***Kocuria palustris* sp. nov. and *Kocuria rhizophila* sp. nov., isolated from the rhizoplane of the narrow-leaved cattail (*Typha angustifolia*)**

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Two Gram-positive, aerobic spherical actinobacteria were isolated from the rhizoplane of narrow-leaved cattail (*Typha angustifolia*) collected from a floating mat in the Soroksár tributary of the Danube river, Hungary. Sequence comparisons of the 16S rDNA indicated these isolates to be phylogenetic neighbours of members of the genus *Kocuria*, family *Micrococcaceae*, in which they represent two novel lineages. The phylogenetic distinctness of the two organisms TA68^T and TAGA27^T was supported by DNA–DNA similarity values of less than 55% between each other and with the type strains of *Kocuria rosea*, *Kocuria kristinae* and *Kocuria varians*. Chemotaxonomic properties supported the placement of the two isolates in the genus *Kocuria*. The diagnostic diamino acid of the cell-wall peptidoglycan is lysine, the interpeptide bridge is composed of three alanine residues. Predominant menaquinone was MK-7(H₂). The fatty acid pattern represents the straight-chain saturated iso-anteiso type. Main fatty acid was anteiso-C_{15:0}. The phospholipids are diphosphatidylglycerol, phosphatidylglycerol and an unknown component. The DNA base composition of strains TA68^T and TAGA27^T is 69.4 and 69.6 mol% G+C, respectively. Genotypic, morphological and physiological characteristics are used to describe two new species of *Kocuria*, for which we propose the names *Kocuria palustris*, type strain DSM 11925^T and *Kocuria rhizophila*, type strain DSM 11926^T.

Keywords: *Kocuria palustris*, *Kocuria rhizophila*, phylogeny, classification

INTRODUCTION

The genus *Kocuria* (Stackebrandt *et al.*, 1995) currently contains four species, i.e. the type species *Kocuria rosea*, and *Kocuria varians*, *Kocuria kristinae* and *Kocuria erythromyxa*. All were originally placed in the genus *Micrococcus*. While the first three species had been recognized as individual species, *K. erythromyxa*, strain UWO 1045, was first called '*Sarcina erythromyxa*', then recognized as a strain of *Micrococcus roseus* and subsequently described as *Deinococcus erythromyxa*, species *incertae sedis* (Brooks & Murray, 1981). Following 16S rDNA analysis the *Micrococcus*

species were shown to form an individual cluster within the *Arthrobacter–Micrococcus* line of descent (Stackebrandt *et al.*, 1980, 1995; Koch *et al.*, 1994); a cluster later described as the family *Micrococcaceae* (Stackebrandt *et al.*, 1997). Based on 16S rDNA analysis and the presence of a unique pattern of chemotaxonomic properties the three *Micrococcus* species were transferred to a new genus *Kocuria*. Later, *Deinococcus erythromyxa* was added to this genus as *K. erythromyxa* when information on the 16S rDNA sequence became available (Rainey *et al.*, 1997). This species is highly related to *K. rosea*, to which it was originally affiliated.

In this communication we report the description of two new species of *Kocuria* isolated from the rhizoplane of *Typha angustifolia* in the Danube river.

The EMBL accession numbers for the sequences of DSM 11925^T and DSM 11926^T are Y16264 and Y16263, respectively.

METHODS

Bacterial strains and cultural conditions. Strains TA68^T and TAGA27^T were isolated from the rhizoplane of the narrow-leaved cattail (*Typha angustifolia*) inhabiting a floating mat on the Soroksár tributary of the Danube river, by plating root mass serially diluted on medium B (Luedeman, 1971) agar plates. The strains were grown on nutrient agar at 28 °C. Strains used for phenotypic comparisons were the type strains of the species *Kocuria rosea* DSM 20447^T, *Kocuria kristinae* DSM 20032^T and *Kocuria varians* DSM 20033^T. *K. erythromyxa* DSM 11630^T was included in fatty acid analyses.

Media. The following media were used in liquid or semisolid state; nutrient agar consisting (l⁻¹) of peptone 5 g, meat extract 3 g and agar (Oxoid) 15 g, adjusted to pH 7.0 and medium B, consisting of starch 20 g, yeast extract 10 g and agar (Oxoid) 15 g, adjusted to pH 7.0.

Morphological studies. Cell and aggregate morphology was studied by phase-contrast microscopy and phase-contrast microphotography of material from surface growth on agar, and by direct observation on the agar surface.

Staining procedures. Gram-staining and acid-fast staining were performed according to Murray *et al.* (1994).

Physiological characterization. The temperature for all physiological tests was 28 °C except for studies concerning the temperature range. The relation to oxygen was studied using stab cultures and agar slant cultures placed in an anaerobic chamber. Oxidase activity was checked by the benzidine (Deibel & Ewans, 1960) and tetramethyl-*p*-phenylenediamine (Tarrand & Gröschel, 1982) tests. Carbohydrate degradation and acid production from carbohydrates and alcohols was determined via the OF-test according to Hugh & Leifson (1953) and by use of API 50CH test strips (bioMérieux). Utilization of various compounds as carbon sources was tested with BIOLOG GP-plate, System Release 3.50, following the manufacturer's instructions. Catalase production was demonstrated on slides by the formation of bubbles after mixing a suspension of the organism with a drop of 3% (v/v) hydrogen peroxide solution. Urease activity, nitrate reduction, aesculin hydrolysis, and hydrolysis of Tween 80 were tested according to published methods (Christensen, 1946; Cowan & Steel, 1974). Decomposition of an emulsion of UV-sterilized cinefilm strips incubated in phosphate buffer was used to verify gelatin hydrolysis. Casein hydrolysis was determined on streak-inoculated agar mixed from 6 ml liquefied agar and 2 ml steamed skimmed milk, DNA hydrolysis on Bacto DNase test agar (Difco), and hydrolysis of starch on inorganic salts starch agar (Difco) after flooding the agar surface with Lugol's solution containing 0.1% (w/v) iodine and 0.2% (w/v) potassium iodide. H₂S production was determined as described by Cowan & Steel (1974). NaCl tolerance was checked by adding NaCl to nutrient broth at final concentrations of 2, 5, 7.5, 10 and 15% (w/v) of NaCl. Antibiotic resistance tests were performed by measuring diameters of inhibition zones on Mueller-Hinton agar plates containing antibiotic disks (SANOFI Diagnostic, Pasteur).

Chemotaxonomic characterization. Purified cell-wall preparations were obtained as described by Schleifer & Kandler (1972). Amino acids and peptides in cell-wall hydrolysates were analysed by two-dimensional TLC on cellulose plates using the solvent systems described by Schleifer & Kandler (1972). The molar ratios of cell-wall amino acids were determined by GC and GC-MS of *N*-heptafluorobutyryl

amino acid isobutyl esters (MacKenzie, 1987). Cellular fatty acids extracted according to Korn-Wendisch *et al.* (1989) were analysed by GC (Groth *et al.*, 1996). Menaquinone profiles were examined by HPLC (Stackebrandt *et al.*, 1995). Polar lipids were extracted as described by Minnikin *et al.* (1979) and identified by two-dimensional TLC followed by spraying with specific reagents (Collins & Jones, 1980).

DNA isolation and determination of G + C content of DNA. The DNA was isolated as described by Cashion *et al.* (1977). The G + C content of the DNA was determined by high-performance liquid chromatography as described by Mesbah *et al.* (1989).

DNA-DNA hybridization. DNA hybridization was carried out according to De Ley *et al.* (1970) with modifications as described by Huß *et al.* (1983) and Escara & Hutton (1980) using a Gilford System 2600 spectrophotometer equipped with a Gilford 2527-R thermoprogrammer and plotter. Renaturation rates were computed by the program TRANSFER.BAS (Jahnke, 1992).

16S rDNA sequence determination and phylogenetic analysis. Genomic DNA extraction, PCR mediated amplification of the 16S rDNA and sequencing of the PCR products were as described by Rainey *et al.* (1996). The sequence reaction products were electrophoresed using a model 373A automatic DNA sequencer (Applied Biosystems). The 16S rDNA sequences were manually aligned with those of members of the class *Actinobacteria* using the ae2 editor (Maidak *et al.*, 1996). Evolutionary distances were calculated by the method of Jukes & Cantor (1969). Phylogenetic dendrograms were reconstructed using the treeing algorithm of De Soete (1983).

Nucleotide sequence accession numbers. Accession numbers for sequences used in the construction of the phylogenetic tree are: *Kocuria rosea* DSM 20447^T, X87556; *Kocuria varians* DSM 20033^T, X87754; *Kocuria kristinae* DSM 20032^T, X80749; *Kocuria erythromyxa* ATCC 187^T, Y11329; *Nesterenkonia halobia* DSM 20541^T, X80747; *Stomatococcus mucilaginosus* DSM 20746^T, X87756; *Rothia dentocariosa* ATCC 19931^T, M59055; *Dermacoccus nishinomiyensis* DSM 20448^T, X87757; *Kytococcus sedentarius* DSM 20547^T, X87755 and *Rubrobacter radiotolerans* JCM 2153^T, U65647. The 16S rDNA sequence of *Micrococcus luteus* was retrieved from the Ribosomal Database Project (Maidak *et al.*, 1996).

RESULTS AND DISCUSSION

Cultural characteristics

Optimal growth for strains TA68^T and TAGA27^T was obtained on nutrient agar at 28 °C under aerobic conditions and visible growth was observed 12 h after inoculation. Colonies were opaque, smooth with irregular edges, and yellow and pale-yellow pigmentation for strains TA68^T and TAGA27^T, respectively. Temperature range for growth on nutrient agar was between 10 and 40 °C for strain TA68^T and between 10 and 30 °C for strain TAGA27^T. Strain TAGA27^T grew in up to 7% (w/v) NaCl, while strain TA68^T grew well at 10% NaCl, sparsely at 15% NaCl, but no growth was detected above 15% NaCl. Both strains grew well between pH 5.7–7.5, but growth was very poor at pH 8.0 and no growth occurred at pH 4.5 or 8.5. Growth was never observed under anaerobic conditions.

Table 1. Phylogenetic distance as determined by 16S rDNA analysis (upper right triangle) and DNA–DNA similarities as determined by hybridization (lower left triangle) of the isolates and three type strains of the genus *Kocuria*

Taxon	Strain TAGA27 ^T	Strain TA68 ^T	<i>K. varians</i>	<i>K. kristinae</i>	<i>K. rosea</i>
Strain TAGA27 ^T	—	97.0	96.9	95.8	97.0
Strain TA68 ^T	30.8	—	98.6	95.8	96.9
<i>K. varians</i>	42.2	52.6	—	95.8	96.6
<i>K. kristinae</i>	37.0	46.6	44.0	—	95.7
<i>K. rosea</i>	46.3	43.0	ND	34.4	—

ND, Not determined.

Fig. 1. 16S rDNA sequence based phylogenetic dendrogram constructed from evolutionary distances (De Soete, 1983) showing the phylogenetic position of isolates TA68^T and TAGA27^T within the radiation of *Kocuria* species. Numbers at branching points refer to bootstrap values (500 trees resampled). Scale bar, inferred nucleotide substitutions per 100 nucleotides.

Maintenance

Serial transfers were done at 4-week intervals on nutrient agar followed by storage at 4 °C. Long-term preservation was achieved by freeze-drying, and maintenance in the vapour phase above liquid nitrogen.

Morphological characteristics

On nutrient agar the cells of TA68^T and TAGA27^T were spherical (1.0–1.5 µm in diameter), occurring in pairs, tetrads and packets. Rarely, larger cells 2.0 µm in diameter were also found. Cells were non-motile. Endospores were not detected.

Staining reactions

Strains TA68^T and TAGA27^T stained Gram-positive and no lysis was observed following treatment with 3% (w/v) KOH. Cells were not acid-fast.

Phylogenetic analysis

Almost complete 16S rDNA sequences comprising 1447 nucleotides for strain TAGA27^T and 1471 nucleotides for strain TA68^T [95.1 and 95.3%, respectively, of the *Escherichia coli* sequence according to Brosius *et al.* (1978)] were determined. Similarity values were calculated for these strains and a representative selection of actinomycete species (not shown). The similarity value between the two strains was 97.6%, while the similarity values determined for the two strains and their closest relatives, which were the type strains of members of the genus *Kocuria* ranged between 95.8 and 98.6% (Table 1, upper-right triangle). The two isolates contained all the signature nucleotides that define the family *Micrococcaceae* to which the genus *Kocuria* belongs phylogenetically.

Table 2. Fatty acid composition of the isolates and the type strains of the genus *Kocuria*

Taxon	Fatty acid composition (%)*														
	i-C _{14:0}	C _{14:0}	i-C _{15:0}	ai-C _{15:0}	C _{15:0}	C _{15:1}	i-C _{16:0}	C _{16:0}	C _{16:1}	i-C _{17:0}	ai-C _{17:0}	ai-C _{17:1}	i-C _{18:1}	C _{18:1}	C _{18:2}
TA68 ^T	1.1	2.4	13.8	48.4			5.9	2.6		1.2	21.1				
TAGA27 ^T	2.2	3.1	1.0	59.2		1.0	3.3	2.1			9.7	3.0	4.6		1.4
<i>K. kristinae</i> †	2.6	1.0	1.6	70.1		12.1	1.7			9.3					
<i>K. varians</i> †	1.4	2.9	1.3	60.3	1.3		11.1	9.6			12.1				
<i>K. rosea</i> †	1.8	1.5	7.6	70.9			1.6	1.6	5.9		4.3	3.0			
<i>K. erythromyxa</i>	1.2	1.8	14.1	63.9			1.4	1.2	6.7		2.4	1.9		1.4	

* Values less than 1% not shown. i, iso; ai, anteiso.

† Data from Stackebrandt *et al.* (1995).

Table 3. Differentiation of the isolates from *Kocuria* species based on biochemical and physiological characteristics

+, Positive; (+), weak positive; –, negative.

Physiological reaction	TA68 ^T	TAGA27 ^T	<i>K. varians</i> *	<i>K. kristinae</i> *	<i>K. rosea</i> *
Gelatinase	+	–	+	(+)	–
Oxidase	–	–	–	–†	–
Starch hydrolysis	–	–	–	–	+
Growth on Simmons' citrate	+	–	(+)	–	–
Urease	–	+	+	–	–
Phosphatase	+	–	–	–	–
Tween 80 hydrolysis	+	–	–	–	–
Aesculin hydrolysis	–	–	–	+	(+)
Arginine dihydrolase	–	–	–	–	–
H ₂ S production	(+)	(+)	–	–	–
NO ₂ [–] from NO ₃ [–]	–	+	–	–	+
Growth in presence of:					
10% NaCl	+	–	–	+	–
15% NaCl	(+)	–	–	–	–
Acid production from:					
D-Mannose	+	–	+	+	–
Galactose	–	+	–	–	–
Lactose	–	+	+†	–	–
Maltose	–	–	–	+	–
Saccharose	+	+	–	+	–
D-Xylose	–	–	–	–	+
L-Arabinose	–	–	–	–	+
Glycerol	–	–	–	+	–
Mannitol	–	–	–	–	+
Sorbitol	–	–	–	+	–
Arbutin	–	–	–	+	–
Salicin	–	–	–	+	–
Trehalose	–	–	–	+	–
Melezitose	–	–	–	+	–
Amidon	–	–	–	+	–
D-Turanose	–	–	–	+	–
Ribose	–	–	+	–	–
β-Gentiobiose	–	–	+	–	–
Utilization of:					
Dextrin	+	–	+	+	–
Glycogen	+	–	+	+	–
Tween 40	+	+	+	+	–
Tween 80	+	+	+	+	–
N-Acetyl-D-galactosamine	–	–	–	+	–
N-Acetyl-D-glucosamine	+	–	–	–	–
Adonitol	+	+	+	+	–
L-Arabinose	+	–	+	+	+
L-Fucose	+	–	+	+	+
meso-Inositol	–	–	–	+	–
Maltose	–	–	+	+	–
D-Mannitol	–	–	–	+	+
D-Mannose	+	–	+	+	+
D-Melibiose	–	–	+	–	–
Sorbitol	–	–	+	+	+
Turanose	+	–	+	+	–
Xylitol	+	–	+	+	–
Methyl-pyruvate	+	–	+	–	–
Inosine	–	+	+	–	–
Glycerol	–	–	–	+	+
L-Glutamic acid	–	–	–	+	–
L-Alanine	–	–	–	+	–

* Data from Stackebrandt *et al.* (1995).† Reaction different from published data (Stackebrandt *et al.*, 1995).

(Stackebrandt *et al.*, 1997). The phylogenetic dendrogram shown in Fig. 1 was constructed from evolutionary distances by the distance matrix method (De Soete, 1983). The 16S rDNA sequence of *Rubrobacter radiotolerans* was used to determine the root. A total of 1350 nucleotides present in all strains between positions 41 and 1458 (*E. coli* positions) were used for the analysis. Strains TA68^T and TAGA27^T grouped amongst species of the genus *Kocuria*. While strain TA68^T was a phylogenetic neighbour of *K. varians* (98.6% sequence similarity), strain TAGA27^T was more distinct, showing between 95.8 and 97% sequence similarity to representatives of *Kocuria*.

DNA–DNA hybridization

To verify the phylogenetically distinct position of strains TA68^T and TAGA27^T as determined by 16S rDNA sequence analysis, the degree of DNA–DNA similarity was determined for these two strains and the type strains of three *Kocuria* species (Table 1, lower left triangle). *K. erythromyxa* was not included because, on the basis of the high 16S rDNA similarity, it can be considered a close relative of *K. rosea*. The DNA–DNA similarity values obtained confirmed the slightly higher degree of relatedness between strain TA68^T and *K. varians* DSM (52.6% similarity) but all DNA similarities were clearly below 70% which is considered to be the threshold value for the delineation of genospecies (Wayne *et al.*, 1987).

Chemotaxonomic characteristics

Strains TA68^T and TAGA27^T contained the peptidoglycan amino acids Lys, Glu and Ala at the molar ratio 1.2:1.0:4.5. From this ratio and from the occurrence of characteristic peptides in the partial hydrolysates of cell walls (data not shown), it was concluded that both strains displayed variation A3 α (Schleifer & Kandler, 1972) with three Ala residues as the interpeptide bridge. The isoprenoid quinones of strain TA68^T were MK-7(H₂), MK-8(H₂), MK-6(H₂) and MK-9(H₂) (peak area ratio, 51:39:4:1). Strain TAGA27^T contains the menaquinones MK-7(H₂), MK-6(H₂) and MK-8(H₂) (peak area ratio, 87:7:2). The polar lipid patterns of both strains consisted of phosphatidylglycerol, diphosphatidylglycerol and one unknown phospholipid. Additionally, strain TA68^T contained one and strain TAGA27^T contained three unknown glycolipids. The cellular fatty acid profiles of both strains were of the branched-chain saturated iso-anteiso type and showed anteiso-C_{15:0} as the predominating component (Table 2). Strain TA68^T is characterized by the additional occurrence of anteiso-C_{17:0} and iso-C_{15:0} in high amounts. By comparison, the type strains of *K. rosea* and *K. erythromyxa* both have fatty acid profiles with remarkably high amounts of iso-C_{15:0} and C_{16:1} fatty acids. The latter fatty acid could not be detected in the profiles of the other *Kocuria* species (Table 2).

Physiological characteristics

For comparison, the type strains of *K. rosea*, *K. varians* and *K. kristinae* were included in the determination of physiological properties of TA68^T and TAGA27^T. *K. erythromyxa* was not included because of its high phylogenetic relatedness to *K. rosea* (Fig. 1). Except for two reactions, the physiological tests of the type strains of the three *Kocuria* species gave results identical with those published in the literature (summarized by Stackebrandt *et al.*, 1995). The two differences were a negative oxidase reaction in *K. kristinae* strain DSM 20032^T, and acid production from lactose in *K. varians* strain DSM 20033^T.

Strains TA68^T and TAGA27^T shared the following physiological properties with strains of the other three *Kocuria* species studied: growth under strictly aerobic conditions; benzidine and catalase tests and growth on inorganic nitrogen were positive; indole-negative, oxidase test and phenylalanine deaminase reaction were negative; acid production from D-glucose and D-fructose; utilization of cellobiose, D-trehalose and glucuronamide was negative. The results of physiological tests in which the isolates differed from each other and/or from the type strains of three species of *Kocuria* are shown in Table 3.

Susceptibility tests to antibiotics gave the following results: the two isolates and the type strains of the three species of *Kocuria* were susceptible to penicillin, sulbactam/ampicillin, amoxicillin, piperacillin, meropenem, cefalexine, cefamandol, cefoperazone, chloramphenicol, erythromycin, clindamycin, netilmicin, vancomycin, trimethoprim; all strains were resistant to nitrofurantoin. Strain TA68^T was resistant to ciprofloxacin while strain TAGA27^T was moderately sensitive.

Description of two new *Kocuria* species

Phylogenetic and chemotaxonomic evidence indicate that the two isolates from the rhizoplane of *Typha angustifolia* represent two new lineages within the genus *Kocuria*. Low to moderate DNA–DNA re-association values obtained for the two isolates and between them and the type strains of the three of the four currently recognized *Kocuria* species confirm their species status. Differentiation of the two new species from each other and from the other *Kocuria* species (little information is available for the moderately radiation-resistant species *K. erythromyxa*; Brooks & Murray, 1981) is achieved by the primary structure of 16S rDNA, composition of fatty acids (Table 2) and physiological properties (Table 3).

Description of *Kocuria palustris* sp. nov.

Kocuria palustris (pa.lus'tris. L.fem. adj. *palustris* marshy, swampy).

The cells are spherical, occurring in pairs, tetrads and packets, 1.0–1.5 μ m in diameter, Gram-positive and

non-motile. Endospores not produced. Not acid-fast. The colonies are pale-yellow, 2.0–3.0 mm in diameter, opaque, smooth with irregular edges with pale-yellow pigmentation. Aerobic. Chemo-organotrophic. No growth above 30 °C. Good growth at pH 5.7–7.7. Catalase, urease benzidine and growth on inorganic nitrogen are positive. Phosphatase, Tween 80 hydrolysis and aesculin hydrolysis are negative. Oxidase, gelatinase, starch hydrolysis, growth on Simmons' citrate, indole, aesculin hydrolysis, arginine dihydrolase and phenylalanine deaminase reaction are negative. H₂S reaction weak. Nitrate reduced to nitrite. Acid production from D-glucose, D-fructose, galactose, lactose and saccharose. No acid production from glycerol, mannitol, sorbitol, ribose, D-xylose, L-arabinose, D-mannose, maltose, β -gentiobiose, D-turanose, arbutine, salicine, trehalose, melezitose or amidon. Utilization of adonitol, glucuronamide, inosine, Tween 40 or Tween 80. No utilization of cellobiose, turanose, xylitol, methyl-pyruvate, dextrin, glycogen, N-acetyl-D-glucosamine, D-trehalose, L-arabinose, D-fructose, L-fucose, N-acetyl-D-galactosamine, meso-inositol, maltose, D-mannitol, D-mannose, D-melibiose, sorbitol, glycerol, L-glutamic acid or L-alanine. Growth at 7% NaCl, but no growth at 10% NaCl. Peptidoglycan contains L-lysine as the diagnostic diamino acid. The interpeptide bridge consists of three alanine residues (variation A3 α). The major menaquinone is MK-7(H₂). The major fatty acid is ai-C_{15:0}. Predominant polar lipids are phosphatidylglycerol and diphosphatidylglycerol. The DNA base composition is 69.6 mol% G+C. Isolated from the rhizosphere of *Typha angustifolia* from a floating mat in the Soroksár tributary of the river Danube, Hungary. The type strain is strain TAGA27^T. It has been deposited at the DSMZ-German Collection of Microorganisms and Cell Cultures as strain DSM 11925^T.

Description of *Kocuria rhizophila* sp. nov.

Kocuria rhizophila (rhi.zo'phi.la. Gr. n. *rhiza* a root; Gr. adj. *philos* loving; M.L. adj. *rhizophila* root-loving).

The cells are spherical, occurring in pairs, tetrads and packets, 1.0–1.5 μ m in diameter, Gram-positive and non-motile. Endospores not produced. Not acid-fast. The colonies are 1.5–2.5 mm in diameter, opaque, smooth with irregular edges with yellow pigmentation. Aerobic. Chemo-organotrophic. No growth above 40 °C. Good growth between pH 5.7–7.7. Catalase, benzidine and growth on inorganic nitrogen positive. Gelatinase, phosphatase, Tween 80 hydrolysis, growth on Simmons' citrate are positive. Oxidase, starch hydrolysis, indole, urease, aesculin hydrolysis, arginine dihydrolase and phenylalanine deaminase reaction are negative. H₂S reaction weak. Nitrate not reduced to nitrite. Acid production from D-glucose, D-fructose, D-mannose and saccharose. No acid production from glycerol, mannitol, sorbitol, ribose, D-xylose, L-arabinose, galactose, lactose, maltose, β -gentiobiose, D-turanose, arbutin, salicin, trehalose, melezitose or

amidon. Utilization of adonitol, L-arabinose, D-fructose, L-fucose, D-glucose, turanose, xylitol, methyl-pyruvate, glucuronamide, dextrin, glycogen, Tween 40, Tween 80 and N-acetyl-D-glucosamine. No utilization of cellobiose, D-trehalose, N-acetyl-D-galactosamine, meso-inositol, maltose, D-mannitol, D-melibiose, sorbitol, inosine, glycerol, L-glutamic acid and L-alanine. Good growth at 10% NaCl. Peptidoglycan contains L-lysine as the diagnostic diamino acid. The interpeptide bridge consists of three alanine residues (variation A3 α). The major menaquinones are MK-7(H₂) and MK-8(H₂). The major fatty acids are ai-C_{17:0}, ai-C_{15:0} and i-C_{15:0}. Predominant polar lipids are phosphatidylglycerol and diphosphatidylglycerol. The DNA base composition is 69.4 mol% G+C. Isolated from the rhizosphere of *Typha angustifolia* from a floating mat on the Soroksár tributary of the river Danube, Hungary. The type strain is strain TA68^T. It has been deposited at the DSMZ as strain DSM 11926^T.

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