Transfer of [*Flexibacter*] *sancti*, [*Flexibacter*] *filiformis*, [*Flexibacter*] *japonensis* and [*Cytophaga*] *arvensicola* to the genus *Chitinophaga* and description of *Chitinophaga skermanii* sp. nov.

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Analysis of the 16S rRNA gene sequences of species currently assigned to the genus *Flexibacter* has shown extensive intrageneric phylogenetic heterogeneity. It has been shown in previous studies that the species [*Flexibacter*] *sancti*, [*Flexibacter*] *filiformis* and [*Flexibacter*] *japonensis* were most closely related to *Chitinophaga pinensis*. In addition, [*Cytophaga*] *arvensicola* and species of the genus *Terrimonas* also clustered into this phylogenetic group. Although the similarities of 16S rRNA gene sequences were low (88·5–96·4 %), there is no evidence for clear phenotypic differences between these organisms that justify assignment to different genera. A proposal is made to transfer these species to the genus *Chitinophaga* as *Chitinophaga sancti* comb. nov., *Chitinophaga filiformis* comb. nov., *Chitinophaga japonenis* comb. nov. and *Chitinophaga arvensicola* comb. nov. on the basis of phylogenetic and phenotypic data. Furthermore, a novel species is described within this genus, *Chitinophaga skermanii* sp. nov., with strain CC-SG1B^T (=CCUG 52510^T=CIP 109140^T) as the type strain.

The monospecific genus *Chitinophaga* was originally proposed by Sangkhobol & Skerman (1981) to include strains of filamentous, chitinolytic, gliding bacteria that transform on ageing into spherical bodies. These bodies were first likened to the microcyst of *Sporocytophaga myxococcoides* (Leadbetter, 1989), but Reichenbach (1992) disputed the formation of microcysts by *Chitinophaga pinensis* and pointed to the similarities between the morphology of *Chitinophaga pinensis* and [*Flexibacter*] *filiformis*. Sly *et al.* (1999) compared the 16S rRNA gene sequences of *Chitinophaga pinensis* and [*Flexibacter*] *filiformis* and found that these two chitinolytic bacteria formed a separate lineage that also included [*Flexibacter*] *sancti*, [*Cytophaga*] *arvensicola* and [*Flavobacterium*] *ferrugineum*, which had already been shown by Nakagawa & Yamasato (1993). Later, Nakagawa *et al.* (2002) showed that [*Flexibacter*] *japonensis* also grouped into this lineage. These authors have previously suggested that [*Flexibacter*] *filiformis*, [*Flexibacter*] *sancti* and [*Cytophaga*] *arvensicola* may constitute a distinct genus on the basis of their phylogenetic relationship as determined from 16S rRNA gene sequence similarities, their strict respiratory metabolism, MK-7 menaquinone content and a base composition in the range 42·8–48·6 mol% G+C.

It was also shown by Takeuchi & Yokota (1992) that [*Flavobacterium*] *ferrugineum* was closely related to this group. Recently, Xie & Yokota (2006) proposed the new genus *Terrimonas* to accommodate [*Flavobacterium*] *ferrigineum* and added a second species to this genus, *Terrimonas lutea*.

Here, we present the characterization of a novel representative of this lineage and propose the formal reclassification of these organisms into the genus *Chitinophaga*.

A yellow-coloured strain, CC-SG1B^T, was isolated from faeces of the millipede *Arthrosphaera magna* collected in India. Subcultivation was done on nutrient agar (Oxoid) at 28 °C for 24 h. On this agar, CC-SG1B^T was able to grow at 10–36 °C, but not at 4 or 45 °C. Growth at 30 °C was also observed on TSA and R2A agar, but not on SS agar (Salmonella-Shigella agar) or MacConkey agar (all from Oxoid). The pH range (pH 4–10 at intervals of 1) and

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain CC-SG1B^T is AJ971483.

requirement for 0, 1, 2, 3, 5 and 7 % NaCl (w/v) was determined using R2A medium. Gram-staining was performed as described by Gerhardt *et al.* (1994). Cell morphology was observed under a Zeiss light microscope at × 1000, using cells that had been grown for 24 h at 28 °C on nutrient agar (Oxoid). Oxidase activity was tested using oxidase reagent (bioMérieux) according to the instructions of the manufacturer. Flexirubin-like pigments were observed by flooding the plates with 20 % (w/v) potassium hydroxide (Fautz & Reichenbach, 1980).

The cells were Gram-negative, rod-shaped, non-spore-forming, non-fluorescent and oxidase-positive. Results on the cell morphology and other details are given in the species description.

The 16S rRNA gene was analysed as described previously (Kämpfer *et al.*, 2003; Young *et al.*, 2005). Analysis of the sequence data was performed by using the software package MEGA version 2.1 (Kumar *et al.*, 2001), after multiple alignment of sequences by CLUSTAL X (Thompson *et al.*, 1997). A distance matrix method (distance options according to the Kimura two-parameter model) using clustering with the neighbour-joining method (Fig. 1) as well as a discrete character-based maximum-parsimony method (data not shown) were performed. In each case, bootstrap values were calculated based on 1000 replications. The 16S rRNA gene sequence of strain CC-SG1B^T was a continuous stretch of 1384 bp. Sequence similarity calculations indicated that strain CC-SG1B^T showed the highest degree of similarity to [*Flexibacter*] *filiformis* ATCC 29495^T (94·8 %) and [*Flexibacter*] *japonensis* IFO 16041^T (94·6 %), which was described by Fujita *et al.* (1996). The similarity to *Chitinophaga pinensis* ACM 2034^T was 93·3 %. Lower sequence similarities (< 94·5 %) were found with all other species of this lineage.

The determination of DNA G+C contents was performed by the methods outlined by Mesbah *et al.* (1989) using a reversed-phase column (Supelco LC-18-S; Supelco). The G+C content of strain CC-SG1B^T was 40·7 mol%.

Chemotaxonomic analyses of respiratory quinones (according to Altenburger *et al.*, 1996) and fatty acids (according to Kämpfer & Kroppenstedt, 1996) were performed. Although respiratory quinones have low resolution within this group, the presence of MK-7 supports affiliation of strain CC-SG1B^T to this group, where all species investigated to date have MK-7 as the major quinone.

The fatty acid profile of strain CC-SG1B^T revealed 15 : 0 iso and 16 : 1ω5*c* as the major fatty acids and 17 : 0 iso 3-OH and 15 : 0 iso 3-OH as the major hydroxy fatty acids. This is in essential agreement with the fatty acid patterns of [*Flexibacter*] *sancti*, [*Flexibacter*] *filiformis*, [*Flexibacter*] *japonenis* and *Chitinophaga pinensis*. The two *Terrimonas* species showed large amounts of 15 : 1 iso H instead of 16 : 1ω5*c* (Table 1), and thus could be clearly differentiated from [*Flexibacter*] *sancti*, [*Flexibacter*] *filiformis*, [*Flexibacter*] *japonenis*, *Chitinophaga pinensis* and strain CC-SG1B^T.

Results of the physiological characterization of CC-SG1B^T are given in the species description, using methods that were described previously (Kämpfer *et al.*, 1991). Additional biochemical tests were performed to assess the carbon source utilization pattern by using Biolog GN2 plates, whilst hydrolysis of 19 substrates was investigated using the API ZYM system and API 20E according to the methods outlined by the manufacturer (bioMérieux). Hydrolysis of chitin was studied by the methods of Smibert & Krieg (1994). The results are given in the species description. Strain CC-SG1B^T was able to utilize many carbohydrates, but organic acids and amino acids were not utilized.

Despite the relatively low 16S rRNA gene sequence similarities of these organisms (88·5–96·4 %), all the strains under study show a remarkable congruence in phenotypic characters. They all produce MK-7 as the major menaquinone and have homospermidine as the predominant polyamine (Hamana & Nakagawa, 2001). The fatty acid profiles were very similar, composed mainly of 15 : 0 iso and 16 : 1ω5*c* as the major fatty acids and 17 : 0 iso 3-OH and 15 : 0 iso 3-OH as the major hydroxy fatty acids (Table 1).

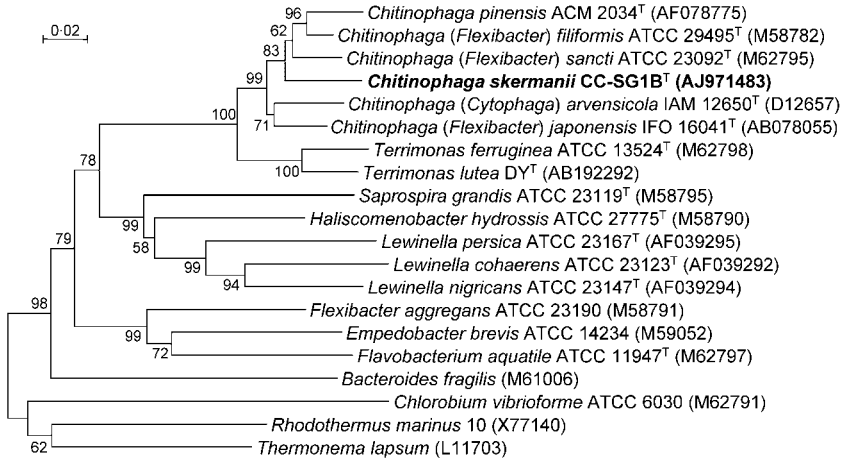

Fig. 1. Phylogenetic analysis based on 16S rRNA gene sequences available from the EMBL database (accession numbers in parentheses) constructed after multiple alignment of data by CLUSTAL X (Thompson *et al.*, 1997). Distances were calculated (distance options according to the Kimura-2 model) and clustering with the neighbour-joining method was performed by using the software package MEGA version 2.1 (Kumar *et al.*, 2001). Bootstrap values based on 1000 replications are listed as percentages at branching points. Bar, 0·02 nucleotide substitutions per nucleotide position.

Table 1. Fatty acid profiles of *Chitinophaga* and *Terrimonas* species

Strains: 1, *Chitinophaga pinensis* DSM 2588^T; 2, *Chitinophaga skermanii* sp. nov. CC-SG1B^T; 3, *Chitinophaga* (*Cytophaga*) *arvensicola* DSM 3695^T; 4, *Chitinophaga* (*Flexibacter*) *japonensis* DSM 13484^T; 5, *Chitinophaga* (*Flexibacter*) *sancti* DSM 784^T; 6, *Chitinophaga* (*Flexibacter*) *filiformis* CCUG 12809^T; 7, *Terrimonas ferruginea* IAM 15098^T; 8, *Terrimonas lutea* DY^T. Data for *T. ferruginea* and *T. lutea* were taken from Xie & Yokota (2006) (confirmed in this study). Values are percentages of total fatty acids.

Fatty acid	1	2	3	4	5	6	7	8
Unknown 13·565	2·6	4·4	3·6	3·1	3·2	2·5	1·3	3·2
13 : 0 iso							0·5	0·5
13 : 0							0·2	0·7
14 : 0 iso							1·1	4·3
14 : 0	0·7	1·8	1·4	0·5	0·7	0·9	0·5	0·4
15 : 0 2-OH			0·3				0·8	0·3
15 : 0 3-OH							0·3	
15 : 0 iso 3-OH	3·1	2·6	3·0	2·4	3·4	3·3	2·2	2·3
15 : 0 iso	30·4	47·3	35·3	40·0	44·0	37·3	28·4	34·8
15 : 0 anteiso			0·6	0·5			0·6	
15 : 1 iso							26·2	21·8
Unknown 11·543		0·8	0·5					
15 : 0	0·4	0·4	0·4				2·7	0·4
Unknown 14·959	0·3	0·4	0·3					
Summed feature 2*		0·4	0·4	0·5				
iso 17 : 1ω9*c*			0·3		1·1			
Summed feature 3	7·7	3·5	3·7	3·3	16·0	11·2	11·2	14·9
Summed feature 4		0·4		1·3	0·8			
16 : 0 10-methyl			0·4	0·9				
16 : 1ω11*c*	1·9	0·4	0·5	1·0	0·9			
16 : 1ω5*c*	33·2	24·4	33·6	22·2	13·5	25·5		
16 : 0 2-OH	0·7			3·0	0·7	1·1		
16 : 0	4·2	3·5	5·1	3·0	4·2	4·3	1·7	1·1
16 : 0 iso			0·3				1·4	
16 : 0 iso 3-OH	0·4	0·4	0·5	0·4			0·7	
16 : 0 3-OH	1·2	1·6	1·7	0·8	0·5	1·2	2·5	3·3
17 : 0 anteiso				0·4				
17 : 0 2-OH			0·4	0·4				
17 : 0 iso	0·4	0·6	0·4	1·8	0·6			
Unknown 16·582	1·1	0·7	0·8	1·1	1·3	0·9	1·3	1·8
17 : 0 iso 3-OH	11·5	5·0	5·9	13·0	9·1	11·8	15·3	14·2

*Summed features are groups of two or three fatty acids that could not be separated. Summed feature 2: 12 : 0 alde/unknown; summed feature 3, 16 : 1ω7*c*/15 : 0 iso 2-OH; summed feature 4, 17 : 1 anteiso B/17 : 1 iso I.

Only a few differences are reported in cell morphology and certain physiological tests (Tables 2 and 3).

From 16S rRNA gene sequencing studies, it is obvious that organisms of this lineage do not belong to the genus *Flexibacter sensu stricto* with the type species *Flexibacter flexilis* (Nakagawa *et al.*, 2002; Sly *et al.*, 1999) or to the genus *Cytophaga sensu stricto* with the type species *Cytophaga hutchinsonii* (Nakagawa *et al.*, 2002; Sly *et al.*, 1999). It should be noted here that species of the phylogenetically related genus *Lewinella* share only 84·7–88·4 % 16S rRNA gene sequence similarity.

For all these reasons, it is proposed to reclassify [*Flexibacter*] *sancti*, [*Flexibacter*] *filiformis*, [*Flexibacter*] *japonenis* and [*Cytophaga*] *arvensicola* to the genus *Chitinophaga* as the new combinations *Chitinophaga sancti* comb. nov., *Chitinophaga filiformis* comb. nov., *Chitinophaga japonensis* comb. nov. and *Chitinophaga arvensicola* comb. nov. A novel species, *Chitinophaga skermanii* sp. nov., is described to accommodate strain CC-SG1B^T.

Emended description of the genus *Chitinophaga* Sangkhobol and Skerman

The description is that of Sangkhobol & Skerman (1981) with the following modifications. A resting stage may be formed. Motility by gliding is possessed by some, but not all species. Some species hydrolyse chitin and some hydrolyse cellobiose.

Description of *Chitinophaga sancti* comb. nov.

Chitinophaga sancti [sanc′ti. L. n. *sanctus* saint; L. gen. n. *sancti* of Saint, perhaps named in honour of Dr Santos Soriano, from whose laboratory the type strain was supplied (the etymology is not clear)].

Basonym: *Flexibacter sancti* Lewin 1969, 199^{AL}.

The description is identical to that given by Lewin (1969) with the additional chemotaxonomic data provided by Reichenbach (1989), Hamana & Nakagawa (2001) and this study. The type strain is ATCC 23092^T = DSM 784^T = HAMBI 1988^T = NBRC 15057^T = LMG 8377^T = VKM B-1428^T.

Description of *Chitinophaga filiformis* comb. nov.

Chitinophaga filiformis (fi.li.for′mis. L. neut. n. *filum* a thread; L. suff. *-formis* like, of the shape of; N.L. fem. adj. *filiformis* thread-shaped).

Basonym: *Flexibacter filiformis* (*ex* Solntseva 1940) Reichenbach 1989.

The description is identical to that given by Reichenbach (1989) with the additional chemotaxonomic data provided by Hamana & Nakagawa (2001) and this study. The type strain is strain Fx e1 Reichenbach^T = ATCC 29495^T = CCUG 12809^T = CIP 106401^T = DSM 527^T = HAMBI 1966^T = NBRC 15056^T.

Description of *Chitinophaga japonensis* comb. nov.

Chitinophaga japonensis (ja.po.nen′sis. N.L. fem. adj. *japonensis* pertaining to Japan).

Table 2. Phenotypic characteristics of *Chitinophaga* and *Terrimonas* species

Strains: 1, *Chitinophaga pinensis* ACM 2034^T; 2, *Chitinophaga skermanii* sp. nov. CC-SG1B^T; 3, *Chitinophaga* (*Cytophaga*) *arvensicola* IAM 12650^T; 4, *Chitinophaga* (*Flexibacter*) *japonensis* NBRC 16041^T; 5, *Chitinophaga* (*Flexibacter*) *sancti* NBRC 15057^T; 6, *Chitinophaga* (*Flexibacter*) *filiformis* NBRC 150656^T; 7, *Terrimonas ferruginea* IAM 15098^T; 8, *Terrimonas lutea* IAM 15284^T. All the strains were isolated from soil and produce acid from glucose; H_2S production is absent from all strains. Major hydroxylated fatty acids in all strains are 17 : 0 iso 3-OH and 15 : 0 iso 3-OH. Data for reference strains were taken from Xie & Yokota (2006), Takeuchi & Yokota (1992), Oyaizu *et al.* (1982), Bernardet *et al.* (1996) and Fujita *et al.* (1996). ND, No data available; HSpd, homospermidine.

Characteristic	1	2	3	4	5	6	7	8
Pigment	Yellow	Yellow	Yellow–orange	Yellow–orange	Golden yellow	Golden yellow	Yellow	Yellow
Cell length (μm)	<40	1–2	0·6–4	2–18	2–15	30–80	1–2	1–2
Gliding movement	+	−	−	+	+	+	−	−
Filamentous shape	+	−	−	+	+	+	−	−
Quinone system	MK-7	MK-7	MK-7	MK-7	ND	ND	MK-7	MK-7
Major polyamine	HSpd	ND	HSpd	HSpd	HSpd	HSpd	HSpd	ND
Major fatty acid*	16 : 1ω5*c*	16 : 1ω5*c*	16 : 1ω5*c*	16 : 1ω5*c*	16 : 1ω5*c*	16 : 1ω5*c*	15 : 1 iso	15 : 1 iso
Oxidase	+	+	+	+	ND	+	+	+
Catalase	+	+	+	+	−	−	+	+
Urease	+	−	−	ND	ND	ND	−	−
Gelatin liquefaction	+	+	−	+	+	+	+	+
Chitin degradation	+	ND	−	−	−	+	−	−
Growth at 37 °C	+	+	−	+	−	+	+	+
Maximum NaCl concentration (%, w/v)	ND	ND	2	2	1	0·3	1	1
DNA G+C content (mol%)	45·2	40·7	46·0	49·8	43·3	45·0	48·9	47·2

*In addition to 15 : 0 iso, which is a major component in all strains. 14 : 0 iso is found only in *Terrabacter* species (in minor amounts), and not in *Chitinophaga* species.

Basonym: *Flexibacter japonensis* Fujita *et al.* 1997.

The description is identical to that given by Fujita *et al.* (1996) and Reichenbach (1989) with the additional chemotaxonomic data provided by Hamana & Nakagawa (2001) and this study. The type strain is strain 758^T = CIP 105790^T = DSM 13484^T = NBRC 16041^T = JCM 9735^T.

Description of *Chitinophaga arvensicola* comb. nov.

Chitinophaga arvensicola [ar.ven′si.co′la. L. adj. *arvensis* belonging to or living in the fields; L. suff. *-cola* from L. n. *incola* inhabitant; N.L. n. *arvensicola* (nominative in apposition) an inhabitant of the fields].

Basonym: *Cytophaga arvensicola* Oyaizu *et al.* 1983.

The description is identical to that given by Oyaizu *et al.* (1982) and Reichenbach (1989) with the additional chemotaxonomic data provided by Hamana & Nakagawa (2001) and this study. The type strain is strain M64^T = ATCC 51264^T = CIP 104804^T = DSM 3695^T = IAM 12650^T = NBRC 14973^T = JCM 2836^T.

Description of *Chitinophaga skermanii* sp. nov.

Chitinophaga skermanii (sker.ma′ni.i. N.L. gen. n. *skermanii* of Skerman, in honour of V. B. D. Skerman, an Australian microbiologist, in recognition of his numerous contributions to the taxonomy of micro-organisms).

Cells are Gram-negative, non-motile, non-spore-forming rods. Aerobic and oxidase-positive. Good growth after 48 h on nutrient agar, tryptic soy agar and MacConkey agar at 30–40 °C. Colonies on nutrient agar are smooth, orange, circular, translucent and shiny with entire edges, becoming mucoid. Orange pigmentation is non-diffusible, non-fluorescent and turns to cherry red upon the addition of 20 % KOH and retains original colour on addition of HCl. Strains are unable to grow at 5 or 42 °C. Growth occurs at pH 5·5–10 and in 7 % (w/v) NaCl. The detailed fatty acid profile is given in Table 1. Positive for β-galactosidase, acetoin production, gelatinase and oxidation of glucose, mannitol and melibiose and negative for arginine dihydrolase, lysine decarboxylase, citrate utilization, H_2S production, urease, tryptophan deaminase, indole production, oxidation of inositol, sorbitol, rhamnose, sucrose, amygdalin and arabinose and cytochrome oxidase activity. Some differentiating tests are given in Table 3 (methods according to Kämpfer *et al.*, 1991). In addition, the following compounds were utilized as sole carbon sources (tested with the Biolog GN system): α-cyclodextrin, dextrin, Tweens 40 and 80, *N*-acetyl-D-galactosamine, *N*-acetyl-D-glucosamine, cellobiose, L-fucose, gentiobiose, α-D-glucose, α-D-lactose, lactulose, maltose, D-mannose, D-melibiose, methyl β-D-glucoside, D-raffinose, sucrose, D-trehalose,

Table 3. Differentiating characters of *Chitinophaga* and *Terrimonas* species

Strains: 1, *Chitinophaga pinensis* DSM 2588^T; 2, *Chitinophaga skermanii* CC-SG1B^T; 3, *Chitinophaga* (*Cytophaga*) *arvensicola* DSM 3695^T; 4, *Chitinophaga* (*Flexibacter*) *japonensis* DSM 13484^T; 5, *Chitinophaga* (*Flexibacter*) *sancti* DSM 784^T; 6, *Chitinophaga* (*Flexibacter*) *filiformis* CCUG 12809^T; 7, *Terrimonas ferruginea* IAM 15098^T; 8, *Terrimonas lutea* DY^T. Data for *T. ferruginea* and *T. lutea* were taken from Xie & Yokota (2006) unless indicated. Assimilation tests were read after 48 h of incubation and hydrolysis of chromogenic substrates after 24 h unless indicated. *o*NP, *o*-Nitrophenyl; *p*NP, *p*-nitrophenyl; *p*NA, *p*-nitroanilide.

Test	1	2	3	4	5	6	7	8
Hydrolysis of:								
*o*NP β-D-galactopyranoside	+	+	+	+	+	+	+	−
*p*NP β-D-glucopyranoside	+	+	+	+	+	+	−	+
*p*NP phenylphosphonate	+	+†	+	+	+	+	+*	−*
*p*NP phosphorylcholine	+	+	+	+	+	+	−*	+*
2-Deoxythymidine-5′-*p*NP phosphate	+	+	+	+	+	+	−*	−*
L-Glutamate-γ-3-carboxy *p*NA	+†	+‡	+	+†	+	+†	−*	−*
L-Proline *p*NA	+†	+‡	+	+†	+	+	+*	−*
Assimilation of:								
N-Acetyl-D-glucosamine	+	+	+	+	−	−	−	+
L-Arabinose	+	−	+†	+	+†	−	−	+
D-Galactose	+	−	−	+	−	−	−	+*
Gluconate	−	−	−	−	+†	−	−*	−*
D-Mannose	+	+	+	+	−	+	+	+
D-Maltose	+	+	+	+	−	+	+	+
α-D-Melibiose	−	+†	+	+	+‡	+†	−	+
L-Rhamnose	+†	−	+	+	−	−	+	−
D-Ribose	−	−	+	−	−	−	−*	−*
Sucrose	+†	−	+†	+	−	+	−	+
Salicin	+†	+	+	+	−	+	−*	−*
D-Trehalose	+	+‡	+†	+	−	+	−	+
D-Xylose	+†	−	+	+	−	+	+	−
Adonitol	−	−	−	+	−	−	+*	−*
Maltitol	+‡	−	−	+†	−	+†	−*	−*

*Data from this study.
†Positive after 7 days of incubation.
‡Positive after 14 days of incubation.

turanose, monomethyl succinate, acetic acid, D-galacturonic acid, α-hydroxybutyric acid, α-ketobutyric acid, DL-lactic acid, succinic acid, DL-alanine, L-alanyl glycine, L-asparagine, L-aspartic acid, L-glutamic acid, glycyl L-aspartic acid, glycyl L-glutamic acid, L-proline, L-serine, L-threonine and glycerol. The following carbon sources are not utilized as sole sources of carbon: D-arabitol, propionic acid, citric acid, glycogen, adonitol, L-arabinose, i-erythritol, D-fructose, D-galactose, *myo*-inositol, D-mannitol, D-psicose, L-rhamnose, D-sorbitol, xylitol, pyruvic acid methyl ester, *cis*-aconitic acid, formic acid, D-galactonic acid lactone, D-glucosaminic acid, D-gluconic acid, D-glucuronic acid, β- and γ-hydroxybutyric acids, *p*-hydroxyphenylacetic acid, itaconic acid, α-ketoglutaric acid, malonic acid, D-saccharic acid, sebacic acid, bromosuccinic acid, quinic acid, succinamic acid, L-pyroglutamic acid, α-ketovaleric acid, glucuronamide, L-alaninamide, D-alanine, L-histidine, hydroxy-L-proline, D-serine, L-leucine, L-ornithine, L-phenylalanine, inosine, uridine, thymidine, DL-carnitine, γ-aminobutyric acid, urocanic acid, phenylethylamine, putrescine, 2-aminoethanol, 2,3-butanediol, DL-α-glycerol phosphate, glucose 1-phosphate and glucose 6-phosphate. Positive test results for enzyme activities are seen for alkaline phosphatase, butyrate esterase, caprylate esterase, leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α-galactosidase, α-glucosidase, β-glucosidase and *N*-acetyl-β-glucosaminidase; negative test results are observed for myristate esterase, α-chymotrypsin, β-galactosidase, β-glucuronidase, α-mannosidase and α-fucosidase.

The type strain is CC-SG1B^T (=CCUG 52510^T=CIP 109140^T), isolated from faeces of the millipede *Arthrosphaera magna*.

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