Algoriphagus aquaeductus sp. nov., isolated from a freshwater pipe

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A Gram-staining-negative, aerobic to microaerophilic, rod-shaped, red-coloured bacterium, strain T4^T, was isolated from a freshwater pipe on Tenerife island. A polyphasic taxonomic study was performed in order to characterize the strain in detail. The isolate is surrounded by a slime capsule, occurs singly, in the form of short chains, or in aggregates, and exhibits catalase and oxidase activities. Growth was observed at 15–42 °C. Optimum growth occurred at pH 8 with mono- and disaccharides, followed by polysaccharides and deoxysaccharides, but the bacterium utilized only a restricted spectrum of alcohols, alditols, amides, amines, carboxylic acids and amino acids. Strain T4^T tolerated concentrations of 0–4 % (w/v) NaCl and contained MK-7 as predominant isoprenoid quinone as well as carotenoids, but lacked pigments of the flexirubin type. The predominant fatty acids were iso-C_{15:0} (32.2 %), summed feature 3 (C_{16:1ω6c} and/or C_{16:1ω7c}; 22.5 %), and iso-C_{17:0} 3-OH (7.9 %). Major polar lipids were phosphatidylethanolamine, phospholipids, aminophospholipids and other lipids of unknown character. The DNA G + C content was approximately 41.8 mol%. The sequence of the 16S-rRNA gene assigned strain T4^T to the CFB group, forming a coherent cluster with species of the genus *Algoriphagus* with the highest similarity of 98.8 % to *Algoriphagus aquatilis* A8-7^T. DNA–DNA hybridization revealed 37.5 % relatedness to strain A8-7^T. Based on morphological, physiological and molecular properties as well as on phylogenetic distinctiveness, strain T4^T should be placed into the genus *Algoriphagus* as a novel species, for which the name *Algoriphagus aquaeductus* sp. nov. (type strain T4^T = DSM 19759^T = LMG 24398^T = NCIMB 14399^T) is proposed.

Isolation of strain T4^T was performed from water samples taken from a freshwater pipe on Tenerife island, Spain. Aliquots of these samples were streaked on half-strength nutrient agar (NA/2) plates, pH 8, and incubated at 30 °C. NA/2 medium contained (l⁻¹ distilled water) 2.5 g peptone, 1.5 g beef extract and 15.0 g agar. Repeated transfers were made until a pure culture of strain T4^T was obtained. Strain T4^T was cultivated routinely at 30 °C for 2–7 days on either solid NA/2 or mineral salt medium (MSM) supplemented with 20.0 g beef extract l⁻¹ (BD Diagnostic Systems) (MSM⁺), both adjusted to pH 8, or in liquid NA/2 or MSM⁺ by shaking at 200 r.p.m. Strain T4^T cannot grow satisfactorily in marine 2216 medium (Difco). MSM, vitamin solution and trace element solution were prepared as described by Bast (2001). Culture conditions were modified by varying the temperature (5–45 °C), salinity (0–15 %, w/v) or pH (5–10), respectively. pH adjustment of

the MSM⁺ medium was done with the appropriate biological buffers. To avoid alkalinization of this medium, the normal NH₄Cl concentration of 1.0 g l⁻¹ was lowered to only 1/10. Growth under anaerobic conditions was determined in MSM, supplemented with either only 5 mM glucose or 5 mM glucose and 10 mM nitrate. Both media were prepared anaerobically under nitrogen atmosphere.

Colony morphology was determined on MSM⁺ agar plates by stereo microscopy (Carl Zeiss Stemi SV 6). Gliding motility was observed at the edge of the colonies by direct microscopy (Carl Zeiss AxioLab). Cell morphology and motility were examined by phase-contrast microscopy (Carl Zeiss AxioLab) and transmission electron microscopy (Carl Zeiss EM 10 A). Ruthenium red was used for staining of a slime layer (Pate & Ordal, 1967). Gram reaction was determined by using the Merck Gram staining kit according to the manufacturer's instructions. The presence of catalase and cytochrome oxidase was determined as described by Süßmuth *et al.* (1987) and by using Merck Bactident oxidase test strips according to the manufacturer's instructions, respectively. The tests were performed after 3–4 days of incubation. Acid production from carbohydrates was

Abbreviation: DDH, DNA–DNA hybridization.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain T4^T is EU161637.

Two supplementary figures, two tables and two text files are available with the online version of this paper.

Table 1. Differential phenotypic characteristics of strain T4^T and closely related species of the genus *Algoriphagus* including *Algoriphagus ratkowskyi* IC025^T, the type species of the genus

Strains: 1, *Algoriphagus aquaeductus* sp. nov. T4^T; 2, *A. alkaliphilus* AC-74^T; 3, *A. aquatilis* A8-7^T; 4, *A. boritolerans* T-22^T; 5, *A. mannitolivorans* JC2050^T; 6, *A. olei* CC-Hsuan-617^T; 7, *A. ratkowskyi* IC025^T. All strains are positive for oxidase, catalase and β -galactosidase activity, and utilization of D-glucose and lactose. All are non-flagellated, have MK-7 as predominant respiratory quinone, are pink-, orange- or red-pigmented, and do not require NaCl for growth. All strains are negative concerning gliding motility, fermentation of glucose, urease activity, and presence of flexirubin-type pigments. Data for reference strains are from Ahmed *et al.* (2007), Bowman *et al.* (2003), Liu *et al.* (2009), Nedashkovskaya *et al.* (2007), Tiago *et al.* (2006), Yi & Chun (2004) and Young *et al.* (2009). +, Positive; w, weakly positive; –, negative; v, variable; ND, not determined.

Characteristic	1	2	3	4	5	6	7
Shape	Short to long rods	Long rods	Short to long rods	Short to long rods	Short rods	Short to long rods	Cocco-bacilli
Size (μm)	0.5–2.5 $\times$ 1.5–15.0	0.5 $\times$ 2.1–3.3	0.2–0.4 $\times$ 1.6–4.0	0.3–0.4 $\times$ 1.2–3.4	0.4–0.5 $\times$ 1.1–1.7	0.4–0.6 $\times$ 0.8–2.5	0.3–0.4 $\times$ 0.3–0.9
Aggregate formation	+	ND	ND	ND	ND	ND	ND
Slime capsule	+	ND	ND	ND	ND	ND	ND
Metabolism	Aerobic to microaerophilic	Strictly aerobic	Strictly aerobic	Strictly aerobic	Strictly aerobic	Strictly aerobic	Strictly aerobic
Nitrate reduction	+	+	–	–	+	–	v
Salinity range (%)	0–4	0–3	0–3	0–3	0–7	0–3	0–6
Temperature range (°C)	15–42	11–39	20–37	17–37	10–40	10–37	–2–25
pH range	7–9	8–11	5.5–10.5	6.5–10.0	6–11	7–9	ND
Hydrolysis of:							
Agar	–	–	ND	–	–	–	v
Casein	+	–	w	ND	–	–	+
DNA	+	+	–	ND	+	–	v
Gelatin	+	+	–	–	+	–	v
Starch	+	+	+	+	+	–	v
Tween 20	+	ND	+	ND	–	–	+
H ₂ S production	–	–	+	–	–	–	–
Acid production from:							
L-Arabinose	–	+	–	–	–	–	+
Cellobiose	–	+	w	+	+	–	+
D-Fructose	–	+	w	–	–	–	+
D-Galactose	–	+	ND	+	–	–	+
D-Glucose	+	+	w	+	–	–	+
Lactose	+	+	w	+	–	–	–
Maltose	+	+	w	+	–	–	+
D-Mannose	+	+	w	+	–	–	+
Melibiose	+	+	w	–	–	–	+
Raffinose	+	–	ND	+	–	–	+
L-Rhamnose	+	–	–	+	–	–	+
Sucrose	+	+	w	–	+	–	–
Trehalose	+	+	w	–	ND	–	+
D- and L-Xylose	–	–	–	–	–	–	+
Utilization of:							
L-Arabinose	–	+	–	–	+	–	+
D-Galactose	+	+	–	+	–	+	+
D-Mannose	+	+	+	+	+	+	+
D-Xylose	ND	–	–	–	+	+	+
Glycerol	+	–	–	ND	–	–	–
myo-Inositol	+	–	–	–	–	–	+
D-Mannitol	–	–	ND	+	+	–	+
Sorbitol	–	+	ND	–	–	–	+
Susceptibility to:							
Ampicillin	+	ND	w	ND	+	ND	–
Benzylpenicillin	+	–	w	+	+	–	–
Carbenicillin	–	ND	+	ND	+	ND	+

Table 1. cont.

Characteristic	1	2	3	4	5	6	7
Kanamycin	–	+	+	–	–	ND	–
Lincomycin	+	ND	ND	ND	+	ND	+
Neomycin	+	ND	ND	ND	–	ND	–
Polymyxin B	+	–	+	ND	–	ND	–
Streptomycin	+	–	+	ND	+	ND	–
Tetracycline	+	–	+	+	+	+	+
DNA G + C content (mol%)	41.8	43.5	43	42.5	42	43	35

*See Supplementary Figure S1.

determined using API 50 CH test strips (bioMérieux) according to the manufacturer's recommendations. Evaluation was performed after two and seven days. The aerobic dissimilation of 95 carbon sources was studied by using the Biolog GN2 MicroPlate system according to the manufacturer's instructions. Antibiotic susceptibility as well as degradation of casein, cellulose (filter paper and CM-cellulose), egg yolk, RNA (method 1) and Tween 20 (method 2) were tested according to the appropriate methods as described by Smibert & Krieg (1994). Hydrolysis of birchwood xylan was determined according to Yoon *et al.* (2004). Hydrolysis of starch, gelatin, urea and agar was tested as described by Süßmuth *et al.* (1987) and Nedashkovskaya *et al.* (2004). The presence of DNase was determined as described by Schreier (1969). The API 10S system (bioMérieux) was used according to the manufacturer's instructions for testing additional enzymic reactions of strain T4^T. Pigment-absorption spectrum analysis was performed spectrophotometrically (model DU640; Beckman), as described by Yoon *et al.* (2004). The presence of flexirubin-like pigments was tested by the method of Güde (1980).

Biomass of strain T4^T from a 2-day-old culture, grown in liquid MSM⁺ medium, was taken for the analysis of isoprenoid quinones as well as for determination of DNA G + C content, 16S rRNA gene sequence and DNA–DNA hybridization (DDH). Isoprenoid quinones were extracted and analysed as described by Komagata & Suzuki (1987). For the analyses of cellular fatty acids and polar lipids, strain T4^T was grown in marine 2216 medium (Difco) for better comparison with results obtained for other species of the genus *Algoriphagus*. Cells were harvested at the beginning of the stationary growth phase and lyophilized. Both analyses were carried out by the Identification Service and Dr Brian Tindall, Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ), Braunschweig, Germany. DNA was isolated as described by Marmur (1961). Concentration and purity of the DNA were examined according to the method of Moore *et al.* (1999). The DNA G + C content (mol%) was determined using the thermal denaturation method (Marmur & Doty, 1962) as a mean value of 36 determinations. DDH was carried out between strain T4^T and *Algoriphagus aquatilis* A8-7^T, the closest relative on the basis

of the results of 16S rRNA gene sequence analyses. Strains T4^T and *A. aquatilis* A8-7^T were cultivated in MSM⁺ and YP medium (Liu *et al.*, 2009), respectively, for DNA isolation before performing DDH. The latter two procedures were performed at the DSMZ according to Cashion *et al.* (1977), De Ley *et al.* (1970) and Huss *et al.* (1983).

Extraction of genomic DNA for 16S rRNA gene sequence determination and PCR were carried out as described by Neilan (1995). PCR products were purified with the Qiagen QIAquick PCR product purification kit according to the manufacturer's instructions, and DNA sequencing was performed by GATC Biotech (Konstanz, Germany). The sequences obtained from amplification were merged together by using Chromas Pro version 1.34 (Technelysium Pty Ltd). The closest relatives of strain T4^T were determined by performing BLAST database searches. Subsequent analyses of the 16S rRNA gene sequence of the new isolate, as well as of closely related sequences, were performed using the ARB software package (version RC 5.1 SVN 6289M; Ludwig *et al.*, 2004) and the corresponding SILVA SSURef 104 database (release October 2010; Pruesse *et al.*, 2007). The nearly complete 16S rRNA sequence of strain T4^T (1398 bp) was aligned automatically using the PT server implemented in the ARB software package, and the alignment was checked manually. Phylogenetic trees were reconstructed according to the neighbour-joining (Saitou & Nei, 1987), maximum-parsimony (Fitch, 1971) and maximum-likelihood (Felsenstein, 1981) methods. The stability of the groupings was estimated by bootstrap analysis (Felsenstein, 1985) of the neighbour-joining and maximum-parsimony methods based on 1000 replications. As suggested by Tindall *et al.* (2010), the alignment as well as the exact parameters for the reconstruction of the phylogenetic trees are given in Supplementary Files S1 (a and b) and S2, respectively, available in IJSEM Online.

If not otherwise stated, all tests were performed in duplicate. Cellular fatty acid and polar lipid analyses as well as the 16S rRNA gene sequence determination were performed only once.

The main morphological, physiological and biochemical properties of strain T4^T are shown in Table 1 or are given in the species description. Table 1 also gives an overview of

Table 2. Cellular fatty acids (%) of strain T4^T and closely related species of the genus *Algoriphagus*, including *A. ratkowskyi* IC025^T, the type species of the genus

Strains: 1, *Algoriphagus aquaeductus* sp. nov. T4^T; 2, *A. alkaliphilus* AC-74^T; 3, *A. aquatilis* A8-7^T; 4, *A. boritolerans* T-22^T; 5, *A. mannitolivorans* JC2050^T; 6, *A. olei* CC-Hsuan-617^T; 7, *A. ratkowskyi* IC025^T. Values for predominant fatty acids are in bold type. Data for reference strains are from Ahmed *et al.* (2007), Bowman *et al.* (2003), Liu *et al.* (2009), Tiago *et al.* (2006), Yi & Chun (2004) and Young *et al.* (2009). Predominant fatty acids are in bold type. ECL, Equivalent chain-length; –, not detected/not reported.

Fatty acid	1	2	3	4	5	6	7
iso-C _{11:0}	–	0.9	–	0.7	–	2.1	–
anteiso-C _{11:0}	–	2.6	–	1.5	1.7	0.8	2.1
iso-C _{13:0}	0.2	–	–	–	–	–	–
Unknown ECL 13.565	–	–	1.7	2.1	–	–	–
Unknown ECL 13.566	–	3.7	–	–	–	–	–
Unknown ECL 14.959	–	–	1.0	–	–	–	–
C _{14:0}	0.6	–	1.4	–	–	–	–
iso-C _{14:0}	0.6	0.3	0.6	0.4	1.2	–	1.4
C _{14:1} ω5c	0.2	–	–	–	–	–	–
C _{15:0}	–	1.6	1.2	2.6	1.7	1.4	1.6
C _{15:0} 3-OH	–	–	3.1	–	–	–	–
iso-C _{15:0}	32.2	32.4	40.3	21.3	28.7	41.0	30.5
anteiso-C _{15:0}	4.1	3.4	4.7	7.0	4.6	1.0	3.6
C _{15:0} 2-OH	0.3	0.5	–	0.6	–	–	–
iso-C _{15:0} 3-OH	3.9	3.2	4.9	2.2	3.6	3.2	2.9
iso-C _{15:1} G	0.6	1.4	1.9	0.5	1.0	6.9	1.1
C _{15:1} ω6c	0.3	1.9	3.1	0.3	2.5	1.7	2.1
C _{16:0}	1.2	0.4	0.9	3.5	–	–	2.9
C _{16:0} 3-OH	2.1	–	–	–	0.6	–	1.9
iso-C _{16:0}	2.0	3.2	2.2	6.5	3.7	0.8	3.4
iso-C _{16:0} 3-OH	1.6	1.3	1.7	1.0	4.0	–	2.8
iso-C _{16:1}	–	–	1.8	–	–	0.6	–
iso-C _{16:1} H	1.2	3.8	–	3.3	2.8	–	1.7
C _{16:1} ω5c	5.8	1.2	2.5	–	1.3	0.6	5.8
Unknown ECL 16.580	–	1.3	–	–	–	–	–
iso-C _{17:0}	0.4	0.8	–	3.2	–	–	–
C _{17:0} 2-OH	0.7	–	–	2.1	0.7	–	–
iso-C _{17:0} 3-OH	7.9	7.4	4.0	7.5	7.9	7.2	9.2
C _{17:1} ω6c	0.9	1.7	2.4	2.5	3.1	1.7	0.5
iso-C _{17:1} ω9c	7.6	14.6	6.0	13.3	5.6	11.2	1.5
anteiso-C _{17:1} ω9c	–	–	–	1.9	–	–	–
iso-C _{19:1} I	–	–	–	–	–	0.6	–
Summed features*							
1	0.2	–	–	–	–	–	–
3	22.50	9.2	12.1	10.0	13.7	7.1	22.3
4	1.7	3.9	–	0.4	4.8	4.3	0.9
8	0.7	–	–	–	–	–	–

*Summed features consist of one or more fatty acids that cannot be separated by the method used. Summed feature 1 contains iso-C_{15:1} H and/or C_{13:0} 3-OH; summed feature 3 contains iso-C_{15:0} 2-OH, C_{16:1}ω6c and/or C_{16:1}ω7c; summed feature 4 contains iso-C_{17:1} I and/or anteiso-C_{17:1} B; summed feature 8 contains C_{18:1}ω7c and/or C_{18:1}ω6c.

differential phenotypic characteristics between strain T4^T and closely related species of the genus *Algoriphagus*, including *Algoriphagus ratkowskyi* IC025^T, the type species of the genus (a comprehensive comparison is shown in Supplementary Table S1).

Best growth was observed on MSM⁺. When strain T4^T was grown on NA/2 agar, smaller colonies with less intense pigmentation were observed. The isolate seemed to be relatively restricted in its utilization of organic compounds as sole carbon sources, because it preferred mono- and disaccharides, followed by oligo-, polysaccharides, and deoxysugars. However, if alcohols, alditols, amides, amines, carboxylic acids or amino acids were supplied, strain T4^T was not able to use most of these carbon sources for growth. Other species of the genus *Algoriphagus* are also relatively restricted in their utilization of organic compounds as sole carbon sources. Strain T4^T could assimilate D-mannitol and myo-inositol, whereas all other members of this genus could not. Strain T4^T produced acids from a broad range of organic compounds. These findings are in accordance with results obtained for other species of the genus *Algoriphagus*. The statements given above about other members of the genus *Algoriphagus* are supported by data from Ahmed *et al.* (2007), Bowman *et al.* (2003), Copa-Patiño *et al.* (2008), Liu *et al.* (2009), Nedashkovskaya *et al.* (2004, 2007), Park *et al.* (2010), Tiago *et al.* (2006), Van Trappen *et al.* (2004), Yi & Chun (2004), Yoon *et al.* (2005a), Yoon *et al.* (2005b), Yoon *et al.* (2006), Yoon *et al.* (2004) and Young *et al.* (2009).

The overall cellular fatty acid profile of strain T4^T was mainly the same as those of closely related species of the genus *Algoriphagus*, with iso-C_{15:0} (32.2%), summed feature 3 (C_{16:1}ω6c and/or C_{16:1}ω7c; 22.5%) and iso-C_{17:0} 3-OH (7.9%) as the predominant fatty acids. A comparison of fatty acids of strain T4^T with those of closely related species of the genus *Algoriphagus*, including *A. ratkowskyi* IC025^T, the type species of the genus, is given in Table 2 (a more comprehensive comparison is shown in Supplementary Table S2). The polar lipid profile consisted of phosphatidylethanolamine, five unknown phospholipids, three unknown aminophospholipids and three unknown lipids (data not shown).

The nearly complete 16S rRNA gene sequence of strain T4^T was used for a BLAST search against GenBank. The result clearly indicated that the isolate belongs to the family *Cyclobacteriaceae* within the CFB group. Sequence similarities between strain T4^T and type strains of closely related species of the genus *Algoriphagus* were 93.3–98.8%. The highest similarity values obtained for strain T4^T and species with validly published names were found with *A. aquatilis* A8-7^T (98.8%), *Algoriphagus olei* CC-Hsuan-617^T (98.1%), *Algoriphagus alkaliphilus* AC-74^T (96.2%), *Algoriphagus mannitolivorans* JC2050^T (96.2%) and *Algoriphagus boritolerans* T-22^T (95%). To test the genomic uniqueness of a novel isolate, Stackebrandt & Ebers (2006) recommend a 16S rRNA gene sequence similarity threshold range of 98.7–99.0% instead of 97.0% as the point at which DNA–DNA

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the position of strain T4^T in the family Cyclobacteriaceae. Bootstrap values (>70%) based on 1000 resamplings are shown. Filled circles indicate that the corresponding nodes were also recovered in trees generated with the maximum-parsimony and maximum-likelihood algorithms. Open circles indicate that the corresponding nodes were also recovered with either the maximum-parsimony or the maximum-likelihood algorithm. The sequence of *Cytophaga hutchinsonii* ATCC 33406^T (GenBank accession no. M58768) was used as an outgroup. Bar, 0.1 substitutions per nucleotide position.

hybridization experiments should be obligatory. Therefore, such experiments were performed and showed that strain T4^T had less than 37.5 % DNA–DNA relatedness with *A. aquatilis* A8-7^T. The recommended criteria for delineating bacterial species state that less than 70 % DNA–DNA relatedness (Wayne *et al.*, 1987) indicates that strains belong to separate species. Meanwhile, it is accepted that different genera contain a number of species that share 16S rRNA gene sequence similarities of significantly higher than 97 % while sharing DNA–DNA relatedness values well below the 70 % cut-off point recommended for the differentiation of genomic species (Kang *et al.*, 2009; Park *et al.*, 2010; Yassin *et al.*, 2010). Therefore, strain T4^T should be placed as a novel species in the genus *Algoriphagus*.

The distinctiveness of strain T4^T is also documented in the phylogenetic tree (Fig. 1). Strain T4^T clustered with *A. aquatilis* A8-7^T (72 % bootstrap support), *A. olei* CC-Hsuan-617^T and *A. mannitolivorans* JC2050^T. A sister group to this clade was formed by *A. alkaliphilus* AC-74^T and *A. boritolerans* T-22^T. The overall tree topology was supported by all tree-making methods used in this study. However, the branching patterns of the species of the genus *Algoriphagus* varied a little depending on the tree-making method used.

The phylogenetic and genetic distinctiveness of strain T4^T, combined with differential phenotypic properties, are both enough to show that this strain is apart from other species of the genus *Algoriphagus*. Thus, on the basis of the phenotypic, chemotaxonomic, phylogenetic and genetic findings, strain T4^T is regarded to represent a novel species of the genus *Algoriphagus*, for which the name *Algoriphagus aquaeductus* sp. nov. (type strain T4^T) is proposed.

Description of *Algoriphagus aquaeductus* sp. nov.

Algoriphagus aquaeductus (a.qua.e.duc'tus. L. gen. masc. n. *aquaeductus* of/from a conduit, a water pipe).

Gram-staining-negative and forms long rod-shaped cells, 0.5–2.5 × 1.5–15.0 µm in size, surrounded by a slime capsule. Cells occur singly, in the form of short chains or in aggregates, are non-spore-forming and non-motile. Aerobic to micro-aerophilic and chemoheterotrophic. Colonies are circular, umbonate, glistening, non-luminescent, butyraceous, opaque and orange with entire margins. Oxidase- and catalase-positive. Optimum temperature for growth is 25–30 °C; no growth occurs at 10 or 45 °C. Optimum growth at pH 8; no growth occurs at pH 6 or 10. Grows with up to 4 % (w/v) NaCl, but best growth occurs without NaCl. Can be classified as mesophilic, neutral to alkaliphilic, and halotolerant. Growth under anaerobic conditions is obtained only when medium is supplemented with nitrate. Absorption maxima of carotenoids occur at 478 nm with shoulders at 449 and 502 nm (see Supplementary Figure S2). Flexirubin-type pigments are absent. The major respiratory quinone is MK-7. Major polar lipids are phosphatidylethanolamine, phospholipids, aminophospholipids and other lipids of unknown character. The predominant fatty acids are iso-C_{15:0}, summed

feature 3 (C_{16:1}ω6c and/or C_{16:1}ω7c) and iso-C_{17:0} 3-OH. Casein, DNA, gelatin, starch, RNA and Tween 20 are hydrolysed, but agar, cellulose (filter paper and CM-cellulose), egg yolk, urea and xylan are not. β-Galactosidase is present, whereas lysine decarboxylase, ornithine decarboxylase and tryptophan deaminase are absent. Indole and H₂S are not produced. Sensitive to (µg per disc) ampicillin (10), chloramphenicol (25), lincomycin (15), neomycin (15), penicillin G (15), polymyxin B (30), rifampicin (20), streptomycin (30), tetracycline (20) and novobiocin (20). Tolerant of carbenicillin (25) and kanamycin (30). Assimilates cellobiose, D-fructose, D-galactose, gentiobiose, α-D-glucose, α-lactose, lactulose, maltose, D-mannose, sucrose, trehalose, turanose, succinic acid monomethyl ester, α-cyclodextrin, dextrin, glycogen, *myo*-inositol, L-asparagine, N-acetyl-D-glucosamine and glycerol, but not melibiose, methyl β-D-glucoside, raffinose, acetic acid, α-ketobutyric acid, α-ketovaleric acid, propionic acid, L-alaninamide, L-alanine, L-glutamic acid, glycyl L-aspartic acid, L-leucine, L-ornithine, L-threonine, α-D-glucose 1-phosphate, D-glucose 6-phosphate, Tween 40, Tween 80, L-arabinose, N-acetyl-D-galactosamine, adonitol, D-arabitol, i-erythritol, L-fucose, D-mannitol, D-psicose, L-rhamnose, D-sorbitol, xylitol, pyruvic acid methyl ester, *cis*-aconitic acid, citric acid, formic acid, D-galactonic acid lactone, D-galacturonic acid, D-gluconic acid, D-glucosaminic acid, D-glucuronic acid, α-hydroxybutyric acid, β-hydroxybutyric acid, γ-hydroxybutyric acid, *p*-hydroxyphenylacetic acid, itaconic acid, α-ketoglutaric acid, DL-lactic acid, malonic acid, quinic acid, D-saccharic acid, sebacic acid, succinic acid, bromosuccinic acid, succinamic acid, glucuronamide, D-alanine, L-alanyl glycine, L-aspartic acid, glycyl L-glutamic acid, L-histidine, hydroxy-L-proline, L-phenylalanine, L-proline, L-pyroglutamic acid, D-serine, L-serine, DL-carnitine, γ-aminobutyric acid, urocanic acid, inosine, uridine, thymidine, phenylethylamine, putrescine, 2-aminoethanol, 2,3-butanediol or DL-α-glycerol phosphate. Acids are produced from D-glucose, D-mannose, lactose, melibiose, maltose, sucrose, trehalose, turanose, gentiobiose, arbutin, aesculin, 5-ketogluconate, raffinose and glycogen, but not from D-arabinose, L-arabinose, D-ribose, L-sorbose, D-lyxose, D-tagatose, D-fructose, D-xylose, L-xylose, cellobiose, D-galactose, N-acetyl-D-glucosamine, L-rhamnose, D-fucose, L-fucose, β-methyl D-xyloside, α-methyl D-mannoside, α-methyl D-glucoside, amygdalin, salicin, melezitose, amidone, inulin, glycerol, erythritol, D-mannitol, D-sorbitol, xylitol, D-arabitol, L-arabitol, D-adonitol, dulcitol, *myo*-inositol, gluconate or 2-ketogluconate. The G + C content of the DNA of the type strain is 41.8 mol%.

The type strain is T4^T (DSM 19759^T = LMG 24398^T = NCIMB 14399^T), isolated from water taken from a freshwater pipe on Tenerife island, Spain.

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