***Corynebacterium terpenotabidum* sp. nov., a bacterium capable of degrading squalene**

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The taxonomic status of *Arthrobacter* sp. Y-11^T, which was described as a squalene-degrading bacterium, was investigated by chemotaxonomic and genetic methods. The strain possesses wall chemotype IV, MK-9(H₂) as the predominant menaquinone, mycolic acids, and straight-chain, saturated and monounsaturated fatty acids, with considerable amounts of tuberculostearic acid. The DNA G+C content is 67.5 mol%. 16S rRNA gene sequence analysis and quantitative DNA–DNA hybridization experiments provided strong evidence that strain Y-11^T represents a new species within the genus *Corynebacterium*, for which the name *Corynebacterium terpenotabidum* sp. nov. is proposed. The type strain of *C. terpenotabidum* is strain Y-11^T (= IFO 14764^T).

Keywords: *Corynebacterium terpenotabidum*, squalene-degrading bacterium

INTRODUCTION

Squalene is a naturally abundant linear triterpene (C₃₀) and an important biosynthetic precursor of steroids and triterpenes in many living organisms. Yamada *et al.* (1975) reported the oxidative degradation of squalene by micro-organisms. A bacterium, strain Y-11^T, capable of degrading squalene was isolated from soil and tentatively named *Arthrobacter* sp. (Yamada *et al.*, 1975, 1977). It was able to grow in a medium containing squalene as a sole carbon source.

Strain Y-11^T is a Gram-positive, non-motile, rod-shaped organism. It possesses cell wall component type IV (*meso*-diaminopimelic acid, arabinose and galactose) (Lechevalier & Lechevalier, 1970), mycolic acids and menaquinone MK-9(H₂), and its DNA has a G+C content of 67.5 mol%. These characteristics limit strain Y-11^T to one of three genera, *Corynebacterium*, *Gordonia* or *Mycobacterium*.

In this paper, the characterization of strain Y-11^T (= IFO 14764^T) is described. On the basis of mor-

phological, physiological and chemotaxonomic characteristics, and DNA–DNA hybridization data, as well as the results of the 16S rDNA sequence analysis, it is concluded that this squalene-degrading organism represents a new *Corynebacterium* species, for which the name *Corynebacterium terpenotabidum* sp. nov. is proposed.

METHODS

Bacterial strains and culture conditions. For chemical and genetic analysis, strain Y-11^T (IFO 14764^T), *Corynebacterium bovis* IFO 15706^T (Collins & Cummins, 1986), *Corynebacterium mycetoides* IFO 15289^T (Collins & Cummins, 1986), *Corynebacterium variabilis* IFO 15286^T (Collins, 1987a), and IFO 14757 (Collins *et al.*, 1989), *Corynebacterium vitrumen* IFO 12143^T (Laneelle *et al.*, 1980), and *Corynebacterium xerosis* IFO 15287^T (Collins & Cummins, 1986) were used. Strain IFO 14757 was a type strain of *Caseobacter polymorphus* (Crombach, 1978), but it has been considered to be a subjective synonym of *C. variabilis* (Collins *et al.*, 1989). All strains were cultured at 28 °C with aerobic shaking in a peptone–yeast extract medium supplemented with brain/heart infusion (PY-BHI medium), which contained 1% peptone, 0.2% yeast extract, 0.2% Bacto brain/heart infusion (Difco), 0.2% NaCl and 0.2% D-glucose (pH 7.2). Cells used for biochemical tests were harvested by centrifugation during the stationary phase, washed with water and lyophilized. To examine the degradation of squalene (Ikeguchi *et al.*, 1988), cells grown in 400 ml SC medium, which contained 0.3% (v/v) salad oil,

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Abbreviation: TBSA, tuberculostearic acid.

The DDBJ accession number for the 16S rRNA sequence of strain Y-11^T (IFO 14764^T) is AB004730.

0.03 % (v/v) squalene and 2 % (v/v) corn steep liquor (pH 7.0), at 30 °C for 65 h were harvested by centrifugation and washed twice with 0.1 M potassium phosphate buffer (pH 7.0).

Morphological, physiological and biochemical characteristics.

Cell morphology was determined by phase-contrast microscopy following cell growth on PY-BHI agar. Motility was determined by the hanging drop method. Unless otherwise indicated, all tests were performed at 28 °C. Catalase activity was determined by the presence of bubbles in a 3 % hydrogen peroxide solution. Oxidase activity was determined by the oxidation of 1 % tetramethyl-*p*-phenylenediamine on filter paper. Organic acid assimilation was studied in a medium containing (1^{-1}) 0.5 % organic acid (sodium salt), 0.02 % D-glucose, 0.01 % yeast extract, 0.01 % Trypticase (BBL), 0.1 % K_2HPO_4 , 0.5 % NaCl, 2 % agar and 12 mg phenol red (pH 7.0). Acid production from carbohydrates was studied in a medium containing 1 % peptone, 0.5 % NaCl, 0.003 % bromocresol purple and 0.5 % carbohydrate (pH 7.2) (Cowan, 1974). Nitrate reduction and hydrolysis of casein, cellulose, aesculin, gelatin, starch, tyrosine and Tween 80 were tested using methods described by Cowan (1974).

Cell chemistry. Cell walls were prepared from about 500 mg (dry weight) bacterial cells as described by Schleifer & Kandler (1972). Amino acids in the acid hydrolysate of the cell walls were identified by two-dimensional chromatography on cellulose TLC plates (Tokyo Kasei) by the method of Harper & Davis (1979) and by HPLC according to the manufacturer's instructions. Cell wall sugars were analysed as described by Mikami & Ishida (1983). The glycolyl test was performed by the method of Uchida & Aida (1977). Fatty acids were extracted from dried cells, purified (Minnikin *et al.*, 1979; Suzuki & Komagata, 1983), and analysed by GLC-MS with a GCMS-QP5000 spectrometer (Shimadzu) combined with a CLASS-5000 MS Workstation computer system. GLC analyses were carried out using a GC-17A gas chromatograph (Shimadzu). A BPX70 capillary column (SGE) containing 70 % cyanopropyl equivalent modified siloxane (50 m $\times$ 0.25 mm) was used at 80 °C for 2 min, 80–150 °C at 15 °C min^{-1} , 150–250 °C at 8 °C min^{-1} , and then 250 °C for 5 min, with helium as carrier gas at a flow rate of 1.4 ml min^{-1} . Mycolic acids were analysed by the method of Minnikin *et al.* (1975). Menaquinones were extracted from dry cells (200 mg) with chloroform-methanol (2:1, v/v), purified by TLC (Kieselgel 60F₂₅₄ plates; Merck) using hexane-diethyl ether (85:15, v/v) as a solvent, extracted with acetone, dried under a nitrogen stream, then analysed by HPLC with a Shimadzu model LC-5A instrument equipped with a Zorbax octyldecyl silane column (150 $\times$ 4.6 mm).

Degradation of squalene. Cells grown in 400 ml SC medium at 30 °C for 65 h were harvested by centrifugation at 6000 *g* for 15 min, washed twice with 0.1 M potassium phosphate buffer (pH 7.0), and resuspended in buffer to give an OD of 10 in a 1 cm light path at 600 nm. The cell suspension (1 ml) and 0.2 ml of squalene were mixed in a test tube and incubated on a reciprocating shaker (150 strokes min^{-1}) at 35 °C for 3 h. The reaction products were analysed by GLC by the method of Ikeguchi *et al.* (1988).

Genetic properties. DNA was obtained by the method of Saito & Miura (1963). The G+C content of the DNA was determined by HPLC of P1 nuclease hydrolysates of genomic DNA (Mesbah *et al.*, 1989; Tamaoka & Komagata, 1984). DNA-DNA hybridization was carried out fluoro-

metrically in microdilution wells using biotinylated DNA (Ezaki *et al.*, 1989).

16S rDNA sequence determination and phylogenetic analysis. 16S rRNA-specific DNA was amplified by PCR and sequenced directly (Hiraishi, 1992; Hiraishi *et al.*, 1994) with a Thermo Sequenase fluorescent-labelled primer cycle sequencing kit with 7-deaza-dGTP (Amersham Life Science) and a Pharmacia ALF DNA sequencer according to the manufacturers' protocols. Nucleotide substitution rates (K_{nuc} values) were calculated (Kimura, 1980), and the phylogenetic tree was constructed by the neighbour-joining method (Saitou & Nei, 1987). The topology of the phylogenetic tree was evaluated by the bootstrap resampling method of Felsenstein (1985) with 1000 replicates.

Nucleotide sequence accession numbers. The DDBJ accession number of the nucleotide sequence data of strain Y-11^T (IFO 14764^T) is AB004730. The sequence was aligned with published sequences from DDBJ, GenBank and EMBL.

RESULTS

Morphological and physiological characteristics

Strain Y-11^T was a Gram-positive, non-acid-fast, non-motile rod. Colonies on PY-BHI agar were circular, had a rough surface and were greyish-white. No aerial mycelia and no diffusible pigments were produced. In young cultures, cells were rod-shaped, (0.5–0.7 by 1.0–1.5 μm) and some were arranged at an angle in a V formation. In older cultures, rods became shorter (0.5–0.7 by 0.6–1.0 μm). The strain grew under aerobic, but not anaerobic conditions. Thiamin and biotin were required for growth. Growth was observed in PY-BHI broth containing 8 % NaCl, but not in 10 % NaCl. Strain Y-11^T utilized fructose, galactose, lactate, mannose and ethanol, but did not produce acid from these carbohydrates. The other phenotypic characteristics of strain Y-11^T are summarized in Table 1.

Chemotaxonomic characteristics

The purified cell wall of strain Y-11^T contained alanine, glutamic acid and *meso*-diaminopimelic acid in a molar ratio of 2.12:1.00:0.97. The main components of the cell wall sugars were arabinose, galactose and mannose in a molar ratio of 2.47:1.71:1.00. The glycan moiety of the cell wall contained acetyl residues. The major fatty acids of strain Y-11^T were C_{16:0} (28 % total cellular fatty acids), C_{18:0} (7 %), C_{18:1} (34 %), C_{16:1} (5 %), C_{17:1} (5 %), and 10-Me-C_{18:0} [tuberculostearic acid (TBSA)] (21 %). The DNA G+C content of strain Y-11^T was 67.5 mol %. The whole-cell methanolysate of strain Y-11^T contained mycolic esters.

Degradation of squalene

Strain Y-11^T was able to degrade linear terpenes including squalene (Willet *et al.*, 1967) and oxidatively cleave the central part of the squalene molecule (Ikeguchi *et al.*, 1988); this regioselective cleavage

Table 1. Phenotypic characteristics of *C. terpenotabidum*

Assimilation of fructose, glucose, mannose, lactate and ethanol is positive. Assimilation of arginine, aspartate, histidine, methylamine, ethylamine, methanol, galactose, lactose, maltose, sucrose, glycerol, sorbitol, mannitol, inositol, citrate, succinate, malonate, pimelate, *m*-hydroxybenzoate and *p*-hydroxybenzoate is negative.

Phenotypic characteristic	Result
Catalase	+
Oxidase	—
OF test	Oxidative
Hydrolysis of:	
Tween 80	+
Starch	—
Gelatin	—
Cellulose	—
Aesculin	—
Tyrosine	—
Acid-fast	—
Urease formation	+
Lysine decarboxylase	—
Ornithine decarboxylase	—
Nitrate reduction	—
Voges-Proskauer test	+
Methyl red test	—
Arginine dihydrolase	—
Growth in:	
0% NaCl	+
8.0% NaCl	+
10.0% NaCl	—

forms two molecules of *trans*-geranylacetone. In contrast, *C. mycetoides* IFO 15289^T, *C. variabilis* IFO 15286^T and 14757, *C. vitrumen* IFO 12143^T, and *C. xerosis* IFO 15287^T did not degrade squalene (data not shown).

Fig. 1. Unrooted phylogenetic tree displaying the relationships of *C. terpenotabidum* IFO 14764^T to reference organisms. The numbers on the branch points of the tree indicate bootstrap values (percentage) derived from 1000 samples (Felsenstein, 1985). Bar, 0.01 K_{nuc} unit.

DNA–DNA relatedness

The levels of DNA–DNA relatedness among strain Y-11^T and *C. bovis* IFO 15706^T, *C. mycetoides* IFO 15289^T, *C. variabilis* IFO 15286^T and 14757, *C. vitrumen* IFO 12143^T, and *C. xerosis* IFO 15287^T was 5–30% (Table 2).

Table 2. DNA base compositions and levels of DNA relatedness between *C. terpenotabidum* and related *Corynebacterium* species

Species	Strain (IFO no.)	G + C content (mol%)	DNA–DNA reassociation (%) with:				
			14764 ^T	15289 ^T	15286 ^T	12143 ^T	15287 ^T
<i>C. terpenotabidum</i>	14764 ^T	67.5	100	9	30	8	8
<i>C. bovis</i>	15706 ^T	68.8	7	ND	ND	ND	ND
<i>C. mycetoides</i>	15289 ^T	63.6	11	100	5	10	13
<i>C. variabilis</i>	15286 ^T	67.0	19	9	100	8	10
<i>C. variabilis</i>	14747	66.8	13	7	84	8	9
<i>C. vitrumen</i>	12143 ^T	63.9	12	11	10	100	12
<i>C. xerosis</i>	15287 ^T	67.3	10	8	5	12	100

ND, Not determined.

Table 3. Levels of 16S rRNA sequence similarity among *C. terpenotabidum* sp. nov., other *Corynebacterium* species and related organisms

Species	Strain*	EMBL no.	16S rRNA similarity (%)
<i>Corynebacterium accolens</i>	CCUG 28779 ^T	X80500	96.2
<i>Corynebacterium afermentans</i> subsp. <i>afermentans</i>	DMMZ 525	X81874	95.4
<i>Corynebacterium afermentans</i> subsp. <i>lipophilum</i>	CIP 103500 ^T	X82055	95.8
<i>Corynebacterium ammoniagenes</i>	CIP 101283 ^T	X84440	96.0
<i>Corynebacterium amycolatum</i>	NCFB 2768 ^T	X84244	96.1
<i>Corynebacterium argenteorotense</i>	CIP 104296 ^T	X83955	96.9
<i>Corynebacterium auris</i>	DMMZ 328 ^T	X82493	95.0
<i>Corynebacterium bovis</i>	NCTC 3224 ^T	X84444	97.2
<i>Corynebacterium callunae</i>	NCIB 10338	X84251	97.2
<i>Corynebacterium cystitidis</i>	NCTC 11863 ^T	X84252	94.7
<i>Corynebacterium diphtheriae</i>	NCTC 11397 ^T	X84248	96.8
<i>Corynebacterium flavesces</i>	NCDO 1320 ^T	X84441	97.4
<i>Corynebacterium glucuronolyticum</i>	DSM 44120 ^T	X86688	93.7
<i>Corynebacterium glutamicum</i>	NCIB 10025 ^T	X84257	97.0
<i>Corynebacterium jeikeium</i>	NCTC 11913 ^T	X84250	96.9
<i>Corynebacterium kutscheri</i>	CIP 103423 ^T	X81871	95.7
<i>Corynebacterium macginleyi</i>	CIP 104099 ^T	X80499	95.9
<i>Corynebacterium matruchotii</i>	DSM 20635 ^T	X84443	94.6
<i>Corynebacterium minutissimum</i>	NCTC 10288 ^T	X84678	96.4
<i>Corynebacterium mycetoides</i>	NCTC 9864 ^T	X84241	95.5
<i>Corynebacterium pilosum</i>	NCTC 11862 ^T	X84246	95.4
<i>Corynebacterium propinquum</i>	CIP 103792 ^T	X84438	95.1
<i>Corynebacterium pseudodiphthereticum</i>	NCTC 11136 ^T	X84258	95.0
<i>Corynebacterium pseudotuberculosis</i>	NCTC 3450 ^T	X84255	96.6
<i>Corynebacterium renale</i>	CIP 103421 ^T	X84249	95.0
<i>Corynebacterium striatum</i>	NCTC 764 ^T	X84442	96.7
<i>Corynebacterium urealyticum</i>	DSM 7109 ^T	X84439	96.7
<i>Corynebacterium variabilis</i>	NCDO 2097 ^T	X53185	98.3
<i>Corynebacterium vitarumen</i>	DSM 20294 ^T	X84680	97.4
<i>Corynebacterium xerosis</i>	DSM 20743 ^T	X84446	97.0
<i>Arthrobacter globiformis</i>	DSM 20124 ^T	M23411	93.2
<i>Dietzia maris</i>	DSM 43672 ^T	X79286	95.5
<i>Gordonia aichiensis</i>	DSM 43978 ^T	X80633	93.9
<i>Gordonia terrae</i>	DSM 43249 ^T	X79286	93.2
<i>Mycobacterium bovis</i>	ATCC 12910 ^T	X55589	94.6
<i>Mycobacterium intracellulare</i>	ATCC 15985	X52927	94.6
<i>Nocardia asteroides</i>	ATCC 3306	X57949	93.6
<i>Rhodococcus erythropolis</i>	DSM 43188	X53203	94.5
<i>Rhodococcus fascians</i>	DSM 20131	X53204	93.4
<i>Rhodococcus rhodochrous</i>	DSM 43241 ^T	X82936	95.1
<i>Tsukamurella paurometabola</i>	DSM 20162 ^T	X53206	93.2

* ATCC, American Type Culture Collection, Manassas, VA, USA; CCUG, Culture Collection of the University of Göteborg, Göteborg, Sweden; CIP, Collection of Institute Pasteur, Paris, France; DMMZ, Culture Collection of the Department of Medical Microbiology, University of Zürich, Zürich, Switzerland; DSM, German Collection of Microorganisms, Braunschweig, Germany; NCDO, National Collection of Dairy Organisms, Reading, UK; NCFB, National Collection of Food Bacteria, Reading, UK; NCIB, National Collection of Industrial and Marine Bacteria, Aberdeen, UK; NCTC, National Collection of Type Cultures, London, UK. T = Type strain.

Phylogenetic analysis

A total of 1499 nucleotides of the 16S rDNA of strain Y-11^T were sequenced, and the primary structure was aligned with sequences of 42 reference coryneform bacteria. Because only partial sequences were available

for some of the reference strains, sequence similarity calculations were based on 957 nucleotides.

Fig. 1 shows an unrooted tree constructed from a matrix of sequence similarities, which clearly demonstrates that strain Y-11^T is a member of the genus

Corynebacterium. Both sequence similarity values and the treeing analysis revealed that the phylogenetically closest corynebacterium to strain Y-11^T is *C. variabilis*; the 16S rDNA sequence similarity was 98.3% (Table 3).

DISCUSSION

From the results of this work, it is evident that strain Y-11^T, which was described as a squalene-degrading bacterium, is a new *Corynebacterium* species.

In the genus *Corynebacterium*, 41 validated species have been previously determined. Comparative analyses of 16S rDNA sequences revealed that the species of the genus *Corynebacterium* form a monophyletic association within the taxa containing chemotype IV and mycolic acid, though there is heterogeneity within this genus (Funke *et al.*, 1997; Pascual *et al.*, 1995; Ruimy *et al.*, 1995). For example, both aerobic and facultatively anaerobic species are included in this genus; some species lack mycolic acid (Collins *et al.*, 1988); some species contain TBSA (Bendinger *et al.*, 1992; Collins *et al.*, 1982; Suzuki & Komagata, 1983) and so on.

Among the 41 validated species, seven *Corynebacterium* species have been known to contain TBSA: *Corynebacterium ammoniagenes* (Collins, 1987b); *C. bovis* (Collins *et al.*, 1988); *Corynebacterium cystitidis*, *Corynebacterium minutissimum* and *Corynebacterium pilosum* (Herrera-Alcaraz *et al.*, 1990); *Corynebacterium urealyticum* (Pitcher *et al.*, 1992); and *C. variabilis* (Collins, 1987a; Collins *et al.*, 1982). In this study, it was clarified that strain Y-11^T is a TBSA-containing corynebacterium.

On the other hand, the generally accepted range of DNA G+C contents for *Corynebacterium* species had

been reported to be 51–63 mol% (Collins & Cummins, 1986). However, G+C contents higher than 63 mol% have been reported in several *Corynebacterium* species: *Corynebacterium afermentans* (66–68 mol%), *C. afermentans* subsp. *afermentans* (66 mol%), *C. afermentans* subsp. *lipophilum* (68 mol%) (Riegel *et al.*, 1993a, b), *Corynebacterium auris* (68–74 mol%) (Funke *et al.*, 1995), *C. bovis* (68–74 mol%) (Riegel *et al.*, 1993b), *C. mycetoides* (68 mol%) (Pitcher, 1983; Riegel *et al.*, 1993b), *C. variabilis* (65 mol%) (Collins, 1987a; Collins *et al.*, 1989), *C. vitarumen* (64.8 mol%) (Collins & Cummins, 1986) and *C. xerosis* (71 mol%) (Riegel *et al.*, 1993b). Table 4 lists some of the characteristics that distinguish strain Y-11^T from these high G+C content corynebacteria. Strain Y-11^T can be distinguished from *C. bovis* and *C. variabilis*, which contain TBSA, in that Y-11^T possesses urease activity, does not reduce nitrate to nitrite and produces acid from mannose. Squalene-degrading ability was not found in *C. bovis* IFO 15706^T, *C. mycetoides* IFO 15289^T, *C. variabilis* IFO 15286^T, *C. vitarumen* IFO 12143^T and *C. xerosis* IFO 15287^T (data not shown), and these phenotypic data clearly support the idea that strain Y-11^T represents a new taxon.

The levels of DNA–DNA relatedness of strain Y-11^T with *C. bovis* IFO 15706^T, *C. mycetoides* IFO 15289^T, *C. variabilis* IFO 15286^T and 14757, *C. vitarumen* IFO 12143^T, and *C. xerosis* IFO 15287^T were less than 30%.

Comparison of the 16S rDNA sequence of strain Y-11^T with those of the 31 species of the genus *Corynebacterium* revealed that the highest level of 16S rDNA sequence similarity was 98.3% with *C. variabilis*.

On the basis of morphological, physiological and chemotaxonomic characteristics, together with DNA–DNA hybridization data and 16S rDNA se-

Table 4. Characteristics useful for differentiating *C. terpenotabidum* from other high G+C content corynebacteria

Data from this study and previous studies (Collins, 1987a; Collins & Cummins, 1986; Collins *et al.*, 1989; Funke *et al.*, 1995; Pitcher *et al.*, 1992; Riegel *et al.*, 1993b). +, 90% or more of strains are positive; –, 90% or more of strains are negative; ND, not determined.

Species	Nitrate reduction	Urease activity	Hydrolysis of aesculin	Acid from:*			Presence of TBSA†
				Fruc	Glc	Man	
<i>C. terpenotabidum</i>	–	+	–	–	–	+	+
<i>C. afermentans</i> subsp. <i>afermentans</i>	–	–	–	ND	–	–	–
<i>C. afermentans</i> subsp. <i>lipophilum</i>	–	–	–	ND	–	–	–
<i>C. auris</i>	–	–	–	ND	–	ND	–
<i>C. bovis</i>	–	–	–	+	+	–	+
<i>C. mycetoides</i>	–	–	–	ND	+	–	–
<i>C. variabilis</i>	+	+	–	–	–	–	+
<i>C. vitarumen</i>	+	+	+	+	+	+	–
<i>C. xerosis</i>	+	–	–	+	+	+	–

* Fruc, fructose; Glc, glucose; Man, mannose.

† TBSA, tuberculostearic acid.

quence comparison data, it is concluded that this squalene-degrading organism, strain Y-11^T, should be a new species of the genus *Corynebacterium*, *Corynebacterium terpenotabidum*. The type strain is strain Y-11^T (=IFO 14764^T).

Description of *Corynebacterium terpenotabidum* sp. nov.

Corynebacterium terpenotabidum (terpeno.ta'bi.dum. L. fem. n. *terpeno* terpene; L. adj. *tabidum* dissolving; M.L. fem. adj. *terpenotabidum* terpene-dissolving).

Cells are Gram-positive, irregular rods 0.5–0.7 µm by 1.0–1.5 µm long in young cultures; some cells are arranged at an angle in a V formation. In old cultures, cells are 0.5–0.7 µm by 0.6–1.0 µm. Rods are Gram-positive, non-acid-fast, non-sporulating and non-motile. No mycelium is produced. Colonies on PY-BHI agar are circular, have a rough surface and are greyish-white. Methyl red test negative. Nitrate is not reduced to nitrite. Growth occurs under aerobic, but not anaerobic conditions. Hugh–Leifson's test in glucose oxidation-fermentation (OF) medium is oxidative. Voges–Proskauer test positive. Catalase and urease are produced, but oxidase, arginine dihydrolase, lysine decarboxylase and ornithine decarboxylase are not. Tween 80 is hydrolysed, but starch, gelatin, casein, cellulose, aesculin and tyrosine are not. Fructose, glucose, mannose, lactate and ethanol are utilized as carbon sources, but galactose, lactose, maltose, sucrose, glycerol, sorbitol, mannitol, inositol, citrate, succinate, malonate, pimelate, *m*-hydroxybenzoate, *p*-hydroxybenzoate, arginine, aspartate, histidine, methylamine, ethylamine and methanol are not. Thiamin and biotin are required for growth. Growth is observed in PY-BHI broth containing 8% NaCl, but not in 10% NaCl. Cell wall peptidoglycan contains *meso*-diaminopimelic acid as the only diamino acid, arabinose, galactose and mannose, as major cell wall sugars. The muramic acids of peptidoglycan occur in the *N*-acetyl form. The predominant isoprenoid quinone is menaquinone MK-9(H₂). Mycolic acids are present. The main straight-chain saturated acids are palmitic acids and the unsaturated fatty acid are oleic acids. High levels of TBSA are present. The G+C content of the DNA is 67.5 mol%. The type strain, strain Y-11^T (=IFO 14764^T), was isolated from soil.

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