Sphingomonas sanxanigenens sp. nov., isolated from soil

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Strain NX02^T, a Gram-negative, non-spore-forming, rod-shaped bacterium, was isolated from soil, and its taxonomic position was investigated using a polyphasic approach. Chemotaxonomic analysis revealed that strain NX02^T possessed Q-10 as the predominant ubiquinone, *sym*-homospermidine as the major polyamine and $C_{18:1}\omega7c$, $C_{16:0}$ and $C_{14:0}$ 2-OH as the major fatty acids. The main polar lipids were sphingoglycolipid, phosphatidylcholine, phosphatidylglycerol, diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylmonomethylethanolamine, phosphatidyldimethylethanolamine and an unidentified glycolipid. The DNA G+C content was 66.4 mol%. Phylogenetic analysis based on 16S rRNA gene sequences showed that strain NX02^T belongs to the α-4 subgroup of the *Proteobacteria*, exhibiting the highest sequence similarity with respect to *Sphingomonas azotifigens* NBRC 15497^T (95.9 %), *Sphingomonas pituitosa* DSM 13101^T (95.8 %) and *Sphingomonas dokdonensis* KCTC 12541^T (95.8 %). On the basis of these results, strain NX02^T represents a novel species of the genus *Sphingomonas sensu stricto*, for which the name *Sphingomonas sanxanigenens* sp. nov. is proposed. The type strain is NX02^T (=DSM 19645^T =CGMCC 1.6417^T).

The genus *Sphingomonas* was first proposed by Yabuuchi *et al.* (1990) and belongs to the family *Sphingomonadaceae* (Kosako *et al.*, 2000). The genus description has been emended by Takeuchi *et al.* (1993, 2001), Yabuuchi *et al.* (2002) and Busse *et al.* (2003). Analysis of the phylogeny, polyamine patterns and fatty acid profiles of members of the genus led to the subdivision of *Sphingomonas* into four separate genera, i.e. *Sphingomonas sensu stricto* and three new genera, *Sphingobium*, *Novosphingobium* and *Sphingopyxis*. Strains belonging to the family *Sphingomonadaceae* have great potential for biotechnological applications, e.g. in the bioremediation and degradation of refractory contaminants and in the production of valuable biopolymers referred to as sphingans. Sphingans, such as gellan (S-60), welan (S-130), rhamsan (S-194), S-88, heteropolysaccharide S-7, S-198, S-657, NW11, PS-P4, GS-1, I-886 and HWR1 (Matsuyama *et al.*, 2003; Seo *et al.*, 2004), have a similar structure, with a linear repeating tetrasaccharide that consists of glucose, glucuronic acid, rhamnose or mannose. Aqueous solutions of sphingans are very viscous or have the ability to form gels.

In this paper, we report the results from our polyphasic taxonomic study on a novel biopolymer-producing bacterium designated strain NX02^T. On the basis of the physiological, chemotaxonomic and phylogenetic data, strain NX02^T represents a novel species of the genus *Sphingomonas sensu stricto*.

Bacteria were isolated from topsoil collected from a cornfield in Xinhe County, PR China. Isolation was performed using the standard dilution plating technique at 30 °C on NK medium (containing, per litre distilled water: 15 g sucrose, 5 g peptone, 3 g beef powder, 1 g yeast extract, 15 g agar; pH 7.0). For purification, colonies of strain NX02^T, which had a distinct mucoid appearance, were picked and then transferred onto new plates. Strain NX02^T produces a novel extracellular biopolymer called sanxan gum, which has thickening and pseudoplastic qualities. Sanxan gum consists of carbohydrates and peptides, and the monosaccharide composition of the carbohydrate portion is similar to that of sphingans (Wang *et al.*, 2008).

A 16S rRNA gene sequence fragment corresponding to positions 6–1540 in the *Escherichia coli* numbering system (Brosius *et al.*, 1978) was amplified using the universal primers 27F (5′-GAGAGTTTGATCCTGGCTCAG-3′) and 1541R (5′-AAGGAGGTGATCCAGCCGCA-3′). A phylogenetic analysis was performed using MEGA, version 3.0

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain NX02^T is DQ789172.

Results of two-dimensional TLC of the polar lipids of strain NX02^T are available as a supplementary figure with the online version of this paper.

(Kumar *et al.*, 2004), after multiple alignment of the data by CLUSTAL_X (Thompson *et al.*, 1997). Distances (with distance options according to the Kimura-2 model) and clustering using the neighbour-joining method were determined using bootstrap percentages based on 1000 replications. The 16S rRNA gene sequence of strain NX02^T was a continuous stretch of 1480 bp. A sequence similarity search of the GenBank/EMBL databases, performed using the FASTA program, revealed that strain NX02^T belongs to the family *Sphingomonadaceae*. The highest sequence similarities were found with respect to strains of established species, including *Sphingomonas azotifigens* NBRC 15497^T (95.9 %), *Sphingomonas pituitosa* DSM 13101^T (95.8 %) and *Sphingomonas dokdonensis* KCTC 12541^T (95.8 %). The neighbour-joining phylogenetic tree (Fig. 1) showed that strain NX02^T clearly belonged to the genus *Sphingomonas sensu stricto* lineage, where it formed a separate branch. This branching pattern demonstrated that strain NX02^T represents a novel species within the genus *Sphingomonas sensu stricto*.

Genomic DNA was isolated and purified using the method of Cashion *et al.* (1977). The G+C content of the genomic DNA was analysed using HPLC after enzymic degradation of the DNA into nucleosides (Mesbah *et al.*, 1989; Tamaoka & Komagata, 1984). DNA–DNA hybridization was carried out using the optical renaturation method (De Ley *et al.*, 1970; Huß *et al.*, 1983; Jahnke, 1992) with a UV-Vis spectrophotometer (Perkin-Elmer) under optimal hybridization conditions (25 °C below the melting temperature of DNA). The DNA G+C content was determined to be 66.4 mol%. The DNA–DNA relatedness between strain NX02^T and *S. azotifigens* NBRC 15497^T was 24 %, i.e. below the value (70 %) considered as the threshold for the delineation of a genospecies (Stackebrandt & Goebel, 1994).

Cell morphology was observed under light and transmission electron microscopy, using cells grown for 3 days at 30 °C (Fig. 2). All other physiological and biochemical tests were performed as described by Li *et al.* (2004) and Lebuhn

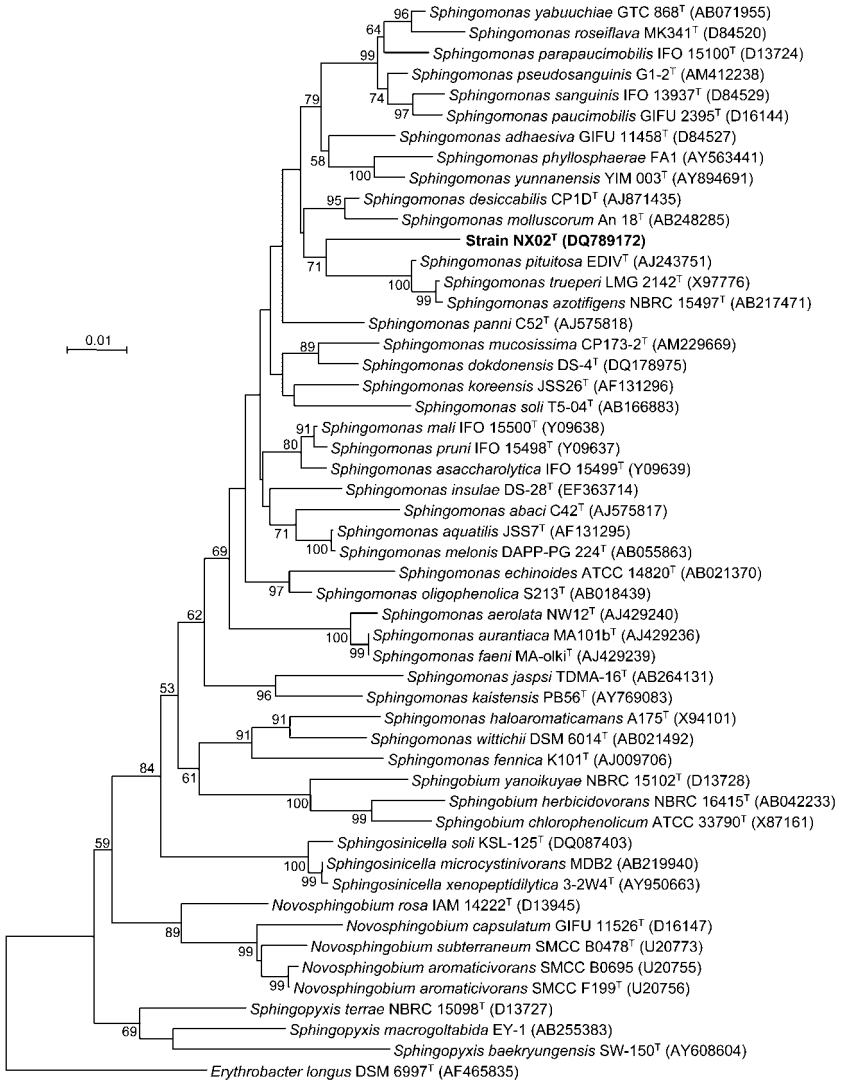

Fig. 1. Neighbour-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationships between strain NX02^T and related taxa. Bootstrap percentages (based on 1000 replicates) are shown at nodes: only values greater than 50 % are shown. The sequence of *Erythrobacter longus* DSM 6997^T was used as the outgroup. Bar, 1 % sequence divergence.

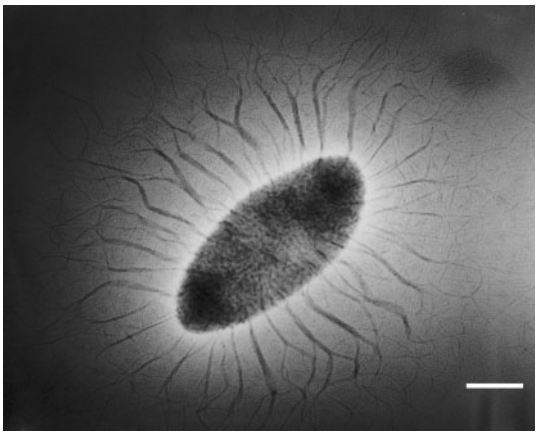

Fig. 2. Transmission electron micrograph of a cell of strain NX02^T. Bar, 500 nm.

et al. (2000). Growth occurred at 4–40 °C and at pH 4.0–8.5, with optima at 28–30 °C and pH 7.0–7.5. Growth occurred in the presence of 0–1.2 % (w/v) NaCl, with optimal growth at 0–0.05 % (w/v). Phenotypic features of strain NX02^T and phylogenetically related species are shown in Table 1. Strain NX02^T could be distinguished from its close relatives on the basis of a combination of phenotypic features. Strain NX02^T was similar to *Sphingomonas desiccabilis* DSM 16792^T in being positive for nitrate reduction, but it differed with regard to the oxidase reaction, the hydrolysis of starch and aesculin and the substrate-assimilation profile. Oxidase activity is absent in strain NX02^T and *S. pituitosa* DSM 13101^T. This is an unusual biochemical trait that has been reported for only a few sphingan-producing strains of the genus *Sphingomonas* (Yabuuchi *et al.*, 1990; Pollock, 1993).

Chemotaxonomic analyses were performed as follows. Respiratory quinones and polar lipids were determined as described by Tindall (1990a, b) and Altenburger *et al.* (1996), respectively, and were carried out by Dr B. J. Tindall and the Identification Service of the Deutsche Sammlung von Mikroorganismen und Zellkulturen (Braunschweig, Germany). Polyamines were extracted as described by Busse & Auling (1988) and analysed according to Busse *et al.* (1997). Fatty acid analysis was performed using the standard method of Sasser (1990): the results were compared with the database of fatty acids in the Sherlock Microbial Identification System (MIDI). The quinone system of strain NX02^T consisted of Q-10 (78 %) and Q-11 (22 %). The polar lipids detected were sphingoglycolipid, phosphatidylcholine, phosphatidylglycerol, diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylmonomethylethanolamine, phosphatidyldimethylethanolamine and an unidentified glycolipid (the two-dimensional thin-layer chromatogram is presented in Supplementary Fig. S1, available in IJSEM Online). The

Table 1. Phenotypic characteristics of strain NX02^T and the type strains of related *Sphingomonas* species

Strains: 1, NX02^T (data from this study); 2, *S. pituitosa* DSM 13101^T (Denner *et al.*, 2001); 3, *S. trueperi* ATCC 12417^T (Kämpfer *et al.*, 1997; Denner *et al.*, 2001); 4, *S. azotifigens* NBRC 15497^T (Xie & Yokota, 2006); 5, *S. dokdonensis* KCTC 12541^T (Yoon *et al.*, 2006); 6, *S. desiccabilis* DSM 16792^T (Reddy & Garcia-Pichel, 2007); 7, *S. molluscorum* CIP 109223^T (Romanenko *et al.*, 2007). +, Positive; −, negative; ND, no data available. All of the strains were positive for catalase activity and negative for indole production and assimilation of citrate.

Characteristic	1	2	3	4	5	6	7
Oxidase	−	−	+	+	+	+	+
Nitrate reduction	+	−	−	−	−	+	−
Hydrolysis of:							
Starch	−	−	+	+	+	+	−
Aesculin	+	+	−	+	+	−	+
Gelatin	+	−	−	−	+	+	−
Assimilation of:							
Acetate	−	+	+	+	+	−	ND
L-Arabinose	+	+	+	+	−	+	+
L-Aspartate	−	−	+	+	ND	−	ND
D-Fructose	−	−	+	+	−	−	ND
D-Glucose	+	+	+	+	−	+	+
L-Glutamic acid	−	ND	+	+	−	−	ND
Lactose	−	+	+	+	ND	−	+
Maltose	−	+	+	+	−	+	+
DNA G+C content (mol%)	66.4	64.5	65.6	66.0–68.0*	66.9	ND	68.3

*Range of values for three strains, including the type strain.

polyamine patterns of strain NX02^T showed a predominance of *sym*-homospermidine and trace amounts of spermidine. The presence of 2-hydroxy fatty acids and the absence of 3-hydroxy fatty acids are common characteristics of members of the family *Sphingomonadaceae* (Busse *et al.*, 1999; Takeuchi *et al.*, 2001). The cellular fatty acids of strain NX02^T mainly comprise $C_{18:1}\omega7c$ (53.8 %), $C_{16:0}$ (15.1 %) and $C_{14:0}$ 2-OH (12.0 %). This profile is consistent with that of the genus *Sphingomonas sensu stricto* (Busse *et al.*, 1999). However, strain NX02^T could be easily distinguished from its closest phylogenetic neighbours, both qualitatively and quantitatively, with regard to certain fatty acids and by the higher levels of $C_{18:1}\omega7c$ (Table 2).

On the basis of morphological and chemotaxonomic data and the results of the 16S rRNA gene sequence analysis, strain NX02^T represents a novel species of the genus *Sphingomonas*, for which the name *Sphingomonas sanxanigenens* sp. nov. is proposed.

Description of *Sphingomonas sanxanigenens* sp. nov.

Sphingomonas sanxanigenens [san.xa.ni.ge′nens. N.L. n. *sanxanum* sanxan gum (an extracellular biopolymer); L.

Table 2. Cellular fatty acid profiles of strain NX02^T and the type strains of related *Sphingomonas* species

Strains: 1, NX02^T (data from this study); 2, *S. pituitosa* DSM 13101^T (Denner *et al.*, 2001); 3, *S. trueperi* ATCC 12417^T (Kämpfer *et al.*, 1997); 4, *S. azotifigens* NBRC 15497^T (Xie & Yokota, 2006); 5, *S. dokdonensis* KCTC 12541^T (Yoon *et al.*, 2006); 6, *S. desiccabilis* DSM 16792^T (Reddy & Garcia-Pichel, 2007); 7, *S. molluscorum* CIP 109223^T (Romanenko *et al.*, 2007). Values are percentages of total fatty acids; –, not detected/not reported.

Fatty acid	1	2	3	4	5	6	7
$C_{14:0}$	0.9	–	–	2.6	0.8	0.8	–
$C_{15:0}$	–	2.6	–	–	–	0.9	1.7
$C_{16:0}$	15.1	11.5	9.8	24.5	19.0	13.4	24.0
$C_{16:1}\omega5c$	1.6	–	–	–	1.3	1.6	–
$C_{16:1}\omega7c$/iso-$C_{15:0}$ 2-OH	8.3	2.1	–	1.2	14.8	18.1	–
$C_{17:1}\omega6c$	1.0	13.0	13.6	1.4	–	6.8	–
$C_{18:1}\omega5c$	–	–	4.0	1.2	–	3.7	–
$C_{18:1}\omega7c$	53.8	54.2*	64.2*	44.7	45.7	37.8	17.7†
$C_{14:0}$ 2-OH	12.0	14.2	6.7	13.3	12.1	4.5	12.8
11-Methyl $C_{18:1}\omega7c$	7.3	–	–	10.9	6.3	–	–

*Reported as summed feature 7 (one or more of $C_{18:1}\omega7c$, $C_{18:1}\omega9t$ and $C_{18:1}\omega12t$).
†Also reported to contain 16.5 % $C_{18:1}\omega9$.

part. adj. *genens* (from L. v. *genere* to produce) producing; N.L. part. adj. *sanxanigenens* sanxan gum-producing].

Cells are rod-shaped, 0.6–0.9 μm wide and 1.5–2.0 μm long and do not exhibit flagella. After 6 days incubation at 30 °C, colonies on NK medium are white, circular, convex, mucoid and 5–6 mm in diameter. Optimum growth occurs at pH 7.0–7.5, 28–30 °C and 0–0.05 % NaCl. Cells are Gram-negative and non-spore-forming. Metabolism is non-fermentative. Positive for catalase and for nitrate reduction. Negative for oxidase, urease and for indole and H_2S production and in the methyl red and Voges–Proskauer tests. Positive for acid coagulation reaction in litmus milk. Hydrolyses aesculin and gelatin but not starch. The following are used as substrates for growth: L-arabinose, cellobiose, dextrin, D-galactose, gentiobiose, α-D-glucose, D-mannose, melibiose, pyruvic acid methyl ester, D-glucuronic acid, β-hydroxybutyric acid, sebacic acid, glycyl L-glutamic acid, raffinose, sucrose, trehalose, bromosuccinic acid, succinamic acid and urocanic acid. The major respiratory lipoquinone is Q-10. The predominant polyamine is s*ym*-homospermidine. The polar lipids contain sphingoglycolipid, phosphatidylcholine, phosphatidylglycerol, diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylmonomethylethanolamine, phosphatidyldimethylethanolamine and an unidentified glycolipid. The cellular fatty acids mainly comprise $C_{18:1}\omega7c$, $C_{16:0}$ and $C_{14:0}$ 2-OH. The DNA G+C content of the type strain is 66.4 mol%.

The type strain, NX02^T (=DSM 19645^T =CGMCC 1.6417^T), was isolated from soil.

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