Sphingomonas mucosissima sp. nov. and *Sphingomonas desiccabilis* sp. nov., from biological soil crusts in the Colorado Plateau, USA

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Two bacterial strains, CP173-2^T and CP1D^T, were isolated from biological soil crusts (BSCs) collected in the Colorado Plateau, USA. Both strains were pigmented, Gram-negative, non-motile rods and produced abundant mucus. They contained C_{16:0}, C_{18:1}ω7c and C_{14:0} 2-OH as the predominant cellular fatty acids, ubiquinone-10 as the isoprenoid quinone and sphingoglycolipid. Based on the above characteristics, the isolates were assigned to the family *Sphingomonadaceae*; 16 rRNA gene signature nucleotides placed them within the genus *Sphingomonas*. Strains CP173-2^T and CP1D^T had a 16S rRNA gene sequence similarity of 96.7% with each other and 91.6–98.9% sequence similarity with other species in the genus, indicating that they represent two separate, and possibly novel, species. The closest species to strains CP173-2^T and CP1D^T were, respectively, *Sphingomonas dokdonensis* (98.9% gene sequence similarity) and *Sphingomonas panni* (97.9%). However, strain CP173-2^T exhibited a DNA–DNA relatedness of only 32.5% with the type strain of *S. dokdonensis*. Similarly, the DNA–DNA relatedness between strain CP1D^T and the type strain of *S. panni* was only 18%. Phenotypic characterization supported this low relatedness. On the basis of this evidence, we propose that the new strains represent two novel species, for which the names *Sphingomonas mucosissima* sp. nov. (with type strain CP173-2^T = ATCC BAA-1239^T = DSM 17494^T) and *Sphingomonas desiccabilis* sp. nov. (with type strain CP1D^T = ATCC BAA-1041^T = DSM 16792^T) are proposed.

Biological soil crusts (BSCs) are formed on the topmost layers of the soil by the entanglement and gluing of mineral particles with micro-organisms and their extracellular polysaccharides (Belnap & Lange, 2001). Most BSCs are dominated by cyanobacteria, with *Microcoleus vaginatus* and *Microcoleus steenstrupii* being the most common phototrophs in the Western arid lands of North America (Bowker *et al.*, 2002; Garcia-Pichel, 2002; Gundlapally & Garcia-Pichel, 2006; Nagy *et al.*, 2005; Yeager *et al.*, 2004). The heterotrophic microbial community of BSCs has only begun to be probed in recent years. Culture-dependent and independent studies on BSCs from the Colorado Plateau (Gundlapally & Garcia-Pichel, 2006) and the Sonoran desert (Nagy *et al.*, 2005) have clearly established the dominance of members of the genera *Actinobacteria*, *Proteobacteria* and

Bacterioidetes among the bacterial chemoorganoheterotrophs and the widespread dominance of members of the genus *Nitrospira* among bacterial ammonia-oxidizing chemoorganolithotrophs (Johnson *et al.*, 2005). However, to date, only two descriptions of heterotrophic isolates from BSCs have been published, namely *Dyadobacter crusticola* (Reddy & Garcia-Pichel, 2005) and *Belnapia moabensis* (Reddy *et al.*, 2006). As a contribution to the study of biodiversity in these communities, we describe two additional isolates belonging to the genus *Sphingomonas* of the class *Alphaproteobacteria*.

The original genus *Sphingomonas*, as proposed by Yabuuchi *et al.* (1990) and emended by Takeuchi *et al.* (1993), was re-evaluated based on phylogenetic analysis, polyamine patterns, fatty acid profiling and nucleotide signature sequences (Pal *et al.*, 2005, 2006; Takeuchi *et al.*, 2001) and is now subdivided into four separate genera: *Sphingomonas sensu stricto*, *Sphingobium*, *Novosphingobium* and *Sphingopyxis*. Members of the genus *Sphingomonas* are yellow-pigmented, non-fermentative, Gram-negative, non-motile or motile rods with a single polar flagellum and are characterized by the presence of a unique sphingoglycolipid with the long-chain base dihydrosphingosin, ubiquinone 10

Abbreviation: BSCs, biological soil crusts.

The GenBank/EMBL/DDJB accession number for the 16S rRNA gene sequences of strains CP173-2^T and CP1D^T are AM229669 and AJ871435, respectively.

A supplementary table detailing 16S rRNA gene sequence similarities between strains CP173-2^T and CP1D^T and other species of the genus *Sphingomonas* is available in IJSEM Online.

(Q-10), 2-hydroxymyristic acid (2-OH $C_{14:0}$) and the absence of 3-hydroxy fatty acids. Species of the genus *Sphingomonas* have great potential for biotechnological applications (Denner *et al.*, 2001; Pollock, 1993).

Strains CP1D^T and CP173-2^T were isolated from biological soil crust samples collected from sandy arid soils in the Colorado Plateau, USA (38° 38' 557" N 109° 38' 910" W and 38° 09' 905" N 109° 44' 509" W), as described earlier (Reddy & Garcia-Pichel, 2005). Orange (CP173-2^T) and yellow (CP1D^T) colonies of pigmented bacteria were picked up from BG11-PGY agar-solidified plates, purified by restreaking and maintained on 10 × BG11-PGY plates. Morphological, biochemical characteristics and fatty acid methyl esters were analysed according to previously described methods (Reddy & Garcia-Pichel, 2005; Reddy *et al.*, 2006). Lipids were extracted and analysed as described by Suresh *et al.* (2004). Quinones were extracted according to the method of Collins *et al.* (1977) and separated by HPLC using the isocratic solvent system methanol/iso-propylether (3 : 1) (Tamaoka *et al.*, 1983; Tamaoka, 1986). *Sphingomonas asaccharolytica* ATCC 51839^T, *Sphingomonas panni* DSM 15761^T and *Sphingomonas dokdonensis* DS-4^T were used as standards for identifying the lipids and quinones. These strains were also used for DNA–DNA hybridization with the two novel strains using the filter hybridization method described by Pandey *et al.* (2002). 16S rRNA gene sequencing and phylogenetic analysis were performed as described previously (Kimura, 1980; Kumar *et al.*, 2001; Reddy & Garcia-Pichel, 2005; Thompson *et al.*, 1994).

Cells of strains CP173-2^T and CP1D^T are Gram-negative, rod-shaped (Fig. 1), non-motile, mucoid and pigmented and contain $C_{16:0}$, $C_{18:1\omega7c}$ and $C_{14:0}$ 2-OH as the major cellular fatty acids, as well as ubiquinone-10 as the isoprenoid quinone. A comparison of the lipid profiles of strains CP1D^T and CP173-2^T with those of *S. asaccharolytica* ATCC 51839^T indicated that they contain, among other lipids, abundant sphingoglycolipid. These traits would place both novel isolates within the family *Sphingomonadaceae*. BLAST similarity analysis based on 16S rRNA gene sequences placed both novel strains clearly within the

genus *Sphingomonas*. In addition, their gene sequences contained the signature sequences C-G, G, G, G-C, U-G, U, U, U, U, A, C, G and C at positions 52–359 (based on the *Escherichia coli* numbering system), 134, 593, 987–1218, 990–1215, 412, 562, 748, 823, 877, 841, 1438 and 1463, respectively, which are characteristic of the genus (Maruyama *et al.*, 2006; Takeuchi *et al.*, 2001). The two novel strains shared a 16S rRNA gene sequence similarity of 96.7 % (see Supplementary Table S1 in IJSEM Online), confirming that they represent separate species belonging to the genus *Sphingomonas* (Stackebrandt & Goebel, 1994). In addition, strain CP1D^T is conspicuously different from strain CP173-2^T in that it is yellow-pigmented, whereas strain CP173-2^T is orange-pigmented; other differentiating characteristics are listed in Table 1.

Strain CP1D^T shared a sequence similarity of 92–97.9 % with other members of the genus *Sphingomonas* (Supplementary Table S1); its closest relative was *S. panni* (97.9 % gene sequence similarity). In addition, the topologies of the 16S rRNA gene sequence phylogenetic trees, constructed using the unweighted pair group method with arithmetic mean (UPGMA), neighbour-joining (NJ), maximum-evolution (ME) and DNA parsimony methods, all strongly supported the affiliation of strain CP1D^T with *S. panni* (Busse *et al.*, 2005) (Fig. 2). However, DNA–DNA hybridization between strain CP1D^T and *S. panni* was only 18 % indicating a clear species separation. This was further confirmed by the phenotypic differences that strain CP1D^T exhibited when compared with *S. panni* (Tables 1 and 2). The differences between these strains were particularly marked with respect to the fatty acid profiles as strain CP1D^T contained higher amounts of $C_{17:1\omega6c}$ and $C_{18:1\omega5c}$ and significantly lower amounts of the major fatty acid $C_{18:1\omega7c}$. Therefore, based on the above characteristics, strain CP1D^T was assigned as the type strain of a novel species, *Sphingomonas desiccabilis* sp. nov.

Strain CP173-2^T showed a 16S rRNA gene sequence similarity of 91.6–98.9 % with other species of the genus *Sphingomonas* (see Supplementary Table S1). The most similar species, with 98.9 % gene sequence similarity, was *S.*

Fig. 1. Transmission electron micrograph of negatively stained cells of (a) *Sphingomonas mucosissima* CP173-2^T and (b) *Sphingomonas desiccabilis* CP1D^T. Note the extracellular mucus as tenuous shadowing around cells. Bars, 1 μm.

Table 1. Phenotypic characteristics that differentiate strains CP1D^T and CP173-2^T from related species of the genus *Sphingomonas*

Taxa: 1, *Sphingomonas desiccabilis* sp. nov. CP1D^T; 2, *S. panni* DSM 15761^T (data from Busse *et al.*, 2005); 3, *Sphingomonas mucosissima* sp. nov. CP173-2^T; 4, *S. dokdonensis* DS-4^T (Yoon *et al.*, 2006); 5, *S. asaccharolytica* Y-345^T (Takeuchi *et al.*, 1995); 6, *Sphingomonas pruni* Y-250^T (Takeuchi *et al.*, 1995); 7, *Sphingomonas mali* Y-351^T (Takeuchi *et al.*, 1995); 8, *Sphingomonas melonis* DSM 14444^T (Buonaurio *et al.*, 2002); 9, *Sphingomonas aquatilis* JSS7^T (Lee *et al.*, 2001); 10, *Sphingomonas koreensis* JSS26^T (Lee *et al.*, 2001); 11, *Sphingomonas abaci* DSM 15867^T (Busse *et al.*, 2005); 12, *Sphingomonas faeni* DSM 14747^T (Busse *et al.*, 2003); 13, *Sphingomonas aerolata* DSM 14746^T (Busse *et al.*, 2003); 14, *Sphingomonas aurantiaca* DSM 14748^T (Busse *et al.*, 2003); 15, *Sphingomonas oligophenolica* CIP 107926^T (Ohta *et al.*, 2004); 16, *Sphingomonas echinoides* DSM 1805^T (Denner *et al.*, 1999). Y, Yellow; LY, light yellow; O, orange; V, variable; NG, not grown; ND, not determined; NR, not reported; +, positive; −, negative; (+), weakly positive.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Temperature range for growth (°C)	15–37	15–37	15–28	10–34	NR	NR	NR	NR	NR	NR	15–28	5–28	5–28	5–28	5–37	NR
Motility	−	−	−	+	−	−	+	−	+	+	−	+	+	+	−	+
Colour	Y	Y	O	Y	Y	Y	LY	Y	Y	Y	O	O	O	O	Y	Y
Biochemical characteristics:																
Oxidase	+	−	+	+	+	+	+	+	+	+	−	+	+	+	+	+
Lipase	+	NR	NG	+	+	+	+	−	NR	NR	NR	−	−	V	NR	−
Gelatinase	+	NR	−	+	−	−	−	−	−	−	NR	−	−	−	+	−
β-Galactosidase	+	+	−	−	+	+	+	+	+	+	+	+	+	+	NR	+
Nitrate reduction	+	NR	−	−	−	−	−	−	−	−	NR	−	−	−	+	+
Hydrolysis of:																
Starch	+	NR	+	+	+	+	−	−	NR	NR	NR	−	−	−	−	+
Aesculin	−	+	−	+	+	+	+	+	+	+	+	+	+	+	NR	+
Assimilation of carbon compounds:																
Acetate	−	NR	+	+	−	−	−	NR	NR	NR	NR	+	+	+	+	−
Alanine	−	−	+	NR	+	+	−	−	NR	NR	−	+	+	+	NR	−
Arabinose	+	−	+	−	+	+	+	+	+	−	−	+	+	+	+	+
Aspartic acid	−	−	−	NR	+	−	+	−	NR	NR	−	+	−	−	NR	−
Cellobiose	+	−	+	+	−	+	+	+	NR	NR	−	+	+	+	+	+
Citrate	−	+	−	−	−	−	−	−	−	−	−	+	V	+	+	−
Fructose	−	−	+	−	−	−	+	+	NR	NR	−	+	+	+	−	−
Fumarate	−	+	−	NR	(+)	+	+	+	NR	NR	+	+	+	+	NR	NR
Galactose	+	−	+	−	−	+	+	+	NR	NR	−	+	+	+	+	+
Glucose	+	−	+	−	+	+	+	+	+	+	−	+	+	+	+	+
Glutamic acid	−	NR	−	−	+	+	+	+	NR	NR	NR	NR	NR	NR	NR	−
Lactose	−	−	−	NR	(+)	+	+	−	NR	NR	−	NR	NR	NR	+	ND
Leucine	−	−	−	NR	−	−	−	NR	NR	NR	−	+	−	+	NR	−
Maltose	+	+	−	−	+	+	+	+	+	+	−	+	+	+	+	+
Mannitol	−	−	−	−	+	−	−	−	NR	NR	−	−	−	−	NR	−
Mannose	+	+	−	+	+	+	+	+	−	−	−	+	+	+	+	−
Melibiose	+	−	+	NR	+	(+)	+	−	−	+	−	+	V	+	NR	−
Proline	+	+	−	NR	+	−	−	+	NR	NR	−	−	−	+	NR	−
Pyruvate	+	+	+	+	−	−	−	NR	NR	NR	−	+	V	+	+	−
Raffinose	+	−	−	NR	−	−	+	−	NR	NR	−	NR	NR	NR	+	ND
Rhamnose	+	−	−	NR	(+)	+	+	+	+	+	−	+	−	−	NR	−
Ribose	+	−	+	NR	NR	NR	NR	−	−	−	−	−	−	−	NR	−
Sucrose	+	−	+	−	(+)	+	+	+	+	+	−	+	+	+	NR	−
Trehalose	−	+	−	+	(+)	+	+	+	NR	NR	−	+	+	+	NR	+
Xylose	+	−	+	−	−	+	+	+	NR	NR	−	+	+	+	+	−

dokdonensis (Yoon *et al.*, 2006), suggesting that strain CP173-2^T could be a further strain of *S. dokdonensis*. Further, the topologies of the phylogenetic trees constructed using different methods suggested a strong affiliation (as supported by the bootstrap values of 88–99 %) of strain

CP173-2^T to *S. dokdonensis* (Fig. 2). However, low relatedness (32.5 %) in DNA–DNA hybridization experiments between strain CP173-2^T and the type strain of *S. dokdonensis*, indicates that the strains represent separate species. In addition, strain CP173-2^T and *S. dokdonensis* exhibited

Fig. 2. Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic relationship between *Sphingomonas mucosissima* sp. nov. CP173-2^T, *Sphingomonas desiccabilis* sp. nov. CP1D^T and other related micro-organisms. Bootstrap values (expressed as a percentage of 1000 replications) >50% are given at the nodes. Bar, 0.02 substitutions per nucleotide position.

several phenotypic differences (morphological and biochemical as well as chemotaxonomic; Tables 1 and 2), further supporting the species separation. Most remarkably, strain CP173-2^T is unique when compared to its closest relatives as it gives a negative result in tests for β -galactosidase and has high proportion of C_{14:0} and C_{16:0} 2-OH. Thus, based on the cumulative differences that strain CP173-2^T exhibited when compared with the recognized species of the genus *Sphingomonas*, we suggest that strain CP173-2^T represents a novel species, for which the name *Sphingomonas mucosissima* sp. nov. is proposed.

It appears that the strains CP1D^T and CP173-2^T could impart some stability to the BSCs they inhabit as they produce very abundant extrapolymeric substances, as evidenced in their mucous appearance in transmission electron micrographs (Fig. 1). Given their extreme environment of origin, these strains are likely to be able to withstand repeated and severe desiccation as well as exposure to temperature extremes and solar radiation. This may make them valuable in biotechnology or bioremediation applications tailored to extreme conditions.

Description of *Sphingomonas mucosissima* sp. nov.

Sphingomonas mucosissima (mu.co.sis'si.ma. L. fem. superlative adj. *mucosissima* slimiest, referring to the appearance of the strains).

Colonies are orange-pigmented, extremely mucoid, convex, round and smooth. Cells are Gram-negative, non-motile rods of 0.75 μ m diameter and 1.7 μ m in length. Grows at 15–30 °C, but not at 37 °C, with an optimum growth temperature of 25 °C and a pH of 7. Can tolerate up to 2.5 % NaCl. Cells are positive for catalase, oxidase, phosphatase and do not grow on test media plates of lipase and urease. Negative result in tests for β -galactosidase, gelatinase, lysine decarboxylase, ornithine decarboxylase, phenylalanine deaminase and arginine dihydrolase activities. Can hydrolyse starch, but not aesculin. Does not reduce nitrate to nitrite and cannot produce H₂S gas. Negative results in methyl red, Voges–Proskauer, indole and Simmons' citrate tests. Can utilize acetate, L-arabinose, D-cellobiose, glucose, D-fructose, D-galactose, D-glucose, glycerol, inulin, D-melibiose,

Table 2. Comparison of fatty acid contents (%) of strains CP173-2^T and CP1D^T with other related species of the genus *Sphingomonas*

Taxa: 1, *Sphingomonas mucosissima* CP173-2^T; 2, *S. dokdonensis* DS-4^T (Yoon *et al.*, 2006); 3, *Sphingomonas desiccabilis* CP1D^T; 4, *S. panni* DSM 15761^T (Busse *et al.*, 2005); 5, *S. asaccharolytica* Y-345^T (Denner *et al.*, 1999); 6, *S. pruni* Y-250^T (Denner *et al.*, 1999); 7, *S. mali* Y-351^T (Denner *et al.*, 1999); 8, *S. melonis* DAPP-PG 224^T (Buonaurio *et al.*, 2002); 9, *Sphingomonas aquatilis* JSS7^T (Lee *et al.*, 2001); 10, *Sphingomonas koreensis* JSS26^T (Lee *et al.*, 2001); 11, *S. abaci* DSM 15867^T (Busse *et al.*, 2005); 12, *S. faeni* DSM 14747^T (Busse *et al.*, 2003); 13, *S. aerolata* DSM 14746^T (Busse *et al.*, 2003); 14, *S. aurantiaca* DSM 14748^T (Busse *et al.*, 2003); 15, *S. oligophenolica* CIP 107926^T (Ohta *et al.*, 2004); 16, *S. echinoides* DSM 1805^T (Denner *et al.*, 1999). +, Detected; ND, not detected; NR, not reported.

Fatty acid	1	2	3	4	5	6	7	8*	9	10	11	12	13	14	15	16
C _{14:0}	10.3	0.8	0.8	1.1	ND	ND	ND	NR	0.7	1.9	ND	2.0	1.9	3.0	3.0	0.9
C _{15:0}	1.4	ND	0.9	1.1	ND	ND	ND	NR	ND	0.2	ND	ND	0.5	0.8	ND	ND
C _{16:0}	7.1	19.0	13.4	17.8	13.3	16.0	11.8	NR	20.6	13.0	12.4	11.2	15.8	15.6	10.0	10.0
C _{17:0}	ND	ND	0.7	ND	ND	ND	ND	NR	ND	ND	ND	ND	ND	0.2	ND	ND
C _{18:0}	4.1	ND	6.1	ND	ND	ND	ND	NR	1.0	0.6	ND	ND	ND	0.3	ND	ND
C _{16:1} ω5c	1.0	1.3	1.6	2.1	ND	ND	ND	NR	0.8	1.3	ND	1.6	2.0	1.8	6.0	0.8
C _{16:1} ω7c/iso-C _{15:0} 2-OH	12.3	14.8	18.1	17.1	ND	ND	ND	NR	4.6	2.1	8.3	29.2	26.8	28.0	5.0	2.5
C _{17:1} ω6c	2.7	ND	6.8	3.6	ND	ND	ND	NR	ND	1.5	1.6	2.6	1.7	3.0	ND	ND
C _{17:1} ω7c	ND	ND	ND	ND	ND	ND	ND	NR	ND	ND	ND	ND	ND	ND	ND	ND
C _{17:1} ω8c	ND	ND	ND	ND	ND	ND	9.3	NR	ND	0.4	ND	ND	ND	0.4	1.0	2.9
C _{18:1} ω5c	0.5	ND	3.7	0.7	ND	ND	ND	NR	1.5	1.8	ND	1.0	0.8	1.0	ND	2.7
C _{18:1} ω7c	33.9	45.7	37.8	51.3	67.3	73.1	70.5	+	59.9	67.0	64.8	41.4	46.0	40.5	56.0	73.1
C _{12:0} 2-OH	ND	ND	ND	ND	ND	ND	ND	NR	ND	ND	ND	0.6	0.6	0.4	ND	ND
C _{14:0} 2-OH	22.3	12.1	4.5	5.3	18.8	10.9	8.4	+	10.9	9.42	12.9	9.7	14.1	10.6	19.0	7.2
C _{15:0} 2-OH	0.4	ND	ND	ND	ND	ND	ND	NR	ND	0.29	ND	ND	ND	ND	ND	ND
C _{16:0} 2-OH	4.1	ND	ND	ND	ND	ND	ND	NR	ND	0.79	ND	ND	ND	ND	ND	ND
C _{17:0} cyclo	ND	ND	ND	ND	ND	ND	ND	NR	ND	ND	ND	ND	0.4	ND	ND	ND
C _{19:0} ω8c cyclo	ND	ND	1.0	0.8	ND	ND	ND	NR	ND	ND	ND	ND	0.7	ND	ND	ND
C _{16:1} 2-OH	ND	ND	ND	ND	ND	ND	ND	NR	ND	ND	ND	ND	0.5	ND	ND	ND
11-Me-C _{18:1} ω7c	ND	6.3	ND	ND	ND	ND	ND	NR	ND	ND	ND	ND	3.5	ND	ND	ND

*Complete data for *S. melonis* is not available.

pyruvate, D-ribose, sucrose, sorbose, sucrose, D-xylose, L-alanine as sole carbon source but not adonitol, citrate, dulcitol, dextran, ethanolamine, fumaric acid, glucuronic acid, *myo*-inositol, lactose, lactic acid, D-levulose, D-maltose, D-mannitol, D-mannose, myristic acid, oxalic acid, raffinose, D-rhamnose, L-sorbose, sorbitol, succinate, trehalose, L-arginine, L-aspartic acid, L-asparagine, L-cysteine, L-glycine, L-glutamine, L-glutamic acid, L-histidine, L-leucine, L-lysine, L-methionine, L-phenylalanine and L-proline. Cells are sensitive to (per disc): azithromycin (30 µg), bacitracin (10 U), ceftriaxone (30 µg), chloramphenicol (30 µg), ciprofloxacin (5 µg), doxycycline (30 µg), gentamicin (10 µg), novobiocin (30 µg), rifampicin (30 µg), tetracycline (30 µg) and vancomycin (30 µg), but resistant to aztreonam (30 µg), carbenicillin (100 µg), cephalothin (30 µg), colistin (10 µg), erythromycin (2 µg), ethambutol (50 µg), ethionamide (30 µg), nitrofurantoin (150 µg), penicillin (10 µg), polymyxin B (300 µg), streptomycin (10 µg), sulfisoxazole (300 µg), sulfathiazole (300 µg) and trimethoprim (5 µg). The fatty acids and their contribution to the total fatty acid content are listed in Table 2. The major lipids present are phosphatidylglycerol (PG), cardiolipin

(DPG), phosphatidyl dimethyl ethanolamine (PDE) and sphingoglycolipid (SGL).

The type strain, strain CP173-2^T (= ATCC BAA-1239^T = DSM 17494^T), was isolated from a biological soil crust from the Colorado Plateau, USA.

Description of *Sphingomonas desiccabilis* sp. nov.

Sphingomonas desiccabilis (de.sic.ca'bi.lis. L. v. *desiccare* to dry up; L. suffix *-abilis* adjectival suffix expressing passive qualities; N.L. fem. adj. *desiccabilis* able to be dried, desiccable).

Colonies are yellow-pigmented, extremely mucoid, convex, round and smooth. Cells are Gram-negative, non-motile, small rods of 0.25 µm in diameter and 0.5 µm in length. Grows at 15–37 °C, with an optimum growth temperature of 25 °C and pH of 7. Can tolerate up to 4 % NaCl. The fatty acids and their contribution to the total fatty acid content are listed in Table 2. Major fatty acids and other metabolic characteristics are the same as those for *Sphingomonas*

mucosissima CP173-2^T, except the following: tests positive for lipase, gelatinase and β -galactosidase, negative in tests for urease and can reduce nitrate to nitrite. Can utilize glucuronic acid, D-maltose, D-mannose, raffinose, D-rhamnose and L-proline as sole carbon source, but not acetate, D-fructose, glycerol or L-alanine. Cells are resistant to gentamicin (10 μ g/disc).

The type strain, strain CP1D^T (= ATCC BAA-1041^T = DSM 16792^T), was isolated from a biological soil crust from the Colorado Plateau, USA.

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