Cesiribacter andamanensis gen. nov., sp. nov., isolated from a soil sample from a mud volcano

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A novel Gram-staining-negative, rod-shaped, non-motile bacterium, strain AMV16^T, was isolated from a soil sample collected from a mud volcano located in the Andaman Islands, India. The cell suspension was pale orange. Cells of strain AMV16^T were positive for catalase, oxidase, lipase, ornithine decarboxylase and lysine decarboxylase and negative for gelatinase and urease. The fatty acids present were anteiso-C_{11:0} (5.4 %), anteiso-C_{12:0} (4.1 %), C_{12:0} (7.0 %), iso-C_{15:0} (14.4 %), anteiso-C_{15:0} (3.4 %), anteiso-C_{16:0} (3.0 %), C_{16:0} (2.6 %), anteiso-C_{17:0} (3.7 %), iso-C_{19:0} (9.7 %), C_{13:1} (13.8 %), iso-C_{15:1} G (15.9 %), iso-C_{16:1} G (11.1 %) and summed feature 5 (anteiso-C_{18:0} and/or C_{18:2}ω6,9c; 5.9 %). Strain AMV16^T contained MK-4 as the major respiratory quinone and diphosphatidylglycerol and phosphatidylethanolamine made up the phospholipids. The G + C content of DNA of strain AMV16^T was 50.9 mol%. BLAST sequence similarity searches based on the 16S rRNA gene sequence indicated that species of the genus *Marivirga* were the nearest phylogenetic neighbours, with pairwise sequence similarity ranging from 89.9 to 90.0 %. Phylogenetic analyses indicated that strain AMV16^T clustered with the type strains of *Marivirga tractuosa* and *Marivirga sericea* at a phylogenetic distance of 14.6 % (85.4 % similarity), distinct from clades representing other genera of the family 'Flammeovirgaceae'. Based on the above-mentioned phenotypic and phylogenetic characteristics, strain AMV16^T is proposed as a representative of a new genus and novel species, *Cesiribacter andamanensis* gen. nov., sp. nov. The type strain of *Cesiribacter andamanensis* is AMV16^T (=DSM 22818^T =CCUG 58431^T).

The systematics of the family 'Flammeovirgaceae' are currently in a state of expansion, with many new genera being described within the last 6 years, including *Fabibacter*, *Limibacter*, *Marinoscillum*, *Perexilibacter*, *Rapidithrix*, *Reichenbachella*, *Marivirga* and *Roseivirga*, from a wide variety of habitats such as decayed wood, sea shells (Srisukchayakul *et al.*, 2007), fresh water (Nedashkovskaya *et al.*, 2010), marine algae (Nedashkovskaya *et al.*, 2005a; Srisukchayakul *et al.*, 2007), sediment (Yoon *et al.*, 2007, 2008), sponges (Lau *et al.*, 2006; Seo *et al.*, 2009) and seawater (Nedashkovskaya *et al.*, 2005b). In the present study, we describe a novel bacterium isolated from a soil sample collected from a mud volcano that is assigned to a new genus that belongs to the family 'Flammeovirgaceae'.

Strain AMV16^T was isolated from a soil sample collected from a mud volcano on Baratang Island, Middle Andamans, India, on 20 February 2009. The sample that yielded strain AMV16^T had a pH of 7.5. For isolation of

bacteria, 100 mg soil sample was plated on ZoBell marine agar medium (ZoBell, 1941) and incubated at room temperature for 15 days. Based on colony morphology, a pale-orange colony was selected and characterized in the present study.

Flexibacter tractuosa DSM 4126^T (now reclassified as *Marivirga tractuosa*, the type species of the genus *Marivirga*; Nedashkovskaya *et al.*, 2010) was procured from the DSMZ; strain AMV16^T was characterized simultaneously with *Marivirga (Flexibacter) tractuosa* DSM 4126^T. Cell morphology and motility were studied using a light microscope. Motility was assessed on TSA containing (l⁻¹) pancreatic digest of casein (17 g), papaic digest of soybean meal (3 g), NaCl (5 g), dipotassium hydrogen phosphate (2.5 g), glucose (2.5 g) and agar (0.4 g) and on motility indole lysine agar slants (cat. no. SL033; HiMedia). Growth at 4, 10, 18, 30, 37 and 40 °C and salt tolerance [0 (without NaCl), 1, 2, 3, 4, 5, 6, 8 and 10 % (w/v) NaCl], biochemical characteristics, carbon assimilation, H₂S production and sensitivity of the culture to antibiotics were determined by previously described

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methods (Lányi, 1987; Smibert & Krieg, 1994). Biochemical characteristics were confirmed with the Hi25 *Enterobacteriaceae* identification kit (cat. no. KB003) and HiCarbohydrate kit parts A, B and C (cat. no. KB009) (HiMedia) according to the manufacturer's protocol. Growth of strain AMV16^T at pH 5, 6, 7, 7.5, 8, 8.5, 9, 9.5, 10, 11 and 12 was assessed on TSA buffered with citric acid/NaOH (for pH 5 and 6), phosphate (pH 7 and 8), glycine/NaOH (for pH 9 and 10) or Tris (for pH 11 and 12).

Fatty acid methyl esters were prepared and analysed by using the Sherlock Microbial Identification System (MIDI) according to the protocol described by Agilent Technologies. For this purpose, strain AMV16^T and *M. tractuosa* DSM 4126^T were grown on marine agar 2216 (Difco) at 30 °C for 2 days. Polar lipids were extracted and analysed according to the method described by Komagata & Suzuki (1987). Menaquinones and polar lipids were determined from freeze-dried cells. Menaquinones were extracted as described by Collins *et al.* (1977) and analysed by HPLC (Groth *et al.*, 1997). DNA was isolated according to the procedure of Marmur (1961) and the G+C content was determined from melting point (T_m) curves (Sly *et al.*, 1986) obtained by using a Lambda 2 UV-Vis spectrophotometer (Perkin Elmer) equipped with the Templab 2.0 software package (Perkin Elmer). *Escherichia coli* DNA was used as a standard in determining the DNA G+C content. For 16S rRNA gene sequencing, DNA was prepared using the Mo Bio microbial DNA isolation kit (Mo Bio Laboratories Inc.) and sequenced as described previously (Lane, 1991). The resultant almost-complete sequence of the 16S rRNA gene contained 1502 nt. The 16S rRNA gene sequence of the isolate was subjected to BLAST sequence similarity search (Altschul *et al.*, 1990) and EzTaxon (Chun *et al.*, 2007) to identify the nearest taxa. All 16S rRNA gene sequences of members of the family 'Flammeovirgaceae' were downloaded from the NCBI database (<http://www.ncbi.nlm.nih.gov>) and aligned using the CLUSTAL_X program (Thompson *et al.*, 1997) and the alignment was then corrected manually. Phylogenetic trees were constructed using two tree-making algorithms, the maximum-likelihood method using the PhyML program (Guindon & Gascuel, 2003) and the neighbour-joining method (Saitou & Nei, 1987) using the PHYLIP package, version 3.5 (Felsenstein, 1993), and the resultant tree topologies were evaluated by bootstrap analysis based on 1000 resamplings using the SEQBOOT and CONSENSE programs in the PHYLIP package. Pairwise evolutionary distances were computed using the DNADIST program with Kimura's two-parameter model as developed by Kimura (1980).

Cells of strain AMV16^T were Gram-negative, non-motile rods, 0.5–0.7 µm wide and 1–3 µm long (Fig. 1), and multiplied by binary fission. Colonies were circular, 0.5–1.5 mm in diameter, smooth, shiny, pale orange, translucent and raised with entire margins on marine agar. The strain was positive for catalase, oxidase, ornithine decarboxylase, lysine decarboxylase and lipase and negative

for DNase, gelatinase and urease. Strain AMV16^T reduced nitrate and hydrolysed aesculin but not starch, cellulose or casein. It was negative for indole production. Growth was observed at 18–37 °C with optimum growth at 30–37 °C, at 0–5 % (w/v) NaCl, with optimum growth at 2–3 %, and at pH 6–8, with optimum growth at pH 7.5. Other characteristics are presented in Table 1. The cellular fatty acid composition of strain AMV16^T showed a spectrum of 12 fatty acids with a pronounced dominance (>4 %) of anteiso-C_{11:0}, anteiso-C_{12:0}, C_{12:0}, iso-C_{15:0}, iso-C_{19:0}, C_{13:1}, iso-C_{15:1} G, iso-C_{16:1} G and summed feature 5 (anteiso-C_{18:0} and/or C_{18:2ω6,9c}) (Table 2). Saturated fatty acids constituted 62.3 % of the total fatty acids. When compared with *M. tractuosa* DSM 4126^T, the number of fatty acids detected in strain AMV16^T was greater and the composition differed considerably (Table 2). The menaquinone present in AMV16^T was MK-4; diphosphatidylglycerol and phosphatidylethanolamine made up the phospholipids. Other characteristics are listed in the species description. The DNA G+C content of strain AMV16^T was 50.9 mol%.

Phylogenetic relationships of strain AMV16^T were ascertained based on 16S rRNA gene sequence similarity with other strains using the BLAST sequence similarity search (NCBI BLAST/EzTaxon). The results indicated that, at the 16S rRNA gene sequence level, strain AMV16^T was close to the phylogenetic neighbours *M. tractuosa* and *M. sericea*, with pairwise sequence similarity to the type strains of 89.9–90.0 %. Phylogenetic analyses based on maximum-likelihood and neighbour-joining trees further indicated that strain AMV16^T clustered with *M. tractuosa* and *M. sericea* at a phylogenetic distance of 14.6 %, distinct from clades representing the genera *Fabibacter*, *Flammeovirga*,

Fig. 1. Electron micrograph of a negatively stained cell of strain AMV16^T. Bar, 0.5 µm.

Table 1. Features that distinguish strain AMV16^T from the closely related *M. tractuosa* DSM 4126^T

Data for both strains are from the present study. Both strains were rod-shaped, positive for oxidase and hydrolysis of aesculin and Tween 20, negative for hydrolysis of agar, casein, cellulose, DNA, starch and urea, phenylalanine deamination, H₂S production, citrate utilization, Voges–Proskauer and methyl red tests and indole production and do not utilize glycine, leucine, isoleucine, phenylalanine, tyrosine, tryptophan, aspartic acid, glutamic acid, threonine, histidine, methionine, glutamine or serine. Both strains are resistant to (μg per disc) amikacin (30), cefazolin (30), co-trimoxazole (25), kanamycin (30), lomefloxacin (30), nalidixic acid (30), nitrofurantoin (300), penicillin G (10), streptomycin (10), tetracycline (30) and tobramycin (10) and sensitive to cefuroxime sodium salt (30), cefotaxime (30) and chloramphenicol (30). Both strains show optimum growth in 2–3 % (w/v) NaCl and grow at 18–37 °C with optimum growth at 30–37 °C. +, Positive; –, negative; w, weak; R, resistant; S, sensitive.

Characteristic	AMV16 ^T	<i>M. tractuosa</i> DSM 4126 ^T
Cell size (μm)	0.5–0.7 × 1–3	0.4–0.5 × 10–50
Colony colour	Pale orange	Dark orange
NaCl concentration for growth (% w/v)	0–5	0.5–6
pH range for growth	6–8	7.0–7.5
Catalase	+	w
Lysine decarboxylase	+	–
Ornithine decarboxylase	+	–
Nitrate reduction	+	–
Hydrolysis of:		
Gelatin	–	+
Tweens 40, 60 and 80	+	–
Acid production from:		
Glucosamine	+	w
Ribose	+	–
Utilization of:		
Glucosamine	+	w
Ribose	+	–
Alanine	–	w
Valine	–	+
Arginine	–	+
Cysteine	–	w
Antibiotic susceptibility (per disc)		
Ampicillin (10 μg)	R	S
Cefoperazone (75 μg)	S	R
Ciprofloxacin (5 μg)	S	R
Erythromycin (15 μg)	R	S
Norfloxacin (10 μg)	S	R
Vancomycin (30 μg)	R	S
Major fatty acids*	ai-C _{11:0} , ai-C _{12:0} , C _{12:0} , i-C _{15:0} , i-C _{19:0} , C _{13:1} , i-C _{15:1} G, i-C _{16:1} G, SF5	i-C _{15:0} , C _{15:1} ω8c, i-C _{15:1} G
Phospholipids†	DPG, PE	PC, PE
Major quinone	MK-4	MK-7

Table 1. cont.

Characteristic	AMV16 ^T	<i>M. tractuosa</i> DSM 4126 ^T
DNA G + C content (mol%)	50.9	35.8

*ai, Anteiso-branched; i, iso-branched; SF5, summed feature 5 (anteiso-C_{18:0} and/or C_{18:2}ω6,9c).

†DPG, Diphosphatidylglycerol; PC, phosphatidylcholine; PE, phosphatidylethanolamine.

Flexithrix, *Limibacter*, *Marinoscillum*, *Perexilibacter*, *Persicobacter*, *Rapidithrix*, *Reichenbachella*, *Roseivirga* and *Thermonema* (Fig. 2).

Strain AMV16^T differs from all the other genera in the family ‘*Flammeovirgaceae*’ by a number of characteristics (Table 3). Based on the 16S rRNA gene sequence phylogeny, the nearest genus in the family ‘*Flammeovirgaceae*’ was

Table 2. Fatty acid profiles of strain AMV16^T and *M. tractuosa* DSM 4126^T

Data for both strains are from the present study following growth on marine agar at 30 °C for 2 days. Results are percentages of the total fatty acids. ND, Not detected.

Fatty acid	Strain AMV16 ^T	<i>M. tractuosa</i> DSM 4126 ^T
C _{10:0}	ND	0.7
iso-C _{11:0}	ND	3.8
anteiso-C _{11:0}	5.4	0.4
C _{11:0}	ND	0.4
anteiso-C _{12:0}	4.1	ND
C _{12:0}	7.0	0.9
iso-C _{13:0}	ND	2.6
C _{13:1}	13.8	2.2
iso-C _{15:0}	14.4	41.8
anteiso-C _{15:0}	3.4	1.1
iso-C _{15:1} G	15.9	35.8
C _{15:1} ω8c	ND	4.0
iso-C _{16:0}	ND	1.8
anteiso-C _{16:0}	3.0	ND
C _{16:0}	2.6	0.7
iso-C _{16:1} G	11.1	0.7
iso-C _{17:0}	ND	0.8
anteiso-C _{17:0}	3.7	ND
anteiso-C _{17:1} ω9c	ND	0.9
iso-C _{19:0}	9.7	ND
Summed feature 5*	5.9	ND

*Summed features are groups of two or three fatty acids that cannot be separated by GLC using the MIDI System. Summed feature 5 contained anteiso-C_{18:0} and/or C_{18:2}ω6,9c.

Fig. 2. Phylogenetic tree based on 16S rRNA gene sequences showing relationships of strain AMV16^T to members of the *Cytophagaceae*. The tree was reconstructed using the maximum-likelihood method. Members of the genus *Flexibacter* are highlighted in bold, in addition to strain AMV16^T. Numbers at nodes are bootstrap percentages from 1000 resamplings. Bar, 0.05 substitutions per nucleotide position.

Marivirga. Strain AMV16^T differed from the genus *Marivirga* with respect to characteristics such as major fatty acids and DNA G + C content (Table 3).

Strain AMV16^T could also be differentiated phenotypically from the closest related species *M. tractuosa*, the type species of the genus *Marivirga* (Table 3). For instance, AMV16^T differed from *M. tractuosa* DSM 4126^T in colony colour, cell size, tolerance of salt, some enzyme activities, hydrolysis of gelatin and Tweens 40, 60 and 80, acid production from carbohydrates, utilization of various carbon sources, antibiotic susceptibility, major fatty acids, phospholipids and DNA G + C content (Table 1). Thus, the cumulative differences that strain AMV16^T exhibits from the species of *Marivirga* unambiguously support the creation of a new genus and species to accommodate strain AMV16^T, for which the name *Cesiribacter andamanensis* gen. nov., sp. nov. is proposed.

Phylogenetic analysis of taxa related to the genus *Flexibacter* of the family *Cytophagaceae* indicated that the genus *Flexibacter* is polyphyletic and its species cluster randomly with different genera (Fig. 2). For instance, *Flexibacter flexilis* IFO 15060^T formed a clade with the genera *Flectobacillus* and *Arcicella*, *Flexibacter ruber* ATCC 23103^T and *Flexibacter elegans* IFO 15055^T formed a clade with the genera *Rhodonellum* and *Microscilla* and the type strains of three other species of *Flexibacter*, namely *Flexibacter roseolus* IFO 16707^T, *Flexibacter litoralis* IFO 15988^T and *Flexibacter polymorphus* IFO 16703^T, formed a distinct clade and branched from the two major clades

within the family *Cytophagaceae*. *M. tractuosa*, which was formerly a member of the genus *Flexibacter*, was recently transferred to the new genus *Marivirga* based on a polyphasic taxonomic approach (Nedashkovskaya *et al.*, 2010). Thus, it is evident the genus *Flexibacter* remains polyphyletic and there is a continuing need to re-evaluate its taxonomic status based on polyphasic taxonomy and comparison with all taxa within the family *Cytophagaceae*.

Description of *Cesiribacter* gen. nov.

Cesiribacter [Ce.si.ri.bac'ter. N.L. n. *cesirum* arbitrary name derived from the acronym CSIR (Council of Scientific and Industrial Research); N.L. masc. n. *bacter* rod; N.L. masc. n. *Cesiribacter* rod named in honour of the CSIR, the national funding agency which has augmented science and technology development in India].

Cells are aerobic and non-motile, Gram-staining-negative, rod-shaped and positive for catalase, oxidase, ornithine decarboxylase, lysine decarboxylase and lipase and negative for DNase, gelatinase and urease. The major fatty acids are anteiso-C_{11:0}, anteiso-C_{12:0}, C_{12:0}, iso-C_{15:0}, iso-C_{19:0}, C_{13:1}, iso-C_{15:1} G, iso-C_{16:1} G and summed feature 5 (anteiso-C_{18:0} and/or C_{18:2ω6,9c}). MK-4 is the predominant respiratory quinone. The phospholipids include diphosphatidylglycerol and phosphatidylethanolamine. The genomic DNA G + C content of the type strain of the type species is 50.9 mol%. The genus is a member of the family 'Flammeovirgaceae', class *Sphingobacteria*, phylum *Bacteroidetes*. The type species is *Cesiribacter andamanensis*.

Table 3. Distinguishing features of strain AMV16^T and other genera within the family 'Flammeovirgaceae'

Taxa: 1, strain AMV16^T (*Cesiribacter* gen. nov.); 2, *Marivirga* (unless indicated, data from Nedashkovskaya *et al.*, 2010); 3, *Fabibacter* (Lau *et al.*, 2006); 4, *Flammeovirga* (Nakagawa *et al.*, 1997); 5, *Flexithrix* (Hosoya & Yokota, 2007; Srisukchayakul *et al.*, 2007); 6, *Limibacter* (Yoon *et al.*, 2008); 7, *Marinoscillum* (Seo *et al.*, 2009); 8, *Perexilibacter* (Yoon *et al.*, 2007); 9, *Persicobacter* (Nakagawa *et al.*, 1997); 10, *Rapidithrix* (Srisukchayakul *et al.*, 2007); 11, *Reichenbachiella* (Nedashkovskaya *et al.*, 2005b); 12, *Roseivirga* (Nedashkovskaya *et al.*, 2005a); 13, *Thermonema* (Hudson *et al.*, 1989). V, Variable; NA, no data available.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13
Cell shape*	R	R	CR	LR	F	R	FTR	R	R	F	R	R	F
Motility	—	Gliding	Gliding	Gliding	Gliding	Gliding	Gliding	Gliding	Gliding	Gliding	+	—	Gliding
Endospore formation	—	—	NA	NA	NA	—	NA	—	—	—	—	—	NA
Pigmentation†	O	O/Y	P	O—RO	GY	O	O/AP	O	P—O	OG	O	O/P	Y
Oxidase/catalase	+/+	+/+	+/+	V/V	NA/—	—/+	+/+	+/+	+/—	+/NA	+/+	+/+	+/+
Major fatty acids‡	ai-C _{11:0} , ai-C _{12:0} , C _{12:0} , i-C _{15:0} , i-C _{19:0} , C _{13:1} , i-C _{15:1} G, i-C _{18:1} G, SF5	i-C _{15:0} , i-C _{15:1} G, C _{15:1} ω8c§	i-C _{15:0} , i-C _{15:1} , i-C _{15:0} 3-OH, i-C _{16:0} 3-OH, i-C _{17:0} 3-OH, SF3	i-C _{15:0} , C _{20:4} ω6,9,12,15c, C _{16:0} 3-OH	C _{16:1} ω5c, i-C _{15:0} 3-OH, i-C _{17:0} 3-OH, C _{16:0}	i-C _{15:0} , C _{16:1} ω7c	C _{16:1} ω5c, SF3	i-C _{15:0} , C _{16:1} ω7c, C _{16:1} ω5c	i-C _{17:1} , C _{16:0} , i-C _{18:1} 3-OH, i-C _{17:0}	C _{16:1} ω5c; i-C _{15:0} 3-OH i-C _{17:0} 3-OH, i-C _{15:0} 3-OH, C _{16:0}	i-C _{15:0} , C _{16:1} ω9	i-C _{15:1} , i-C _{15:0} , ai-C _{15:0} , i-C _{17:0} 3-OH	i-C _{15:0} , i-C _{17:0} 3-OH
DNA G+C content (mol%)	50.9	36–37	42.5	31–36	37	27.9	41–44	43	40–42	40–43	44.5	40.1–43.7	47–50.9
Isolation source	S	FW	MSP	M	SSS	MS	MSP	SW	M	SS	SW	GA	HS

*CR, Curved rod; F, filament; FTR, flexible thread-like rod; LR, long rod; R, rod.

†AP, Apricot; GY, golden yellow; O, orange; OG, olive grey; P, pink; RO, reddish orange; Y, yellow.

‡ai, Anteiso-branched; i, iso-branched; SF3, summed feature 3 (iso-C_{15:0} 2-OH and/or C_{16:1}ω7c); SF5, summed feature 5 (anteiso-C_{18:0} and/or C_{18:2}ω6,9c).

§Data from this study for *M. tractuosa* DSM 4126^T.

||FW, Fresh water; GA, green alga; HS, hot spring; M, marine; MS, marine sediment; MSP, marine sponge; S, soil; SS, sea shell; SSS, seashore silt; SW, seawater.

Description of *Cesiribacter andamanensis* sp. nov.

Cesiribacter andamanensis (an.da.ma.nen'sis. N.L. masc. adj. *andamanensis* of or belonging to Andaman Islands, India, referring to the isolation of the type strain).

Displays the following properties in addition to those given in the genus description. Cells are 0.5–0.7 µm wide and 1–3 µm long, occur singly and multiply by binary fission. Colonies on marine agar are circular, 0.5–1.5 mm in diameter, smooth, shiny, pale orange, translucent and raised with entire margins. Grows at 18–37 °C with an optimum temperature of 30–37 °C and tolerates up to 5.0% NaCl (w/v). Grows at pH 6–8. Tryptophan deaminase activity is not present. Indole is not produced. The methyl red and Voges–Proskauer reactions are negative. Starch and casein are not hydrolysed but Tweens 20, 40, 60 and 80 and aesculin are hydrolysed. Nitrate is reduced and H₂S gas is not produced. Produces acid from glucosamine and ribose but not from L- or D-arabinose, xylose, rhamnose, cellobiose, melibiose, sucrose, raffinose, trehalose, glucose, lactose, maltose, fructose, galactose, mannose, inulin, mannitol, methyl α-D-glucoside, melezitose, methyl α-D-mannoside, malonate, adonitol, sodium gluconate, glycerol, salicin, dulcitol, inositol, sorbitol or xylitol after 1 week of incubation at optimum temperature and pH. Assimilates glucosamine and ribose but not L- or D-arabinose, xylose, rhamnose, cellobiose, melibiose, sucrose, raffinose, trehalose, glucose, lactose, maltose, fructose, galactose, mannose, inulin, mannitol, methyl α-D-glucoside, melezitose, methyl α-D-mannoside, malonate, adonitol, sodium gluconate, glycerol, salicin, dulcitol, inositol, sorbitol or xylitol. Susceptible to (µg per disc unless indicated) cefotaxime (30), chloramphenicol (30), ciprofloxacin (5), cefuroxime (30) and cefoperazone (75) and resistant to amikacin (30), ampicillin (10), cefazolin (30), colistin (10), co-trimoxazole (25), erythromycin (15), penicillin G (10), polymyxin B (50 U), kanamycin (30), lomefloxacin (30), nalidixic acid (30), nitrofurantoin (300), streptomycin (10), tetracycline (30), tobramycin (10) and vancomycin (30). The cellular fatty acid composition of the type strain is detailed in Table 2.

The type strain, AMV16^T (=DSM 22818^T =CCUG 58431^T), was isolated from a soil sample collected from a mud volcano on Baratang Island, Middle Andamans, India.

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