Deefgea rivuli gen. nov., sp. nov., a member of the class *Betaproteobacteria*

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Two strains, designated WB 3.4-79^T and WB 3.3-25, were isolated from a hard-water sample collected from the Westerhöfer Bach, Lower Saxony, Germany. The strains shared 100 % DNA–DNA relatedness, indicating membership of the same genospecies. This close relationship was supported by identical 16S rRNA gene sequences and high similarities in fatty acid composition and biochemical characteristics. The G + C content of the genomic DNA of strain WB 3.4-79^T was 48.5 mol% and the predominant ubiquinone was Q-8. Major polar lipids were phosphatidylethanolamine and phosphatidylglycerol. Major fatty acids (> 10 %) were C_{16:0} and C_{16:1 ω 7c}. Polyhydroxybutyrate and polyphosphate granules as well as unidentified enterosomes and a polar organelle are visible by electron microscopy. Comparative 16S rRNA gene sequence analysis indicated that the isolates were placed within the class *Betaproteobacteria*, remotely related to *Chitinibacter tainanensis* DSM 15459^T, *Silvimonas terrae* KCTC 12358^T, *Formivibrio citricus* DSM 6150^T and *Iodobacter fluvialis* DSM 3764^T. On the basis of phylogenetic and phenotypic distinctness, we propose a novel genus, *Deefgea* gen. nov., with *Deefgea rivuli* sp. nov. as the type species. The type strain of *Deefgea rivuli* is strain WB 3.4-79^T (= DSM 18356^T = CIP 109326^T).

During the investigation of the prokaryotic diversity of a hard-water creek, with emphasis on the participation of bacteria in the formation of tufa, hundreds of organisms were isolated from rivulet water which, on R2A agar, showed either the capacity for swarming or colonies that had a slimy appearance. Most of the swarming bacteria (~40 %) and many of the slime-producing bacteria were members of the genus *Flavobacterium* (Brambilla *et al.*, 2007; Cousin *et al.*, 2007), while other strains with the slimy phenotype were affiliated to various classes of the *Proteobacteria* on the basis of partial 16S rRNA gene sequences (unpublished results). Phylogenetic analysis demonstrated the close affiliation of most water isolates to described species (>98 % 16S rRNA gene sequence similarity), and only a few were more distantly related. In this communication we present the characterization of two of these strains which are affiliated to the class *Betaproteobacteria*.

Strains WB 3.4-79^T and WB 3.3-25 were isolated from sampling site 3 (Brambilla *et al.*, 2007) of the Westerhöfer

Bach on the western slopes of the Harz Mountains in Lower Saxony, Germany. Creek water was spread on R2A plates (Difco) which were incubated at 10 or 18 °C for 4 days. Single slimy colonies on the plates were purified by transferring them onto new plates and incubating again under the same conditions. The isolates were cultured routinely on R2A agar at 28 °C and maintained as a glycerol suspension (20 %, w/v) at –70 °C. Strains were preserved in the long term as freeze-dried cultures or in liquid nitrogen.

Ultrastructural analysis

Mid-exponential phase cells of strain WB 3.4-79^T were prepared as ‘whole-mount’ samples either shadow-cast (Fig. 1a, b) or negatively stained (Fig. 1c), following a general protocol (Yakimov *et al.*, 1998; Golyshina *et al.*, 2000). Cells were also embedded in epoxy resin (Spurr, 1969) and ultrathin-sectioned. Energy-filtered transmission electron microscopy (EFTEM) was done with a CEM 902 instrument (Zeiss) at 80 kV in the elastic bright-field mode (Lünsdorf *et al.*, 2001, 2006).

On ultrastructural analysis by EFTEM, whole-mount bacterial cells typically appeared as rods, 1.9–3.7 µm in length (mean 2.8 ± 0.7 µm, *n* = 12) and 0.7–0.9 µm in width (mean 0.8 ± 0.1 µm, *n* = 21). Cells generally showed one and

Abbreviation: EELS, electron energy loss spectroscopy.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain WB 3.4-79^T is AM397080.

Results of EELS and a 16S rRNA gene sequence-based maximum-likelihood tree are available as supplementary material in IJSEM Online.

Fig. 1. Transmission electron microscopy of strain WB 3.4-79^T showing 'whole mount' shadow-cast (a, b) and negatively stained (c) bacteria. Cells appear enveloped in a greyish slime matrix, which occasionally shows fibre-like protrusions (open arrowheads). Darkish spots within this matrix represent drying artefacts. An individual flagellum (fl) is inserted at a cell pole, which appears slightly flattened (c, double arrows) relative to the opposite, conical cell end (large arrow). (d, e) Uranyl acetate-post-stained ultrathin sections reveal cells to contain large amounts of polyhydroxybutyrate (phb), often torn out of the section, leaving holes behind (asterisks). Large electron-dense inclusions represent 'enterosomes' (es) associated with or adjacent to clusters of polyphosphate granules (pp). po, Polar organelle; cm, cytoplasmic membrane; om, outer membrane. Bars, 1.0 µm (a–d) and 150 nm (e).

occasionally two flagella inserted at one cell pole [monopolar, mono(bi)trichous flagellation], which measured 3.3–5.3 µm in length (mean 4.4 ± 0.7 µm, $n=12$) (Fig. 1a–c). Individual cells were surrounded by a slime layer, variable in thickness. In negatively stained cells, the slime layer can be visualized as an electron-dense halo (Fig. 1c) and in a platinum-shadowed preparation as a greyish amorphous rim at the cell periphery that occasionally showed radiant extrusions (Fig. 1a, open arrowheads).

Analysis of ultrathin sections showed the cell wall of strain WB 3.4-79^T to be outlined by an outer and cytoplasmic membrane (Fig. 1e), characteristic of Gram-negative bacteria. In contact with the cytoplasmic membrane at the cytoplasmic face, a regularly structured layer was occasionally found, which is isomorphic to 'polar organelles'. These have been described in *Sphaerotilus natans* (and other bacteria), and have been assumed to play a role in energy supply in this polytrichous monopolarly flagellated bacterium, based on their ATPase and cytochrome oxidase

activities (Tauschel, 1985). Additionally, three morphotypes of intracellular inclusions, polyhydroxybutyrate (phb), polyphosphate (pp) and enterosomes (es) (Fig. 1d, e), are present. Electron-transparent polyhydroxybutyrate inclusions filled most of the cellular volume and were often torn out during the sectioning process. Polyphosphate granules, intensely stained and small in size, were interspersed as small clusters within the cytoplasm or were associated with the surface of large, electron-dense inclusions, 170–200 nm in size. Electron energy loss spectroscopy (EELS) revealed distinctly the presence of phosphorus in both small and large dark cellular inclusions (see Supplementary Fig. S1 in IJSEM Online). EELS also revealed the electron density to be based mainly on uranium, added as a stain during the dehydration process. A closer view of these large inclusions revealed the interior to be filled with a fine particulate matrix that, after low-frequency filtering or fast Fourier transformation, revealed a faint structural order, indicative of residual crystallinity (see Supplementary Fig. S1f–h). Residual crystallinity can also be deduced from the

polyhedral contours of these inclusions. EELS and high-resolution elemental mapping showed the presence of phosphorus and nitrogen as the main constituents of these inclusions, supplemented by small amounts of calcium (Supplementary Fig. S1b–e). Nitrogen, as an indicator element of proteins, and the weak structural order of the particulate matrix indicate that these dark inclusions can be considered ‘enterosomes’ in the general sense (Cannon *et al.*, 2001). The presence of a distinct outer proteinaceous shell could not be observed and thus they differ at the structural level from typical ‘polyhedral bodies’. Further biochemical and physiological analysis has to be done to differentiate whether these inclusions represent ‘carboxysomes’ in a specific sense (Cannon *et al.*, 2001) or, because of the presence of calcium and phosphate, analogues to the ‘acidocalcisomes’ of *Agrobacterium tumefaciens* (Seufferheld *et al.*, 2003) or general ‘metabolosomes’ (Brinsmade *et al.*, 2005).

Genomic and phylogenetic characterization

Genomic DNA was extracted using the DNeasy Tissue kit (Qiagen) following the manufacturer’s instructions. The 16S rRNA gene was amplified as described by Rainey *et al.* (1996) using the primers 10–30 forward and 1500 reverse. PCR products were purified with the QIAquick PCR purification kit (Qiagen) and sequenced directly by using the CEQ Dye Terminator cycle sequencing kit and on a CEQ 8000 Genetic Analysis system. 16S rRNA gene sequences were aligned with corresponding sequences from the DSMZ database using the ae2 editor (Maidak *et al.*, 1997). Evolutionary distances were calculated by the method of Jukes & Cantor (1969). A distance analysis dendrogram was reconstructed by the neighbour-joining and maximum-likelihood algorithms (Felsenstein, 1993) and by the algorithm of De Soete (1983). Bootstrap analysis was used to evaluate the tree topology by performing 500 resamplings (Felsenstein, 1985).

Nearly complete 16S rRNA gene sequences (1508 nt) were obtained from strains WB 3.4-79^T and WB 3.3-25. As the two sequences were identical, only that of strain WB 3.4-79^T was analysed further. Preliminary comparison against the 16S rRNA gene sequences in GenBank by BLAST (Altschul *et al.*, 1997) indicated that strain WB 3.4-79^T belonged to the

Chitinibacter–Iodobacter branch of the family *Neisseriaceae*, class *Betaproteobacteria*. The sequence of strain WB 3.4-79^T was then included in the DSMZ database of 16S rRNA gene sequences and similarity values were determined. On the basis of these values, the closest described type strains were *Chitinibacter tainanensis* BCRC 17254^T (93.8%), *Formivibrio citricus* DSM 6150^T (92.6%), *Silvimonas terrae* KCTC 12358^T (91.9%) and *Iodobacter fluviatilis* ATCC 33051^T (92.3%). The 16S rRNA gene sequence similarity between strain WB 3.4-79^T and other members of the order *Neisseriales* was less than 90%. Strain WB 3.4-79^T and the four type strains indicated above formed a monophyletic clade with a high bootstrap value (99%), which was in accordance with the different treeing algorithms employed. While strain WB 3.4-79^T branched adjacent to *Chitinibacter tainanensis* BCRC 17254^T according to the neighbour-joining and De Soete analyses (Fig. 2), maximum-likelihood analysis showed strain WB 3.4-79^T and *Formivibrio citricus* DSM 6150^T to be phylogenetic neighbours (Supplementary Fig. S2).

Data from the literature (compiled by Stackebrandt & Ebers, 2006) indicate that strains may belong to different genospecies even if they share 100% 16S rRNA gene sequence similarity. Therefore, the genomic relatedness between the two novel strains was determined by the spectrophotometric DNA–DNA reassociation method. DNA was isolated as described by Marmur (1961) and was fragmented by ultrasonication (Bandelin Sonoplus) for 2 min at 170 μm_{ss} . DNA–DNA hybridization was carried out as described by De Ley *et al.* (1970), with the modifications of Huß *et al.* (1983) and Escara & Hutton (1980), using a model Cary 100 Bio UV/VIS spectrophotometer equipped with a Peltier-thermostatted 6 × 6 multicell changer and a temperature controller with *in-situ* temperature probe (Varian). The G + C content of the DNA of the two strains was determined according to Mesbah *et al.* (1989). The DNA relatedness of strains WB 3.4-79^T and WB 3.3-25 was 100%. The G + C content of strain WB 3.4-79^T was 48.5 mol% (two determinations).

Analyses of chemotaxonomic properties

Except for fatty acid analysis, biomass for chemotaxonomic studies was prepared by growing the strain in shake flasks in

Fig. 2. Additive phylogenetic tree (neighbour-joining), based on 16S rRNA gene sequences, showing the nearest neighbours of strain WB 3.4-79^T within the family *Neisseriaceae*, class *Betaproteobacteria*. Numbers at branch points indicate percentage bootstrap values from 1000 datasets. Only bootstrap values greater than 60% are shown. Bar, 5% difference in nucleotide sequences, as determined by measuring the lengths of the horizontal lines connecting any two organisms.

marine broth 2216 (Difco) at 28 °C for 2 days. Cultures were checked for purity, harvested by centrifugation and freeze-dried. Polar lipids and isoprenoid quinones were extracted following the procedure of Minnikin *et al.* (1984). The polar lipids were separated by TLC using the standard method (Minnikin *et al.*, 1984), whereas the quinone extract was filtered and reduced to dryness by a stream of dry nitrogen. The dried preparation was dissolved in 200 µl isopropanol and filtrated using a Dyna Gard 0.2 µl syringe filter. Aliquots (5 µl) were separated by HPLC following a described method (Kroppenstedt & Mannheim, 1989). Fatty acids of *Chitinibacter tainanensis* DSM 15459^T, *Formivibrio citricus* DSM 6150^T and *Silvimonas terrae* DSM 18233^T were extracted and analysed (Miller, 1982; Sasser, 1990) according to the standard protocol of the Microbial Identification System (MIDI Inc., 1999). As *Formivibrio citricus* DSM 6150^T does not grow anaerobically on TSBA medium, medium DSM 505 (DSMZ, 2001) was used to obtain biomass for fatty acid extraction. The same protocol was also reported for *Silvimonas terrae* KCTC 12358^T (Yang *et al.*, 2005). Extracts were analysed by using a Hewlett Packard model HP6890A gas chromatograph equipped with a flame-ionization detector as described by Kämpfer & Kroppenstedt (1996).

Ubiquinone 8 was the only isoprenoid quinone present. Phosphatidylethanolamine and phosphatidylglycerol were the major polar lipids. Diphosphatidylglycerol occurred in smaller amounts. The fatty acid composition is compiled in Table 1.

Phenotypic characterization

Cultural properties such as colony size, shape and colour were determined after 3 days incubation at 28 °C on R2A (Difco 218263). Conventional biochemical tests were performed according to standard methods (Smibert & Krieg, 1994). The data obtained are indicated in the species description and in Table 2. Accumulation of poly-β-hydroxybutyrate was determined as described by Ostle & Holt (1982). Physiological and biochemical tests were performed on the two isolates and *Chitinibacter tainanensis* DSM 15459^T at 28 °C using API 20NE, API 20E and API 50CH strips (bioMérieux) and Biolog GN microplates (Oxoid). All tests were inoculated with cells grown on R2A. API strips were used according to the manufacturer's instructions; utilization reactions were observed for 5 days. Acid production from carbohydrates was tested on API 50CH strips with bioMérieux medium E. Utilization of carbohydrates was determined on API 50CH strips with modified AUX medium in which growth factors and amino acids were replaced by a solution containing [(1 distilled water)⁻¹]: phosphate buffer, 40 mM; (NH₄)₂SO₄, 2 g; MgSO₄·7H₂O, 6 g; CaCl₂·2H₂O, 0.066 g; agar, 1.5 g; yeast extract, 0.1 g; trace element solution, 1 ml; vitamin solution, 5 ml. Results of Biolog GN plates did not change over incubation times of 1–4 days. Wells showing a photometric value above 25 or 80 units were scored as weak and positive, respectively.

Table 1. Comparison of fatty acid profiles of strains WB 3.4-79^T and WB 3.3-2.5 and their phylogenetically closest relatives

Strains: 1, WB 3.4-79^T; 2, WB 3.3-2.5; 3, *Chitinibacter tainanensis* DSM 15459^T; 4, *Silvimonas terrae* KCTC 12358^T (data from Yang *et al.*, 2005); 5, *Formivibrio citricus* DSM 6150^T. Data are from this study unless indicated. Values are percentages of total fatty acids; fatty acids that make up <1 % in all strains are not shown. –, Not detected.

Fatty acid	1	2	3	4	5
C _{12:0}	2.7	2.8	2.6	3.8	5.3
C _{12:0} 3-OH	2.5	2.5	4.3	—	—
C _{14:0} 3-OH	2.0	—	—	2.9	9.5
C _{14:1}	—	—	—	—	1.2
C _{14:0}	2.0	2.6	—	8.0	1.6
C _{15:1ω6c}	1.5	2.3	1.1	—	—
C _{15:0}	2.9	3.9	1.3	3.5	—
C _{16:1ω7c}	60.1	59.6	61.3	16.5	57.7
C _{16:0}	20.7	18.4	15.1	27.2	11.9
C _{16:0} 3-OH	—	—	1.6	—	—
C _{18:1ω7c}	3.4	3.0	7.7	13.9	10.8
C _{17:0} cyclo	—	—	—	18.3	—
C _{19:0} methyl	—	—	1.7	—	—

Cultural characteristics

The novel strains grew well on R2A agar, Bacto tryptic soy broth agar without glucose (BTS; BD 286226), H3P agar (DSMZ medium 428) and Columbia agar with 5 % sheep blood (BD 254005) at 28 °C. The temperature optimum was tested for strain WB 3.4-79^T in BTS medium for 72 h, using a temperature gradient incubator model TN-3 (Toyo Kagaku Sangyo) in 1 °C steps, ranging from –1 to 40 °C. Growth was observed between 4 and 32 °C over 72 h. The optimum temperature was 23–28 °C. Cells began to lyse above 29 °C after 22 h; growth was delayed by 24 h at temperatures between 4 and 12 °C. Motility was observed over the whole temperature range.

The pH range for growth was tested in buffered R2A medium at 28 °C between pH 5.1 and 9.5, with steps of about 0.3 pH. Growth of strain WB 3.4-79^T occurred at pH 5.8–8.5, with an optimum around pH 7.3–7.6.

Salt tolerance of strain WB 3.4-79^T was tested on R2A supplemented with 0.5, 1, 2, 4, 6, 8 and 10 % (w/v) NaCl at 28 °C. Good growth was observed after 3 days incubation at 0.5 %, while growth was weak on agar containing 1 % NaCl. No growth occurred at 2 % NaCl or above.

Tests for chemolithoautotrophic growth were done in mineral medium 81 (DSMZ, 2001) at 28 °C for 7 days under reduced (H₂/N₂/CO₂/air; 70:10:10:10 by vol.) and aerobic conditions. Hydrogen and oxygen served as electron donor and acceptor, respectively. Growth was positive under both conditions and cells grew to similar densities.

Table 2. Characters that distinguish strains WB 3.4-79^T and WB 3.3-2.5 from their closest phylogenetic relatives

Strains: 1, WB 3.4-79^T and WB 3.3-2.5; 2, *Chitinibacter tainanensis* DSM 15459^T; 3, *Silvimonas terrae* KCTC 12358^T; 4, *Formivibrio citricus* DSM 6150^T. Phenotypic tests were based on API 20NE and API 50CH strips (columns 1 and 2), API 20NE and API 32GN strips (Yang *et al.*, 2005) (column 3) or API 20A strips (Tanaka *et al.*, 1991) (column 4). w, Weak reaction; ND, not determined or no data available.

Property	1	2	3	4
Morphology	Rods, straight to slightly curved	Rods, straight to slightly curved	Rods, singly or in pairs	Curved rods, singly or in pairs
Number of polar flagella	One, rarely two	One or two	One	One
Catalase	+	+	+	—
Relation to O ₂	Facultatively anaerobic	Strictly aerobic	Facultatively anaerobic	Strictly anaerobic
Anaerobic growth on R2A or in R2A broth	+	w	+	—
Acid production from:				
Glucose in OF test	—	w	ND	ND
Glucose in API 20NE strips	—	+	+	ND
Sucrose in API 20E strips	+	—	—	ND
Growth at 40 °C	—	+	+	—
Gelatin hydrolysis	—	+ (after 5 days)	ND	—
Chitin hydrolysis	—	+	+	ND
Utilization of (API 50CH):				
Ribose	+	—	—	ND
Sucrose	+	—	+	ND
N-Acetylglucosamine	w	—	+	ND
Assimilation of β-hydroxybutyric acid (Biolog)	w	—	ND	ND
DNA G+C content (mol%)	48.5	56	58	59

Antibiotic-sensitivity tests were performed by using filter-paper discs containing 15 different antibiotics and concentrations. Discs were placed on R2A plates spread with WB 3.4-79^T culture and were then incubated at 28 °C for 3 days. Susceptibility was scored as positive at zone diameters above 13 mm, intermediate susceptibility at 10–12 mm and resistance at less than 10 mm. The reactions are indicated in the species description.

Strains WB 3.4-79^T and WB 3.3-2.5 are virtually identical in all taxonomic criteria used. They were isolated from the same site and may be considered clones, enriched on different growth media. The novel taxon can be distinguished from all neighbours by its significantly lower G+C content and in addition from *Chitinibacter tainanensis* (Chern *et al.*, 2004) by the lack of chitin and gelatin hydrolysis, lack of growth at 40 °C, lack of C_{16:0} 3-OH and C_{19:0} methyl fatty acids and by some phenotypic reactions. It differs from *Silvimonas terrae* (Yang *et al.*, 2005) by the lack of hydrolysis of chitin, starch and cellulose, lack of growth at 40 °C, lack of C_{17:0} cyclo and C_{14:0} 3-OH fatty acids and in the quantities of C_{16:0} fatty acid and those summed in features 4 and 7. While strains WB 3.4-79^T and WB 3.3-2.5 are facultatively anaerobic, *Formivibrio citricus* (Tanaka *et al.*, 1991) is strictly anaerobic. Due to this feature, only the API 20A (anaerobe) tests could be performed on the latter organism. Based on phylogenetic, cultural and physiological distinctness, we propose the genus *Deefgea* gen. nov. and *Deefgea rivuli* sp. nov. as new taxa, with strain WB 3.4-79^T as the type strain of *Deefgea rivuli*.

Description of *Deefgea* gen. nov.

Deefgea [De.ef.ge'a. N.L. fem. n. *Deefgea* arbitrary name derived from the acronym DFG for Deutsche Forschungsgemeinschaft (German Science Foundation)].

Cells are Gram-negative, rod-shaped (0.7–0.8 × 3–4 µm) and facultatively anaerobic. They occur mostly singly (Fig. 1a) and are motile by means of a single flagellum (Fig. 1b) or rarely two polar flagella. Colonies on R2A are circular, convex and pearl white. Catalase and oxidase are positive. Contain polyhydroxybutyrate and polyphosphate granules. The predominant quinone is Q-8. Polar lipids are phosphatidylethanolamine and phosphatidylglycerol. Major cellular fatty acids (> 10 %) are C_{16:0} and C_{16:1ω7c}. The G+C content of the DNA is 49 mol%. Based on 16S rRNA gene sequence analysis, *Deefgea* belongs to the class *Betaproteobacteria*, family *Neisseriaceae*, showing a distant relatedness to *Chitinibacter tainanensis*, *Silvimonas terrae* and *Formivibrio citricus*. The type species is *Deefgea rivuli*.

Description of *Deefgea rivuli* sp. nov.

Deefgea rivuli (ri'vu.li. L. gen. masc. n. *rivuli* of/from a rivulet, a small brook).

In addition to the characters that define the genus, it has the following characteristics. Cells have one round end and one pointed end; in older cultures, larger cells (4–7 µm) are occasionally present. Cells are highly motile at temperatures below 10 °C. Colonies on R2A agar are 1–2.5 mm in

diameter, opaque with a smooth, shiny surface and butyrous with entire margins. Similar characteristics define colonies formed on Columbia agar (grey–white, umbonate, 3.2–4 mm in diameter), H3P (cream–white, 0.5–0.7 mm) and BTS (cream–white, 1.0–2.2 mm). Unspecified enterosomes and a polar organelle are present in the cytoplasm. No acid production in OF test under oxic or anoxic conditions. Grows at 4 °C but not above 32 °C. No growth above 2 % NaCl (w/v). pH optimum is between pH 7.3 and 7.6. Grows chemolithoautotrophically under aerobic and reduced conditions. Positive in API 20NE strips for reduction of nitrate to nitrite and utilization of glucose, *N*-acetylglucosamine and gluconate (all substrates utilized weakly). Tests positive in API 20E strips for acidification of glucose (only transiently after 24 h; realkalinization after 48 h) and acid production from sucrose. Substrates utilized in API 50CH with AUX medium are ribose, glucose, fructose, *N*-acetylglucosamine, sucrose and gluconate. Substrates positive in Biolog plates are dextrin, *N*-acetylglucosamine, D-fructose and β -D-glucose; weakly positive for D-mannose, methylpyruvate and β -hydroxybutyric acid. No degradation of chitin, cellulose, casein, starch or xylan. Resistant (per disc) to penicillin G (10 IU), oxacillin (5 μ g), ampicillin (10 μ g), cephalothin (30 μ g), cefotaxime (30 μ g), piperidic acid (20 μ g), erythromycin (15 μ g), vancomycin (30 μ g) and lincomycin (15 μ g); intermediately susceptible to norfloxacin (10 μ g), ofloxacin (5 μ g) and colistin (10 μ g); susceptible to tetracycline (30 μ g), chloramphenicol (30 μ g), imipenem (10 μ g) and doxycycline (30 μ g).

The type strain, WB 3.4-79^T (=DSM 18356^T=CIP 109326^T), was isolated from water of the Westerhöfer Bach, near Westerhof, Lower Saxony, Germany (51° 45' 49" N 10° 05' 31.7" E).

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