**Hyphomonas sediminis** sp. nov., isolated from marine sediment

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Received: 29 April 2022 / Accepted: 10 July 2022 / Published online: 25 July 2022
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**Abstract** A Gram-staining-negative, aerobic and pear-shaped bacterial strain, designated WL0036\(^T\), was isolated from coastal sediment sample collected in Nantong city, Jiangsu province of China (120° 51′ 13″ E, 32° 6′ 26″ N) in October 2020. Strain WL0036\(^T\) was found to grow at 20–37 °C (optimum, 28 °C) with 0–9.0% NaCl (optimum, 2.5–4.0%) and displayed alkaliphilic growth with the pH range of pH 6.0–10.0 (optimum, pH 7.0–8.0). The polar lipids profile of strain WL0036\(^T\) included phosphatidylcholine, phosphatidylethanolamine, glycolipid and an unidentified lipid. The major isoprenoid quinone was determined to be Q-11 and the major fatty acids were C\(_{16:0}\), 11-methyl-C\(_{18:1}\)\(\omega 7\)\(^c\), and summed features 8 (C\(_{18:1}\)\(\omega 6\)\(^c\) and/or C\(_{18:1}\)\(\omega 7\)\(^c\)). The G+C content of genomic DNA was 61.8%. Phylogenetic trees constructed based on 16S rRNA gene sequence and bac120 gene set (a collection of 120 single-copy protein sequences prevalent in bacteria) indicted that strain WL0036\(^T\) clustered with strains *Hyphomonas neptunium* ATCC 15444\(^T\) and *H. polymorpha* PS728\(^T\). The average nucleotide identities between strain WL0036\(^T\) and strains *H. neptunium* ATCC 15444\(^T\) and *H. polymorpha* PS728\(^T\) were 80.7% and 81.2%, respectively. Strain WL0036\(^T\) showed 22.8% and 23.2% of digital DNA-DNA hybridization identities with *H. neptunium* ATCC 15444\(^T\) and *H. polymorpha* PS728\(^T\), respectively. As inferred from the phenotypic and genotypic characteristics and the phylogenetic trees, strain WL0036\(^T\) ought to be recognized as a novel species in genus *Hyphomonas*, for which the name *Hyphomonas sediminis* sp. nov. is proposed. The type strain is WL0036\(^T\) (=MCCC 1K05843\(^T\) = JCM 34658\(^T\) = GDMCC 1.2413\(^T\)).

**Keywords** *Hyphomonas sediminis* sp. Nov. · Marine sediment · bac120 tree
Introduction

The genus *Hyphomonas* was originally proposed by Pongratz 1957. The cells of the genus *Hyphomonas* are Gram-staining-negative, aerobic, heterotrophic and nonsporeforming. The daughter cells are oval to pear-shaped, smaller than the body of the mother cell, moving through polar lateral flagella. Hyphae rarely branch during normal growth (Pongratz 1957). At the time of writing, the genus *Hyphomonas* includes 12 species, of which 11 have been validly published according to the List of Prokaryotic names with Standing in Nomenclature (LPSN) server (https://lpsn.dsmz.de/ genus/ hyphomonas, accessed on March 30, 2022) (Parte 2018): *H. polymorpha* (Moore et al. 1984); *H. neptunium* (Moore et al. 1984); *H. oceanitis* (Weiner et al. 1985); *H. jannaschiana* (Weiner et al. 1985); *H. adhaerens* and *(Weiner et al. 2000); H. johnsonii* (Weiner et al. 2000); *H. atlanticus* (Li et al. 2016c); *H. beringensis* (Li et al. 2014a); *H. pacifica* (Li et al. 2016), *H. rosenbergii* (Weiner et al. 2000) and *H. chukchiensis* (Li et al. 2014a). Nevertheless, *H. rosenbergii* was recommended to be place on the reject list because the 16S rRNA gene sequence of *H. rosenbergii* ATCC 43869T shared a similarity of 92.8% with the primitive sequence (Lai et al. 2015; Li et al. 2014b). Members of the genus *Hyphomonas* are primarily spread in the marine environment, which include pelagic areas, offshore areas and deep-sea thermal springs.

To investigate the application potential of the bacteria from offshore areas of Jiangsu province, China, a novel bacterium, designated WL0036T, was isolated from a marine sediment sample of Nantong city. In the present study, we conducted a polyphasic taxonomic study to clarify the taxonomic position of strain WL0036T.

Materials and methods

Isolation and culture condition

Strain WL0036T was isolated from a marine sediment sample collected in Nantong city, Jiangsu province of China (120° 51′ 13″ E, 32° 6′ 26″ N) in October 2020. Prior to isolation, the sample was stored in 4 °C refrigerator. For isolation, 2 g sample was diluted in sterile physiological saline (per litre of water: 9.0 g sodium chloride, Sangon Biotech, China) (18 mL), and then incubated in a constant temperature shaker incubator at 28 °C for 1 h. The suspension was diluted to 10−3 and 100 µL were spread on plates of the marine agar medium 2216E (Hopebio, China, per litre: 5.0 g peptone, 1.0 g yeast extract, 15.0 g agar, 0.01 g ferric phosphate, 25 g sea salt, 0.5 g NaOH). After incubation at 28 °C for 5 days, colonies were picked up and streaked on tryptose soya agar (TSA, per litre: 15.0 g tryptone (Sangon Biotech, China), 5.0 g soy papain digest (Sangon Biotech, China), 15.0 g agar (Sangon Biotech, China)) medium supplemented with 2.5% sea salt (Baojiao, China) to obtain pure cultures. Subsequently, the bacterium was maintained on TSA (Difco) medium supplemented with 2.5% sea salt and also stored at −80 °C in 20.0% (v/v) glycerol.

Genome sequencing and annotation

For 16S rRNA gene amplification by PCR, genomic DNA was extracted by using the Ezup column bacterial genomic DNA purification kit (Sangon Biotech, China). The crude extract was used as DNA template for PCR as described previously (Weisburg et al. 1991) with 27F (5′-AGAGTTTGATCCT TGGCTCAG-3′) and 1492R (5′-AAGGAGGTG ATCCAGGTC-3′) primers. The almost full-length 16S rRNA gene sequence was compiled using SeqMan software (DNASTAR) and ultraseq through the EzbioCloud (https://www.ezbiocloud.net/) server (Yoon et al. 2017) to retrieve sequences of the most closely related types strains. Whole-genome shotgun sequencing of strain WL0036T was performed using paired-end sequencing method with Hiseq X platform (Illumina) at Magigene Company, Guangzhou, China. The whole genome was assembled using SPAdes version 3.10.1 (Nurk et al. 2013) in UGENE software package (Okonechnikov et al. 2012). Following the proposed minimal standards for the use of genome data for the taxonomy of prokaryote (Goris et al. 2007; Richter and Rosselló-Móra 2009), the average nucleotide identity (ANI) and the digital DNA-DNA hybridization (dDDH) were used to compare strain WL0036T and related type species genome sequences. The ANI values was calculated by ANI calculator using the OrthoANIu algorithm on the EzBioCloud website (https://www.ezbiocloud.net/) (Yoon et al. 2017) and the dDDH values was calculated using the
Genome-to-Genome Distance Calculator (http://ggdc.dsmz.de/ggdc.php/) (Meier-Kolthoff et al. 2013). Genome annotation was conducted by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (Tatusova et al. 2016), ulpha online server (https://eggnog-mapper.Embl.de/) (Huerta-Cepas et al. 2017) and KEGG online server (https://www.kegg.jp/blastkoala/) (Kanehisa et al. 2016). The results of genetic analysis for drug resistance was obtained through the Comprehensive Antibiotic Resistance Database (CARD) website (https://card.mcmaster.ca/) (Alcock et al. 2020). The G+C content of genomic DNA was calculated based on the EzBioCloud server from the draft genome sequence.

Phylogenetic analysis

Phylogenetic trees based on 16S rRNA gene sequence were reconstructed by the ulphate-joining (NJ) (Saitou and Nei 1987), minimum-evolution (ME) (Pardi et al. 2010), and maximum-parsimony (MP) (Fitch 1971) methods using MEGA X software (Kumar et al. 2018) after multiple sequence alignments. The evolutionary distance matrix of the phylogenetic tree was commonly calculated using Kimura’s two-parameter model (Kimura 1980). Confidence values for tree branches were determined by bootstrap analysis based on 1000 resamples (Felsenstein 1985). Genome-based phylogenies of supermatrix and supertree approaches from protein sequences of the bac120 gene set (a collection of 120 single-copy protein sequences prevalent in bacteria) were constructed by using Easy-CGTree version 3.0 (https://github.com/zdf1987/EasyCGTree) as described previously (Zhang et al. 2020). The genome sequences of the strains of interest were downloaded from the NCBI genome database (https://www.ncbi.nlm.nih.gov/genome/) and detailed information is listed in Suppl. Table S1.

Morphology, physiology, and biochemical analysis

A Gram Stain kit (Solarbio, China) was used for testing the Gram reaction. The cell morphology of the bacterium was observed by transmission electron microscopy (JEM, 2100) using cells grown in TSA (Difco) medium supplemented with 2.5% sea salt for 48 h at 28 °C. Motility was determined by observing growth of cells in test tubes containing TSB medium with 0.3% agar after 3 days of incubation at 28 °C. Anaerobic growth was tested in an anaerobic chamber (Oxoid, UK) with the atmosphere generation system (AnaeroGen, Oxoid, UK) for 10 days on TSA medium plates which supplemented with 2.5% sea salt. To determine the development conditions of the strain WL0036T, growth at various temperatures (4, 10, 20, 28, 37, 45, and 50 °C) was tested in TSA medium supplemented with 2.5% sea salt. Adjusting pH values (pH 4.0–12.0, with 1.0 increments), using NaOH solution (1.0%, w/v) and HCl solution (1.0%, w/v) to adjust pH in the tryptic soy broth (TSB, per litre: 15.0 g tryptone (Sangon Biotech, China), 5.0 g soy papain digest (Sangon Biotech, China), 25.0 g sea salt) medium. To investigate the tolerance to NaCl, growth at various NaCl concentrations (0, 1.5, 2.5, 4.0, 7.0, 9.0, 11.0 and 13.0%) was investigated in TSA medium (per litre: 15.0 g tryptone, 5.0 g soy papain digest).

Catalase activity was detected by observing whether bubbles were produced using 3.0% hydrogen peroxide. Oxidase activity was determined with the use of 1.0% tetramethyl-β-phenylenediamine. Additional biochemical tests were performed using the BIOLOG GEN III microtest system (Biolog, USA), API 20NE and API ZYM systems (bioMérieux, France) in addition to adjusting the salinity to 2.5% with sea salt when culturing strain WL0036T according to the manufacturer’s instructions.

Chemotaxonomic characterization

The strain WL0036T and the two reference strains H. neptunium ATCC 15444T and H. polymorpha PS728T were incubated in TSB medium supplemented with 2.5% sea salt at 28 °C for three days, and then the biomass was collected for fatty acid characterization. Cellular fatty acids was methylated and sulphated using the Sherlock Microbial Identification System (MIDI) according to a previously described method and the manufacturer’s instructions (Sasser 1990). The polar lipid profile and isoprenoid quinones were determined using cells grown on TSB medium containing 2.5% sea salt at 28 °C for 3 days. Two-dimensional thin-layer chromatography was performed following previously demonstrated methods to detect polar lipids in cells (Collins and Jones 1980; Minnikin et al. 1984). Phosphomolybdic acids were used for determination of all polar lipids, ninhydrin for phospholipids containing amino or glucosamine,
and anisaldehyde and α-naphthol were used for glycolipids. Isoprenoid quinones were extracted (Collins et al. 1977) and sulphate using reversed phase HPLC as described previously (Tamaoka 1986).

Results and discussion

Phylogenetic analysis

The complete 16S rRNA gene sequence of strain WL0036T was 1292 bp (accession number, OL605964) a length of 1072 bp was used to construct the 16SrRNA evolutionary tree of the strain. The results from the EzBioCloud server suggested that the 16S rRNA gene sequence of strain WL0036T exhibited the highest similarities to those of H. polymorpha PS728T (98.3%) and H. neptunium ATCC 15444T (97.8%). By using the maximum-parsimony method, the phylogenetic tree (Fig. 1) denoted that strain WL0036T clustered with H. polymorpha PS728T, H. rosenbergii VP-6T and H. neptunium ATCC 15444T, and the clade of these four taxa was closely related to the rest members of the genus Hyphomonas. Meanwhile, the phylogenetic position of strain WL0036T was well supported (bootstrap value > 70.0%) in the sulphate-joining tree, and it agreed with the trees of sulphate-joining method (Suppl. Fig. S1) and the minimum-evolution method (Suppl. Fig. S2) with high confidence (bootstrap values > 70).

In order to further explore the relationships among strain WL0036T and related species within the genus Hyphomonas, the bac120 tree constructed following the method of the supermatrix (Fig. 2) demonstrated that strain WL0036T formed a clade and clustered with the reference strains H. polymorpha PS728T and H. neptunium ATCC 15444T. Meanwhile, the phylogenetic tree based on 119 universal protein coding genes of the bac120 set among the strains of interest (Suppl. Fig. S3) showed that strain WL0036T also formed a clade with H. polymorpha PS728T and H. neptunium ATCC 15444T, which was supported

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**Fig. 1** Maximum-parsimony phylogenetic tree based on 16S rRNA gene sequence showing the relationship between strain WL0036T and its closest relatives. Bootstrap values (expressed as percentages of 1000 replications) of above 70% are shown at the branch nodes. The black dots indicate branches that were also recovered using the minimum-evolution and neighbor-joining methods. Species with no valid publication are marked with double-quote. The GenBank/EMBL/DDJB accession numbers are indicated in the brackets at the end of the tip labels. *Escherichia coli* JCM 1649T is used as out group. The Figure is from this study.

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Fig. 2  Maximum-likelihood phylogenetic tree based on concatenated protein sequences of bac120 gene set showing the relationship between strain WL0036\textsuperscript{T} and its closest relatives. Bootstrap values are based on 1000 replicates and shown at the branch nodes. Escherichia coli JCM 1649\textsuperscript{T} is used as out group. Bar, 0.1 substitutions per nucleotide position. The bioproject accession numbers are indicated in the brackets at the end of the tip labels. The refseq assembly accession number of the strain is listed in Suppl. Table S1. The Figure is from this study.

by 113 of the 119 genes (95.0\%) used in supertree method. This result was corresponding to that of the supermatrix method and those based on 16S rRNA gene sequence. Consequently, these findings support that strain WL0036\textsuperscript{T} was a member of genus *Hyphomonas*.

Genomic features

The draft genome of strain WL0036\textsuperscript{T} was comprised of 4 contigs with a size of 3498010 bp. The G+C content of genomic DNA was 61.8\%. Automated annotation by NCBI PGAP recognized 3302 protein-coding sequences, 6 rRNA genes, 41 tRNA genes and 3 RNA genes of other type. The 16S rRNA gene sequence (locus tag K1X12_16485) on the genome was identical to the Sanger sequence.

The annotation of KEGG indicated that strain WL0036\textsuperscript{T} had 12 genes involved in sulphate metabolism (ko00920): *KIX12_RS02220* (cysI), *KIX12_RS02210* (cysH), *KIX12_RS12225* (cysE), *KIX12_RS05225* (metA), *KIX12_RS07770* (cysN), *KIX12_RS07775* (cysD), *KIX12_RS10865* (seet), *KIX12_RS04790* (cysQ), *KIX12_RS03670* (cysK), *KIX12_RS00130* (tauD), *KIX12_RS16560* (metZ), *KIX12_RS14335* (sqr), of which *KIX12_RS02220* (cysI), *KIX12_RS02210* (cysH) and *KIX12_RS07770* (cysN) may confer assimilatory sulphate reduction; 27 genes were involved to flagellar assemblies (ko02040), of which 10 were involved in coding flagellar hook-basal body and flagellar basal body complex protein, and cells of strain WL0036\textsuperscript{T} with a single polar flagella (Suppl. Fig. S4). And in the BIOLOG GEN III tests after 48 h of incubation at 28 °C, all three strains were resistant to nalidixic acid (Suppl. Table S2).

The ANI values between strain WL0036\textsuperscript{T} and strains *H. neptunium* ATCC 15444\textsuperscript{T} and *H. poly morpha* PS728\textsuperscript{T} were 80.7\% and 81.2\%, respectively (Table 1), all of which the ANI values were below threshold for species boundaries (95.0–96.0\%) (Richter and Rosselló-Móra, 2009). Strain WL0036\textsuperscript{T} showed dDDH values of 22.8\% and 23.2\% with
The cells of strain WL0036\textsuperscript{T} were Gram-staining-negative, aerobic, motile and pear-shaped with a single polar flagellum. Slight yellow, round and smooth colonies were observed on TSA medium with 2.5% sea salt for 3 days at 28 °C. More results on phenotypic characteristics were listed in Table 2 and Suppl. Table S2.

Chemotaxonomic characteristics

Strain WL0036\textsuperscript{T} exhibited a polar lipid profile consisting of phosphatidylcholine (PC),...
phosphatidylethanolamine (PE), glycolipid (GL) and an unidentified lipid (L) (Fig. S5). The predominant cellular fatty acids (> 10%) of strain WL0036T were C\textsubscript{16:0} (27.6%), 11-methyl-C\textsubscript{18:1}ω7c (12.1%), and summed features 8 (C\textsubscript{18:1ω6c} and/or C\textsubscript{18:1ω7c}) (35.0%) (Suppl. Table S3), which was resemblance to that of the strains of the geuns *Hyphomonas* (Li et al. 2016). The compositions of cellular fatty acid contents (> 1%) of WL0036T and the neighboring type strains were presented in Suppl. Table S2. The predominant isoprenoid quinone was ubiquinone-11 (Q-11), in addition to a small amount of ubiquinone-10 (3.5%), which was identical to that of the two neighboring type strains (Moore et al. 1984).

**Taxonomic conclusions**

The phylogenetic analysis from 16S rRNA gene sequence and bac120 gene set suggested that strain WL0036T should be a member of the genus *Hyphomonas* (Figs. 1, 2). Characterization by physiological and biochemical experiments showed that strain WL0036T shared many common traits with the two neighboring type strains. Meanwhile, there are some variations between them, for example: in chemical composition, the reference strain *Hyphomonas polymorpha* DSM 2665\textsuperscript{T} has two more major fatty acids than the strain WL0036\textsuperscript{T} (Suppl. Table S3); in terms of polar lipids, the reference strain *Hyphomonas polymorpha* DSM 2665\textsuperscript{T} has one less polar lipid than strain WL0036\textsuperscript{T}, and these chemical characteristics clearly distinguish strain WL0036\textsuperscript{T} from the reference strain *Hyphomonas polymorpha* DSM 2665\textsuperscript{T}. And strain WL0036\textsuperscript{T} was significantly distinguished from the two neighboring type strains in terms of its capability to utilize gelatin and L-arginine as carbon sources and its positive activity for α-chymotrypsin (Table 2). Beside of the evidence above, strain WL0036\textsuperscript{T} also can be distinguished from *H. neptunium* ATCC 15444\textsuperscript{T} and *H. polymorpha* PS728\textsuperscript{T} by other phenotypic differences (Suppl. Table S2). For example, strain WL0036\textsuperscript{T} is negative for utilization of N-acetyl-D-glucosamine, N-acetyl-β-D-mannosamine, D-cellbiose, gentiobiose, D-glucose-6-PO\textsubscript{4}, D-malic acid, L-malic acid, D-melibiose, β-methyl-D-glucoside and L-rhamnose as carbon sources, positive for utilization of acetate, acetoacetic acid and α-keto-glutaric acid as carbon sources, negative for resistance of aztreonam, α-glucosidase, lincomycin, β-rockulosidase, D-serine, tetrozolium blue, troleandomycin, trypsin, valine arammatase and vancomycin, which can clearly distinguish the strain WL0036\textsuperscript{T} from the strain *H. neptunium* ATCC 15444\textsuperscript{T}; strain WL0036\textsuperscript{T} is positive for utilization of L-arginine, L-aspartic acid, D-fucose, L-fucose, D-fructose-6-PO\textsubscript{4}, gelatin, glycol- L-histidine and L-prolin as carbon sources, negative for utilization of L-butryic acid, L-lactic acid, D-malic acid, L-malic acid and methyl Pyruvate, negative for resistance of fusidic acid, troleandomycin, tetrozolium blue, lincomycin and vancomycin, which can clearly distinguish the strain WL0036\textsuperscript{T} from the strain *H. polymorpha* PS728\textsuperscript{T}.

Based on the results of phenotypic, phylogenetic, the ANI values and the dDDH values, strain WL0036\textsuperscript{T} was suggested to be clearly distinguished from *H. polymorpha* PS728\textsuperscript{T} and *H. neptunium* ATCC 15444\textsuperscript{T}. Consequently, strain WL0036\textsuperscript{T} was proposed as a novel species in the genus *Hyphomonas*, for which the name *Hyphomonas sediminis* sp. Nov. is proposed.

**Description of *Hyphomonas sediminis* sp. Nov.**

*Hyphomonas sediminis* [se.di’mi.nis. L. gen. neut. n. sediminis, of sediment]  

Cells are Gram-staining-negative, aerobic, motile and pear-shaped. Cells grow well on TSA medium with 2.5% sea salt, marine agar medium 2216E. Growth occurs at 20–37 °C (optimum 28 °C), pH 6.0–10.0 (optimum 7.0–8.0) and with 0–9.0% NaCl (optimum 2.5–4.0%). Cells are positive for both oxidase and catalase. The strain showed negative reactions (API 20NE) in the assimilation of L-arabinose, N-acetylglucosamine, capric acid, D-glucose, malic acid, D-maltose, D-mannose, D-mannitol, potassium gluconate, phenylacetic acid and trisodium citrate, showed positive reactions (API 20NE) in the enzyme assays of hydrolysis of esculin and indole production, negative for arginine dihydrolase, D-glucose fermentation, hydrolysis of gelatin, hydrolysis of urea, nitrate reduction and 4-nitrophenyl β-D-galactopyranoside (PNPG). In the API ZYM tests, positive for chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, lipase (C14) and α-mannosidase, but negative for N-acetyl glucosaminidase, acid phosphatase,
alkaline phosphatase, cystine aramase, esterase (C4), esterase lipase (C8), α-glucosidase leucine arylamidase, β-rockulosisidase, naphthol-AS-BI-phosphohydrolase, trypsin, β-uronic acid glycase and valine aramase. In the BIOLOG GEN III tests, positive for utilization of L-arginine, L-aspartic acid, L-butyric acid D-fructose-6-PO₄, D-fucose, L-fucose, gelatin, L-glutamic acid, glycyl-L-proline, (> 10%) are C₁₆:₀, 11-methyl-C₁₈:₁ respiratory quinone. The major cellular fatty acids tests are all negative. The polar lipid profile consists lurite, rifamycin SV and sodium butyrate; the rest tests are all negative. The polar lipid profile consists of phosphatidylcholine, phosphatidylethanolamine, glycolipid and an unidentified lipid. Q-11 is the sole respiratory quinone. The major cellular fatty acids (> 10%) are C₁₆:₀, 11-methyl-C₁₈:₁ω₇c, and summed features 8 (C₁₈:₁ω₇c and/or C₁₈:₁ω₇c).

The type strain, WL0036T (= MCCC 1K05843T = JCM 34658T = GDGCC 1.2413T), the DNA G+C content of genomic DNA is 61.8%. The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequence and the draft genome sequence of strain WL0036T are OL605964 and JAIEZP0000000000, respectively.

**Author contributions** DFZ and WJL designed research and project outline. LW and DFZ performed isolation, deposition and polyphasic taxonomy. DFZ, LW and WH performed genome analysis. LW, WJL AHZ and DFZ drafted the manuscript. AHZ, WH, ZYG, JKH and CL revised the manuscript. All authors read and approved the final manuscript.

**Funding** This research was supported by the National Natural Science Foundation of China (No. 31900001), the China Postdoctoral Science Foundation (2020M671312) and the Fundamental Research Funds for the Central Universities (B210202140).

**Data availability** All of the data supporting the conclusions of this article are included within the article and its additional files. The genome datasets and the 16S rRNA gene sequence of *Hyphomonas sediminis* WL0036T generated during the current study are available in the GenBank/EMBL/DDBJ repository under accession number JAIEZP0000000000 and OL605964. Other datasets used and/or analyzed during the current study are available from the corresponding author upon reasonable request. Other genome sequence data detailed information was listed in Suppl. Table S1.

**Declarations**

**Competing interests** The authors declare no competing interests.

**Ethical approval** This article does not contain any studies with human participants or animals performed by any of the authors.

**References**

Alcock BP et al (2020) CARD 2020: antibiotic resistance surveillance with the comprehensive antibiotic resistance database. Nucleic Acids Res 48:517–525. https://doi.org/10.1093/nar/gkz935

Collins MD, Jones D (1980) Lipids in the classification and identification of coryneform bacteria containing peptidoglycans based on 2, 4-diaminobutyric acid. J Appl Bacteriol 48:459–470. https://doi.org/10.1111/j.1365-2672.1980.tb01036.x

Collins MD et al (1977) Distribution of menaquinones in actinomycetes and corynecbacteria. J Gen Appl Microbiol 100:221–230. https://doi.org/10.1099/0022287-100-2-221

Felsenstein J (1985) Confidence limits on phylogenies: an approach using the bootstrap. Evolution 39:783–791. https://doi.org/10.1111/j.1558-5646.1985.tb00420.x

Fitch WM (1971) Toward defining the course of evolution: minimum change for a specific tree topology. Syst Biol 20:406–416. https://doi.org/10.2307/2412116

Goris J, Konstantinidis KT, Klappenbach JAJM et al (2007) DNA-DNA hybridization values and their relationship to whole-genome sequence similarities. Int J Syst Evol Microbiol 57:81–91. https://doi.org/10.1099/ijs.0.64483-0

Huerta-Cepas J, Forlund K, Coelho LP et al (2017) Fast genome-wide functional annotation through orthology assignment by eggNOG-Mapper. Mol Biol Evol 34:2115–2122. https://doi.org/10.1093/molbev/msx148

Kanehisa M, Sato Y, Kawashima M et al (2016) KEGG as a reference resource for gene and protein annotation. Nucleic Acids Res 44:457–462. https://doi.org/10.1093/nar/gkv1070

Kimura M (1980). A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. J Mol Evol 16:111–120. https://doi.org/10.1007/BF01731581

Kumar S et al (2018) MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol 35:1547–1549. https://doi.org/10.1093/molbev/msy096

Lai Q et al (2015) 2000. request for an opinion. Int J Syst Evol Microbiol 65:321–321. https://doi.org/10.1099/0.066118-0

Li C, Lai Q, Li G et al (2014a) Hyphomonas beringensis sp. nov. and *Hyphomonas chukchiensis* sp. nov., isolated from surface seawater of the bering sea and chukchi sea. Antonie van Leeuwenhoek 106:657–665. https://doi.org/10.1007/10.1371/journal.pone.0101394

Li C, Lai Q, Li G et al (2014b) Multilocus sequence analysis for the assessment of phylogenetic diversity and biogeography in hyphomonas bacteria from diverse marine environments. PLoS ONE 9:101394–101394. https://doi.org/10.1371/journal.pone.0101394
Li C, Lai Q, Li G et al (2014c) *Hyphomonas atlantica* sp. nov., isolated from the Atlantic ocean and emended description of the genus *Hyphomonas*. Syst Appl Microbiol 37:423–428. https://doi.org/10.1007/s10482-016-0712-7

Li X, Li C, Lai Q et al (2016) *Hyphomonas pacifica* sp. nov., isolated from deep sea of the Pacific ocean. Antonie Van Leeuwenhoek 109:1111–1119. https://doi.org/10.1007/s10482-016-0712-7

Meier-Kolthoff JP, Auch AF, Klenk H-P et al (2013) Genome sequence-based species delimitation with confidence intervals and improved distance functions. BMC Bioinform 14:60. https://doi.org/10.1186/1471-2105-14-60

Minnin DE, O’Donnell AG, Goodfellow M et al (1984) An integrated procedure for the extraction of bacterial isoprenoid quinones and polar lipids. J Microbiol Methods 2:233–241. https://doi.org/10.1016/0167-7012(84)90018-6

Moore RL, Weiner RM, Gebers R (1984) Notes: Genus *Hyphomonas* Pongratz 1957 nom. rev. emend., *Hyphomonas polymorpha* Pongratz 1957 nom. rev. emend., and *Hyphomonas neptunium* (Leifson 1964) comb. nov. emend. (*Hyphomicrobium neptunium*). Int J Syst Bacteriol 34:71–73. https://doi.org/10.1099/00207713-34-1-71

Nurk S et al (2013) Assembling single-cell genomes and mini-metagenomes from chimeric MDA products. J Comput Biol 20:714–737. https://doi.org/10.1089/cmb.2013.0084

Okonechnikov K, Golosova O, Fursov M et al (2012) Unipro UGENE: a unified bioinformatics toolkit. Bioinformatics 28:1166–1167. https://doi.org/10.1093/bioinformatics/bts091

Pardi F, Guillemot S, Gascuel O (2010) Robustness of phylogenetic inference based on minimum evolution. Bull Math Biol 72:1820–1839. https://doi.org/10.1007/s11538-010-9510-y

Parte AC (2018) LPSN-list of prokaryotic names with standing in nomenclature (bacterio.net), 20 years on. Int J Syst Evol Microbiol 68:1825–1829. https://doi.org/10.1099/ijsem.0.002786

Pongratz E (1957) D’une bactérie pédiculée isolée d’un pus de sinus. Pathobiology 20:593–608. https://doi.org/10.1159/000160167

Richter M, Rosselló-Móra R (2009) Shifting the genomic gold standard for the prokaryotic species definition. Proc Natl Acad Sci USA 106:19126–19131. https://doi.org/10.1073/pnas.0906412010

Saitou N, Nei M (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol Biol Evol 4:406–425. https://doi.org/10.1093/oxfordjournals.molbev.A010454

Sasser M (1990) Identification of bacteria by gas chromatography of cellular fatty acids, MIDI technical note 101. Microbial ID Inc, Newark

Tamaoka J (1986) Analysis of bacterial menaquinone mixtures by reverse-phase high-performance liquid chromatography. Meth Enzymol 123:251–256. https://doi.org/10.1016/s0076-6879(86)23028-1

Tatusova T et al (2016) NCBI prokaryotic genome annotation pipeline. Nucleic Acids Res 44:6614–6624. https://doi.org/10.1093/nar/gkw569

Weiner RM, Devine RA, Powell DM et al (1985) *Hyphomonas oceanitis* sp. nov., *Hyphomonas hirschiana* sp. nov., and *Hyphomonas jannaschiana* sp. nov. Int J Syst Bacteriol 35:237–243. https://doi.org/10.1099/00207713-35-3-237

Weiner RM et al (2000) *Hyphomonas adhaerens* sp. nov., *Hyphomonas johnsonii* sp. nov. and *Hyphomonas rosenbergii* sp. nov., marine budding and prosthecate bacteria. Int J Syst Evol Microbiol 50:459–469. https://doi.org/10.1099/00207713-50-2-459

Weisburg WG, Barns SM, Pelletier DA et al (1991) 16S ribosomal DNA amplification for phylogenetic study. J Bacteriol 173:697–703. https://doi.org/10.1128/jb.173.2.697-703.1991

Yoon S-H, Ha S-M, Kwon S et al (2017) Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and whole-genome assemblies. Int J Syst Evol Microbiol 67:1613–1617. https://doi.org/10.1099/ijsem.0.001755

Zhang D-F, Cui X-W, Zhao Z et al (2020) *Sphingomonas hominis* sp. nov., isolated from hair of a 21-year-old girl. Antonie Van Leeuwenhoek 113:1523–1530. https://doi.org/10.1007/s10482-020-01460-z

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