Fibrisoma limi gen. nov., sp. nov., a filamentous bacterium isolated from tidal flats

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An orange-pigmented, Gram-staining-negative, non-motile, filament-forming, rod-shaped bacterium (BUZ 3^T) was isolated from a coastal mud sample from the North Sea (Fedderwardersiel, Germany) and characterized taxonomically using a polyphasic approach. According to 16S rRNA gene sequence data, it belonged to the family *Cytophagaceae*, exhibiting low 16S rRNA gene sequence similarity (<90%) with members of the genera *Spirosoma*, *Rudanella* and *Fibrella*. The DNA G + C content was 52.0 mol%. The major fatty acids were summed feature 3 (comprising C_{16:1}ω7c and/or iso-C_{15:0} 2-OH), C_{16:1}ω5c and iso-C_{17:0} 3-OH. The major polar lipids consisted of phosphatidylethanolamine and several aminolipids. On the basis of phenotypic, chemotaxonomic and phylogenetic data, it is proposed that strain BUZ 3^T represents a novel genus and species, for which the name *Fibrisoma limi* gen. nov., sp. nov. is proposed. The type strain is BUZ 3^T (=DSM 22564^T =CCUG 58137^T).

The family *Cytophagaceae* constitutes a phylogenetically diverse group within the phylum *Bacteroidetes* (Ludwig *et al.*, 2008) and contains 18 genera at the time of writing. Recently, two new genera were proposed: *Rudanella*, described by Weon *et al.* (2008), and *Fibrella*, described by Filippini *et al.* (2011). Novel species of the genus *Spirosoma* have also been characterized recently, namely *Spirosoma rigui* (Baik *et al.*, 2007), *Spirosoma panaciterrae* (Ten *et al.*, 2009), *Spirosoma spitsbergense* and *Spirosoma luteum* (Finster *et al.*, 2009).

Strains BUZ 3^T and BUZ 4 were isolated from a mud sample from tidal flats in Fedderwardersiel (53° 35' 59" N, 8° 21' 23" E, elevation 0 m), on the North Sea coast of Germany, while searching for agar-degrading bacteria. Colonies were isolated on a selective nutrient agar (Difco, Becton Dickinson) with 50 µg kanamycin ml⁻¹. The strains were cultured on R2A plates (Reasoner & Geldreich, 1985) and maintained for long-term storage at -80 °C in a glycerol suspension (1:1 mixture of glycerol and cell culture).

Bacterial genomic DNA was extracted using lysis buffer (KCl, Tris-base, Tween 20, pH 8) as described by Svercel *et al.* (2009). PCR was carried out with the universal

bacterial primers 27F and 1525R in a Techne TC 512 thermal cycler (Barloworld Scientific). Sequencing was performed both in-house (ABI 3730 Sequencer) and at an external facility (Microsynth, Switzerland). The sequences were assembled and edited manually using Geneious Pro 3.6.2. software. Phylogenetic analysis was performed with the software package MEGA version 4.1 (Kumar *et al.*, 2001) following multiple alignment of data by CLUSTAL_X2 (Thompson *et al.*, 1997). Phylogenetic trees were reconstructed by using the neighbour-joining, minimal evolution, maximum-parsimony and maximum-likelihood algorithms. Evolutionary distances were computed using the Kimura-2 model and the maximum composite likelihood method. Maximum-likelihood analysis was performed using Garli (Zwickl, 2006). These analyses were performed using 1000 bootstrap resamplings.

Comparison of a 1430 bp fragment of the 16S rRNA gene with sequences deposited in GenBank indicated that the strains belong to the family *Cytophagaceae*, showing the highest level of sequence similarity to *S. panaciterrae* Gsoil 1519^T (89.5%), *Spirosoma rigui* WPCB118^T (89.4%), *S. linguale* LMG 10896^T (88.1%), *Rudanella lutea* 5715S-11^T (86.7%) and *Fibrella aestuarina* BUZ 2^T (86.0%). These values are lower than the threshold level of 95% that is generally used to delineate a new genus (Ludwig *et al.*, 1998). Fig. 1 shows that strain BUZ 3^T forms a distinct clade in the neighbour-joining phylogenetic tree supported by a high bootstrap value, in line with the other

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain BUZ 3^T is GQ355622.

Two supplementary figures are available with the online version of this paper.

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship of strain BUZ 3^T with representative members of the family *Cytophagaceae*. Bootstrap values (expressed as percentages of 1000 replications) greater than 70 % are shown at branch nodes. Accession numbers are given in parentheses. The tree was rooted using *Rhodothermus marinus* DSM 4252^T as the outgroup. Filled circles indicate that the corresponding branches were also recovered in the maximum-likelihood tree. Bar, 0.02 substitutions per nucleotide position.

phylogenetic inference methods employed (data not shown). The type strains of the type species of the genera *Spirosoma*, *Rudanella* and *Fibrella* were selected as reference strains and studied in parallel to the novel isolate in all phenotypic tests.

Comparison of strains BUZ 3^T and BUZ 4 based on DNA–DNA hybridization analysis (99.7 % reassociation value), 16S rRNA gene sequences (99.6 % similarity) and phenotypic profile (carbon utilization, growth conditions and enzyme production) indicated that they belong to the same species. The only difference detected between strain BUZ 3^T and strain BUZ 4 was the intensity of colony colour on R2A. Strain BUZ 3^T was taken as type strain and characterized with a polyphasic approach.

The Gram reaction was determined using the KOH test as described by Tindall *et al.* (2007). Bacterial cell morphology and gliding motility (Bernardet *et al.*, 2002) were observed under a light microscope (BX-51; Olympus) from liquid cultures grown in *Spirosoma* medium (SM; DSMZ Medium 7) for 1 day. For transmission (CM100; Philips) and scanning (Gemini; Zeiss) electron microscopy, cells were grown for 3 days in R2A broth at 30 °C. Cells for transmission electron microscopy were high-pressure frozen (EMPact2; Leica Microsystems) and freeze-substituted with anhydrous acetone with 2 % OsO₄ (EMAFS2; Leica) before embedding in Epon (Sigma). For scanning electron microscopy, cells were chemically fixed with 2.5 % glutaraldehyde in PBS, dehydrated with a graded ethanol series, critical point dried and coated with 5 nm platinum. The presence of flagella was assessed by transmission electron microscopy after negative staining with 2 % aqueous phosphotungstic acid.

Physiological and biochemical tests were performed at 30 °C unless otherwise indicated. Catalase activity was determined by adding a drop of 3 % H₂O₂ to colonies. Oxidase activity was assessed by using the bioMérieux kit according to the manufacturer's protocol. Flexirubin-type pigments were detected based on a colour shift after exposure to 20 % (w/v) KOH solution (Reichenbach, 1992).

Pigments were extracted as described by Gosink *et al.* (1998) using 99 % ethanol. The absorption spectrum

between 350 and 800 nm was measured with a spectrophotometer (SpectraMax 384 Plus; Molecular Devices) after incubation for 20 min in the dark.

Growth was tested in R2A, SM, nutrient broth (NB; Becton Dickinson), 0.2 % peptone water and 0.5 % yeast water and on trypticase soy agar (TS; Becton Dickinson), yeast extract tryptone agar (YT; Becton Dickinson), blood agar (Merck) and MacConkey agar (Merck). Since strain BUZ 3^T grew well in R2A and SM broths, these two media were used for further analysis. Physiological and biochemical properties of strain BUZ 3^T were determined using API 20NE, API 20E, API 50CH and API ZYM strips (bioMérieux) following the manufacturer's instructions. API 50CH strips were inoculated with cells suspended in AUX medium (bioMérieux). API 20NE, API 20E and API 50CH strips were inspected after 3 and 7 days at 30 °C, whereas API ZYM strips were read after 5 h at 37 °C. Some of the substrates included in the API 50CH strip, namely glucose, arabinose, lactose and maltose, were also tested by the conventional method using blue green algae medium (BG 11; Rippka *et al.*, 1979) as minimal medium with 0.2 % (w/v) substrate. The temperature range for growth was determined in R2A broth by growing cultures at 4, 10, 15, 20, 30, 37 and 40 °C. The pH range for growth was examined in SM broth adjusted to pH 5.0–11.0 (at 1 pH unit intervals) using KHPO₄ and K₂HPO₄ prior to autoclaving. Higher pH was reached with additional NaOH. The pH was verified after autoclaving with pH strips. Growth at different temperatures and pH was observed for up to one week. Additionally, tolerance of sodium chloride was tested on R2A plates adjusted to 0–10 % NaCl (at 0.5 % intervals). Anaerocult C (Merck) was used for generating an oxygen depleted (5–7 % O₂) and carbon dioxide enriched (8–10 % CO₂) atmosphere in anaerobe jars. Growth was monitored for up to one week. Hydrolysis of starch, xylan, CM-cellulose, pectin, amylopectin, agar and agarose was tested by adding 0.5 % of the respective polysaccharide to nutrient agar solidified with gellan gum. After 3 to 5 days of incubation, the plates were flooded with iodine solution. A positive test was indicated by a colourless area around cell growth. Hydrolysis of casein was tested on milk agar prepared according to the

Table 1. Phenotypic properties of strain BUZ 3^T and the type strains of its closest neighbours

All data are from this study except for the DNA G + C contents of *Rudanella lutea* DSM 1938^T and *S. linguale* DSM 74^T, which are taken from Weon *et al.* (2008), and of *Fibrella aestuarina* BUZ 2^T, taken from Filippini *et al.* (2011). In the API ZYM strip, all strains are positive for alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α -chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, β -glucosidase and *N*-acetyl- β -glucosaminidase activities. All strains are negative for lipase (C14) and β -glucuronidase activities. All strains are catalase positive. In API 20NE and API 20E strips, all strains are negative for indole and H₂S production, glucose fermentation, arginine dihydrolase, urease, lysine decarboxylase and ornithine decarboxylase activities, nitrate reduction, citrate utilization, oxidation of D-glucose, D-mannitol, inositol, D-sorbitol, L-rhamnose, sucrose, melibiose, amygdalin and L-arabinose, and assimilation of D-mannitol, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. All strains are positive for aesculin hydrolysis and β -galactosidase activity. In API 50CH strips, all strains are positive for aesculin assimilation and negative for glycerol, erythritol, D-arabinose, L-xylose, D-adonitol, L-sorbose, L-rhamnose, dulcitol, inositol, D-mannitol, D-sorbitol, xylitol, D-tagatose, D- and L-fucose, D- and L-arabitol and potassium 5-ketogluconate assimilation. All strains are positive for amylopectin hydrolysis. All strains are resistant to amikacin, colistin, gentamicin, kanamycin and polymyxin B. All strains are sensitive to amoxicillin, amoxicillin/clavulanic acid, chloramphenicol, ciprofloxacin, penicillin G, rifampicin, streptomycin and tetracycline. +, Positive; w, weakly positive; –, negative.

Characteristic	BUZ 3 ^T	<i>Spirosoma linguale</i> DSM 74 ^T	<i>Rudanella lutea</i> DSM 1938 ^T	<i>Fibrella aestuarina</i> BUZ 2 ^T
Cell morphology	Rods and filaments	Ring-like and horseshoe-shaped	Rods and filaments	Rods and filaments
Colony colour	Orange	Yellow	Orange	Pink
Carotenoid pigment peaks (max. in bold)	450, 476 nm	450 , 476 nm	450, 476 , 506 nm	482 , 506 nm
Temperature range (°C)	10–40	4–37	10–40	10–40
pH range (optimum)	6–7	6–8 (8)	6.0–11.0 (7)	6–8 (7)
Tolerance to NaCl (%)	0–2	0–1.25	0–2	0–0.5
Growth on peptone	–	–	w	–
Oxidase activity	–	+	–	–
Hydrolysis of:				
Gelatin	+	–	–	+
Starch	w	w	w	+
CM-cellulose	–	–	–	+
Agar	+	–	–	+
Xylan	w	–	+	+
Casein	w	–	+	+
Agarose	+	–	–	+
Assimilation of (API20NE and 50CH):				
D-Glucose	–	+	–	+
L-Arabinose	–	w	–	+
D-Mannose	–	+	–	+
N-Acetylglucosamine	–	+	–	+
Maltose	–	+	–	+
D-Fructose	–	+	–	+
Raffinose	–	+	–	+
Potassium gluconate	–	–	–	w
Methyl β -D-xylopyranoside	–	–	–	+
D-Lyxose	–	+	–	–
Glycogen	–	–	–	+
Arbutin	–	–	–	+
D-Ribose	–	–	–	+
D-Xylose	–	+	–	+
D-Galactose	–	+	–	+
Methyl α -D-mannopyranoside	–	+	–	+
Methyl α -D-glucopyranoside	–	+	–	+
Amygdalin	–	+	–	w
Salicin	–	+	–	+
Cellobiose	–	+	–	+
Lactose	–	+	–	+
Melibiose	–	+	–	+
Sucrose	–	+	–	+

Table 1. cont.

Characteristic	BUZ 3 ^T	<i>Spirosoma linguale</i> DSM 74 ^T	<i>Rudanella lutea</i> DSM 19387 ^T	<i>Fibrella aestuarina</i> BUZ 2 ^T
Trehalose	—	+	—	+
Inulin	—	+	—	+
Melezitose	—	+	—	+
Starch	—	+	—	+
Gentiobiose	—	w	—	+
Turanose	—	+	—	+
Potassium 2-ketogluconate	—	—	—	w
Enzymic activity (API ZYM)				
α-Fucosidase	—	—	—	+
α-Mannosidase	+	+	—	+
α-Glucosidase	+	+	—	+
α-Galactosidase	+	+	—	+
β-Galactosidase	+	+	—	+
Susceptibility to vancomycin	Intermediate	Sensitive	Sensitive	Resistant
DNA G + C content (mol%)	52.0	51–53	55	56.5

Sigma recipe (15 g agar, 10 ml fresh milk, 5 g peptone and 1 g yeast extract l⁻¹) as described elsewhere (Filippini *et al.*, 2011).

Susceptibility to antibiotics was determined by using the disc-diffusion method on R2A plates. The following antibiotics (bioMérieux) were tested (µg per disc, unless indicated): amikacin (30), amoxicillin (10), amoxicillin/clavulanic acid (20/10), chloramphenicol (30), ciprofloxacin (5), colistin (30 U), gentamicin sulfate (10), kanamycin (30), penicillin G (10 U), polymyxin B (300 U), rifampicin (30), streptomycin (10), tetracycline (30) and vancomycin (30). Results were interpreted according to the guidelines set forth by the Clinical and Laboratory Standards Institute (CLSI, 2008).

Strain BUZ 3^T produced an orange pigment with wavelength absorbance spectral peaks at 450 and 476 nm, a spectrum similar to that of *S. linguale* DSM 74^T but with the major peak at 476 nm (see Supplementary Figure S1 available in IJSEM Online). *Rudanella lutea* DSM 19387^T produced a third peak at 506 nm in addition to the two peaks mentioned above. The pink-coloured *Fibrella aestuarina* BUZ 2^T had two peaks at 482 and 506 nm, with a major peak at 482 nm. All of these peaks are in the range reported for carotenoid pigments (Asker *et al.*, 2007).

Phenotypic characteristics of strain BUZ 3^T are given in Table 1 and in the genus and species descriptions.

For fatty acid analysis, strains BUZ 3^T, *R. lutea* DSM 19387^T, *S. linguale* DSM 74^T and *Fibrella aestuarina* BUZ 2^T were grown in SM broth for three days at room temperature. Fatty acids were analysed by the Identification Service of the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ, Braunschweig, Germany) according to the standard protocol of the MIDI/Hewlett Packard Microbial Identification System (Sasser, 1990). Respiratory quinone and polar lipid analyses, determination of the DNA

G + C content of strain BUZ 3^T and DNA–DNA hybridization between strains BUZ 3^T and BUZ 4 were also carried out by the DSMZ and Dr B. J. Tindall.

Cellular fatty acid profiles of strain BUZ 3^T and its closest relatives are shown in Table 2. The dominant fatty acids of strain BUZ 3^T were summed feature 3 (comprising C_{16:1}ω7c and/or iso-C_{15:0} 2-OH; 29.3%), C_{16:1}ω5c (23.2%) and iso-C_{17:0} 3-OH (13.7%). Although the overall fatty acid compositions of the four strains were rather similar, strain BUZ 3^T could be distinguished from its closest phylogenetic neighbours by smaller proportions of summed feature 3 and C_{16:0} 3-OH, and larger proportions of C_{16:1}ω5c, iso-C_{17:0} 3-OH, C_{17:0} 2-OH, C_{16:0} 2-OH and anteiso-C_{15:0}.

Menaquinone 7 (MK-7) was the only respiratory quinone found in strain BUZ 3^T, similar to members of the genera *Spirosoma* and *Fibrella*. MK-7 was also the major respiratory quinone in *R. lutea* DSM 19387^T, but a small amount of MK-6 was also found.

The major polar lipid of strain BUZ 3^T was phosphatidyl-ethanolamine, but several unidentified aminolipids and aminophospholipids were also detected (Supplementary Fig. S2). The polar lipid profile of strain BUZ 3^T shared several similarities with that of *Fibrella aestuarina* BUZ 2^T (Filippini *et al.*, 2011), which was isolated from the same location, whereas the profile of strain BUZ 3^T exhibited more differences from the profiles of *S. linguale* DSM 74^T and *R. lutea* DSM 19387^T, published by Weon *et al.* (2008). Strain BUZ 3^T possessed an aminolipid (AL3) that was absent in *Fibrella aestuarina*, while lacking a phospholipid (PL2) that was present in *Fibrella aestuarina*. Besides these two differences, the profiles of strain BUZ 3^T and *Fibrella aestuarina* were similar. In comparison to *S. linguale*, strain BUZ 3^T contained three aminophospholipids instead of one and three aminolipids (AL) instead of two. In particular, AL3 was not present in *S. linguale*. Moreover, strain BUZ 3^T

Table 2. Fatty acid content (%) of strain BUZ 3^T and its closest neighbours

Strains: 1, BUZ 3^T; 2, *Spirosoma linguale* DSM 74^T; 3, *Rudanella lutea* DSM 19387^T; 4, *Fibrella aestuarina* BUZ 2^T. Values for fatty acids amounting to <1 % of the total fatty acids in all strains are not shown. tr, Trace amounts (<1 %); ND, not detected. All data are from this study; bacteria were grown in SM broth at room temperature for 3 days.

Fatty acid	1	2	3	4
Straight-chain				
C _{15:0}	tr	tr	1.1	1.0
C _{16:0}	3.8	3.7	4.3	9.8
Branched saturated				
iso-C _{13:0}	ND	2.0	ND	ND
iso-C _{15:0}	8.9	7.9	8.3	11.9
iso-C _{16:0}	tr	tr	1.3	1.3
iso-C _{17:0}	tr	tr	tr	3.4
anteiso-C _{15:0}	4.9	2.0	1.8	2.1
anteiso-C _{17:0}	tr	tr	tr	1.7
Hydroxy				
iso-C _{15:0} 3-OH	2.7	2.6	2.3	1.3
C _{16:0} 2-OH	2.5	ND	tr	ND
C _{16:0} 3-OH	tr	2.2	3.6	1.6
C _{17:0} 2-OH	1.7	tr	tr	tr
iso-C _{17:0} 3-OH	13.7	7.5	6.8	9.3
Mono-unsaturated				
C _{16:1} ω5c	23.2	18.1	21.2	17.5
iso-C _{17:1} ω9c	1.5	tr	tr	1.2
Summed feature 3*	29.3	46.1	42	33.1
Summed feature 4	1.3	tr	tr	tr
Unknown 16.582	1.2	tr	tr	tr

*Summed features are groups of two or three fatty acids that could not be separated by GLC using the MIDI system. Summed feature 3 comprised C_{16:1}ω7c and/or iso-C_{15:0} 2-OH. Summed feature 4 comprised iso-C_{17:1} I and/or anteiso-C_{17:1} B.

showed a reduced number of unspecified lipids (L): only two were detected in comparison to the seven observed in *S. linguale*. The number of unspecified lipids also distinguished strain BUZ 3^T from *R. lutea*. The latter presented five such lipids in its profile. Both *S. linguale* and *R. lutea* had the lipids labelled as L3, L7 and L9 (Weon *et al.*, 2008) as dominant lipids in their profiles. These were missing in the profile of strain BUZ 3^T. Additionally, strain BUZ 3^T differed from *R. lutea* by the presence of aminophospholipids and AL3, both absent in *R. lutea*.

The DNA G+C content of strain BUZ 3^T was 52.0 mol%, which is in the range reported for members of the genus *Spirosoma* (Larkin & Borrall, 1984). This value is slightly lower than those determined for members of the genera *Fibrella* (Filippini *et al.*, 2011) and *Rudanella* (Weon *et al.*, 2008).

Based on this polyphasic analysis, we propose that strain BUZ 3^T represents a novel genus and species in the family

Cytophagaceae, for which the name *Fibrisoma limi* gen. nov., sp. nov. is proposed.

Description of *Fibrisoma* gen. nov.

Fibrisoma [Fi.bri.so'ma. L. n. *fibra* a fibre, filament; -i-connecting vowel; Gr. neut. n. *soma* body; N.L. neut. n. *Fibrisoma* filamentous body (bacterium)].

Gram-staining-negative and non-motile rods able to form filaments. Cells are facultatively anaerobic. Catalase-positive and oxidase-negative. Nitrate is not reduced. Carotenoid-type pigments are produced but flexirubin-type pigments are not produced. The predominant cellular fatty acids are summed feature 3 (C_{16:1}ω7c and/or iso-C_{15:0} 2-OH), C_{16:1}ω5c and iso-C_{17:0} 3-OH. The major polar lipid is phosphatidylethanolamine, but three unidentified aminophospholipids and three aminolipids also occur. The only respiratory quinone is MK-7. The DNA G+C content of the type strain of the type species is 52.0 mol%. Phylogenetically, the genus belongs to the family *Cytophagaceae* within the phylum *Bacteroidetes*. The type species is *Fibrisoma limi*.

Description of *Fibrisoma limi* sp. nov.

Fibrisoma limi (li'mi. L. gen. n. *limi* of/from mud).

Displays the following properties in addition to those given in the genus description. After 1 day of growth in SM, filaments are 1.1 µm in diameter and 6.9–86.2 µm in length (Fig. 2). In the earlier exponential growth phase, lengths of up to 366 µm can be reached. Colonies on R2A are orange, convex and circular with regular edges. Flagellar and gliding motility are absent. Growth occurs in R2A, SM, NB, 0.5 % yeast water and on YT but not on blood, MacConkey and TS agars or in peptone water. The pH range for growth is 6.0–7.0. The temperature range for growth within 1 week is 10–40 °C (optimum 20–30 °C). Does not require NaCl for growth but tolerates up to 2 % (w/v) NaCl. Agar, agarose and amylopectin are hydrolysed and starch, casein and xylan are weakly hydrolysed (as shown by haloes around the colonies). Pectin and CM-cellulose are not hydrolysed. In the API ZYM strip, trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, α-glucosidase, alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase, β-glucosidase, N-acetyl-β-glucosaminidase and α-mannosidase activities are present; lipase (C14), β-glucuronidase and α-fucosidase activities are absent. In the API 20NE strip, positive reactions are observed for β-galactosidase, aesculin assimilation and gelatin hydrolysis; negative reactions for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase and urease activities, and assimilation of glucose, arabinose, mannose, mannitol, N-acetylglucosamine, maltose, potassium gluconate, capric acid, adipic acid, malate, trisodium citrate and phenylacetic acid. In the API 20E strip, negative results are

Fig. 2. Cellular morphology of strain BUZ 3^T. Cells are rod-shaped and form filaments; light micrograph (a), scanning electron micrograph (b) and transmission electron micrograph (c). Bars, 20 µm (a), 2 µm (b) and 0.5 µm (c).

observed for arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase and urease activities, citrate utilization, and H₂S and indole production. In the API 50CH strip after 7 days of incubation, aesculin is the only substrate assimilated; all other substrates are not assimilated. No growth on glucose, arabinose, lactose or maltose in BG 11 medium. Resistant to amikacin (30 µg), colistin (30 U), gentamicin (10 µg), kanamycin (30 µg) and polymyxin B (300 U). Sensitive to amoxicillin (10 µg), amoxicillin/clavulanic acid (20/10 µg), chloramphenicol (30 µg), ciprofloxacin (5 µg), penicillin G (10 U), rifampicin (30 µg), streptomycin (30 µg) and tetracycline (30 µg). Intermediate sensitivity to vancomycin (10 µg).

The type strain, BUZ 3^T (=DSM 22564^T =CCUG 58137^T), was isolated from mud in a tidal flat on the North Sea Coast of Germany.

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