Novosphingobium soli sp. nov., isolated from soil

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A yellow-pigmented, Gram-negative, rod-shaped, non-spore-forming bacterium, strain CC-TPE-1^T, was isolated from oil-contaminated soil near an oil refinery located in Kaohsiung County, Taiwan. 16S rRNA gene sequence analysis of strain CC-TPE-1^T showed highest sequence similarity to *Novosphingobium naphthalenivorans* TUT562^T (98.1%), *N. panipatense* SM16^T (97.9%) and *N. mathurense* SM117^T (97.6%) and lower (<97%) sequence similarity to all other *Novosphingobium* species. DNA–DNA hybridizations of strain CC-TPE-1^T with *N. naphthalenivorans* DSM 18518^T, *N. panipatense* SM16^T and *N. mathurense* SM117^T showed low relatedness of 30% (reciprocal 35%), 29.1% (reciprocal 30.6%) and 35% (reciprocal 23.6%), respectively. The major respiratory quinone was ubiquinone Q-10, the predominant fatty acid was C_{18:1}ω7c (49.9%) and three 2-hydroxy fatty acids, C_{14:0} 2-OH (8.2%), C_{15:0} 2-OH (2.45%) and C_{16:0} 2-OH (1.05%), were detected. Polar lipids consisted mainly of phosphatidylethanolamine, phosphatidylglycerol, phosphatidylcholine, phosphatidyl-dimethylethanolamine, two sphingoglycolipids, phosphatidylmonomethylethanolamine and several unidentified lipids, and a yellow pigment was also detected. The polyamine pattern contained the single major compound spermidine. Characterization by 16S rRNA gene sequence analysis, physiological parameters, pigment analysis and polyamine, ubiquinone, polar lipid and fatty acid compositions revealed that strain CC-TPE-1^T represents a novel species of the genus *Novosphingobium*, for which we propose the name *Novosphingobium soli* sp. nov., with the type strain CC-TPE-1^T (=DSM 22821^T =CCM 7706^T =CCUG 58493^T).

The genus *Novosphingobium* was proposed as a consequence of the dissection of the genus *Sphingomonas* (Yabuuchi *et al.*, 1990), which was based on phylogenetic and chemotaxonomic analyses (Takeuchi *et al.*, 2001). At the time of writing, 18 *Novosphingobium* species have been described with validly published names: the type species *Novosphingobium capsulatum* (Yabuuchi *et al.*, 1990), *N. rosa* (Takeuchi *et al.*, 1995), *N. aromaticivorans*, *N. stygium* and *N. subterraneum* (Balkwill *et al.*, 1997), *N. subarcticum* (Takeuchi *et al.*, 2001) (which has been reported to be a later

heterotypic synonym of *N. resinovorum*; Lim *et al.*, 2007), *N. hassiacum* (Kämpfer *et al.*, 2002), *N. tardaugens* (Fujii *et al.*, 2003), *N. pentaromativorans* (Sohn *et al.*, 2004), *N. taihuense* (Liu *et al.*, 2005), *N. lentum* (Tiirola *et al.*, 2005), *N. nitrogenifigens* (Addison *et al.*, 2007), *N. resinovorum* (Lim *et al.*, 2007), *N. naphthalenivorans* (Suzuki & Hiraishi, 2007), *N. acidiphilum* (Glaeser *et al.*, 2009), *N. mathurense* and *N. panipatense* (Gupta *et al.*, 2009) and *N. indicum* (Yuan *et al.*, 2009). *Novosphingobium* species have been isolated from a wide variety of habitats including soil, coastal and freshwater sediments (Balkwill *et al.*, 1997; Sohn *et al.*, 2004; Liu *et al.*, 2005), activated sludge/wastewater treatment plants (Neef *et al.*, 1999; Fujii *et al.*, 2003) and a contaminated ground-water bioremediation reactor (Tiirola *et al.*, 2002).

Abbreviations: pNA, *p*-nitroanilide; pNP, *p*-nitrophenyl.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain CC-TPE-1^T is FJ425737.

Strain CC-TPE-1^T was isolated from oil-contaminated soil near an oil refinery located in Kaohsiung County, Taiwan. The strain showed single cells and formed small yellow colonies (<0.5 mm) with a smooth surface after 48 h at 25 °C on nutrient agar. Cell morphology was investigated by phase-contrast microscopy for cells grown on nutrient agar at 25 °C. During exponential growth, rod-shaped cells of strain CC-TPE-1^T were 1.6 ± 0.4 µm long and 0.8 ± 0.1 µm wide and motile in the early exponential growth phase. Cells stained Gram-negative and were positive for cytochrome oxidase in a delayed reaction as determined by using an oxidase test (Merck). Endospores could not be detected.

For 16S rRNA gene sequencing, chromosomal DNA was extracted as described by Pitcher *et al.* (1989) and a 1461 bp fragment of the 16S rRNA gene was amplified using primers targeting conserved regions of the 16S rRNA gene, 8F (positions 8–27, *Escherichia coli* numbering; Brosius *et al.*, 1981) and 1492R (1492–1510; Lane, 1991). Sequencing of the DNA fragment was done with primers 8F and 1492R and two additional reverse primers, 907R (907–926) and 1100R (1100–1115) (Lane, 1991), using the Big Dye terminator cycle sequencing reaction kit and an ABI Prism 310 Genetic Analyzer (Applied Biosystems). DNA sequences were processed in the software package MEGA (Kumar *et al.*, 2004) and phylogenetic analysis was performed with the ARB software package (Ludwig *et al.*, 2004). Similarities were calculated on the basis of a pairwise comparison (ARB software) and phylogenetic trees were obtained by the neighbour-joining and maximum-likelihood methods including bootstrap values based on 1000 replicates. Comparison of the 16S rRNA gene sequence of strain CC-TPE-1^T revealed highest similarity to *N. naphthalenivorans* TUT562^T (98.1 %), *N. panipatense* SM16^T (97.9 %) and *N. mathurensis* SM117^T (97.6 %) and lower (<97 %) sequence similarity to representatives of all other *Novosphingobium* species (Fig. 1). DNA–DNA hybridization experiments with strain CC-TPE-1^T and the type strains of the three species given above were done as described previously (Kämpfer *et al.*, 2002) and revealed low relatedness values of 30 % (reciprocal 35 %) to *N. naphthalenivorans* DSM 18518^T, 29.1 % (reciprocal 30.6 %) to *N. panipatense* SM16^T and 35 % (reciprocal 23.6 %) to *N. mathurensis* SM117^T.

Further characterization of strain CC-TPE-1^T was performed using a substrate assimilation panel and enzyme tests with chromogenic substrates [*p*-nitrophenyl (pNP) and *p*-nitroanilide (pNA)-linked substrates] (Kämpfer *et al.*, 1991). Results of comparative characterizations are given in Table 1. The results showed that strain CC-TPE-1^T can be clearly distinguished from the most closely related *Novosphingobium* species.

Fatty acids were analysed from biomass grown on tryptone soy agar as described by Kämpfer & Kroppenstedt (1996). The detailed fatty acid profile of strain CC-TPE-1^T is shown in Table 2. The dominant fatty acid of CC-TPE-1^T

Fig. 1. Phylogenetic tree calculated using the neighbour-joining method indicating the phylogenetic relationship of strain CC-TPE-1^T to members of other *Novosphingobium* species. The sequence of *Erythrobacter longus* JCM 6170^T was used as an outgroup. Numbers at nodes indicate percentages of bootstrap support based on 1000 resampled datasets. Bar, 5 substitutions per 1000 nucleotide positions.

was C_{18:1}ω7c (49.9 %); three 2-hydroxy fatty acids, C_{14:0} 2-OH (8.2 %), C_{15:0} 2-OH (2.45 %) and C_{16:0} 2-OH (1.05 %), could be detected in small amounts, but no 3-hydroxy fatty acids were detected (Table 2). Takeuchi *et al.* (2001) distinguished the genus *Novosphingobium* from the genera *Sphingomonas sensu stricto*, *Sphingopyxis* and *Sphingobium* by the absence of major 2-hydroxy fatty acids other than C_{14:0} 2-OH. However, strain CC-TPE-1^T contained rather similar amounts of C_{14:0} 2-OH, C_{15:0} 2-OH and C_{16:0} 2-OH fatty acids, which was also reported for *N. hassiacum* W-51^T and *N. acidiphilum* FSW06-204d^T (Kämpfer *et al.*, 2002; Glaeser *et al.*, 2009).

For polyamine, quinone and polar lipid analyses, cells were grown on PYE agar (0.3 % peptone from casein, 0.3 % yeast extract, pH 7.2, supplemented with 3 % salts used for seawater aquaria). Quinones and polar lipids were extracted and analysed by the methods described by Tindall (1990a, b) and Altenburger *et al.* (1996) and polyamines as described by Busse & Auling (1988). For HPLC analyses of the quinones and polyamines, the apparatus described by Stolz *et al.* (2007) was used. The quinone system consisted of ubiquinones Q-10 (79 %) and Q-9 (21 %). The polyamine pattern contained the major compound spermidine [25.5 µg (g dry weight)⁻¹] and trace amounts of spermine [<0.1 µg (g dry weight)⁻¹]. The polar lipid profile (Fig. 2) consisted of the major lipids phosphatidylethanolamine, phosphatidylglycerol, phosphatidylcholine, phosphatidylidimethylethanolamine, phosphatidylmonomethylethanolamine and two sphingoglycolipids and minor amounts of an unidentified glycolipid, two aminolipids and two lipids not stained by any of the specific spray reagents used. Surprisingly,

Table 1. Differentiation of strain CC-TPE-1^T and type strains of closely related *Novosphingobium* species

Strains: 1, CC-TPE-1^T; 2, *N. naphthalenivorans* DSM 18518^T; 3, *N. panipatense* SM16^T; 4, *N. mathurense* SM117^T; 5, *N. capsulatum* ATCC 14666^T [data from Tirola *et al.* (2005), obtained with the same method]. –, Negative; +, positive; (+), weakly positive. Data were obtained in this study, unless indicated otherwise. All strains were positive for hydrolysis of L-alanine pNA and 2-deoxythymidine-5'-pNP phosphate and for assimilation of D-glucose*† and L-proline†; all strains were negative for hydrolysis of pNP β-D-galactopyranoside and pNP β-D-xylopyranoside and for assimilation of L-sorbose, D-mannitol*† and citrate*.

Characteristic	1	2	3	4	5
Hydrolysis of:					
Aesculin	–	(+)*	–†	+†	+
pNP α-D-glucopyranoside	–	+	+	+	+
bis-pNP phosphate	+	–	+	+	+
pNP phenylphosphonate	+	–	+	+	+
pNP α-D-glucuronide	+	–	–	+	+
Assimilation of:					
L-Arabinose	+	+*	(+)+	+†	(+)
D-Fructose	(+)	–	(+)+	+†	–
D-Galactose	–	–	(+)+	+†	+
Maltose	–	+*	(+)+	+†	+
L-Rhamnose	–	–	–†	+†	+
Sucrose	–	–	(+)+	+†	+
Acetate	+	–	–	+	–
L-Malate	+	–	–	–	+
Pyruvate	+	+	+	+	–
L-Histidine	–	–	(+)+	+†	+
L-Leucine	+	–	+	–	+

*Result in accordance with that published for *N. naphthalenivorans* DSM 18518^T by Suzuki & Hiraishi (2007).

†Result in accordance with those published for *N. panipatense* SM16^T and *N. mathurense* SM117^T by Gupta *et al.* (2009).

diphosphatidylglycerol, usually found in representatives of the *Sphingomonadaceae*, could not be detected. Unfortunately, *N. naphthalenivorans* was not analysed for this trait and, hence, it is not known whether the absence of diphosphatidylglycerol from the lipid profile of CC-TPE-1^T is useful for differentiation from its close relatives. A yellow pigment spot that gave a positive reaction with α-naphthol was also detected, indicating the presence of a sugar moiety in the pigment. However, strain CC-TPE-1^T shares the chemotaxonomic traits listed in the genus description (Takeuchi *et al.*, 2001), including a polyamine pattern with the major compound spermidine (*sym*-homospermidine absent), ubiquinone Q-10 and a polar lipid profile showing sphingoglycolipids. A combination of the observed chemotaxonomic and physiological differences (absence of diphosphatidylglycerol, production of three hydroxylated fatty acids and several physiological features) warrant the proposal of a separate species to accommodate strain CC-TPE-1^T.

Table 2. Whole-cell fatty acid profiles of strain CC-TPE-1^T and type strains of closely related *Novosphingobium* species

Strains: 1, CC-TPE-1^T; 2, *N. naphthalenivorans* DSM 18518^T; 3, *N. panipatense* SM16^T; 4, *N. mathurense* SM117^T; 5, *N. capsulatum* ATCC 14666^T [data from Kämpfer *et al.* (2002), obtained with the same method]. Data are from this study, unless indicated. Values represent percentages of total fatty acids; –, not detected. Double bonds are located by counting from the methyl (ω) end of the carbon chain.

Fatty acid	1	2	3	4	5
Saturated fatty acids					
C _{14:0}	–	–	–	0.5	–
C _{15:0}	0.6	0.9	–	0.5	–
C _{16:0}	7.3	6.0	6.5	5.4	8.1
C _{17:0}	–	0.9	–	–	–
C _{18:0}	0.8	–	–	–	–
Unsaturated fatty acids					
C _{16:1ω5c}	1.9	1.4	3.4	2.8	1.7
C _{17:1ω8c}	1.7	1.6	–	–	–
C _{17:1ω6c}	11.0	15.2	2.4	5.2	–
C _{18:1ω7c}	49.9	52.0	57.9	61.2	64.8
C _{18:1ω5c}	0.8	0.8	–	1.4	–
11-Methyl C _{18:1ω7c}	7.6	–	0.6	1.2	–
Hydroxy fatty acids					
C _{13:0} 2-OH	0.7	0.4	–	–	–
C _{14:0} 2-OH	8.2	7.1	7.7	6.2	14.7
C _{15:0} 2-OH	2.4	3.2	–	0.4	–
C _{16:0} 2-OH	1.0	1.4	1.4	4.1	–
iso-C _{16:0} 3-OH	–	–	–	1.3	–
Summed feature 3*	6.3	9.0	19.4	25.7	6.7

*Summed features represent groups of two or three fatty acids that could not be separated by GLC in the MIDI System. Summed feature 3 contains C_{16:1ω7c} and/or iso-C_{15:0} 2-OH.

Description of *Novosphingobium soli* sp. nov.

Novosphingobium soli (so'li. L. neut. gen. n. *soli* of soil, the source of the type strain).

The species shares all the characteristics of the genus as given by Takeuchi *et al.* (2001). Cells are rod-shaped, 1.6 ± 0.4 µm long and 0.8 ± 0.1 µm wide in the mid-exponential phase, and motile in the early exponential phase. Growth is observed on peptone/yeast extract (PYE) agar and nutrient, tryptone soy and R2A agars. On nutrient agar, circular yellow colonies are formed after incubation for 2–3 days at 25 °C. Cells stain Gram-negative and are positive for cytochrome oxidase and catalase-negative. Endospores are not observed. On nutrient agar, growth occurs at 4–32 °C, but not at 37 or 42 °C, and at pH 4.5–7.0, but not at pH 3.5 or 8.5. Hydrolyses L-alanine pNA, L-glutamate-γ-carboxy pNA and L-proline pNA and is positive for the assimilation of L-arabinose, D-fructose (weak), D-glucose, trehalose, D-xylose, acetate, DL-3-hydroxybutyrate, pyruvate, L-leucine and L-proline. Negative for assimilation of cellobiose, D-galactose, maltose, D-mannose, L-rhamnose,

Fig. 2. Total polar lipid profile of strain CC-TPE-1^T after two-dimensional TLC and detection with molybdatophosphoric acid. PC, Phosphatidylglycerol; PDE, phosphatidyl dimethylethanolamine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PME, phosphatidylmonomethylethanolamine; SGL1, 2, sphingoglycolipids; GL1, unidentified glycolipid; AL1, 2, unknown aminolipids; L1, 2, unknown polar lipids; yPig, yellow pigment staining positively with α -naphthol.

sucrose, L-malate, 2-oxoglutarate, L-sorbose, D-mannitol, citrate, DL-lactate, DL-3-aminobutyrate, benzoate, 4-hydroxybenzoate, L-histidine and L-phenylalanine. Polar lipid profile consists of the predominant lipids phosphatidylethanolamine, phosphatidylglycerol, phosphatidylcholine, phosphatidyl dimethylethanolamine, phosphatidylmonomethylethanolamine and two sphingoglycolipids and minor amounts of an unidentified glycolipid, two aminolipids and two polar lipids not stained by any of the specific spray reagents used; diphosphatidylglycerol is absent. The polyamine pattern contains the major amine spermidine and the quinone system contains ubiquinone Q-10 with moderate amounts of Q-9. The fatty acid profile consists of the major component C_{18:1} ω 7c; three 2-hydroxy fatty acids, C_{14:0} 2-OH, C_{15:0} 2-OH and C_{16:0} 2-OH, are also found in small amounts, but no 3-hydroxy fatty acids are detected.

The type strain, CC-TPE-1^T (=DSM 22821^T =CCM 7706^T =CCUG 58493^T), was isolated from oil-contaminated soil near an oil refinery located in Kaohsiung County, Taiwan.

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