Description of *Sphingosinicella xenopeptidilytica* sp. nov., a β -peptide-degrading species, and emended descriptions of the genus *Sphingosinicella* and the species *Sphingosinicella microcystinivorans*

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A Gram-negative, rod-shaped bacterium, strain 3-2W4^T, was isolated from the aeration tank of a wastewater treatment plant in Zurich and was found to have the exceptional capacity to degrade synthetic β -peptides. 16S rRNA gene sequence analysis showed that strain 3-2W4^T is closely related to *Sphingosinicella microcystinivorans* Y2^T, but DNA–DNA hybridization experiments between these two strains revealed that they belong to two different species. The two strains displayed different fingerprints after PCR analysis using the repetitive primers BOX, ERIC and REP. Strain 3-2W4^T did not degrade microcystin, which is a characteristic trait of *Sphingosinicella microcystinivorans* Y2^T. Like *Sphingosinicella microcystinivorans* Y2^T, strain 3-2W4^T had the following characteristics: fatty acids comprising mainly C_{18:1 ω 7c}, summed feature 3 (C_{16:1 ω 7c} and/or iso-C_{15:0} 2-OH) and C_{16:0}, the presence of ubiquinone Q-10 and *sym*-homospermidine as the predominant polyamine compound. The polar lipid profiles of the two strains were almost identical, consisting of phosphatidylethanolamine, phosphatidylmonomethylethanolamine, phosphatidylglycerol and sphingoglycolipid. Strain 3-2W4^T and *Sphingosinicella microcystinivorans* Y2^T utilized the β -peptides H- β hVal- β hAla- β hLeu-OH and H- β hAla- β hLeu-OH as sole carbon and energy sources and shared β -peptidyl aminopeptidase activity in common, which distinguishes them from *Sphingomonas* and *Sphingopyxis* type strains. On the basis of these results, strain 3-2W4^T represents a novel species of the genus *Sphingosinicella*, for which the name *Sphingosinicella xenopeptidilytica* sp. nov. is proposed. The type strain is 3-2W4^T (= DSM 17130^T = CCUG 52537^T). The descriptions of the genus *Sphingosinicella* and the species *Sphingosinicella microcystinivorans* are emended.

The synthesis of β -peptides composed of β -homoamino acids with proteinogenic side-chains was achieved for the first time by Seebach *et al.* (1996). Since then, knowledge has accumulated about the structural properties of β -peptides, their synthesis on the basis of homologated β -amino acids (Seebach *et al.*, 2004), their pharmaceutical applications

(Kritzer *et al.*, 2004; Stephens *et al.*, 2005) and their biological stability (Frackenpohl *et al.*, 2001; Lelais & Seebach, 2003; Seebach *et al.*, 1998). β -Amino acids are found in many biological molecules, such as microcystin, paclitaxel (Taxol), carnosine and bestatin, but β -peptides composed solely of β -homoamino acids do not occur in nature. Although β -peptides are of synthetic origin and exhibit extremely high resistance to enzymic degradation, different bacterial consortia have been shown to have the capacity to grow on these substrates (Schreiber *et al.*, 2002). Recently, strain 3-2W4^T was isolated from one of these mixed cultures and it was shown that this strain utilized the

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain 3-2W4^T is AY950663.

A two-dimensional thin-layer chromatogram of the polar lipids of strain 3-2W4^T is available as a supplementary figure in IJSEM Online.

β -tripeptide H- β hVal- β hAla- β hLeu-OH as a sole source of carbon and energy (Geueke *et al.*, 2005). The inoculum for the enrichment culture originated from the aeration tank of a wastewater treatment plant at Leutschenbach in Zurich, Switzerland. Here we report on the classification of strain 3-2W4^T within a novel species of *Sphingosinicella*, based on analyses of its 16S rRNA gene sequence, chemotaxonomic characteristics and physiological traits.

Genomic DNA was extracted with the AquaPure genomic DNA purification kit (Bio-Rad). The 16S rRNA gene sequence of strain 3-2W4^T was amplified by a PCR using the primers 16S 6F (5'-GGAGAGTTAGATCTTGGCTCA-3') and 16S 1510R (5'-GTGCTGCAGGGTTACCTTGTTACG-ACT-3'). The PCR product was cloned into pGEM-T Easy, sequenced and a continuous stretch of 1411 bp was obtained. The 16S rRNA gene sequence of strain 3-2W4^T was compared with sequences in the databases by means of a BLAST search: the highest levels of similarity were found with respect to *Sphingosinicella microcystinivorans* Y2^T (99.9%) (Maruyama *et al.*, 2006) and *Sphingomonas suberifaciens* IFO 15211^T (94.6%), the latter being a strain that will probably be classified within another genus on the basis of its separate phylogenetic position. Values of $\leq 94.2\%$ were found with respect to the type strains of *Sphingomonas* and *Sphingopyxis* species. Like *Sphingosinicella microcystinivorans* Y2^T, strain 3-2W4^T exhibited all of the characteristic 16S rRNA signature nucleotides of the genus *Sphingomonas* and showed a single difference with respect to the signatures of the genus *Sphingopyxis* (Takeuchi *et al.*, 2001). Additionally, we identified eight signature nucleotides that distinguish *Sphingosinicella* strains from other members of the

Table 1. Signatures in the 16S rRNA gene sequences of *Sphingosinicella* strains (including unnamed strains sharing more than 97% similarity with *Sphingosinicella microcystinivorans* Y2^T) useful for differentiation from all other species of the family *Sphingomonadaceae*

Positions are given according to *Escherichia coli* numbering.

Position	<i>Sphingosinicella</i>	Other members of the <i>Sphingomonadaceae</i>
412	A	U
562	C	U
748	A	U*
823	G	U
877	C	A†
841	U	C‡
1463	A	U or C§
1438	U	G or A

*G for *Sphingomonas phyllosphaerae*, A for *Sphingomonas suberifaciens*.

†U for *Sphingomonas echinoides*.

‡A for *Sphingopyxis baekryungensis*; gap for most *Novosphingobium* strains.

§G for *Sphingomonas echinoides*.

Sphingomonadaceae (Table 1). Phylogenetic analysis of nearly full-length 16S rRNA gene sequences of strain 3-2W4^T and *Sphingosinicella microcystinivorans* Y2^T confirmed that they are closely related to each other and that the genus *Sphingosinicella* forms a distinct phylogenetic lineage in comparisons with selected type strains of the family *Sphingomonadaceae* (Fig. 1).

Strain 3-2W4^T was subcultured on nutrient agar (Biolife) at 30 °C. Liquid cultures were incubated at 25 °C in nutrient broth or minimal medium. The minimal medium used to measure the pH and NaCl tolerances was composed of the following (l⁻¹): 0.2 mM CaCl₂, 2 mM MgSO₄, 1 g NaCl, 2 g Na₂HPO₄·2H₂O, 1 g KH₂PO₄, 0.7 g (NH₄)₂SO₄ and 0.1 g yeast extract. It was supplemented with a trace element solution (1 ml l⁻¹) and a vitamin solution (2 ml l⁻¹) according to Schreiber *et al.* (2002). NaCl and pH tolerances were measured in minimal medium with isoleucine (1 g l⁻¹) as the main carbon source. To adjust the pH of the medium, the phosphate salts were omitted and universal buffer (according to Teorell & Stenhagen, 1938) was used for pHs in the range 4–12. Growth at different salinities was measured for NaCl concentrations between 0 and 3% (w/v). Carbon-source utilization was examined as described

Fig. 1. Neighbour-joining phylogenetic tree of the type strains of the genus *Sphingosinicella* and selected type strains of the genera *Sphingomonas*, *Sphingopyxis*, *Novosphingobium*, *Sphingobium* and other members of the *Alphaproteobacteria*. *Rhodospirillum rubrum* DSM 467^T was used as the outgroup. The alignment was performed with the program CLUSTAL W (Chenna *et al.*, 2003) and ambiguous nucleotides and gaps were removed with the program BioEdit, version 5.0.6. The total alignment length was 1299 bp. Phylogenetic analyses were performed using the PHYLIP package (version 3.6). Numbers at the nodes show bootstrap values higher than 700, based on DNA distance analyses of 1000 resampled datasets. Bar, 0.1 substitutions per nucleotide position.

previously (Kämpfer *et al.*, 1991). Additionally, physiological and biochemical characteristics were examined using the API 20NE and API 20E kits according to the manufacturer's instructions (bioMérieux). Gram stains were performed at the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ; Braunschweig, Germany) according to Cerny (1976) and Gregersen (1978); the hydrolysis of starch, Tween 80 and DNA was measured according to Gerhardt *et al.* (1981). Strain 3-2W4^T and *Sphingosinicella microcystinivorans* Y2^T utilized many amino acids and some organic acids as sources of carbon and energy, but they did not grow on any of the sugars and polyalcohols tested (Table 2). The only characteristics that distinguish strain 3-2W4^T from *Sphingosinicella microcystinivorans* Y2^T concerned the intensity of growth on β -homovaline, citrate and DL-lactate and the reduction of nitrate to nitrite (Table 2).

Recently, the β -peptidyl aminopeptidase of strain 3-2W4^T was isolated and characterized and its coding sequence (*bapA*) analysed (Geueke *et al.*, 2005). This enzyme is responsible for the ability of strain 3-2W4^T to utilize the synthetic β -peptides H- β hVal- β hLeu- β hAla-OH and H- β hAla- β hLeu-OH as sole sources of carbon, nitrogen and energy (Geueke *et al.*, 2005). The two β -peptides were synthesized according to Schreiber *et al.* (2002). To determine whether this unusual enzymic activity might be characteristic of the genus *Sphingosinicella*, *Sphingosinicella microcystinivorans* Y2^T, 20 type strains of *Sphingomonas* and six type strains of *Sphingopyxis* species were tested for the ability to utilize both β -peptides as sole sources of carbon and energy. Strain 3-2W4^T and *Sphingosinicella microcystinivorans* Y2^T assimilated the two β -peptides, but none of the reference strains did. Moreover, a copy of the *bapA* gene was detected in the genome of *Sphingosinicella microcystinivorans* Y2^T (Geueke *et al.*, 2006). These observations indicate that utilization of β -peptides distinguishes strain 3-2W4^T and *Sphingosinicella microcystinivorans* Y2^T from *Sphingomonas* and *Sphingopyxis* species.

The degradation of microcystin by strain 3-2W4^T was investigated, since this feature is an exceptional trait of *Sphingosinicella microcystinivorans* (Maruyama *et al.*, 2006; Park *et al.*, 2001; Saito *et al.*, 2003). Strain 3-2W4^T was cultivated in nutrient broth, the cells were harvested in the late-exponential phase by centrifugation and disrupted by ultrasonication and the crude extract was incubated with microcystin-LR, which is the most common type of microcystin. Under these conditions, no degradation was observed. To support this result, we screened for the occurrence of the genes *mlrA*, *mlrB*, *mlrC* and *mlrD*, because they code for three peptidases and an oligopeptide transporter protein that are involved in the degradation of microcystin (Bourne *et al.*, 2001; Saito *et al.*, 2003). The following primer pairs were used to probe for the *mlrA*, *mlrB*, *mlrC* and *mlrD* genes, respectively: 5'-GACCCGATGTTCAAGATGCT-3' and 5'-CTCCTCCACAAATCAGGAC-3'; 5'-ACNTCGAAGCAGTTTACAGC-3'

Table 2. Characteristics of strain 3-2W4^T useful for differentiation from *Sphingosinicella microcystinivorans* Y2^T

Strains: 1, 3-2W4^T; 2, *Sphingosinicella microcystinivorans* Y2^T. +, Positive; –, negative; (+), weakly positive. Both strains grew on acetate, azelate, 4-aminobutyrate, DL-3-hydroxybutyrate, propionate, suberate, L-alanine, L-aspartate, L-histidine, L-leucine, L-ornithine, L-phenylalanine, L-serine, L-tryptophan, L-valine, β -alanine, L- β -homovaline, L- β -homoleucine, L- β -homovaline, L-isoleucine, L-glutamate, L-arginine, L-lysine, L-proline, L-threonine, but not on N-acetylgalactosamine, N-acetyl-D-glucosamine, L-arabinose, p-arbutin, D-cellobiose, D-fructose, D-galactose, D-glucose, D-mannose, D-maltose, α -D-melibiose, L-rhamnose, D-ribose, sucrose, salicin, D-trehalose, D-xylose, adonitol, i-inositol, maltitol, D-mannitol, D-sorbitol, putrescine, *cis*- and *trans*-aconitate, glycerol, adipate, caprate, fumarate, gluconate, itaconate, malate, mesaconate, oxoglutarate, succinate, L-cysteine, L-tyrosine, L-methionine, glycine, glycyl-glycine, 3-hydroxybenzoate or 4-hydroxybenzoate. Both strains hydrolysed bis-p-nitrophenyl phosphate, p-nitrophenyl phenylphosphonate, p-nitrophenyl phosphorylcholine, 2-deoxythymidine 5'-p-nitrophenyl phosphate, L-alanine p-nitroanilide, L-glutamate- γ -3-carboxy p-nitroanilide and L-proline p-nitroanilide, but not aesculin, gelatin, o-nitrophenyl β -D-galactopyranoside, p-nitrophenyl β -D-glucuronide, p-nitrophenyl α -D-glucopyranoside, p-nitrophenyl β -D-glucopyranoside or p-nitrophenyl β -D-xylopyranoside. They did not exhibit urease or arginine dihydrolase activity. They were unable to produce acid from glucose, lactose, sucrose, D-mannitol, dulcitol, salicin, adonitol, inositol, sorbitol, L-arabinose, raffinose, rhamnose, maltose, D-xylose, trehalose, cellobiose, methyl D-glucoside, erythritol, melibiose, D-arabitol and D-mannose. Formation of indole from tryptophan was not detected for either strain. Both strains grew on R2A agar plates and exhibited positive reactions for oxidase and catalase activities. The genes *bapA* and *mlrD* were detected by PCR in both strains, but *mlrC* did not yield a PCR product in either strain.

Characteristic	1	2
Assimilation of:		
DL-Lactate	+	(+)
Citrate	+	(+)
L- β -Homovaline	(+)	+
Reduction of nitrate	+	–
Degradation of microcystin	–	+
Two red pigment spots in the polar lipid extract	+	–
Growth at 2.5 % (w/v) NaCl	+	–
Detection by PCR of:		
<i>mlrA</i>	–	+
<i>mlrB</i>	–	+
<i>puf</i>	–	+

and 5'-AAGTAATTGGTGTDDACGTA-3'; 5'-AATWCNT-TCTCACCTSTGCC-3' and 5'-CCACCGCCGGGGT-TGACC-3'; and 5'-GAGATGTGGGAGVSC TTC-3' and 5'-CCMAGWGTGCCGCAGAYCAGCGG-3'. Genes *mlrA*, *mlrB* and *mlrC*, which encode enzymes responsible for the degradation of microcystin, were not detected in the genome of strain 3-2W4^T, but *mlrA*, *mlrB* and *mlrD* were

present in strain Y2^T (Table 2). Additionally, the absence of *mlrA* in strain 3-2W4^T was demonstrated by Southern hybridization with DIG-High Prime DNA Labelling and Detection starter kit II (Roche). The probe was composed of 806 bp and was amplified from genomic DNA of strain Y2^T by a PCR using the above-mentioned primers. From the results of the degradation and genetic experiments, we can conclude that strain 3-2W4^T is not capable of utilizing microcystin.

PCR experiments with the genomic DNA of *Sphingosinicella microcystinivorans* Y2^T and strain 3-2W4^T and the primers 5'-TGTCCGAGATCATCACSRTYTGC-3' and 5'-TTGCCGTABCGGATCGAGAA-3' showed that the former contained *puf* genes, which encode subunits of the photosynthetic reaction centre. These genes could not be detected in strain 3-2W4^T (Table 2).

For the analysis of quinones, polar lipids and polyamines, the cells were cultivated aerobically in PYE medium (0.3 %, w/v, casein peptone; 0.3 %, w/v, yeast extract; pH 7.2) at 25 °C. Respiratory quinones and polar lipids were determined according to Tindall (1990) and Altenburger *et al.* (1996); polyamines were analysed according to Busse & Auling (1988) and Busse *et al.* (1997). Fatty acids were analysed at the DSMZ with the MIDI Sherlock Microbial Identification System (version 4.5). The fatty acids of strain 3-2W4^T comprised C_{18:1}ω7c (42.1 %), summed feature 3 (C_{16:1}ω7c and/or iso-C_{15:0} 2-OH) (35.9 %), C_{16:0} (10.5 %), C_{14:0} 2-OH (4.3 %), C_{16:1}ω5c (3.2 %) and C_{14:0} (1.1 %). Traces (≤ 1 %) of C_{17:1}ω6c, C_{18:1}ω5c, iso-C_{16:0} 3-OH and 11-methyl C_{18:1}ω7c were detected. A very similar fatty acid profile was detected for *Sphingosinicella microcystinivorans* Y2^T: C_{18:1}ω7c (45.2 %), summed feature 3 (C_{16:1}ω7c and/or iso-C_{15:0} 2-OH) (31.9 %), C_{16:0} (7.0 %), C_{14:0} 2-OH (7.5 %), C_{16:1}ω5c (3.4 %), C_{14:0} (1.5 %), C_{17:1}ω6c (1.4 %) and C_{18:1}ω5c (1.2 %). Traces (< 0.7 %) of C_{16:0} 2-OH, C_{18:1}ω5c, iso-C_{16:0} 3-OH and C_{18:0} were identified. This result was also in excellent agreement with data reported for *Sphingosinicella microcystinivorans* (Maruyama *et al.*, 2006). The quinone system of strain 3-2W4^T consisted exclusively of ubiquinone Q-10 and the predominant polyamine was *sym*-homospermidine, both of which are characteristic of the genera *Sphingomonas sensu stricto* and *Sphingosinicella* (Busse *et al.*, 1999; Maruyama *et al.*, 2006; Takeuchi *et al.*, 2001). The polar lipid profiles of strain 3-2W4^T and *Sphingosinicella microcystinivorans* Y2^T were almost identical, confirming their high degree of relatedness. They consisted of the major compounds phosphatidylethanolamine, phosphatidylmonomethylethanolamine, phosphatidylglycerol and sphingoglycolipid, moderate amounts of diphosphatidylglycerol and minor to trace amounts of two unknown phospholipids, an unknown aminophospholipid and an unknown polar lipid. One of the unknown phospholipids showed the same chromatographic behaviour as PL3, which is present in the majority of species of the *Sphingomonadaceae*, as reported by Busse *et al.* (1999). Within the family *Sphingomonadaceae*, the lack of

phosphatidyl dimethylethanolamine in polar lipid extracts has been reported only for *Sphingomonas echinoides* DSM 1805^T, *Sphingopyxis witflariensis* DSM 14551^T and *Sphingopyxis macrogoltabidus* DSM 8826^T; *Sphingomonas echinoides* DSM 1805^T was the only strain also lacking phosphatidylcholine. These observations, as well as the presence of the major compound phosphatidylmonomethylethanolamine, underscore the unique polar lipid profiles of strain 3-2W4^T and *Sphingosinicella microcystinivorans* Y2^T (Busse *et al.*, 1999, 2003, 2005; Denner *et al.*, 2001; Kämpfer *et al.*, 2002b, c; Liu *et al.*, 2005; Pal *et al.*, 2005; Tirola *et al.*, 2005; Zhang *et al.*, 2005). Hence, this characteristic might be specific for members of the genus *Sphingosinicella*. However, this assumption has to be verified by isolating and analysing further species of the genus. The presence of two red pigment spots in addition to two yellow spots visible after two-dimensional TLC of the lipid extract clearly distinguished strain 3-2W4^T from *Sphingosinicella microcystinivorans* Y2^T (see Supplementary Fig. S1 available in IJSEM Online).

DNA-association studies were performed between strain 3-2W4^T and *Sphingosinicella microcystinivorans* Y2^T using two different methods. The microplate method described by Ziemke *et al.* (1998) was modified slightly: for nick translation, 2 µg DNA was labelled for 3 h at 15 °C. The second DNA–DNA hybridization experiment (De Ley *et al.*, 1970; Huß *et al.*, 1983) was performed by the identification service of the DSMZ. With the microplate method, strain 3-2W4^T and *Sphingosinicella microcystinivorans* Y2^T exhibited 40.6 % (reciprocal, 51.9 %) DNA–DNA relatedness, whereas hybridization experiments performed at the DSMZ resulted in 33 ± 7 % DNA–DNA relatedness. These observations confirmed the results of a previous study that reported slightly higher hybridization results when the microplate method was used (Kämpfer *et al.*, 2002a). However, the results clearly indicate that the two strains belong to different species, despite their almost identical 16S rRNA gene sequences.

We performed PCRs using the repetitive primers BOX, ERIC and REP to fingerprint the genomes of strain 3-2W4^T and *Sphingosinicella microcystinivorans* Y2^T using Expand long template polymerase (Roche Diagnostics) and primers REP1R-I, REP2-I, ERIC1R, ERIC2 and BOXA1R (Louws *et al.*, 1994). The banding patterns from these PCR experiments clearly showed differences between the two strains (Fig. 2). A band of approximately 1.9 kb became visible for both strains after BOX-PCR; this band was much more prominent for strain 3-2W4^T, whereas additional products appeared for *Sphingosinicella microcystinivorans* Y2^T. The fingerprints after ERIC-PCR and REP-PCR show striking differences. However, the REP-fingerprint of both strains exhibited two bands of approximately 1.2–1.3 kb.

The high levels of 16S rRNA gene sequence similarity and the similar chemotaxonomic features for strain 3-2W4^T and *Sphingosinicella microcystinivorans* Y2^T showed that strain 3-2W4^T should be classified within the genus *Sphingosinicella*. Moreover, our experiments indicated that strain 3-2W4^T is unable to degrade microcystin, in contrast to

Fig. 2. PCR fingerprints from genomic DNA of strain 3-2W4^T and *Sphingosinicella microcystinivorans* Y2^T. The BOX-PCR (lanes 1 and 2), ERIC-PCR (lanes 3 and 4) and REP-PCR (lanes 5 and 6) patterns are shown. The resulting electrophoretic patterns of strain 3-2W4^T (lanes 1, 3 and 5) and *Sphingosinicella microcystinivorans* Y2^T (lanes 2, 4 and 6) are illustrated. The PCR program was started with one initial cycle at 94 °C for 2 min, followed by 10 cycles of denaturation at 94 °C for 10 s, annealing at 44, 52 or 53 °C for 30 s with the REP, ERIC and BOX primers, respectively, and extension at 68 °C for 4 min. The elongation times for the next 25 cycles were extended to 4 min plus 20 s for each successive cycle. The reaction was stopped after subsequent incubation at 68 °C for 7 min. The gel was loaded with 5 µl PCR mixture. M, Markers.

Sphingosinicella microcystinivorans, for which this capacity is a major characteristic (Maruyama *et al.*, 2006). In view of the results of the DNA–DNA hybridization experiments between strain 3-2W4^T and *Sphingosinicella microcystinivorans* Y2^T, the absence of genes important in the degradation of microcystin, the presence of two red compounds in the pigment composition and the ability to reduce nitrate show that strain 3-2W4^T represents a novel species of the genus *Sphingosinicella*, for which we propose the name *Sphingosinicella xenopeptidilytica* sp. nov.

In this study, we have demonstrated that *Sphingosinicella xenopeptidilytica* 3-2W4^T and *Sphingosinicella microcystinivorans* Y2^T utilize the β -peptides H- β hVal- β hLeu- β hAla-OH and H- β hAla- β hLeu-OH as sole carbon and energy sources. Growth on these unusual substrates is the only trait that distinguishes the two strains from strains of the genera *Sphingopyxis* and *Sphingomonas sensu stricto*. In addition, we have provided the complete polar lipid profiles of these two strains. In view of these findings, an emended description of the genus *Sphingosinicella* is justified and is given below.

Emended description of *Sphingosinicella* Maruyama *et al.* 2006

The genus is as described by Maruyama *et al.* (2006), with the following emendations and modifications. Cells utilize

the β -peptides H- β hVal- β hAla- β hLeu-OH and H- β hAla- β hLeu-OH as sole carbon and energy sources and exhibit β -peptidyl aminopeptidase activity. The polar lipid profiles comprise the major compounds phosphatidylethanolamine, phosphatidylmonomethylethanolamine, phosphatidylglycerol and sphingoglycolipid, moderate amounts of diphosphatidylglycerol and minor to trace amounts of two unknown phospholipids, an unknown aminolipid and an unknown polar lipid. Eight nucleotides of the 16S rRNA gene sequence are typical signatures (Table 1). Degradation of microcystin is variable among species.

Emended description of *Sphingosinicella microcystinivorans* Maruyama *et al.* 2006

The species shares the characteristics listed in the emended genus description. Data listed in Table 2 add to the original species description. Growth is observed at temperatures in the range 20–37 °C, at pH 5.6 and 9.7 and at 0 and 2 % NaCl (w/v).

Description of *Sphingosinicella xenopeptidilytica* sp. nov.

Sphingosinicella xenopeptidilytica [xe'no.pep'ti.di.ly'ti.ca. Gr. adj. *xenos* foreign; N.L. n. *peptidum* peptide; N.L. adj. *lyticus* -a -um dissolving; N.L. fem. adj. *xenopeptidilytica* lysing foreign (xenobiotic) peptides].

Colonies are pale yellow, circular and convex. Cells are aerobic and 0.6–0.8 $\times$ 1.5–2.5 µm in size. Gram-negative, as determined by KOH and aminopeptidase tests. Growth occurs at temperatures between 5 and 37 °C, with an optimum between 20 and 37 °C on nutrient agar, but not at 44 °C. Cells grow in liquid minimal medium at pH 5.6–9.7 and at salinities of 0–2.5 % (w/v) but not at higher NaCl concentrations or on Bacto marine agar 2216 (Becton Dickinson). H₂S is formed. Starch, Tween 80 and DNA are not hydrolysed. Microcystin is not degraded and the relevant genes, *mlrA*, *mlrB* and *mlrC*, are not present. Other physiological and biochemical characteristics are shown in Table 2. The main fatty acids are C_{18:1 ω 7c}, summed feature 3 (C_{16:1 ω 7c} and/or iso-C_{15:0} 2-OH) and C_{16:0}. The polar lipid profile is the same as that given in the emended genus description. The quinone system is ubiquinone Q-10 and the predominant polyamine is sym-homospermidine. In addition to yellow components, the pigment composition contains also two red spots.

The type strain, 3-2W4^T (DSM 17130^T=CCUG 52537^T), was isolated from the aeration tank of a wastewater treatment plant in Zürich, Switzerland.

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