Nafulsella turpanensis gen. nov., sp. nov., a member of the phylum *Bacteroidetes* isolated from soil

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A Gram-staining-negative, rod-shaped, gliding and pale-pink-pigmented bacterium, designated strain ZLM-10^T, was isolated from a soil sample collected from an arid area in Xinjiang province, China, and characterized in a taxonomic study using a polyphasic approach. The novel strain grew optimally at 30–37 °C and in the presence of 2 % (w/v) sea salts. The only respiratory quinone detected was MK-7 and the major cellular fatty acids were summed feature 3 (iso-$C_{15:0}$ 2-OH and/or $C_{16:1}\omega7c$), iso-$C_{15:0}$ and iso-$C_{17:0}$ 3-OH. The polar lipids consisted of diphosphatidylglycerol, phosphatidylethanolamine, an unidentified aminolipid and two unidentified aminophospholipids. The DNA G+C content was 45.4 mol%. Flexirubin-type pigments were not produced. Phylogenetic analysis based on 16S rRNA gene sequences showed that strain ZLM-10^T was a member of the phylum *Bacteroidetes* and appeared most closely related to *Cesiribacter roseus* 311^T (90.2 % sequence similarity), *Marivirga sericea* LMG 13021^T (89.2 %), *Cesiribacter andamanensis* AMV16^T (89.1 %) and *Marivirga tractuosa* DSM 4126^T (89.1 %). On the basis of phenotypic and genotypic data and phylogenetic inference, strain ZLM-10^T should be classified as a novel species of a new genus in the family *Flammeovirgaceae*, for which the name *Nafulsella turpanensis* gen. nov., sp. nov. is proposed. The type strain of the type species is ZLM-10^T (=CCTCC AB 208222^T=KCTC 23983^T).

The family *Flammeovirgaceae* belongs to the phylum *Bacteroidetes* and was first proposed by Garrity & Holt (2001) in the second edition of *Bergey's Manual of Systematic Bacteriology*. Recently, the description of the family *Flammeovirgaceae* was formally established by Yoon *et al.* (2011a). At the time of writing, the family *Flammeovirgaceae* incorporates the genera *Aureibacter*, *Cesiribacter*, *Fabibacter*, *Flammeovirga*, *Flexithrix*, *Fulvivirga*, *Limibacter*, *Marivirga*, *Perexilibacter*, *Persicobacter*, '*Porifericola*', *Rapidithrix*, *Reichenbachiella*, *Roseivirga*, *Sediminitomix* and '*Tunicatimonas*' (Ludwig *et al.*, 2010; Nedashkovskaya *et al.*, 2010; Srinivas *et al.*, 2011; Yoon *et al.*, 2011a, b, 2012). In the present study, we report on the taxonomic characterization of a pale-pink-pigmented bacterium, designated strain ZLM-10^T, that was isolated from a soil sample collected from an arid area in Xinjiang province, China. Based on phenotypic and genotypic data and phylogenetic analysis, it is proposed that the new isolate represents a novel species in a new genus of the family *Flammeovirgaceae*.

For strain isolation, the soil sample was thoroughly suspended in sterile water and serial dilutions were spread on marine agar 2216 (MA; Difco). Isolation was achieved after incubation at 30 °C for 1 week. Strain ZLM-10^T was routinely cultivated on the same medium at 30 °C and preserved at −80 °C in marine broth 2216 (MB; Difco) supplemented with 20 % (v/v) glycerol.

Genomic DNA of strain ZLM-10^T was prepared according to the procedure of Wilson (1987) with the modification by Cleenwerck *et al.* (2002). Genomic DNA G+C content was determined by HPLC (UltiMate 3000; Dionex) according to the method of Mesbah *et al.* (1989). The 16S rRNA gene sequence of strain ZLM-10^T was amplified by PCR with the bacterial universal primers 27f and 1527r (Lane, 1991), and the PCR products were sequenced commercially, by Invitrogen Biotechnology. Identification

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain ZLM-10^T is JN899241.

A supplementary figure is available with the online version of this paper.

of phylogenetic neighbours and calculation of pairwise 16S rRNA gene sequence similarities were achieved using the EzTaxon-e server (http://eztaxon-e.ezbiocloud.net/; Kim *et al.*, 2012). Phylogenetic analysis was performed using version 4.1 of the MEGA package (Tamura *et al.*, 2007), after multiple alignment of the data within CLUSTAL_X (Thompson *et al.*, 1997). Phylogenetic distances were calculated by the neighbour-joining method (Saitou & Nei, 1987), using the Kimura two-parameter model (Kimura, 1980), and by the maximum-parsimony method (Fitch, 1971), using the close-neighbour-interchange algorithm (search level=2, random additions=100). Each resultant tree was evaluated by bootstrap analysis on the basis of 1000 replications (Felsenstein, 1985).

The almost-complete 16S rRNA gene sequence (1441 nt) of strain ZLM-10^T was determined. Comparative 16S rRNA gene sequence analysis revealed that strain ZLM-10^T was affiliated with the family *Flammeovirgaceae* within the phylum *Bacteroidetes*, and exhibited the highest sequence similarities to *Cesiribacter roseus* 311^T (90.2 %), *Marivirga sericea* LMG 13021^T (89.2 %), *Cesiribacter andamanensis* AMV16^T (89.1 %) and *Marivirga tractuosa* DSM 4126^T (89.1 %). All other species of the family *Flammeovirgaceae* with validly published names were more distantly related, showing 16S rRNA gene sequence similarities of <88.9 %. In the phylogenetic tree based on the neighbour-joining algorithm, strain ZLM-10^T was clustered with members of the genera *Cesiribacter* and *Marivirga* but was clearly separated from these two genera (Fig. 1). The overall topology of the maximum-parsimony tree was essentially the same as that of the neighbour-joining tree (data not shown). The genomic DNA G+C content of strain ZLM-10^T was 45.4 mol%, which differs from the DNA G+C contents of its phylogenetically closest relatives (Table 1). These results suggest that strain ZLM-10^T represents a novel genus within the family *Flammeovirgaceae*.

Growth was evaluated at 30 °C on several standard bacteriological media: marine agar 2216 (MA; Difco), R2A agar (Difco), trypticase soy agar (TSA; Difco), nutrient agar (NA; Difco) and MacConkey agar (Difco). Cell morphology was examined by transmission electron microscopy (H-8100; Hitachi) using cells from the exponential growth phase. The cells were negatively stained with 1 % (w/v) phosphotungstic acid and the grids were examined after being air-dried. Gram staining of cells was carried out according to the classical Gram procedure described by Doetsch (1981). Gliding motility was determined as described by Bowman (2000). The presence of flexirubin-type pigments was investigated using the bathochromatic shift test, with 20 % (w/v) KOH (Bernardet *et al.*, 2002; McCammon & Bowman, 2000). The temperature range and optimum for growth were assessed at 4, 7, 10, 15, 20, 25, 30, 37, 40, 42, 45 and 50 °C on MA for up to 1 week. The pH range and optimum for growth were tested in MB medium at pH 4.0–11.0, by using 0.1 M citric acid/0.1 M sodium citrate (for pH 4.0–5.0), 0.1 M KH_2PO_4/0.1 M NaOH (for pH 6.0–8.0), 0.1 M $NaHCO_3$/0.1 M Na_2CO_3 (for pH 9.0–10.0) or 0.05 M Na_2HPO_4/0.1 M NaOH (for

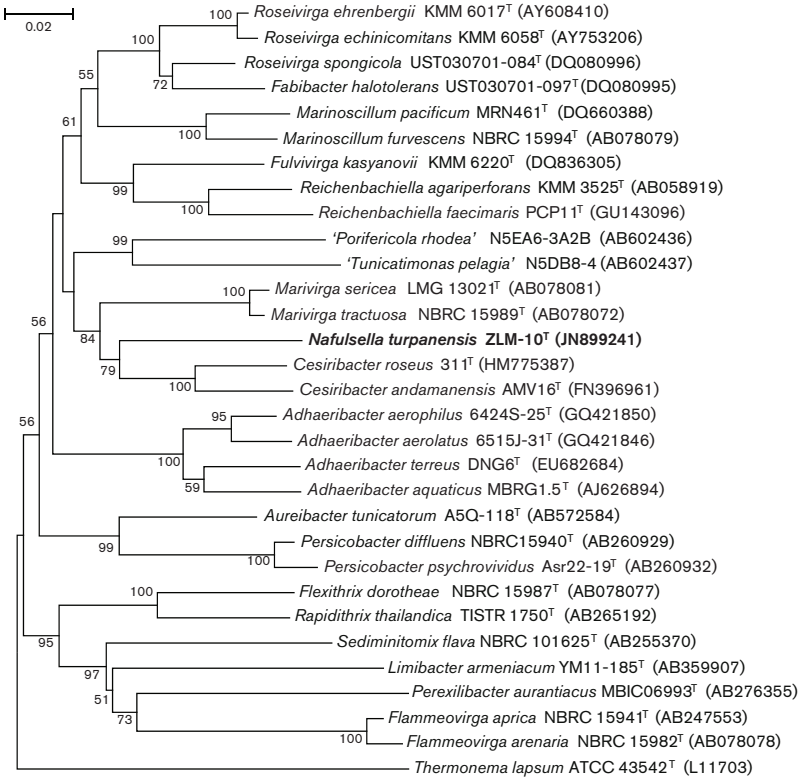

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationships between strain ZLM-10^T and related taxa. Bootstrap values >50% (based on 1000 replications) are shown at branching points. *Thermonema lapsum* ATCC 43542^T was used as the outgroup. Bar, 0.02 substitutions per nucleotide position.

Table 1. Features that distinguish strain ZLM-10^T from the closely related *Cesiribacter roseus* 311^T and *Marivirga tractuosa* DSM 4126^T

Strains: 1, ZLM-10^T; 2, *C. roseus* 311^T; 3, *M. tractuosa* DSM 4126^T. All data were from this study except for the genomic DNA G+C contents of strains 2 and 3, which were taken from Liu *et al.* (2012) and Nedashkovskaya *et al.* (2010), respectively. All three strains are positive for growth on MA, hydrolysis of gelatin, and catalase, alkaline phosphatase, esterase (C4), esterase lipase(C8), leucine arylamidase, valine arylamidase, naphthol-AS-BI-phosphohydrolase and α-glucosidase activities. All strains are negative for growth on MacConkey agar, H_2S and indole production, citrate utilization, arginine dihydrolase, urease, ornithine decarboxylase, lysine decarboxylase, β-glucuronidase, α-mannosidase and α-fucosidase activities, and acid production from L-arabinose, D-mannitol, D-galactose, D-mannose, L-rhamnose, glycerol, D-xylose, D-arabinose and lactose. +, Positive; −, negative; W, weakly positive.

Characteristic	1	2	3
Motility	Gliding	+	Gliding
Oxidase	+	−	+
Growth on:			
R2A agar	−	+	W
0.1× TSA	−	+	−
TSA	−	−	+
NA	−	−	W
Temperature range for growth (°C)	10–45	4–37	10–40
Salinity range (%, w/v)	0.5–6*	0–3	0.5–6
Production of flexirubin-type pigments	−	+	+†
Hydrolysis of:			
Aesculin	−	+	+
Starch	+	+	−
Nitrate reduction	−	+	−
Voges–Proskauer reaction	+	−	−
Tryptophan deaminase	−	+	−
Acid production from:			
D-Glucose	+	−	−
D-Fructose	+	−	−
D-Ribose	W	W	−
Maltose	+	W	−
Sucrose	W	−	−
Trehalose	−	W	−
Enzyme activities (API ZYM):			
Lipase (C14)	W	−	−
Cystine arylamidase	+	−	+
Trypsin	+	−	−
Acid phosphatase	+	−	+
α-Galactosidase	−	+	−
α-Chymotrypsin	−	−	+
β-Galactosidase	−	−	+
β-Glucosidase	−	−	+
N-Acetyl-β-glucosaminidase	−	+	−
DNA G+C content (mol%)	45.4	47.1	36.1

*Strain ZLM-10^T did not grow with NaCl as the only salt; the values given refer to sea salts.
†Negative result reported by Nedashkovskaya *et al.* (2010).

pH 11.0) as buffer. Growth in the absence of NaCl and in the presence of 0.5–10.0 % (w/v) NaCl (at 0.5 % intervals) was investigated in peptone–yeast extract (PY) medium that contained (l^{-1}) 2.5 g Bacto peptone and 0.5 g yeast extract. Growth was also determined in PY medium containing sea salts (Sigma) at 0–10.0 % (w/v) (in increments of 0.5 %). Growth under anaerobic conditions was determined after 2 weeks of incubation on MA in an anaerobic jar containing an AnaeroGen anaerobic system envelope (Oxoid). Oxidase activity was determined by using 1 % (w/v) tetramethyl-*p*-phenylenediamine. Catalase activity was detected by assessing the production of bubbles after the addition of a drop of 3 % (v/v) H_2O_2. Hydrolysis of casein and starch was assessed according to the methods of Smibert & Krieg (1994). Hydrolysis of carboxymethycellulose (0.1 %, w/v), chitin from crab shells (1 %, w/v) and tyrosine (0.5 %, w/v) was also assessed. Acid production from carbohydrates was determined as described by Leifson (1963). Activities of constitutive enzymes and other physiological properties were determined by using API 20E, API 20NE and API ZYM strips (bioMérieux) according to the manufacturer's instructions, except that all of the suspension media used for strain ZLM-10^T were supplemented with 2 % (w/v) sea salts. Antimicrobial susceptibility testing was performed by the agar-diffusion method using antibiotic-impregnated discs, as described by Buczolits *et al.* (2002).

At 30 °C, strain ZLM-10^T grew well on MA but not on R2A agar, TSA, NA or MacConkey agar. Cells of strain ZLM-10^T were strictly aerobic, Gram-staining-negative, gliding and rod-shaped (Fig. 2). Strain ZLM-10^T did not grow in PY medium containing NaCl (at $\leqslant$10 %, w/v) as the only salt but did grow in PY medium supplemented with 0.5–6.0 % (w/v) sea salts (optimum, 2.0 %). Flexirubin-type pigments were not produced. Other phenotypic features of strain ZLM-10^T are summarized in the species description. Strain ZLM-10^T differed from its closest phylogenetic relative, *Cesiribacter roseus* 311^T, in several phenotypic characteristics, including its mode of motility, temperature range for growth, tolerance of salt, hydrolysis of aesculin, nitrate reduction, Voges–Proskauer reaction, acid production

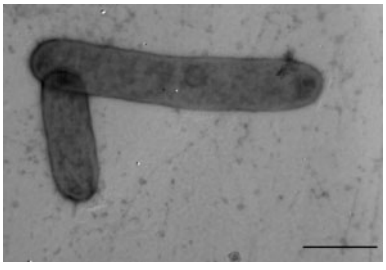

Fig. 2. Transmission electron micrograph showing the general morphology of negatively stained cells of strain ZLM-10^T after growth for 36 h at 30 °C on MA. Bar, 800 nm.

Table 2. Distinguishing features of strain ZLM-10^T and genera within the family *Flammeovirgaceae*

Taxa: 1, strain ZLM-10^T (data from this study); 2, *Cesiribacter* (Srinivas *et al.*, 2011; Liu *et al.*, 2012); 3, *Marivirga* (Nedashkovskaya *et al.*, 2010); 4, *Aureibacter* (Yoon *et al.*, 2011a); 5, *Fabibacter* (Lau *et al.*, 2006); 6, *Flammeovirga* (Takahashi *et al.*, 2006; Hosoya & Yokota, 2007a; Xu *et al.*, 2012); 7, *Flexithrix* (Lewin, 1970; Hosoya & Yokota, 2007b); 8, *Fulvivirga* (Nedashkovskaya *et al.*, 2007; Nupur *et al.*, 2012); 9, *Limibacter* (Yoon *et al.*, 2008); 10, *Perexilibacter* (Yoon *et al.*, 2007); 11, *Persicobacter* (Muramatsu *et al.*, 2010); 12, '*Porifericola*' (Yoon *et al.*, 2011b); 13, *Rapidithrix* (Srisukchayakul *et al.*, 2007); 14, *Reichenbachiella* (Nedashkovskaya *et al.*, 2003, 2005a; Cha *et al.*, 2011); 15, *Roseivirga* (Nedashkovskaya *et al.*, 2005b, c, 2008; Lau *et al.*, 2006); 16, *Sediminitomix* (Khan *et al.*, 2007); 17, '*Tunicatimonas*' (Yoon *et al.*, 2012). +, Positive; −, negative; W, weakly positive; V, variable; ND, no data available.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Gliding motility	+	−	+	−	+	+	+	V	+	+	+	−	+	+	V	−	−
Nitrate reduction	−	+	−	−	−	+	−	V	−	−	+	−	ND	−	V	+	−
Oxidase	+	V	+	+	+	V	+	+	+	+	−	−	+	+	+	+	−
Catalase	+	+	+	+	+	V	+	+	+	+	+	+	−	+	+	+	+
Hydrolysis of:																	
Gelatin	+	V	+	+	−	V	−	V	+	+	+	+	+	V	+	+	−
Starch	+	V	−	+	W	V	−	V	−	−	W	−	+	+	−	+	−
Casein	+	V	V	ND	−	V	−	V	ND	ND	ND	ND	ND	V	−	−	−
Voges–Proskauer reaction	+	−	−	−	+	+	−	ND	−	−	ND	+	ND	ND	V	ND	−
Growth at 45 °C	+	−	−	−	−	−	−	−	−	−	V	−	ND	−	−	−	−
Enzyme activities (API ZYM):																	
Acid phosphatase	+	−/ND	+	+	+	+	+	ND	+	+	ND	+	+	+	+	+	+
Alkaline phosphatase	+	+/ND	+	+	+	+	+	ND	+	+	ND	+	+	+	+	+	+
Leucine arylamidase	+	+/ND	+	+	+	+	+	ND	+	+	ND	+	+	+	+	+	+
Valine arylamidase	+	+/ND	+	+	+	+	+	ND	+	+	ND	+	+	+	+	+	+
Esterase (C4)	+	+/ND	+	+	+	W	+	ND	−	−	ND	+	+	V	+	ND	+
α-Fucosidase	−	−/ND	−	−	−	−	+	ND	−	−	ND	−	+	−	−	ND	−
DNA G+C content (mol%)	45.4	47.1 –50.9	36.1 –37.1	36.2	42.5	31–36	35.6	55.1 –59.9	27.9	43.0	42.0 –43.8	43.0	40 –43	39.6 –44.5	40.2 –43.7	38	52.6

from carbohydrates and some enzyme activities (Table 1). Strain ZLM-10^T could also be differentiated phenotypically from *Marivirga tractuosa* DSM 4126^T, the type species of the genus *Marivirga* (Table 1). The phenotypic features differentiating strain ZLM-10^T from related members of the family *Flammeovirgaceae* are shown in Table 2.

The respiratory quinones of strain ZLM-10^T were extracted and identified by HPLC, as described by Xie & Yokota (2003). Polar lipids of strain ZLM-10^T were extracted and analysed as described by Tindall (1990). For this, 6.75 ml of chloroform/methanol/saline [0.3 % (w/v) NaCl in water] (1 : 2 : 0.8, by vol.) was added to 100 mg freeze-dried cells. The preparation was stirred overnight before the cell debris was pelleted by centrifugation. Polar lipids were recovered into the chloroform phase, by adjusting the chloroform/methanol/saline mixture to a ratio of 1 : 1 : 0.9 (by vol.), and then dried under nitrogen. The dried polar lipids were resuspended in chloroform/methanol (2 : 1, v/v) and separated by two-dimensional TLC. The total lipids and specific functional groups were detected using 5 % (w/v) ethanolic molybdophosphoric acid (total lipids), Zinzadze reagent (phosphate), ninhydrin (free amino groups), periodate-Schiff (α-glycols), Dragendorff's reagent (quaternary nitrogen) and anisaldehyde-sulfuric acid (glycolipids). For cellular fatty acid analysis, samples of cell biomass of strain ZLM-10^T, *Cesiribacter roseus* 311^T and *Marivirga tractuosa* DSM 4126^T were harvested at late-exponential growth phase from MA plates incubated at 30 °C. The physiological age of the three cultures was standardized according to the protocol given by MIDI (http://www.microbialid.com/PDF/TechNote_101.pdf). Fatty acids were saponified, methylated and extracted using the standard protocol of version 6.0 of the Sherlock Microbial Identification System (MIDI), analysed by GC (6890N; Hewlett Packard) and identified using the TSBA6 database of the Microbial Identification System (Sasser, 1990).

The only isoprenoid quinone detected in strain ZLM-10^T was menaquinone 7 (MK-7). The polar lipid profile (Fig. S1, available in IJSEM Online) consisted mainly of phosphatidylethanolamine but diphosphatidylglycerol and two unidentified aminophospholipids occurred at moderate levels and trace amounts of an unidentified aminolipid (AL1) were also detected. The major fatty acids of strain ZLM-10^T were summed feature 3 ($C_{16:1}\omega7c$ and/or $C_{16:1}\omega6c$; 26.4 %), iso-$C_{15:0}$ (20.3 %) and iso-$C_{17:0}$ 3-OH (12.0 %). In addition, $C_{16:1}\omega5c$ (5.7 %), anteiso-$C_{15:0}$ (5.5 %), summed feature 9 (iso-$C_{17:1}\omega9c$ and/or 10-methyl $C_{16:0}$; 4.4 %) and iso-$C_{17:0}$ (4.0 %) were detected in moderate amounts. As shown in Table 3, the fatty acid profile of strain ZLM-10^T was distinct from that of

Table 3. Cellular fatty acid contents (%) of strain ZLM-10^T, *Cesiribacter roseus* 311^T and *Marivirga tractuosa* DSM 4126^T

Strains: 1, ZLM-10^T; 2, *C. roseus* 311^T ; 3, *M. tractuosa* DSM 4126^T. All data from this study; the three strains were cultured on MA at 30 °C and cells at late-exponential growth phase were used. Fatty acids amounting to <1 % of the total fatty acids in all three strains are not listed. TR, Trace (<1 %); −, not detected.

Fatty acid	1	2	3
iso-$C_{13:0}$	TR	TR	1.0
iso-$C_{14:0}$	TR	−	2.8
iso-$C_{15:1}$ G	TR	2.9	−
iso-$C_{15:0}$	20.3	21.6	31.0
anteiso-$C_{15:0}$	5.5	TR	TR
iso-$C_{16:1}$ H	TR	−	4.8
iso-$C_{16:0}$	2.1	TR	12.8
$C_{16:1}\omega5c$	5.7	32.1	−
$C_{16:0}$	3.5	1.3	1.1
iso-$C_{15:0}$ 3-OH	3.0	2.9	4.5
iso-$C_{17:0}$	4.0	2.9	TR
anteiso-$C_{17:0}$	1.2	TR	−
$C_{17:1}\omega6c$	TR	TR	2.2
iso-$C_{16:0}$ 3-OH	TR	TR	4.0
$C_{16:0}$ 3-OH	TR	TR	2.0
iso-$C_{17:0}$ 3-OH	12.0	14.3	9.7
$C_{17:0}$ 2-OH	1.0	TR	−
Summed features*			
3	26.4	1.0	6.0
4	2.1	14.6	−
8	1.6	−	−
9	4.4	−	12.4

*Summed features are groups of two or three fatty acids that cannot be separated by GLC using the MIDI system. Summed feature 3 contained $C_{16:1}\omega7c$ and/or $C_{16:1}\omega6c$; summed feature 4 contained anteiso-$C_{17:1}$ B and/or iso-$C_{17:1}$ I; summed feature 8 contained $C_{18:1}\omega7c$ and/or $C_{18:1}\omega6c$; summed feature 9 contained iso-$C_{17:1}\omega9c$ and/or 10-methyl $C_{16:0}$.

Cesiribacter roseus 311^T, the novel strain having summed feature 9 as well as significantly smaller amounts of $C_{16:1}\omega5c$ and summed feature 4 and significantly larger amounts of summed feature 3 and anteiso-$C_{15:0}$. Fatty acid profiles also allowed strain ZLM-10^T to be differentiated from *Marivirga tractuosa* DSM 4126^T, the novel strain having $C_{16:1}\omega5c$ as well as a significantly smaller amount of summed feature 9 and significantly larger amounts of summed feature 3 and anteiso-$C_{15:0}$.

Based on the phenotypic and genotypic data and the relatively low levels of 16S rRNA gene sequence similarity between strain ZLM-10^T and members of related genera of the family *Flammeovirgaceae*, strain ZLM-10^T represents a novel species of a new genus in the family *Flammeovirgaceae*, for which the name *Nafulsella turpanensis* gen. nov., sp. nov. is proposed.

Description of *Nafulsella* gen. nov.

Nafulsella (Na.ful.sel′la. N.L. fem. dim. n. *Nafulsella* arbitrary name derived from the acronym, NAFULS, used for the Northwest A&F University College of Life Sciences, where the type species was identified).

Cells are rod-shaped, Gram-stain-negative and strictly aerobic. Motile by gliding. Catalase- and oxidase-positive. Flexirubin-type pigments are not detected. Negative for nitrate and nitrite reduction. The major respiratory menaquinone is MK-7. Predominant cellular fatty acids are summed feature 3 (iso-$C_{15:0}$ 2-OH and/or $C_{16:1}\omega7c$), iso-$C_{15:0}$ and iso-$C_{17:0}$ 3-OH. The major polar lipid is phosphatidylethanolamine. The type species of the genus is *Nafulsella turpanensis*.

Description of *Nafulsella turpanensis* sp. nov.

Nafulsella turpanensis (tur.pan.en′sis. N.L. fem. adj. *turpanensis* of or pertaining to Turpan, the city in Xinjiang province, north-western China where the type strain was isolated).

Cells are strictly aerobic, Gram-stain-negative rods that measure approximately 0.5–0.6 μm in width and 1.4–3.2 μm in length and are motile by gliding. Colonies grown on MA for 3 days are pale pink, smooth, circular, flat and 1–2 mm in diameter, with clear margins. Growth occurs at 10–45 °C (optimum 30–37 °C), at pH 6–9 (optimum, pH 7) and in the presence of 0.5–6 % (w/v) sea salts (optimum, 2 %). Unable to grow with NaCl as the sole salt. Hydrolyses gelatin, starch and casein but not aesculin, carboxymethylcellulose, chitin or tyrosine. Positive for acetoin production (Voges–Proskauer reaction). Negative for H_2S production, citrate utilization, indole production and arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, urease and tryptophan deaminase activities (API 20E). Negative for the assimilation of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid (API 20NE). Acid is produced from D-glucose, maltose, sucrose (weakly), D-fructose and D-ribose (weakly) but not from D-mannitol, glycerol, D-arabinose, L-arabinose, D-xylose, D-galactose, D-mannose, L-rhamnose, lactose or trehalose. In API ZYM tests, positive for alkaline phosphatase, esterase (C4), esterase lipase (C8), lipase (C14) (weakly), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase and α-glucosidase activities, but negative for α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, β-glucosidase, *N*-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase activities. Susceptible to (μg per disc unless indicated otherwise) ampicillin (10), penicillin G (10 IU), carbenicillin (100), chloramphenicol (30), doxycycline (30), erythromycin (15), lincomycin (15), tetracycline (30) and vancomycin (30), but resistant to gentamicin (10), kanamycin (30), neomycin (30) and

streptomycin (10). The only respiratory quinone is MK-7. The polar lipids consist of diphosphatidylglycerol, phosphatidylethanolamine, an unidentified aminolipid and two unidentified aminophospholipids. The major fatty acids are summed feature 3 ($C_{16:1}\omega7c$ and/or $C_{16:1}\omega6c$), iso-$C_{15:0}$ and iso-$C_{17:0}$ 3-OH. The detailed fatty acid composition is given in Table 3.

The type strain, ZLM-10^T (=CCTCC AB 208222^T=KCTC 23983^T), was isolated from a soil sample collected from an arid area in Turpan city, Xinjiang province, north-western China. The genomic DNA G+C content of the type strain is 45.4 mol%.

Acknowledgements

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