Staphylococcus massiliensis sp. nov., isolated from a human brain abscess

Mouhamad Al Masalma, Didier Raoult and Véronique Roux

Correspondence
Véronique Roux
vroux91@live.fr

Laboratoire de Bactériologie – Virologie, Hôpital de la Timone, URMITE CNRS-IRD UMR 6236, IFR48, 264 rue Saint-Pierre, 13385 Marseille, Cedex 05, France

Gram-positive, catalase-positive, coagulase-negative, non-motile, non-fermentative and novobiocin-susceptible cocci were isolated from a human brain abscess sample (strain 5402776^T). This novel strain was analysed by a polyphasic taxonomic approach. The respiratory quinones detected were MK-7 (93 %) and MK-6 (7 %) and the major fatty acids were C_{15:0} iso (60.5 %), C_{17:0} iso (8.96 %) C_{15:0} anteiso (7.93 %) and C_{19:0} iso (6.78 %). The peptidoglycan type was A3α L-Lys-Gly₂₋₃-L-Ser-Gly. Based on cellular morphology and biochemical criteria, the new isolate was assigned to the genus *Staphylococcus*, although it did not correspond to any recognized species. The G + C content of the DNA was 36.6 mol%. Phylogenetic analysis based on 16S rRNA gene sequence comparisons showed that the new isolate was most closely related to *Staphylococcus piscifermentans*, *Staphylococcus condimenti*, *Staphylococcus carnosus* subsp. *carnosus*, *S. carnosus* subsp. *utilis* and *Staphylococcus simulans* (97.7 %, 97.6 %, 97.6 %, 97.6 % and 96.5 % sequence similarity, respectively). Comparison of *tuf*, *hsp60*, *rpoB*, *dnaJ* and *sodA* gene sequences was also performed. In phylogenetic analysis inferred from *tuf*, *dnaJ* and *rpoB* gene sequence comparisons, strain 5402776^T clustered with *Staphylococcus pettenkoferi* (93.7 %, 82.5 % and 89 % sequence similarity, respectively) and on phylogenetic analysis inferred from *sodA* gene sequence comparisons, it clustered with *Staphylococcus chromogenes* (82.8 %). On the basis of phenotypic and genotypic data, this isolate represents a novel species for which the name *Staphylococcus massiliensis* sp. nov. is proposed (type strain 5402776^T=CCUG 55927^T=CSUR P23^T).

Staphylococci are ubiquitous bacteria in nature that are able to colonize or infect a wide range of animals. Currently the genus *Staphylococcus* consists of more than 50 recognized species and subspecies. Coagulase-positive *Staphylococcus aureus* subsp. *aureus* and coagulase-negative staphylococci are among the most commonly isolated bacterial species in the clinical microbiology laboratory. Coagulase-negative staphylococci have long been regarded as skin commensals and their role as pathogens has been recognized only recently, especially in patients with indwelling devices such as prosthetic valves and catheters (Huebner & Goldmann, 1999; Von Eiff *et al.*, 2002). During the last decade, several coagulase-negative staphylococci have been isolated from animals (Pantůček *et al.*, 2005; Spargser *et al.*, 2003) and clinical samples (Trülsch *et al.*, 2007; Zakrzewska-Czerwinska *et al.*, 1995). In this report, we describe a novel coagulase-negative

species belonging to the genus *Staphylococcus* that was isolated from a human brain abscess sample.

In December 2005, a 52-year-old man underwent neurosurgical intervention for the treatment of a brain tumour. He developed fever, headache and an aggravation of existing neurological symptoms. Magnetic resonance imaging and computerized tomography revealed a frontal brain abscess. Antibiotic therapy was begun with a combination of imipenem, gentamicin and vancomycin. The abscess was drained and samples of the pus were sent to our laboratory for cultural and molecular investigations. A bacterial strain was isolated on blood agar at 37 °C in an aerobic atmosphere. Gram staining revealed Gram-positive cocci that occurred singly, in pairs and in clusters. The isolate (strain 5402776^T) was identified using a Vitek 2 instrument and Gram-positive card (bioMérieux) as *Leuconostoc mesenteroides* subsp. *cremoris* with a probability of 93 %. API 20 Staph strip inoculation (bioMérieux) was performed and an identification of *Kocuria varians* was obtained. 16S rRNA gene sequence determination was conducted and a comparison with the GenBank database showed that strain 5402776^T was a member of the genus *Staphylococcus*. It was initially suspected to be a contaminant because it was sensitive to gentamicin and vancomycin.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA sequence of *Staphylococcus massiliensis* sp. nov. 5402776^T is EU707796.

Additional phylogenetic trees based on *tuf*, *hsp60*, *rpoB*, *dnaJ* and *sodA* gene sequences are available as supplementary figures with the online version of this paper.

Antimicrobial susceptibility was determined according to the CLSI (formerly National Committee for Clinical Laboratory Standards; NCCLS) criteria. The novel isolate was sensitive to oxacillin, gentamicin, clindamycin, ofloxacin, rifampicin, fosfomycin, vancomycin, teicoplanin and trimethoprim/sulfamethoxazole. The strain showed intermediate susceptibility to fusidic acid.

Colony morphology and haemolytic activity were observed after 48 h growth on 5 % sheep blood agar at 37 °C. Colonies were white, glossy, circular, bulging, non-haemolytic and 1–3 mm in diameter. Growth was tested at different temperatures (25, 30, 37, 45 and 50 °C) using sheep blood agar. Growth occurred between 25 °C and 45 °C, but optimum growth was obtained at 37 °C. Growth was tested in an anaerobic atmosphere created using the GENbag anaer incubation system (bioMérieux), a microaerophilic atmosphere created using the GENbag microaer incubation system, in the presence of air and also in the presence of 5 % CO₂. Growth occurred in all atmospheres but was weak in microaerophilic and anaerobic atmospheres. Growth in different NaCl concentrations was tested in trypticase soy broth (TSB; Becton Dickinson) supplemented with 2, 5, 7, 10 and 15 % (w/v) NaCl. The novel strain was able to grow in NaCl concentrations from 2 % to 15 % (w/v).

The size and ultrastructure of the cells were determined by electron microscopy. Cells were grown in liquid TSB medium for 48 h at 37 °C and stained with 1 % (w/v) phosphotungstic acid. The samples were examined using a transmission electron microscope (Morgagni 268D; Philips) at an operating voltage of 60 kV. The cells were cocci of 0.5–0.8 µm in diameter.

Coagulase activity was investigated using Staph Aureus Fumouze kit (Fumouze Diagnostics) and was negative. Catalase activity was determined by the ID colour catalase test kit (bioMérieux) and was positive. Oxidase activity was assayed by applying the cells to moistened discs impregnated with dimethyl-*p*-phenylene diamine (bioMérieux) and was negative. Clumping factor activity was investigated using the Slidex Staph Plus test (bioMérieux) and was negative. Biochemical characteristics were determined using API ZYM strips, API 50 CH strips combined with API 50 CHB/E medium, API 20 Staph strips and ID 32 Staph strips (bioMérieux) according to the manufacturer's instructions. Additional characteristics were tested using the Biolog system. Bacterial growth was obtained on BUG (Biolog Universal Growth) agar + blood (Biolog) medium. Suspension of the bacterial cells was performed using sterile GP/GN inoculation fluid (Biolog) and samples were dispensed to GP2 Microplates (Biolog) according to the manufacturer's instructions. Incubation was carried out at 36 °C in an aerobic atmosphere for 21 h.

The phenotypic characteristics of the novel strain were compared with those of *Staphylococcus piscifermentans* CIP 103958^T, *Staphylococcus condimenti* CIP 105760^T, *Staphylococcus carnosus* subsp. *carnosus* CIP 103274^T and

S. carnosus subsp. *utilis* CIP 105758^T, which were identified as the most closely related species by 16S rRNA gene sequence analysis, and with those of *Staphylococcus pettenkoferi* CIP 107711^T and *Staphylococcus chromogenes* CIP 81.59^T, which were identified as the most closely related species when *tuf*, *rpoB*, *dnaJ* gene sequences and *sodA* gene sequences were analysed, respectively. The distinctive traits of the novel isolate are presented in Table 1 and Table 2. The results of additional tests are given in the species description. Phenotypically, the most closely related strain to strain 5402776^T was *S. pettenkoferi* CIP 107711^T but differences were apparent for acid production from glycerol, D-glucose, D-fructose, sucrose and trehalose. Differences were also noted for enzymic activities such as esterase (C4), esterase lipase (C8) and acid phosphatase. Nitrate reduction was positive for strain 5402776^T but was negative for *S. pettenkoferi* CIP 107711^T.

Analysis of respiratory quinones by HPLC and polar lipids by two-dimensional TLC was carried out by the DSMZ Identification Service and Dr Brian Tindall, DSMZ, Braunschweig, Germany. Respiratory lipoquinones were extracted from 100 mg freeze-dried cell material as described by Tindall (1990a, b). Respiratory lipoquinones were separated into their different classes (menaquinones and ubiquinones) by TLC on silica gel, using hexane:tert-butylmethylether (9:1, v/v) as the solvent. UV-absorbing bands corresponding to menaquinones or ubiquinones were removed from the plate and further analysed by HPLC at 269 nm. The respiratory quinones were MK-7 (93 %) and MK-6 (7 %). Preparation and determination of cellular fatty acids were carried out according to the procedures given for the Sherlock Microbial identification system (MIDI). The major fatty acids were C_{15:0} iso (60.5 %), C_{17:0} iso (8.96 %), C_{15:0} anteiso (7.93 %) and C_{19:0} iso (6.78 %). The determination of the peptidoglycan structure was carried out as described by Schleifer (1985) and Schleifer & Kandler (1972) with the modification that TLC on cellulose was applied instead of paper chromatography. Quantitative analysis of amino acids was performed after derivatization by GC and GC/MS according to MacKenzie (1987). The total hydrolysate (4 M HCl, 16 h, 100 °C) of the peptidoglycan contained the amino acids lysine (Lys), alanine (Ala), glycine (Gly), serine (Ser) and glutamic acid (Glu) in molar ratios of around 1.0:1.5:3.5:0.9:1.0. The identity of the amino acids was confirmed by GC/MS. The partial hydrolysate (4 M HCl, 0.75 h, 100 °C) of the peptidoglycan contained (in addition to the amino acids) the peptides L-Ala→D-Glu, Gly→Gly, Gly→L-Lys, L-Lys→D-Ala and Gly→L-Lys→D-Ala. It was concluded that strain 5402776^T showed the A3α L-Lys-Gly₂₋₃-L-Ser-Gly peptidoglycan type (type A11.3 according to <http://www.dsmz.de/microorganisms/main.php?content id=35>). The interpeptide bridge, consisting of oligoglycine peptides, was characteristic of the genus *Staphylococcus*. The DNA G + C content was determined by using the HPLC method of Mesbah *et al.* (1989). The value found for strain 5402776^T was 36.6 mol%.

Table 1. Characteristics that differentiate the novel strain from the different species tested in this study

Taxa: 1, strain 5402776^T; 2, *S. pettenkoferi* CIP 107711^T; 3, *S. chromogenes* CIP 81.59^T; 4, *S. piscifermentans* CIP 103958^T; 5, *S. condimentis* CIP 105760^T; 6, *S. carnosus* subsp. *carnosus* CIP 103274^T; 7, *S. carnosus* subsp. *utilis* CIP 105758^T. +, Positive; –, negative; w, weakly positive.

Characteristic	1		2		3		4		5		6		7	
	24 h	48 h	24 h	48 h	24 h	48 h	24 h	48 h	24 h	48 h	24 h	48 h	24 h	48 h
Acid production from (API 50 CH):														
N-Acetylglucosamine	–	–	–	–	w	+	+	+	+	+	+	+	w	+
Aesculin	–	–	–	–	–	–	+	+	–	–	–	–	–	–
Arbutin	–	–	–	–	–	–	w	+	–	–	–	–	–	–
D-Fructose	–	–	w	+	+	+	–	+	+	+	+	+	+	+
D-Galactose	–	–	–	–	+	+	+	+	w	+	w	+	–	–
D-Glucose	–	–	w	+	+	+	+	+	+	+	+	+	+	+
Glycerol	–	–	–	w	w	+	–	–	–	–	w	+	–	–
D-Lactose	–	–	–	–	+	+	+	+	+	+	+	+	–	–
Maltose	–	–	–	–	–	–	+	+	–	–	–	–	–	–
D-Mannitol	–	–	–	–	–	–	–	–	w	+	+	+	–	–
D-Mannose	–	–	–	–	+	+	–	–	+	+	+	+	–	–
Melezitose	–	–	–	–	–	–	+	+	–	–	–	–	–	–
D-Ribose	–	–	–	–	+	+	–	–	–	+	–	–	–	–
D-Sorbitol	–	–	–	–	–	–	–	–	w	+	w	+	–	–
Sucrose	–	–	–	w	+	+	+	+	–	–	–	–	–	–
Trehalose	–	–	–	w	+	+	+	+	+	+	+	+	+	+
Turanose	–	–	–	–	–	–	w	+	–	–	–	–	–	–
Enzyme activities:														
Acid phosphatase	–		+		+		+		+		+		+	
Alkaline phosphatase	–		–		+		–		+		+		–	
Arginine dihydrolase	–		–		+		+		+		+		+	
Esterase (C4)	w		+		+		+		+		+		+	
Esterase lipase (C8)	w		+		w		+		+		+		–	
β-Galactosidase	–		–		–		+		+		+		–	
α-Glucosidase	–		–		–		+		–		–		+	
β-Glucosidase	–		–		–		+		–		–		–	
Naphthol-AS-BI-phosphohydrolase	–		–		–		–		–		+		w	
Urease	–		–		–		+		+		–		–	
Resistance to novobiocin	–		–		–		+		+		+		+	
Nitrate reduction	+		–		+		+		+		+		+	

For nucleotide sequence analysis, bacterial DNA was extracted using the MagNA Pure LC DNA isolation kit III (Roche) with the MagNA Pure LC instrument as described by the manufacturer. the 16S rRNA gene was PCR-amplified using the universal primer pair fD1 and rp2 (Weisburg *et al.*, 1991). The *tuf*, *hsp60*, *rpoB*, *dnaJ* and *sodA* genes were also PCR-amplified as previously described (Ghebremedhin *et al.*, 2008; Shah *et al.*, 2007). PCR products were purified using the NucleoFast 96 PCR kit (Macherey–Nagel) according to the manufacturer's recommendations. Sequencing reactions were carried out using the Big Dye Terminator, version 1.1, cycle sequencing kit (Perkin-Elmer) according to the manufacturer's instructions. Sequencing products were purified and sequences were analysed on an ABI PRISM 3130x Genetic Analyzer (Applied Biosystems). The sequences obtained were compared with database sequences (GenBank) using BLAST. Gene sequences were aligned using the multi-sequence alignment program CLUSTAL_X (1.8). Phylogenetic

relationships with closely related species were determined using MEGA version 4 (Tamura *et al.*, 2007). Distance matrices were determined following the assumptions described by Kimura (1980) and were used to elaborate dendrograms using the neighbour-joining method (Saitou & Nei, 1987). The maximum-parsimony algorithm was also used to infer phylogenetic relationships. A bootstrap analysis was performed to investigate the stability of the tree obtained. Bootstrap values were obtained for a consensus tree based on 100 randomly generated trees. The tree topology was the same with the two methods.

Based on 16S rRNA sequence comparisons, a value $\leq 97\%$ has been suggested as the threshold to separate species (Stackebrandt *et al.*, 2002). However, increasingly, novel species have been described with higher similarity values (Kuisiene *et al.*, 2008; Mun *et al.*, 2008; Song *et al.*, 2007; Zhou *et al.*, 2008) and recently Stackebrandt & Ebers

Table 2. GP2 MicroPlate results

Taxa: 1, strain 5402776^T; 2, *S. pettenkoferi* CIP 107711^T; 3, *S. chromogenes* CIP 81.59^T; 4, *S. piscifermentans* CIP 103958^T; 5, *S. condimenti* CIP 105760^T; 6, *S. carnosus* subsp. *carnosus* CIP 103274^T; 7, *S. carnosus* subsp. *utilis* CIP 105758^T. +, Positive; –, negative; w, weakly positive; v, variable.

Characteristic	1	2	3	4	5	6	7
Acetic acid	–	–	–	–	–	–	+
N-Acetyl-D-glucosamine	–	–	–	–	–	+	+
Adenosine	+	–	–	+	–	+	+
Adenosine 5'-monophosphate	–	–	–	–	–	+	–
L-Alaninamide	v	–	–	–	–	–	–
D-Alanine	–	–	–	+	+	v	+
L-Alanyl glycine	–	–	–	+	–	–	+
L-Arabinose	w	–	–	–	–	–	+
D-Arabitol	–	–	–	+	–	–	–
2'-Deoxyadenosine	+	–	–	+	–	+	+
Dextrin	–	–	–	+	+	+	+
D-Fructose 6-phosphate	–	+	–	–	–	–	–
D-Fructose	–	–	+	+	+	+	+
D-Galactose	–	–	–	+	v	–	–
D-Gluconic acid	–	–	–	+	+	+	–
D-Glucose 6-phosphate	–	+	–	–	–	–	–
L-Glutamic acid	+	+	–	+	+	–	+
DL- α -Glycerol phosphate	–	–	–	+	+	–	–
α -Hydroxybutyric acid	–	–	+	–	–	–	+
γ -Hydroxybutyric acid	–	–	–	v	–	–	–
Inosine	w	–	–	–	–	+	+
α -Ketovaleric acid	+	+	+	+	w	+	+
D-Lactic acid methyl ester	–	–	–	–	v	–	–
Maltose	–	–	–	+	–	–	–
Maltotriose	–	–	–	+	–	–	–
D-Mannitol	–	–	–	–	–	+	–
D-Mannose	–	–	+	–	+	+	–
Melezitose	–	–	–	+	–	–	–
β -Methyl D-glucoside	–	–	+	–	–	–	–
3-Methyl D-glucose	–	–	–	–	+	+	+
D-Psicose	–	–	+	+	+	+	+
L-Pyrogutamic acid	+	–	–	+	–	v	–
D-Ribose	+	–	+	+	+	+	+
L-Serine	+	–	+	+	+	+	+
Sucrose	–	+	+	+	–	–	–
Thymidine	–	–	–	+	+	+	+
Thymidine 5'-monophosphate	–	–	–	–	v	+	–
Trehalose	–	+	+	+	+	+	+
Turanose	–	–	–	+	–	–	v
Tween 40	–	–	–	–	–	–	+
Uridine	–	–	–	+	+	+	+
Uridine 5'-monophosphate	–	–	–	–	+	+	–
D-Xylose	–	–	+	–	–	–	+

(2006) proposed that a cut-off value of 98.7 % should be applied to define novel species on the basis of 16S rRNA gene sequence comparisons. This new cut-off value was confirmed by Achtman & Wagner (2008). Based on 16S rRNA gene sequence similarity (calculated with MEGA version 4), the highest value between the novel strain and other species of the genus *Staphylococcus* was 97.7 % with *S.*

piscifermentans. The similarity values between the novel strain and recognized species of the genus *Staphylococcus* ranged from 99.9 % to 95.8 % (median value, 97.3 %). Based on 16S rRNA gene sequence comparisons, strain 5402776^T represented a novel species of the genus *Staphylococcus* (Fig. 1). In the phylogenetic analyses inferred from *tuf*, *dnaJ* and *rpoB* gene sequence comparisons, strain 5402776^T clustered with *S. pettenkoferi* (see Supplementary Figs S1, S2 and S3 in IJSEM Online). The sequence similarity values were 93.7 %, 82.5 % and 89 %, respectively. In the phylogenetic analysis inferred from *sodA* gene sequences, strain 5402776^T clustered with *S. chromogenes* (82.8 %) and in the phylogenetic analysis inferred from the *hsp60* gene sequences, strain 5402776^T formed a distinct subline within the genus *Staphylococcus* (see Supplementary Figs S4 and S5).

Based on the results described above, we suggest that the novel strain isolated from a human brain abscess represents a novel species of the genus *Staphylococcus* species, for which the name *Staphylococcus massiliensis* sp. nov. is proposed.

Description of *Staphylococcus massiliensis* sp. nov.

Staphylococcus massiliensis (mas.si.li.en'sis. L. masc. adj. *massiliensis* of Massilia, the old Roman name for Marseille, from where the type strain was isolated).

Cells are Gram-positive, 0.5–0.8 μ m in diameter, non-spore-forming, non-motile and occur singly, in pairs and in clusters. Growth occurs preferentially in aerobic atmospheres. After 48 h on 5 % sheep blood agar, colonies are white, glossy, circular, regular, bulged, non-haemolytic and 1–3 mm in diameter. The temperature range for growth is 25–45 °C, with optimum growth between 30 °C and 37 °C. Grows at 37 °C in TSB containing 0–15 % (w/v) NaCl. Coagulase-negative, catalase-positive, oxidase-negative, novobiocin-susceptible and negative in tests for the presence of clumping factor. Using API ZYM, activities of esterase (C4) and esterase lipase (C8) are weakly positive. No activities for alkaline phosphatase, lipase (C14), acid phosphatase, β -galactosidase, leucine arylamidase, valine arylamidase, α -glucosidase, cystine arylamidase, trypsin, α -chymotrypsin, naphthol-AS-BI-phosphohydrolase, α -galactosidase, β -glucuronidase, β -glucosidase, N-acetyl- β -glucosaminidase, α -mannosidase or α -fucosidase are detected. Using the API Rapid ID32 Staph system, reduction of nitrates is positive. No activities for urease, arginine dihydrolase, ornithine decarboxylase, β -galactosidase, arginine arylamidase, alkaline phosphatase, pyrrolidonyl arylamidase or β -glucuronidase. Negative results for aesculin hydrolysis and acetoin production. All reactions for fermentation of sugars are negative: D-glucose, D-fructose, D-mannose, D-lactose, trehalose, D-mannitol, raffinose, D-ribose, cellobiose, D-sucrose, turanose, N-acetylglucosamine and L-arabinose. Using API 50 CH after an incubation time of 48 h, acid is not produced from D-

Fig. 1. Phylogenetic tree inferred from 16S rRNA gene sequence comparisons (1264 nt fragment). Numbers at nodes are the percentages of 100 resamplings that support the shown topology. *Macrococcus bovicus*, *Gemella morbillorum* and *Streptococcus pneumoniae* were used as the outgroup. Bootstrap values >50% are indicated at nodes. Bar, 0.02 nucleotide changes per nucleotide position.

galactose, D-glucose, D-fructose, maltose, D-lactose, sucrose, trehalose, D-xylose, melezitose, turanose, D-lyxose, D-ribose, D-mannose, glycerol, erythritol, D-arabinose, L-arabinose, L-xylose, D-adonitol, methyl β -D-xylopyranoside, L-sorbose, L-rhamnose, dulcitol, inositol, D-mannitol, D-sorbitol, methyl α -D-mannopyranoside, methyl α -D-glucopyranoside, N-acetylglucosamine, amygdalin, arbutin, aesculin ferric citrate, salicin, cellobiose, D-melibiose, inulin, raffinose, starch,

glycogen, xylitol, gentiobiose, D-tagatose, D-fucose, L-fucose, D-arabitol, L-arabitol, potassium gluconate, potassium 2-ketogluconate or potassium 5-ketogluconate. Using the Biolog GP2 Microplate, the following tests are positive, α -D-glucose, D-ribose, α -ketovaleric acid, L-lactic acid, pyruvic acid methyl ester, pyruvic acid, L-alanine, L-glutamic acid, L-pyroglyutamic acid, L-serine, glycerol, adenosine and 2'-deoxyadenosine. L-Arabinose and inosine are weakly posi-

tive. L-Alaninamide is variable. The following tests are negative: α -cyclodextrin, β -cyclodextrin, dextrin, glycogen, inulin, mannan, Tween 40, Tween 80, N-acetyl-D-glucosamine, N-acetyl- β -D-mannosamine, amygdalin, D-arabitol, arbutin, cellobiose, D-fructose, L-fucose, D-galactose, D-galacturonic acid, gentiobiose, D-gluconic acid, myo-inositol, α -D-lactose, lactulose, maltose, maltotriose, D-mannitol, D-mannose, melezitose, melibiose, methyl α -D-galactoside, methyl β -D-galactoside, 3-methyl D-glucose, methyl α -D-glucoside, methyl β -D-glucoside, methyl α -D-mannoside, palatinose, D-psicose, raffinose, L-rhamnose, salicin, sedoheptulosan, D-sorbitol, stachyose, sucrose, D-tagatose, trehalose, turanose, xylitol, D-xylose, acetic acid, α -hydroxybutyric acid, β -hydroxybutyric acid, γ -hydroxybutyric acid, p-hydroxyphenylacetic acid, α -ketoglutaric acid, lactamide, D-lactic acid methyl ester, D-malic acid, L-malic acid, succinic acid monomethyl ester, propionic acid, succinamic acid, succinic acid, N-acetyl-L-glutamic acid, D-alanine, L-alanyl glycine, L-asparagine, glycyl L-glutamic acid, putrescine, 2,3-butanediol, thymidine, uridine, adenosine 5'-monophosphate, thymidine 5'-monophosphate, uridine 5'-monophosphate, D-fructose 6-phosphate, α -D-glucose 1-phosphate, D-glucose 6-phosphate and DL- α -glycerol phosphate. The respiratory quinones are MK-7 (93 %) and MK-6 (7 %), and the major fatty acids are C_{15:0} iso, C_{17:0} iso, C_{15:0} anteiso and C_{19:0} iso. The peptidoglycan type is A3 α L-Lys-Gly₂₋₃-L-Ser-Gly.

The type strain, 5402776^T (=CCUG 55927^T=CSUR P23^T), was isolated from a human brain abscess. The DNA G + C content of the type strain was 36.6 mol%.

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