acids C₁₅:₀ iso 3-OH, C₁₇:₁₋₀₈c and C₂₀:₁₋₀₉t distinguished the novel strains from species of the genus Pseudaminobacter. In contrast to the novel strains, species of the genus Mesorhizobium contained high amounts of fatty acids C₁₆:₀ and C₁₈:₀ and low levels of summed feature 7. The absence of 11 methyl C₁₈:₁₋₀₇c and C₁₂:₀ cyclo fatty acids distinguished novel strains DSM 9103ᵀ and LPM-₄ᵀ from the members of the genus Mesorhizobium.

For analysis of the cellular phospholipids, the novel strains were grown in minimal medium E containing 1 g l⁻¹ EDTA in batch culture at 28°C. Cells of strains LPM-₄ᵀ and DSM 9103ᵀ in the exponential growth phase (4 days) were harvested by centrifugation at 5000 g for 20 min. Cellular phospholipids were extracted using chloroform:methanol (1:2, v/v). The suspension was stirred for 1 h in an ice bath and was then centrifuged (5000 g, 20 min) to separate the two phases. The extraction procedure was performed twice and the upper phases were combined. Chloroform (2 ml) and distilled water (2 ml) were added to the supernatant with careful shaking for 15 min in an ice bath. The mixture was then centrifuged and three phases were separated. The lower phase containing the polar lipids was evaporated at 30°C and dissolved in 200 μl chloroform. Polar lipids were separated by two-dimensional TLC (Kieselgel 60, 10 × 10 cm, Merck) using the solvent systems chloroform:methanol:water (65:25:4) for the first dimension, followed by chloroform:methanol:acetic acid:water (85:12:15:4) for the second dimension. Polar lipids were analysed as described by Tindall (1990). Non-specific detection of total lipids on the two-dimensional TLC plates was performed with iodine vapours. To detect lipids carrying free amino groups, the plates were sprayed with 0.2% (w/v) ninhydrin dissolved in acetone followed by heating of the plates at 120°C. To detect phospholipids, two reagents were used: (i) 5 ml 60% w/v perchloric acid, 10 ml 1 M HCl and 25 ml 4% (w/v) ammonium molybdate (Skidmore & Entemann, 1962); (ii) 10% CuSO₄ in 8% H₃PO₄ (Andreev & Galchenko, 1983) as seen in Supplementary Fig. S1 (available at IJSEM Online).

The polar lipids of strains DSM 9103ᵀ and LPM-₄ᵀ were phosphatidylcholine (PC), phosphatidylglycerol (PG), phosphatidylethanolamine (PE), phosphatidyldimethyl-ethanolamine (PDE), phosphatidylmonomethylethanolamine (PME) and diphosphatidylglycerol (DPG) (see Supplementary Fig. S1). This polar lipid profile was similar to those reported for species of the related genera Aminobacter, Pseudaminobacter and Mesorhizobium. The presence of the unknown phospholipids (PL₁–PL₃) and the unidentified aminophospholipid (APL) distinguished strains DSM 9103ᵀ and LPM-₄ᵀ from members of the genera Aminobacter and Pseudaminobacter. Strains DSM 9103ᵀ and LPM-₄ᵀ did not contain the Mesorhizobium-specific ornithine lipid, which was not reported to contain a phosphate group (Choma & Komaniecka, 2002).

Polyamines of strains LPM-₄ᵀ and DSM 9103ᵀ were extracted according to the methods of Tkachenko et al. (2006). The dansylated polyamines were separated by using HPLC (Waters) equipped with two model 510 HPLC pumps, a U6K injector and a reversed-phase column (Hypersil ODS 1961, 250 × 4.6 mm, 5 μm particles) as described by Altenburger et al. (1996). The polyamine patterns for strains DSM 9103ᵀ and LPM-₄ᵀ were similar and consisted of large amounts of triamine sym-homospermidine [30.2 μmol (g dry wt)⁻¹], putrescine [6.5 μmol (g dry wt)⁻¹] and spermidine [5.3 μmol (g dry wt)⁻¹]. The genera Aminobacter and Mesorhizobium are characterized by the presence of sym-homospermidine as the predominant compound, high amounts of putrescine and low amounts of spermidine. The major polyamines of the genus Pseudaminobacter are spermidine [32.2 μmol (g dry wt)⁻¹], sym-homospermidine [18.6 μmol (g dry wt)⁻¹] and putrescine [15.6 μmol (g dry wt)⁻¹] (the level of polyamines given for the type species Pseudaminobacter salicylatoxidans BN12ᵀ; Kämpfer et al., 1999). Strains DSM 9103ᵀ and LPM-₄ᵀ could be distinguished from members of the genus Pseudaminobacter by the minor amounts of putrescine and spermidine.

Ubiquinones were extracted and purified according to Collins (1985). Analysis was performed by MS (MX-1310; Finnigan). The quinone system of strains DSM 9103ᵀ and LPM-₄ᵀ comprised major amounts of Q-10 (98%) and minor amounts of Q-9. This pattern was in agreement with the ubiquinone pattern reported for the type species of the genera Aminobacter (Urakami et al., 1992), Pseudaminobacter (Kämpfer et al., 1999) and Mesorhizobium (Jarvis et al., 1982, 1997).

DNA was isolated and purified according to Marmur (1961). DNA–DNA relatedness was determined as described previously (Doronina et al., 2000). DNA–DNA relatedness between strains DSM 9103ᵀ and LPM-₄ᵀ was 37%. The DNA–DNA relatedness value between strains LPM-₄ᵀ and
BNC1 was 51%, indicating that the strains belong to separate species.

Other EDTA-degrading strains appear to be very closely related or even identical to strain DSM 9103T (Nörtemann, 1999, 2005; Nörtemann et al., 2004). In particular, strain BNC1, described formerly as *Mesorhizobium* sp. BNC1 and for which the genome has already been sequenced by the Joint Genome Institute (see http://cmr.jcvi.org/tigr-scripts/CMR/GenomePage.cgi?org=ntms05), exhibited 100% relatedness in DNA–DNA hybridizations with strain DSM 9103T. This result means that the possibility that these organisms are identical cannot be excluded. A more detailed comparative study of strains DSM 9103T, BNC1 and ANP11 is in progress.

The DNA–DNA relatedness values of strains DSM 9103T and LPM-4T with *Aminobacter aminovorans* DSM 7048T and *Mesorhizobium loti* DSM 2626T were low (10–11%). Hence, the results of the DNA–DNA hybridizations demonstrated that strains DSM 9103T, BNC1 and LPM-4T were clearly separated from representatives of the genera *Aminobacter* and *Mesorhizobium*.

DNA G + C content was determined by using the thermal denaturation (*Tm*) method with a spectrophotometer (DU-8B; Beckman) at a heating rate of 0.5 °C min⁻¹. The calculation was performed according to Owen & Lapage (1976) using the equation: mol G + C = (Tm 2.08) - 106.4. The DNA of *Escherichia coli* K-12 was used as a standard. The DNA G + C contents of strains LPM-4T and DSM 9103T were found to be 60.8 and 63.1 mol% (*Tm*), respectively.

The 16S rRNA genes of the novel strains were amplified and sequenced (Lane, 1991). The 16S rRNA gene sequences were aligned against those of representative taxa of the class *Alphaproteobacteria* (see Supplementary Figs S2–S4), the novel EDTA-degrading bacteria represented a separate branch within the class *Alphaproteobacteria*.

Based on phenotypic and genotypic characteristics, strains DSM 9103T and LPM-4T should be placed in a separate new genus for which the name *Chelativorans* gen. nov. is proposed. Strains DSM 9103T and LPM-4T represent novel species within this genus for which the names *Chelativorans multitrophicus* gen. nov., sp. nov. and *Chelativorans oligotrophicus* sp. nov. are proposed, respectively. The key properties that differentiate the new genus from related genera of the class *Alphaproteobacteria* are listed in Table 1. Members of the genus *Chelativorans* gen. nov. can be distinguished from the genus *Aminobacter* by their inability to grow on methyalted amines due to the absence of the appropriate C₅ enzymes, by the phospholipid and fatty acid profiles, by reproduction by binary fission, by the requirement for biotin and by the absence of PHB granules.

Members of the genus *Chelativorans* gen. nov. can be distinguished from those of the genus *Mesorhizobium* by physiological differences, by some differences in the cellular fatty acids, by the absence of PHB granules and the presence of aminophospholipid (APL) in the polar lipid profile. Members of the genus *Mesorhizobium* are able to invade the root hairs of a wide range of plants and instigate the production of root nodules where atmospheric nitrogen can be reduced. However, a PCR amplification test using primers specific for the *nifH* gene (Fedorov et al. 2008) was negative in the novel strains, suggesting that they were not diazotrophs. In addition, representatives of the genera *Mesorhizobium* and *Aminobacter* are commonly pleomorphic and motile. Due to poor phenotypic descriptions for the genera *Aquamicrobium* and *Defluvibacter*, it is difficult to compare them with members of the genus *Chelativorans* gen. nov. However, these taxa are clearly distant phylogenetically (94.6–95.2% gene sequence similarity). Organisms that share 16S rRNA gene sequence similarities of lower than 95% are usually regarded as belonging to separate bacterial genera (Stackebrandt & Goebel, 1994). Formal descriptions of the new genus and the two novel species are given below.

**Description of Chelativorans gen. nov.**

*Chelativorans* (Che.la’ti.vor.ans. N.L. n. chelatum a chelate; L. part. adj. vorans devouring; N.L. masc. n. Chelativorans a bacterium digesting metal chelates).

According to 16S rRNA gene sequence analysis, strains DSM 9103T and LPM-4T showed 99.3% similarity. They were closely related to members of the genera *Aminobacter* (94.8–95.9%), *Mesorhizobium* (94.2–96.9%) and *Pseudaminobacter* (95.0–95.7%) (Fig. 2 and Supplementary Fig. S2). The genera *Aminobacter* and *Mesorhizobium* had the highest sequence similarity (94.6–98.2%) followed by *Aminobacter* and *Pseudaminobacter* (96.4–97.0%) and *Mesorhizobium* and *Pseudaminobacter* (93.1–97.2%). The 16S rRNA gene sequence of strain DSM 9103T was most similar (99.9% similarity) to that of strain BNC1 (Fig. 2 and Supplementary Fig. S2). Both of these strains could be included as members of the same species as suggested previously on the basis of the morphological, cytophysiological and biochemical data for strain BNC1 (Nörtemann, 1992; Bohuslavek et al., 2001). In the phylogenetic trees (see Fig. 2 and Supplementary Figs S2–S4), the novel EDTA-degrading bacteria represented a separate branch within the class *Alphaproteobacteria*.
Gram-negative, asporogenous, non-pleomorphic, rod-shaped and often found as pairs of cells. Non-motile. Multiply by binary fission. Form small white colonies (0.1–0.3 mm in diameter) on EDTA/mineral salt agar incubated for 7 days at 30°C. Electron-dense inclusions found in EDTA-grown cells are thought to represent intracellular precipitates consisting of calcium and magnesium phosphates which are absent in fumarate-grown cells. PHB granules are absent. Oxidase- and catalase-positive. Do not reduce nitrate to nitrite. Do not fix atmospheric nitrogen. Mesophilic and neutrophilic; optimal pH and temperature for growth are 6.5–7.5 and 25–35°C, respectively. Strictly aerobic with respiratory metabolism. Facultative or obligate utilizers of EDTA as the carbon, nitrogen and energy source. Do not utilize methanol and methylated amines as the carbon, nitrogen and energy source. Incapable of autotrophic or methylotrophic growth. Biotin is required as a growth factor. Oxidize EDTA by monooxygenase consuming flavin mononucleotide (FMN) H2 delivered by a NADH2:FMN oxidoreductase. The major cellular fatty acids are summed feature 7 (consisting of C18:1ω7c, C18:1ω9t and/or C18:1ω12t) and C19:0 cyclo ω8c. Hydroxy fatty acids such as C12:0 3-OH, C13:0 3-OH and C15:0 iso 3-OH are absent. The major ubiquinone is Q-10. Predominant polar lipids are PC, PG, PE, PDE, PME and DP. Mesorhizobium-specific ornithine lipid is absent. The major polyamine is sym-homospermidine and small amounts of spermidine and putrescine are detected. The DNA G+C content is 60–64 mol% (Tm). The genus is a member of the class Alphaproteobacteria. The type species is Mesorhizobium loti.

**Description of Chelativorans multitrophicus** sp. nov.

Chelativorans multitrophicus (mu.1tiтроphi.cs. L. adj. multitus many; Gr. adj. trophikos nursing, tending; N.L. masc. adj. multitrophicus utilizing many growth substrates).
Table 1. Main characteristics that differentiate the genera Chelativorans, Aminobacter, Mesorhizobium, Pseudaminobacter, Aquamicrobium and Defluvibacter

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*Data from this study.
+ Data from Hamana et al., 1990.
ND Data are for Pseudaminobacter salicylatoxidans BN12ᵀ (Kämpfer et al., 1999).

Exhibits the following properties in addition to those given in the genus description. Facultative EDTA-utilizing rods of 0.5–1.0 × 0.7–2.0 μm. Grows on glucose, lactate, glutamate, fumarate, succinate, acetate, nitrolotriacetate, iminodiacetate, N,N′-ethylenediaminediacetate, and ethylenediaminedisuccinate as the sole carbon and energy sources. No growth on diethylenetriaminepentaacetate or hydroxyethyleneaminetriacetate. The generation time with EDTA as the source of carbon, nitrogen and energy at pH 7.0 and 30 °C is 14 h. Good, but slow growth on complex media at low concentrations of organic compounds, such as Plate Count Broth at one third of the normal strength. No growth in the presence of 3% (w/v) NaCl. Able to degrade uncomplexed EDTA and Ca²⁺, Ba²⁺, Mg²⁺, Mn²⁺, Pb²⁺, Cu²⁺ or Zn²⁺-EDTA complexes, but not Fe³⁺-EDTA complex. Resistant to oxacillin, ampicillin and lincomycin, but sensitive to gentamicin, streptomycin, novobiocin, nalidixic acid and neomycin. Shows α-ketoglutarate dehydrogenase activity.

The type strain, DSM 9103ᵀ (=VKM B-2394ᵀ), was isolated from a mixture of soil extracts and activated sludge samples taken from various industrial wastewater treatment plants (Switzerland). The DNA G+C content of the type strain is 63.1 mol% (Tₘ).

Description of Chelativorans oligotrophicus sp. nov.
Chelativorans oligotrophicus (o.li.go.tro’phicus. Gr. adj. oligos little; Gr. adj. trophikos nursing, tending; N.L. masc. adj. oligotrophicus utilizing only a few growth substrates).

Exhibits the following properties in addition to those given in the genus description. Obligate EDTA-utilizing rods of 0.5–1.0 × 0.7–2.0 μm. The generation time of the strain grown with EDTA as the source of carbon, nitrogen and energy at pH 7.0 and 32–34 °C is 7 h. Able to degrade uncomplexed EDTA and Mn³⁺, Ca²⁺, Mg²⁺ and Ba²⁺-EDTA and slowly degrade Zn²⁺-EDTA, but not Pb²⁺, Cu²⁺ or Fe³⁺-EDTA. Does not grow on peptone/yeast extract medium, nutrient broth, nutrient agar or in medium containing carbohydrates (D-glucose, D-fructose) or amino acids, or ethanol or methanol or organic acids (acetate, fumarate, succinate and citrate). Resistant to oxacillin, ampicillin, novobiocin, lincomycin, nalidixic acid and neomycin, but sensitive to gentamicin and streptomycin. Has multiple enzymic lesions in the central carbon metabolism. The tricarboxylic acid cycle is deficient in α-ketoglutarate dehydrogenase activity. The activities of 6-phosphofructokinase (ATP/PPI) are also absent.
The type strain, LPM-4T (=VKM B-2395T =DSM 19276T), was isolated from municipal sewage sludge samples taken near Pushchino, Moscow region, Russia. The DNA G+C content of the type strain is 60.8 mol% (Tm).

Acknowledgements

The authors wish to thank Drs T. I. Chistyakova, N. E. Suzina, I. G. Minkevich, E. Lang, C. Spröer and Ms W. Palme for their help. Special thanks are due to Professor P. Kämpfer, Dr J. Euzéby and anonymous reviewers for their valuable comments and advice. This work was supported by grants RFBR 06-04-49580a and Ministry of Education and Science RF RNP 2.1.1. 605.

References


