Description of *Sinomonas soli* sp. nov., reclassification of *Arthrobacter echigonensis* and *Arthrobacter albidus* (Ding et al. 2009) as *Sinomonas echigonensis* comb. nov. and *Sinomonas albida* comb. nov., respectively, and emended description of the genus *Sinomonas*

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A novel actinomycete strain, designated CW 59^T, was isolated from a polluted forest soil sample in Anhui Province, China. Cells were strictly aerobic, non-motile, bent rods. The strain grew optimally at 30–37 °C and pH 6.0–8.0. The major fatty acids were ai-C_{15:0} (34.7%), i-C_{15:0} (11.6%) and ai-C_{17:0} (14.9%); the predominant respiratory quinone was MK-9(H₂), with MK-8(H₂) present as a minor component. The polar lipid composition of strain CW 59^T consisted of diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol, two glycolipids and phosphatidylmonomethylethanolamine (minor component). The whole-cell sugars contained galactose, mannose, ribose and glucose; the major amino acids of the cell-wall were lysine, alanine and glutamic acid. The genomic DNA G + C content was 66.9 mol%. Phylogenetic analysis showed that CW 59^T belonged to the genus *Sinomonas* and grouped with members of the species *Sinomonas atrocyanea*, *Sinomonas flava*, *Arthrobacter echigonensis* and *Arthrobacter albidus*. 16S rRNA gene sequence similarities of CW 59^T to *S. atrocyanea* DSM 20127^T, *S. flava* CW 108^T, *A. echigonensis* LC10^T and *A. albidus* LC13^T were 99.5, 99.3, 98.2 and 98.0%, respectively. DNA–DNA hybridization of the isolate showed relatedness values of 58.3% (DSM 20127^T), 41.8% (CW 108^T), 21.6% (LC10^T) and 25.5% (LC13^T) with its four closest neighbours. The taxonomic relationships of strains LC10^T and LC13^T with the genus *Sinomonas* were further clarified by means of a direct experimental comparison; results showed that strains LC10^T and LC13^T showed the same major fatty acid, polar lipid, cell-wall amino acid, whole-cell sugar and respiratory quinone compositions as members of the genus *Sinomonas*. Based on phenotypic, chemotaxonomic and phylogenetic analysis, it is proposed that: strain CW 59^T represents a novel species of the genus *Sinomonas*, *Sinomonas soli* sp. nov., with CW 59^T (=CCTCC AB 207193^T=KCTC 19389^T) as the type strain; and the type strains of *A. echigonensis* and *A. albidus* should be reclassified as *Sinomonas echigonensis* comb. nov. and *Sinomonas albida* comb. nov., respectively. An emended description of the genus *Sinomonas* is given.

The genus *Sinomonas* (type species *Sinomonas flava*) was first proposed by Zhou et al. (2009) with the description of the

newly isolated strain *S. flava* CW 108^T and the reclassification of *Arthrobacter atrocyaneus* as *Sinomonas atrocyanea* (type strain DSM 20127^T) (Zhou et al., 2009; Kuhn & Starr, 1960). Shortly after the description of the genus *Sinomonas* was published, two novel species *Arthrobacter echigonensis* and *Arthrobacter albidus* were proposed (Ding et al., 2009), but strains of these species showed high 16S rRNA gene

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A supplementary figure is available with the online version of this paper.

sequence similarity values (>98 %) with strains of *S. flava* and *S. atrocyanea*, and the four species formed a deep separate lineage within the family *Micrococcaceae*. However, no conclusive evidence regarding their taxonomic relationships based on polyphasic taxonomy studies has been provided thus far.

During a project to investigate bacterial diversity from a polycyclic aromatic hydrocarbon-polluted forest soil sample from Anhui Province (China), one actinomycete strain, designated CW 59^T, was isolated and subjected to a polyphasic taxonomic study along with the four of its closest phylogenetic neighbours. Strain CW 59^T showed high 16S rRNA gene sequence similarities to *S. atrocyanea* DSM 20127^T (99.5 %) and *S. flava* CW 108^T (99.3 %), but the novel isolate displayed obviously different morphological and physiological characteristics from these two strains. In order to determine the phylogenetic and taxonomic relationships between strain CW 59^T, *A. echigonensis* and *A. albidus*, and species of the genus *Sinomonas*, morphological, physiological and chemotaxonomic characteristics of type strains belonging to these species were determined. DNA–DNA hybridization reactions were also performed between CW 59^T and its four closest relatives. Results from this polyphasic taxonomic study indicated that strain CW 59^T represents a novel species of the genus *Sinomonas*, for which the name *Sinomonas soli* sp. nov. is proposed; it is also proposed that *A. echigonensis* and *A. albidus* should be reclassified as members of the genus *Sinomonas* as *Sinomonas echigonensis* comb. nov. and *Sinomonas albida* comb. nov., respectively, and an emended description of the genus *Sinomonas* is given.

Strain CW 59^T was isolated using the medium and methods described by Zhou *et al.* (2007) from a polluted forest soil sample. The pure culture was preserved in 25 % (v/v) glycerol at –80 °C. *S. atrocyanea* DSM 20127^T and *S. flava* CW 108^T, as used in previous studies (Zhou *et al.*, 2009) were obtained from our laboratory, and *A. echigonensis* LC10^T (=CCTCC AB 206017^T) and *A. albidus* LC13^T (=CCTCC AB 206018^T) were obtained from the China Center for Type Culture Collection (CCTCC). These four most closely related type strains were used as reference strains for DNA–DNA hybridization and for analysis of chemotaxonomic markers and physiological characteristics.

In order to investigate the morphological, biochemical and physiological characteristics, the five strains were routinely cultivated on TYB and PYES media at 30 °C (Zhou *et al.*, 2009; Wieser *et al.*, 2002). Unless otherwise indicated, phenotypic characteristics were studied using standard procedures (Smibert & Krieg, 1994; Zhou *et al.*, 2007). Dark blue pigment production was determined on YDC agar as described by Kuhn & Starr (1960). Morphological characteristics of strain CW 59^T were observed by light microscopy (model XTL-3400; Olympus) and transmission electron microscopy (model H-7650; Hitachi) after incubation for 24 h at 30 °C on TYB agar. Electron microscopy preparations were performed as described by Yoon *et al.*

(2003). For the various physiological tests, API 20E and API 50 CHB test strips (bioMérieux) were applied according to the manufacturer's instructions.

PCR amplification of the 16S rRNA gene sequence was performed as described by Li *et al.* (2007). The 16S rRNA gene sequence was manually aligned with reference sequences retrieved from GenBank following BLAST searches. Phylogenetic trees were constructed using the software package MEGA version 3.1 (Kumar *et al.*, 2004) after multiple alignment of sequence data by CLUSTAL_X (Thompson *et al.*, 1997). The corrected evolutionary distance was calculated according to Kimura's two-parameter model (Kimura, 1980, 1983) and clustering was based on the neighbour-joining and maximum-parsimony methods. Bootstrap analysis was used to evaluate the tree topology by performing 1000 resamplings (Felsenstein, 1985).

Genomic DNA was prepared for determination of G + C content and DNA–DNA hybridization tests following the procedure of Marmur (1961). The DNA G + C content was determined by reverse-phase HPLC according to Mesbah *et al.* (1989). DNA–DNA hybridizations were carried out using the optical renaturation method (Jahnke, 1992; Huß *et al.*, 1983; De Ley *et al.*, 1970). DNA–DNA hybridizations were performed with CW 59^T and the four reference type strains; five replicate experiments were carried out. Bacterial biomass collected for chemotaxonomic analysis was cultivated on tryptic soy agar (TSA) at 30 °C for 24 h. Respiratory quinones were extracted from lyophilized cells and the extracts were purified and analysed by HPLC using the procedures reported by Hu *et al.* (2001). Procedures for identification of cell-wall amino acids and whole-cell sugars were as described by Stanek & Roberts (1974). Cellular fatty acid analysis was performed as described by Sasser (1990) using the Microbial Identification System (MIDI, Sherlock Version 6.0) with database TSBA 6.00. Polar lipids were extracted, examined by two-dimensional TLC and identified using the procedures of Minnikin *et al.* (1984).

Strain CW 59^T showed good growth on PYES and TYB agar and moderate growth was observed on Luria–Bertani agar (Oxoid). As observed with the type strains of *S. atrocyanea* and *S. flava*, strain CW 59^T showed obvious growth at temperatures up to 42 °C on PYES (or TYB) medium, but not at 45 °C. Cells of CW 59^T were non-motile, bent rods (0.5–1.0 µm in width and 1.2–4.5 µm in length, as calculated by transmission electron microscopy) after cultivation for 24 h. Metamorphic characteristics of bacterial cells (rod–coccus growth cycle) were observed for CW 59^T and other type strains of the genus *Sinomonas* at various growth stages (or under different cultural conditions). Phenotypic properties useful for distinguishing CW 59^T from its four phylogenetic neighbours are shown in Table 1 and the detailed characteristics of strain CW 59^T are summed up in the species description.

The almost complete 16S rRNA gene sequence of strain CW 59^T was determined. Phylogenetic analysis based on 16S rRNA gene sequences showed that strain CW 59^T

Table 1. Morphological and physiological characteristics of five type strains of the genus *Sinomonas*

Strains: 1, *Sinomonas soli* CW 59^T; 2, *Sinomonas flava* CW 108^T; 3, *Sinomonas atrocyanea* DSM 20127^T; 4, *Sinomonas echigonensis* LC10^T; 5, *Sinomonas albida* LC13^T. +, Positive; –, negative; (+), weakly positive.

Characteristic	1	2	3	4	5
Colony colour on: *					
YDC agar at 25 °C	PY	PY	DB	CW	CW
TYB or PYES agar	PY	PY	GW	PY	PY
API 20E					
Citrate acid	(+)	+	–	–	–
Catalase	+	(+)	+	(+)	–
Urease	(+)	+	–	–	–
Tween 80	(+)	+	(+)	+	+
Nitrate reduction	–	+	+	–	–
API 50CHB					
Glycerol	–	+	–	(+)	+
Erythritol	–	+	–	–	–
Ribose	–	(+)	–	–	–
Methyl β-D-xyloside	–	+	+	–	+
D-Glucose	–	+	+	(+)	+
Sorbitol	–	(+)	–	–	+
N-Acetylglucosamine	(+)	–	–	–	+
Salicin	+	–	–	(+)	+
Cellobiose	–	(+)	–	(+)	+
Maltose	–	(+)	–	(+)	+
Sucrose	+	(+)	+	–	+
Melezitose	–	(+)	–	–	+
Turanose	+	(+)	(+)	–	(+)
2-Ketogluconate	–	+	–	–	–

*CW, Creamy white; DB, dark blue; GW, grey white; PY, pale yellow.

clearly belonged to the genus *Sinomonas* and clustered with strains of *S. atrocyanea*, *S. flava*, *A. echigonensis* and *A. albidus* in the phylogenetic tree (Fig. 1; Supplementary Fig. S1, available in IJSEM Online). 16S rRNA gene sequence similarities between CW 59^T and the four reference strains DSM 20127^T, CW 108^T, LC10^T and LC13^T were 99.5, 99.3, 98.2 and 98.0 %, respectively. Due to the high 16S rRNA gene sequence similarities between CW 59^T and its four closest neighbours, DNA–DNA hybridizations were required to clarify their relatedness (Stackebrandt & Goebel, 1994). The DNA–DNA relatedness values between CW 59^T and the reference strains were 58.3 % (DSM 20127^T), 41.8 % (CW 108^T), 21.6 % (LC10^T) and 25.5 % (LC13^T), respectively, values which are significantly lower than the threshold value of 70 % that is commonly accepted for the definition of a novel bacterial species (Stackebrandt & Goebel, 1994).

The DNA G + C content of strain CW 59^T was 66.9 mol% and the major fatty acids consisted of ai-C_{15:0}, i-C_{15:0} and ai-C_{17:0}. All five strains studied had the same major fatty acids (content >10 %); detailed fatty acid profiles are given in Table 2. The respiratory quinone system of CW 59^T was

the same as that of *S. flava* CW 108^T and consisted of MK-9(H₂) as the predominant respiratory quinone, with MK-8(H₂) as a minor component; LC10^T and LC13^T also contained MK-9(H₂) as the predominant respiratory quinone, but had MK-10(H₂) as a minor component. The polar lipid composition of CW 59^T was similar to that of *S. flava* and consisted of diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol and two glycolipids, with phosphatidylmonomethylethanolamine as a minor component (two glycolipids were not listed in the previous publication for *S. flava*) (Zhou *et al.*, 2009). Diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol and two glycolipids were detected in strains LC10^T and LC13^T, but phosphatidylmonomethylethanolamine was not detected. Strains CW 59^T and CW 108^T contained the whole-cell sugars galactose, mannose, ribose and glucose and the cell-wall amino acids were lysine, alanine and glutamic acid. Strains LC10^T and LC13^T displayed almost the same whole-cell sugars (galactose, mannose, ribose and glucose were detected for strains LC10^T and LC13^T, and glucosamine was also detected as a minor component in LC13^T) as *S. flava* and similar cell-wall amino acids (lysine, alanine and serine) as strain CW 108^T (Zhou *et al.*, 2009; Ding *et al.*, 2009).

Although phylogenetic analysis and chemotaxonomic characteristics (major fatty acids, polar lipids and respiratory quinones, etc.) supported assignment of strain CW 59^T to the genus *Sinomonas*, differences in physiological and biochemical characteristics, i.e. dark blue pigment production, nitrate reduction, and utilization of methyl β-D-xyloside, D-glucose, N-acetylglucosamine and salicin, indicate that strain CW 59^T is not a member of any described species of the genus *Sinomonas*. Furthermore, differences in fatty acid composition were also observed between strain CW 59^T and type strains of *Sinomonas* species (Table 2). Morphological, physiological and chemotaxonomic characteristics combined with DNA–DNA hybridization results support the proposal that strain CW 59^T represents a novel species of genus *Sinomonas*, *Sinomonas soli* sp. nov.

In the present work, comparisons between LC10^T, LC13^T and type strains of species of the genus *Sinomonas* based on a polyphasic approach were carried out to elucidate their taxonomic relationships. Phylogenetic analysis indicated that two *Arthrobacter* strains (LC10^T and LC13^T) showed high 16S rRNA gene sequence similarity values (>98 %) with the three *Sinomonas* strains CW 59^T, CW 108^T and DSM 20127^T, and the five strains formed a deep lineage that was separate from other *Arthrobacter* species in the family *Micrococcaceae* (Fig. 1; Supplementary Fig. S1). Chemotaxonomically, LC10^T and LC13^T showed the same predominant respiratory quinone [MK-9(H₂)], major fatty acids (ai-C_{15:0}, i-C_{15:0} and ai-C_{17:0}), major whole-cell sugars (galactose, mannose, ribose and glucose), diagnostic diamino acid (lysine) and major polar lipids (diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol and two glycolipids) as the strains of *Sinomonas*

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences, showing the position of *Sinomonas soli* CW 59^T and related taxa in the family Micrococcaceae. Bootstrap values are shown as percentages of 1000 replicates; only values above 50 % are shown. GenBank accession numbers are shown in parentheses. Bar, 1 nt substitution per 100 nt.

studied. Phylogenetic data and chemotaxonomic results described above strongly support the transfer of *A. echigonensis* and *A. albidus* to the genus *Sinomonas* as *Sinomonas echigonensis* comb. nov. and *Sinomonas albida* comb. nov., respectively.

In this study, the presence of phosphatidylmonomethyl-ethanolamine as a minor polar lipid was not detected in the newly proposed combinations *S. echigonensis* and *S. albida*. Catalase activity was negative for *Sinomonas albida* in this study. Additionally, differences in the minor respiratory quinone [MK-10(H₂)] and cell-wall amino acid components (i.e. the presence of serine) were observed between the two species *S. echigonensis* and *S. albida* and the other *Sinomonas* strains studied; an emended description of the genus *Sinomonas* is thus proposed.

Emended description of the genus *Sinomonas*

Sinomonas (Si.no.mo'nas. M.L. n. *Sina* China; L. fem. n. *monas* a unit, monad; N.L. fem. n. *Sinomonas* a bacterium isolated from China).

Cells are Gram-positive (or variable), aerobic, mesophilic and rod-shaped; a rod-coccus cycle may be observed. Oxidase activity is negative and catalase activity is variable. Major fatty acids are ai-C_{15:0}, i-C_{15:0} and ai-C_{17:0}. The predominant respiratory quinone is MK-9(H₂). Polar lipids

consist of diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol and two glycolipids. The peptidoglycan type is A3 α (peptidoglycan diagnostic diamino acid is lysine) and whole-cell sugars are galactose, mannose, ribose and glucose. The DNA G+C content is 66.9–71.8 mol%. The type species is *Sinomonas flava*.

Description of *Sinomonas soli* sp. nov.

Sinomonas soli (so'li. L. gen. n. *soli* of soil, the source of the type strain).

Cells are Gram-positive (or variable), aerobic, mesophilic and rod-shaped; a rod-coccus cycle may be observed. Colonies are circular, convex and pale yellow in colour after 24 h cultivation at 30–37 °C on TYB, YDC or PYES agar. Growth occurs at 15–42 °C (optimum 30–37 °C) and pH 5.0–9.0 (optimum pH 6.0–8.0). Dark blue pigment is not produced on YDC agar at 25–30 °C. Growth occurs with 0–3 % (w/v) NaCl, but not with 4 % (w/v) NaCl. Catalase activity is present and oxidase activity is absent. Tween 80 is hydrolysed weakly, but casein and tyrosine are not hydrolysed. β -Galactosidase activity is present; weak activities of urease and lipase are also present, but arginine dihydrolase, tryptophan deaminase, ornithine decarboxylase and lysine decarboxylase activities are absent. Nitrate and nitrite are not reduced, citrate is utilized weakly but

Table 2. Cellular fatty acids of *Sinomonas soli* CW 59^T and four related type strains of the genus *Sinomonas*

Strains: 1, *Sinomonas soli* CW 59^T; 2, *Sinomonas flava* CW 108^T; 3, *Sinomonas atrocyanea* DSM 20127^T; 4, *Sinomonas echigonensis* LC10^T; 5, *Sinomonas albida* LC13^T. Data for CW 108^T and DSM 20127^T were obtained from Zhou *et al.* (2009) and data for the other three type strains were from the present study; all strains were grown on TSA medium and fatty acids were analysed under the same conditions. Major fatty acids are indicated in bold. ND, Not detected.

Fatty acid	1	2	3	4	5
i-C _{14:0}	0.6	ND	1.4	0.7	0.6
C _{14:0}	2.1	1.3	ND	0.1	0.3
i-C_{15:0}	11.6	30.6	13.9	14.1	13.0
ai-C_{15:0}	34.7	35.9	36.3	58.9	41.3
i-C _{16:0}	3.3	1.9	7.2	4.7	6.8
C _{16:0}	9.8	4.3	1.6	0.4	1.9
i-C _{17:0}	2.2	3.2	6.0	2.4	5.6
ai-C_{17:0}	14.9	15.4	30.2	17.8	29.4
C _{18:1ω9c}	5.0	0.6	ND	ND	ND
C _{18:0}	7.8	2.2	1.0	0.1	0.10
Summed features:*					
3	0.6	1.0	ND	ND	ND
8	3.9	0.6	ND	0.1	ND

*Fatty acids that could not be separated by GC using Microbial Identification System (Microbial ID) software were considered as summed features. Summed feature 3 contains C_{16:1 ω 7c} and/or C_{16:1 ω 6c}; summed feature 8 contains C_{18:1 ω 7c} and/or C_{18:1 ω 6c}.

gelatin is not hydrolysed. Voges–Proskauer test is positive; indole and H₂S are not produced (API 20E tests). *N*-Acetylglucosamine, aesculin, D-fructose, inositol, D-mannose, mannitol, salicin, sucrose and turanose are utilized in API 50 CHB tests. D-Adonitol, amygdalin, D-arabinose, L-arabinose, D-arabitol, L-arabitol, arbutin, cellobiose, dulcitol, erythritol, D-fucose, L-fucose, D-galactose, D-gentiobiose, D-glucose, glycerol, glycogen, inulin, lactose, D-lyxose, maltose, melezitose, melibiose, methyl β -D-xylopyranoside, methyl α -D-mannopyranoside, methyl α -D-glucopyranoside, potassium gluconate, potassium 2-ketogluconate, potassium 5-ketogluconate, raffinose, L-rhamnose, D-ribose, L-sorbose, sorbitol, starch, D-tagatose, trehalose, xylitol, D-xylose and L-xylose are not assimilated in API 50CHB tests. Polar lipids comprise diphosphatidylglycerol, phosphatidylglycerol, phosphatidyl-inositol and two glycolipids, with phosphatidylmonomethyl-ethanolamine as a minor component. Whole-cell sugars contain galactose, mannose, ribose and glucose. The fatty acid profile contains C_{14:0}, i-C_{15:0}, ai-C_{15:0}, i-C_{16:0}, C_{16:0}, i-C_{17:0}, ai-C_{17:0}, C_{18:0}, C_{18:1 ω 9c} and summed feature 8 (C_{18:1 ω 7c} and/or C_{18:1 ω 6c}).

The type strain is CW 59^T (=CCTCC AB 207193^T=KCTC 19389^T), isolated from a polluted forest soil sample in Anhui Province, China. The DNA G+C content of the type strain is 66.9 mol% (HPLC).

Description of *Sinomonas echigonensis* comb. nov.

Sinomonas echigonensis (echi.go.nen'sis. N.L. fem. adj. *echigonensis* pertaining to the Echigo region, Japan).

Basonym: *Arthrobacter echigonensis* Ding *et al.* 2009.

The description is as given for the genus and *Arthrobacter echigonensis* by Ding *et al.* (2009) with the following additions. Dark blue pigment is not produced on YDC agar at 25–30 °C. Weak activities of β -galactosidase and arginine dihydrolase are present, but urease, tryptophan deaminase, ornithine decarboxylase and lysine decarboxylase activities are absent. Nitrate is not reduced, citrate is not utilized and gelatin is not hydrolysed. Indole and H₂S are not produced (API 20E tests). *N*-Acetylglucosamine, aesculin, amygdalin, D-arabitol, arbutin, cellobiose, D-fructose, D-glucose, glycerol, inulin, maltose, mannitol, melezitose, methyl α -D-mannopyranoside, methyl α -D-glucopyranoside, salicin, starch, sucrose and turanose are utilized in API 50CHB tests. D-Adonitol, D-arabinose, L-arabinose, L-arabitol, dulcitol, erythritol, D-fucose, L-fucose, D-galactose, D-gentiobiose, glycogen, inositol, lactose, D-lyxose, D-mannose, melibiose, methyl β -D-xylopyranoside, potassium gluconate, potassium 2-ketogluconate, potassium 5-ketogluconate, raffinose, L-rhamnose, D-ribose, L-sorbose, sorbitol, D-tagatose, trehalose, xylitol, D-xylose and L-xylose are not utilized in API 50CHB tests.

The type strain is LC10^T (=IAM 15385^T=CCTCC AB 206017^T), isolated from a filtration substrate made from volcanic rock from Niigata, Japan.

Description of *Sinomonas albida* comb. nov.

Sinomonas albida (al'bi.da. L. fem. adj. *albida* whitish, referring to the colour of the colonies).

Basonym: *Arthrobacter albidus* Ding *et al.* 2009.

The description is as given for the genus and *Arthrobacter albidus* by Ding *et al.* (2009) with the following additions. Dark blue pigment is not produced on YDC agar at 25–30 °C. Negative for catalase and oxidase. β -Galactosidase activity is present, weak arginine dihydrolase activity is also present, but urease, tryptophan deaminase, ornithine decarboxylase and lysine decarboxylase activities are absent. Nitrate is not reduced, citrate is not utilized and gelatin is not hydrolysed. Indole and H₂S are not produced (API 20E tests). *N*-Acetylglucosamine, D-adonitol, aesculin, amygdalin, L-arabinose, arbutin, cellobiose, dulcitol, D-fructose, D-galactose, D-gentiobiose, D-glucose, glycerol, inositol, inulin, lactose, maltose, mannitol, D-mannose, melezitose, melibiose, methyl α -D-mannopyranoside, methyl α -D-glucopyranoside, methyl β -D-xylopyranoside, raffinose, L-rhamnose, salicin, starch, L-sorbose, L-sorbitol, sucrose, trehalose, turanose, D-xylose and L-xylose are utilized in API 50CHB tests. D-Arabinose, D-arabitol, L-arabitol, erythritol, D-fucose, L-fucose, glycogen, D-lyxose, potassium gluconate, potassium 2-ketogluconate, potassium 5-ketogluconate, D-ribose, D-tagatose and xylitol are not utilized in API 50CHB tests.

Whole-cell sugars contain galactose, mannose, ribose and glucose, with glucosamine as a minor component.

The type strain is LC13^T (=IAM 15386^T=CCTCC AB 206018^T), isolated from a filtration substrate made from volcanic rock from Niigata, Japan.

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