Hydrotalea flava gen. nov., sp. nov., a new member of the phylum *Bacteroidetes* and allocation of the genera *Chitinophaga*, *Sediminibacterium*, *Lacibacter*, *Flavihumibacter*, *Flavisolibacter*, *Niabella*, *Niastella*, *Segetibacter*, *Parasegetibacter*, *Terrimonas*, *Ferruginibacter*, *Filimonas* and *Hydrotalea* to the family *Chitinophagaceae* fam. nov.

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Three bacterial strains, designated CCUG 51397^T, CCUG 53736 and CCUG 53920, isolated from water samples taken at different locations in southern Sweden were studied to determine their taxonomic position using a polyphasic approach. Comparative analysis of 16S rRNA gene sequences showed that these bacteria had <93 % sequence similarity to all described species of the genera *Sediminibacterium*, *Lacibacter*, *Flavihumibacter*, *Flavisolibacter*, *Niabella*, *Niastella*, *Segetibacter*, *Parasegetibacter*, *Terrimonas*, *Ferruginibacter*, *Filimonas* and *Chitinophaga*. The three organisms grouped most closely with *Sediminibacterium salmoneum* NJ-44^T but showed only 92.5 % sequence similarity to this strain, the only recognized species of this genus. The fatty acid profiles showed large amounts of iso-$C_{15:0}$, iso-$C_{17:0}$ 3-OH and iso-$C_{15:1}$ G with smaller amounts of iso-$C_{15:0}$ 3-OH, iso-$C_{16:0}$ 3-OH and other fatty acids, which differentiated the novel strains from related genera. Biochemical tests performed on strains CCUG 51397^T, CCUG 53736 and CCUG 53920 also gave different results from those of *Sediminibacterium salmoneum* NJ-44^T and other related genera. Based on this evidence, strains CCUG 51397^T, CCUG 53736 and CCUG 53920 represent a novel species of a new genus, for which the name *Hydrotalea flava* gen. nov., sp. nov. is proposed. The type strain of *Hydrotalea flava* is CCUG 51397^T (=CCM 7760^T). A formal allocation of the genera *Sediminibacterium*, *Lacibacter*, *Flavihumibacter*, *Flavisolibacter*, *Niabella*, *Niastella*, *Segetibacter*, *Parasegetibacter*, *Terrimonas*, *Ferruginibacter*, *Filimonas* and *Chitinophaga* to the family *Chitinophagaceae* fam. nov. is also proposed.

Three bacterial strains, designated CCUG 51397^T, CCUG 53736 and CCUG 53920, were isolated from different water samples taken in July 2005 and November and December 2006 in southern Sweden and were studied using a polyphasic approach. Cells of the isolates were Gram-reaction-negative and formed orange-pigmented colonies. From the results of initial 16S rRNA gene sequence analysis, it was evident that these strains, which had identical 16S rRNA gene sequences, could be allocated to the phylum *Bacteroidetes*. The most closely related species was found to be *Sediminibacterium salmoneum* (Qu & Yuan, 2008) with a 16S rRNA gene sequence similarity of 92.5 % to the three strains. Lower 16S rRNA gene sequence similarites were found with representatives of the genera *Chitinophaga* (Sangkhobol & Skerman, 1981), *Terrimonas* (Xie & Yokota, 2006), *Niastella* (Weon *et al.*, 2006), *Niabella* (Kim *et al.*, 2007), *Flavisolibacter* (Yoon & Im, 2007), *Segetibacter* (An *et al.*, 2007), *Parasegetibacter* (Zhang *et al.*, 2009), *Lacibacter* (Qu *et al.*, 2009), *Ferruginibacter* (Lim *et al.*, 2009), *Filimonas* (Shiratori *et al.*, 2009) and *Flavihumibacter* (Zhang *et al.*, 2010). All of these genera formed a distinct cluster in the 16S rRNA gene sequence-based tree and showed some phenotypic similarities. Here, we propose that these three novel strains represent a novel genus, *Hydrotalea* gen. nov., and in addition formally propose that the genera *Chitinophaga*, *Sediminibacterium*, *Lacibacter*, *Flavihumibacter*, *Flavisolibacter*, *Niabella*, *Niastella*,

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains CCUG 51397^T, CCUG 53736 and CCUG 53920 are FN665659, FN665660 and FN665661, respectively.

Segetibacter, *Parasegetibacter*, *Terrimonas*, *Ferruginibacter*, *Filimonas* and *Hydrotalea* be moved to the family *Chitinophagaceae* fam. nov.

Strains CCUG 51397^T, CCUG 53736 and CCUG 53920 were isolated from water samples from different locations in southern Sweden. Initial isolation was done on blood agar (Oxoid) at 37 °C. Subcultivation was done on Nutrient agar (NA, Oxoid) at 30 °C for 24 h. Gram-staining was performed following the standard procedure as described by Gerhardt *et al.* (1994). Cell morphology was examined with a Zeiss light microscope at ×1000 magnification using cells that had been grown for 24 h at 30 °C on NA.

The 16S rRNA gene was analysed as described by Kämpfer *et al.* (2003). DNA extraction was carried out using the GenElute Plant Genomic DNA kit (Sigma) according to the manufacturer's instructions. The 16S rRNA gene was PCR-amplified using the primer pair 27F (5′-GAGTTTGATCMTGGCTCAG-3′) and MR 1492R (5′-ACGGYTACCTTGTTACGACTT-3′) (Lane, 1991) and the following cycle conditions: an initial step of 95 °C for 3 min followed by 28 cycles of 94 °C for 1 min, 57.3 °C for 45 s and 72 °C for 2 min and a final step of 72 °C for 15 min. The PCR product was purified with the QIAquick PCR purification kit (Qiagen) according to the manufacturer's instructions and sequenced with standard sequencing primers for the 16S rRNA gene. Phylogenetic analysis was performed using the ARB software package (version December, 2007; Ludwig *et al.*, 2004) and the corresponding SILVA SSURef 100 database (version August, 2009; Pruesse *et al.*, 2007). Trees were reconstructed using the maximum-likelihood method with fastDNAmL (Olsen *et al.*, 1994) without filters. Similar results were obtained with both the neighbour-joining and maximum-parsimony methods (data not shown). The almost complete 16S rRNA gene sequences of the three strains were compared by distance calculations (pairwise distances) using the ARB software package (version December, 2007; Ludwig *et al.*, 2004). The 16S rRNA gene sequences of the three novel strains were identical. The results of further calculations indicated that the closest relative of the strains was *Sediminibacterium salmoneum* NJ-44^T with 92.5 % sequence similarity. Lower sequence similarities were found to sequences of all described species of the genera *Chitinophaga*, *Lacibacter*, *Flavihumibacter*, *Flavisolibacter*, *Niabella*, *Niastella*, *Segetibacter*, *Parasegetibacter*, *Ferruginibacter*, *Filimonas* and *Terrimonas*, all of which formed a distinct cluster with the novel isolates (see Fig. 1). For fatty acid analysis, the strains were grown on R2A agar at 28 °C for 48 h. Fatty acids were extracted and analysed according to Kämpfer & Kroppenstedt (1996). The fatty acid profiles of strains CCUG 51397^T, CCUG 53736 and CCUG 53920 were similar, although some differences could be observed. The three strains produced iso-$C_{15:0}$, iso-$C_{17:0}$ 3-OH and iso-$C_{15:1}$ G as major fatty acids. In addition, iso-$C_{13:0}$, iso-$C_{17:1}\omega 9c$ and iso-$C_{15:0}$ 3-OH were produced in moderate amounts. The presence of iso-$C_{13:0}$ was mostly unique to the three strains when compared with the fatty acid profiles of representatives of related genera. *Sediminibacterium salmoneum* NJ-44^T produced iso-$C_{14:0}$ instead of iso-$C_{13:0}$ and anteiso-$C_{15:1}$ A, which was not found in the three novel strains. Furthermore, iso-$C_{17:1}\omega 9c$ was absent in *S. salmoneum* NJ-44^T. In addition, several other, mainly

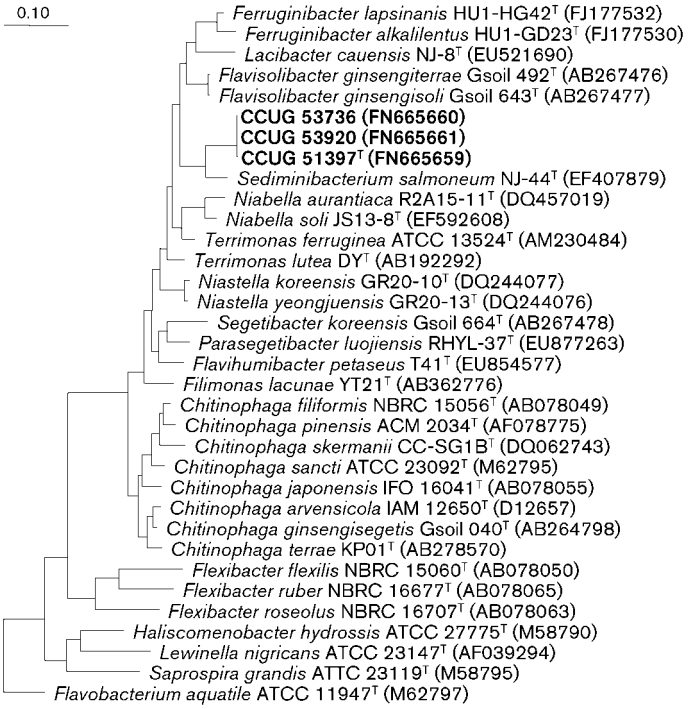

Fig. 1. Phylogenetic analysis of strains CCUG 51397^T, CCUG 53736 and CCUG 53920 and closely related species based on 16S rRNA gene sequences available from the EMBL database (accession numbers are given in parentheses). The phylogenetic tree was reconstructed using the ARB software package (version, December 2007; Ludwig *et al.*, 2004) and the corresponding SILVA SSURef 100 database (version, August 2009; Pruesse *et al.*, 2007). Tree reconstruction was performed using the maximum-likelihood method with fastDNAmL (Olsen *et al.*, 1994) and no conservatory filter. Sequence similarities between type strains of the family *Chitinophagaceae* ranged from 99.5 to 87.6 %; sequence similarities between type strains of the family *Chitinophagaceae* and closely related type strains of the phylum *Bacteroidetes*, ranged from 76.5 to 82.6 %. Bar, 0.1 substitutions per nucleotide position.

Table 1. Cellular fatty acid compositions of strains CCUG 51397^T, CCUG 53736 and CCUG 53920 and type strains of related species

Taxa: 1, CCUG 51397^T; 2, CCUG 53736; 3, CCUG 53920; 4, *Sediminibacterium salmoneum* NJ-44^T; 5, *Flavisolibacter ginsengiterrae* Gsoil 492^T; 6, *Flavisolibacter ginsengisoli* Gsoil 643^T; 7, *Lacibacter cauensis* NJ-8^T; 8, *Flavihumibacter petaseus* T41^T; 9, *Terrimonas ferruginea* IAM 15098^T; 10, *Terrimonas lutea* IAM 15284^T; 11, *Niabella aurantiaca* R2A15-11^T; 12, *Niastella yeongjuensis* DSM 17621^T; 13, *Niastella koreensis* DSM 17620^T; 14, *Segetibacter koreensis* Gsoil 664^T; 15, *Chitinophaga pinensis* ACM 2034^T; 16, *Filimonas lacunae* YT21^T; 17, *Parasegetibacter luojiensis* RHYL-37^T; 18, *Ferruginibacter alkalilentus* HU1-GD23^T; 19, *Ferruginibacter lapsinanis* HU1-HG42^T. Data for reference strains were taken from Qu & Yuan (2008), Yoon & Im (2007), Qu *et al.* (2009), Zhang *et al.* (2010), Xie & Yokota (2006), Kim *et al.* (2007), Weon *et al.* (2006), Kämpfer *et al.* (2006), An *et al.* (2007), Shiratori *et al.* (2009), Zhang *et al.* (2009), Lim *et al.* (2009). Some of the strains listed were grown under different culture conditions (see footnotes). Values are percentages of total fatty acids. Fatty acids amounting to less than 1 % of total fatty acids in all strains studied are not listed. tr, Trace (<1 %).

Fatty acid	1	2	3	4*	5†	6†	7*	8*	9‡	10‡	11*	12*	13*	14§	15	16‖	17¶	18*	19*
Unknown 11.543	0.5	0.9	0.4															1.5	
Unknown 13.565	8.4	11.3	7.4	1.5			4.2	1.5	1.3	3.2				2.1	2.6	tr		2.1	1.1
Unknown 16.582	1.7	1.7	1.3	tr			1.5		1.3	1.8	1.2	1.6	1.4		1.1	1.9			
iso-$C_{13:0}$	4.2	5.2	4.3													tr		tr	3.2
iso-$C_{14:0}$				2.5			tr		1.1	4.3						tr		tr	
iso-$C_{14:1}$ E		0.3																	
$C_{14:0}$			0.5											1.0			2.0	tr	
$C_{13:1}$ AT 12 13	0.4	0.6	0.7																
iso-$C_{15:1}$G	8.2	11.5	3.8	24.1			15.4	13.3			22.3	14.7	15.6			18.3		22.3	21.7
iso-$C_{15:1}$					5.3	4.4			26.2	21.8				14.4			14.7		
anteiso-$C_{15:1}$A				7.4													3.7		
iso-$C_{15:0}$	34.8	30.8	18.7	17.5	45.9	31.2	27.8	33.8	28.4	34.8	33.7	30.6	26.8	23.4	30.4	25.2	19.5	30.4	32.1
anteiso-$C_{15:0}$	1.7	1.7	3.6	9.5	5.9	5.0	tr		tr		1.6	3.3	4.9				3.3	2.0	
$C_{15:0}$	0.6	0.6	3.4	tr			4.7	8.0	2.7	tr				1.1	tr			2.1	
iso-$C_{16:0}$	0.7	0.7	4.4	1.1			tr		1.4				1.0			tr	3.0	1.1	
$C_{15:1}\omega6c$			0.7												1.9				
$C_{16:1}\omega11c$															1.9				
iso-$C_{16:1}$ H			1.6																
$C_{16:1}\omega5c$				tr			1.6	5.8				1.2		12.5	33.2	3.0			
$C_{17:1}\omega8c$			0.6																
$C_{17:1}\omega6c$			1.3																
$C_{18:1}\omega7c$							1.9												
iso-$C_{17:1}\omega9c$	5.9	4.0	4.5		1.3														
$C_{16:0}$	0.9	0.7	1.9	1.2	5.5	7.5		2.2	1.7	1.1	3.5	2.9	2.6	8.5	4.2	4.7	10.1	2.6	3.3
anteiso-$C_{16:0}$																		1.9	1.5
iso-$C_{13:0}$ 3-OH														1.6			5.2		
iso-$C_{14:0}$ 3-OH			0.5																
iso-$C_{15:0}$ 3-OH	4.0	4.5	3.5	7.4	1.4	1.0	2.7	3.9	2.2	2.3	2.9	1.9	1.3		3.1	2.7		8.8	4.6
$C_{15:0}$ 2-OH	0.4	0.4	1.0	1.9					tr	tr									
$C_{15:0}$ 3-OH			1.8																
iso-$C_{16:0}$ 3-OH	1.2	1.4	6.2	7.7					tr						tr		1.8	3.2	
$C_{16:0}$ 2-OH			0.3			2.9										tr			
$C_{16:0}$ 3-OH	0.9	0.8	1.9	1.8			tr	2.7	2.5	3.3	2.4	2.3	1.3		1.2	3.9		2.1	2.7
iso-$C_{17:0}$ 3-OH	16.9	15.0	15.5	7.7	13.7	11.8	14.5	12.9	15.3	14.2	15.5	27.1	29.4	14.5	11.5	22.6	16.3	15.1	15.6
$C_{17:0}$ 2-OH	0.5	0.4	1.8	2.2								2.6	3.5				1.3		
$C_{17:0}$ 3-OH			1.4				tr	1.1					1.2						
iso-$C_{17:0}$		1.3	1.3		3.1	9.1	1.2						1.6		tr	tr	1.1		
anteiso-$C_{17:0}$						1.0													
$C_{18:0}$						2.0	tr							1.9			3.9		
Summed features#																			
2		0.9			2.7	2.5													
3	4.7	3.8	6.0	tr	10.5	6.2	13.9	1.5	11.2	14.9	10.6	5.3	4.3	6.6	7.7	13.6	3.1	4.0	14.3
4	1.0	1.1			1.4	3.1	1.2							3.9					

*Cells were grown at 28 °C in R2A broth/R2A medium (Weon *et al.*, 2006; Kim *et al.*, 2007; Qu & Yuan, 2008; Qu *et al.*, 2009; Zhang *et al.*, 2010).

†Cells were grown for 3 days on one-tenth-strength trypticase soy agar (TSA) (temperature not specified) (Yoon & Im, 2007).
‡Cells were grown for 3 days at 29 °C on TSA (Xie & Yokota, 2006).
§Cells were grown for 3 days on one-tenth-strength TSA (temperature not specified) (An *et al.*, 2007).
||Cells were grown for 72 h at 30 °C on R2A agar (Shiratori *et al.*, 2009).
¶Cells were grown for 4 days at 30 °C on R2A agar (Zhang *et al.*, 2009).
#Summed features are combinations of fatty acids that cannot be separated by the MIDI system. Summed feature 2 comprises iso-$C_{16:1}$ I, $C_{14:0}$ 3-OH and /or $C_{12:0}$ aldehyde; summed feature 3 comprises iso-$C_{15:0}$ 2-OH and/or $C_{16:1}\omega7c$; summed feature 4 comprises iso-$C_{17:1}$ I and/or anteiso-$C_{17:1}$ B.

quantitative, differences in the fatty acid profiles allowed further differentiation of the three novel strains from the genus *Sediminibacterium*. The qualitative and quantitative differences between fatty acid profiles of representatives of each genus (Table 1) could also be used for differentiation at the genus level.

Results of physiological and biochemical characterization using methods described previously (Kämpfer *et al.*, 1991, 2010) are given in Table 2 and in the species description. Strains CCUG 51397^T, CCUG 53736 and CCUG 53920 showed identical biochemical profiles; they were oxidase- and catalase-positive, did not show β-galactosidase or urease activities and were able to utilize sucrose and D-xylose, melibiose and L-rhamnose weakly but not L-arabinose or trehalose. Differential characteristics of the three novel strains and representatives of related genera are shown in Table 2. On the basis of the phylogenetic, chemotaxonomic, physiological and biochemical evidence, strains CCUG 51397^T, CCUG 53736 and CCUG 53920 represent a novel species in a new genus (Tables 1 and 2), for which the name *Hydrotalea flava* gen. nov., sp. nov. is proposed.

Description of *Chitinophagaceae* fam. nov.

Chitinophagaceae (Chi.ti.no.pha.ga.ce′a.e. N.L. fem. n. *Chitinophaga* type genus of the family; L. suff. *-aceae* ending to denote a family; N.L. fem. pl. n. *Chitinophagaceae* the *Chitinophaga* family).

This family is defined, in part, on the basis of 16S rRNA gene sequence similarities. Cells are often thin, rod-shaped and usually non-motile. Swarming motility may occur. Aerobic or facultatively anaerobic. Limited fermentative capabilities are observed in some members. Menaquinones are of the MK-7 type and a typical fatty acid profile contains iso-$C_{15:0}$, iso-$C_{17:0}$ 3-OH and iso-$C_{15:1}$ G as important characteristic components. The family comprises the genera *Chitinophaga*, *Sediminibacterium*, *Lacibacter*, *Flavihumibacter*, *Flavisolibacter*, *Niabella*, *Niastella*, *Segetibacter*, *Parasegetibacter*, *Terrimonas*, *Ferruginibacter*, *Filimonas* and *Hydrotalea*. The type genus is *Chitinophaga* Sangkhobol and Skerman, 1981.

Description of *Hydrotalea* gen. nov.

Hydrotalea (Hy.dro.ta.le′a. Gr. n. *hydros* water; L. fem. n. *talea* a rod; N.L. fem. n. *Hydrotalea* a rod isolated from water).

Cells are Gram-reaction-negative, aerobic, non-motile, thin rods, 1.5–2.0 × 0.2–0.8 μm. Oxidase-positive. Good growth occurs after 24 h of incubation on nutrient agar and R2A agar at 25–30 °C. Major fatty acids are iso-$C_{15:0}$, iso-$C_{17:0}$ 3-OH and iso-$C_{15:1}$ G. In addition, iso-$C_{13:0}$, iso-$C_{17:1}\omega9c$ and iso-$C_{15:0}$ 3-OH are produced in moderate amounts and are characteristic of the genus. The DNA G+C content of the type strain of the type species, *Hydrotalea flava*, is 42 mol%.

Description of *Hydrotalea flava* sp. nov.

Hydrotalea flava (fla′va. L. fem. adj. *flava* golden-yellow).

The description is the same as for the genus with the following additional characteristics. On NA, colonies are orange–yellow and circular with an entire margin. Good growth on R2A agar and NA; moderate growth on tryptone soy agar; no growth on MacConkey's agar. Grows at 20, 25, 28, 30 and 37 °C; no growth at 4, 10, 15 and 40 °C. L-Alanine-*p*-nitroanilide, *p*-nitrophenyl-β-D-galactopyranoside, *p*-nitrophenyl-α- and β-D-glucopyranoside, bis-*p*-nitrophenyl-phosphate, bis-*p*-nitrophenyl-phenyl-phosphonate, bis-*p*-nitrophenyl-phosphoryl-choline, L-aniline-*p*-nitroanilide, γ-L-glutamate-*p*-nitroanilide and L-proline-*p*-nitroanilide are hydrolysed on the basis of the method described by Kämpfer *et al.* (1991). *p*-Nitrophenyl-β-D-glucuronide and *p*-nitrophenyl-β-D-xylopyranoside are not hydrolysed. Arbutin, D-cellobiose, D-fructose, D-galactose, melibiose and L-rhamnose are used as sole carbon sources (weak positive results after 72 h incubation) on the basis of the method described by Kämpfer *et al.* (1991). The following compounds are not assimilated: *N*-acetylgalactosamine, *N*-acetylglucosamine, L-arabinose, D-glucose, D-gluconate, maltose, D-mannose, L-rhamnose, D-ribose, sucrose, salicin, trehalose, D-xylose, adonitol, *myo*-inositol, maltitol, D-mannitol, D-sorbitol, putrescine, acetate, *cis*- and *trans*-aconitate, pyruvate, fumarate, DL-3-hydroxybutyrate, DL-lactate, adipate, azelate, 4-aminobutyrate, citrate, glutarate, itaconate, L-malate, mesaconate, 2-oxoglutarate, propionate, suberate, L-alanine, β-alanine, L-aspartate, L-leucine, L-ornithine, L-proline, L-serine, L-histidine, L-phenylalanine, L-serine, L-tryptophan, 3-hydroxybenzoate and phenylacetate. No acids are produced from D-glucose, lactose, sucrose, D-mannitol, dulcitol, salicin, adonitol, *myo*-inositol, sorbitol, L-arabinose, raffinose, L-rhamnose, maltose, D-xylose, trehalose, cellobiose, methyl-D-glucoside, erythritol, melibiose, D-arabitol and D-mannose.

Table 2. Differential characteristics of strains CCUG 51397^T, CCUG 53737, CCUG 53920 and type strains of related species

Taxa: 1, CCUG 51397^T, CCUG 53737, CCUG 53920; 2, *Sediminibacterium salmoneum* NJ-44^T; 3, *Flavisolibacter ginsengiterrae* Gsoil 492^T; 4, *Flavisolibacter ginsengisoli* Gsoil 643^T; 5, *Lacibacter cauensis* NJ-8^T; 6, *Flavihumibacter petaseus* T41^T; 7, *Terrimonas ferruginea* IAM 15098^T; 8, *Terrimonas lutea* IAM 15284^T; 9, *Niabella aurantiaca* R2A15-11^T; 10, *Niastella yeongjuensis* DSM 17621^T; 11, *Niastella koreensis* DSM 17620^T; 12, *Segetibacter koreensis* Gsoil 664^T; 13, *Chitinophaga pinensis* ACM 2034^T; 14, *Filimonas lacunae* YT21^T; 15, *Parasegetibacter luojiensis* RHYL-37^T; 16, *Ferruginibacter alkalilentus* (5 strains); 17, *Ferruginibacter lapsinanis* HU1-HG42^T. Data for reference strains were taken from Xie & Yokota (2006), Kim *et al.* (2007), Weon *et al.* (2006), Kämpfer *et al.* (2006), Qu & Yuan (2008), Shiratori *et al.* (2009), Zhang *et al.* (2009), Lim *et al.* (2009). +, Positive; −, negative; W, weakly positive; ND, no data available.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Pigmentation*	O	SP	Y	Y	O	Y	SR	Y	O	M	LY	Y	Y	LY	GY	R	R
Production of:																	
Flexirubin-type pigments	−	−	ND	ND	−	ND	ND	ND	+	−	−		ND	−	−	−	−
H_2S	−	+	−	−	+	+	−	−	ND	ND	ND	−	−	ND	ND	−	−
Oxidase	+	+	+	−	+	W	+	+	−	+	−	+	+	+	+	+	+
Catalase	+	+	−	+	+	+	W	W	+	−	−	+	+	+	+	+	+
β-Galactosidase	+	+	+	+	+	ND	+	−	+	+	+	−	ND	+	+	ND	ND
Urease	−	−	−	−	−	−	−	−	−	−	−	+	+	+	−	ND	ND
Gliding motility	−	+	−	−	+	−	−	−	−	+	+	−	+	+	+	−	−
Nitrate reduction	−	−	−	−	−	−	+	+	−	−	−	−	ND	−	−	−	−
Growth at 37 °C	+	+	−	+	+	+	+	+	ND	−	+	−	+	−	+	−	−
Highest NaCl tolerance (%)	4.0	1.0	3.0	1.0	1.0	1.0	1.0	1.0	3.0	ND	ND	3.0	ND	<1.0	1.0	<0.5	<0.5
Assimilation of:																	
L-Arabinose	−	−	+	−	−	+	−	+	+	−	−	−	+	+	+	W	−
Trehalose	−	+	ND	ND	+	+	−	+	ND	ND	ND	ND	ND	−	ND	+	−
D-Xylose	−	−	ND	ND	−	+	+	−	ND	ND	ND	ND	ND	ND	ND	+	−
Melibiose	W	+	+	−	+	+	−	+	+	−	−	W	−	−	−	W	−
Sucrose	−	+	+	+	+	+	−	+	+	−	−	−	+	−	+	+	+
L-Rhamnose	W	−	+	−	+	+	+	−	+	−	−	+	+	−	−	−	−
DNA G+C content (mol %)	42.0	ND	ND	42.7	46.6	48.1	48.9	47.2	45.0	44.3	45.8	40.4	45.2	45.2	39.7	38.5–39.5	38.5–39.5

*LY, Light yellow; M, milky; O, orange; SP, salmon pink; SR, salmon red; Y, yellow; GY, golden-yellow; R, rusty.

The type strain, CCUG 51397^T (=CCM 7760^T), was isolated from a water sample in southern Sweden.

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