Pseudonocardia abyssalis sp. nov. and Pseudonocardia oceani sp. nov., two novel actinomycetes isolated from the deep Southern Ocean

Jonathan Parra, Sylvia Soldatou†, Liam M. Rooney‡ and Katherine R. Duncan*
sediment cores were obtained by the PS **Polarstern** (2002) during the ANDEEP II expedition. KRD168T was isolated from dark greenish-grey silty clay collected in the North Weddell Kosminski Fracture Zone (62° 57.56′ S 27° 53.23′ W) at a depth of 4539 m, while KRD185T was isolated from greenish-grey silty clay collected in the Weddell Abyssal Plain (65° 19.88′ S 48° 5.58′ W) at a depth of 4060 m [18]. The strains were isolated on artificial seawater agar (SW; Instant Ocean sea salt 18 g l⁻¹, agar 14 g l⁻¹) using the stamping method [19]. The strains were routinely cultured on ISP2 agar [20] supplemented with artificial seawater (18 g l⁻¹) and stored at −80 °C as glycerol suspensions (20%).

### 16S rRNA GENE PHYLOGENY

The almost-complete 16S rRNA gene sequences of strains KRD168T and KRD185T were obtained by PCR amplification using the 3-IDT (Integrated DNA Technology) primers FC27 (5′-AGAGTTTGTATCCTGGCTCAG-3′) and RC1492 (5′-TACGGCTACCTTGTTACGACTT-3′) [21]. Sequences were compared to those within the National Center for Biotechnology Information (NCBI) database using the Basic Local Alignment Search Tool (BLAST) [22], and EzBioCloud [23]. A multiple alignment of all the sequences was achieved by using CLUSTAL X 2.1 [24], and their evolutionary relationships were assessed using neighbour-joining tree [25] reconstructions based on the Tamura–Nei model [26] using MEGA X [27] with 1000 bootstrap replications [28]. The nearly complete (93.1%) 16S rRNA gene sequence of strain KRD168T was found to be closely related to *Pseudonocardia carthageonis* ATCC 15777T (99.6%), *Pseudonocardia hydrocarbonoxydans* NRRL B-16171T (99.4%), and *Pseudonocardia seranimata* YIM 63233T (99.3%). Similarly, the nearly complete (95.0%) 16S rRNA gene sequence of strain KRD185T was closely related to *Pseudonocardia broussonetiae* Gen01T (99.6%), *P. petroleophila* ATCC 15777T (98.9%), *P. hydrocarbonoxydans* NRRL B-16171T (98.4%) and *P. seranimata* YIM 63233T (98.4%).

The neighbour-joining phylogenetic tree (Fig. 1) showed that both isolates formed a monophyletic group with *P. petroleophila* ATCC 15777T, *P. seranimata* YIM 63233T and *P. broussonetiae* Gen01T. In particular, strain KRD168T, *P. seranimata* YIM 63233T and *P. petroleophila* ATCC 15777T were part of the same branch, while strain KRD185T and *P. broussonetiae* Gen01T formed a second branch. This topology was also supported by the maximum-likelihood and maximum-parsimony trees (Fig. S1, available in the online version of this article).

### GENOME FEATURES

A modified organic DNA extraction protocol [29] was performed for DNA isolation from strains KRD168T and KRD185T. Genomic DNA was sequenced at MicrobesNG for short-read sequencing. Genomic DNA libraries were prepared using a Nextera XT Library Prep Kit and sequenced on the Illumina HiSeq platform. Genomic DNA was also sequenced at NU-OMICS using PacBio technology for long-read sequencing. The polymerase binding reaction to SMRTBell template was performed using the Sequel Binding kit 2.1 and sequenced using a PacBio Sequel instrument with a 10 h movie capture time. Next, the BAM files of circular consensus sequencing reads were used for assembly in HGAP (v.4).

For strain KRD168T, long reads were assembled using Flye [30] (v.2.8.1). Then, the short reads were mapped over the assembly using Bowtie2 [31] (v.2.4.2), and the produced BAM files were used for improving the genome using Pilon [32] (v.1.23) by correcting bases, fixing misassemblies and filling gaps. As a result, a complete genome sequence was obtained with 1150.6× genome coverage, comprising a chromosome sequence of 6273229 bp and a plasmid of 32760 bp, and with a G+C content of 73.44 mol%. For strain KRD185T, a consensus assembly was created to reduce the number of contigs. To this end, long reads were first assembled using HGAP [33] (v.4), Flye (v.2.8.1), Canu [34] (v.2.1.1) and Raven [35] (v.1.2.2). Then, a consensus assembly was obtained with Flye using the ‘subassemblies’ mode. Finally, the consensus long-read assembly was integrated within Unicycler [36] (v.0.4.8), with SPAdes [37] (v.3.14.1) and Pilon (v.1.23) as dependencies, to create a hybrid assembly including short-read data. As a result of this strategy, an assembly made up of a chromosome of 6661555 bp, and presumably two plasmids of 99100 and 61150 bp, was obtained. The genome coverage for strain KRD185T was 217.1×, and the G+C content was 73.98 mol%.

Finally, the quality of both assemblies was evaluated using QUAST [38] (v.5.0.2), while their completeness was evaluated using BUSCO [39] (v.3.0.2) (Table S1).

To assess the genomic distance between strains KRD168T and KRD185T and other publicly available *Pseudonocardia* genomes (Table S2), digital DNA–DNA hybridization (dDDH) values were calculated with the Genome-to-Genome Distance Calculator (GGDC) [40] (v.2.1) using formula 2, while pairwise whole-genome average nucleotide identity (ANI) values were calculated using FastANI [41] (v.1.3). The calculated values (Fig. 2) showed that strain KRD168T and *P. petroleophila* CGMCC 4.1532T had a dDDH of 43.5% and an ANI of 91.8%, whilst strain KRD185T and *P. broussonetiae* Gen01T showed dDDH and ANI values of 51.7% and 93.7%, respectively. In both cases, the ANI values were below the recommended inter-species boundary value of 95% [41, 42]. Furthermore, the dDDH values also support the inter-species delimitation as they were below the threshold value of 70% [43]. Hence, despite the high sequence similarity (>99.5%) observed in the 16S rRNA gene between strain KRD168T and *P. petroleophila* ATCC 15777T, and between strain KRD185T and *P. broussonetiae* Gen01T, the whole-genome sequence relatedness indicated that strains KRD168T and KRD185T represent two novel species.

A genome-scale phylogenetic tree (Fig. 2) based on multilocus sequence analysis was reconstructed using autoMLST [44]. The list of used protein-coding genes can be found in Table S3. This analysis confirmed the evolutionary relationship between strains KRD168T and KRD185T, *P. petroleophila* CGMCC 4.1532T and *P. broussonetiae* Gen01T. Moreover, it
suggested a recent common ancestor between this monophyletic group and *Pseudonocardia thermophila* DMS 43832\(^T\) [1]. Interestingly, although the 16S rRNA gene phylogeny suggested a more distant relationship, the whole-genome analysis showed that *P. hydrocarbonoxydans* NBRC 14498\(^T\) [45] is closely related to strains KRD168\(^T\) and KRD185\(^T\).

**PHYSIOLOGY AND CHEMOTAXONOMY**

The colony morphology of strains KRD168\(^T\) and KRD185\(^T\), as well as *P. petroleophila* DSM 43193\(^T\) and *P. hydrocarbonoxydans* DSM 43281\(^T\), was examined when cultured on ISP2, ISP3, ISP4 and ISP5 media [20] (Fig. S2). Salinity and pH tolerance analysis of the strains was carried out on modified ISP2 and ISP5 at pH 4–10 (Table S4) and with 0–20% (w/v) NaCl. The strains were able to grow on all tested media with no diffusible pigments produced. Despite their marine origin, strains KRD168\(^T\) and KRD185\(^T\) did not display a particularly high halotolerance in comparison with their closest relatives as they both grew well at an NaCl concentration of 3%, which was 1% less than *P. petroleophila* DSM 43193\(^T\) and 1% more than *P. hydrocarbonoxydans* DSM 43281\(^T\) (Table 1). Moreover, salt was not a requirement for growth.

Analyses of fatty acids, metabolic activity, respiratory quinones, polar lipids and whole-cell sugars were carried out by the Identification Service of the Leibniz Institute DSMZ – German Collection of Microorganisms and Cell Cultures. For these analyses, strains were cultivated in GYM medium (28°C for 8–14 days). Fatty acid analysis was performed using the Sherlock MIS (MIDI) system after conversion into fatty acid methyl esters [46, 47]. The fatty acids of the genus *Pseudonocardia* suggested a recent common ancestor between this monophyletic group and *Pseudonocardia thermophila* DMS 43832\(^T\) [1]. Interestingly, although the 16S rRNA gene phylogeny suggested a more distant relationship, the whole-genome analysis showed that *P. hydrocarbonoxydans* NBRC 14498\(^T\) [45] is closely related to strains KRD168\(^T\) and KRD185\(^T\).
acid annotations and quantification were made by the MIS Standard Software (Microbial ID) using the Aerobic Bacteria Library (TSBA v6.10). Metabolic activity was determined using the API 20E and API ZYM systems (bioMérieux). Polar lipids and respiratory quinones were extracted from freeze-dried cells cultured in YEME broth and analysed by chromatography [48]. Analysis of whole-cell sugars and detection of isomers of 2,6-diaminopimelic acid (Dpm) and 2,6-diamino-3-hydroxypimelic acid (OH-Dpm) were performed by TLC [49, 50].

The observed morphology of strains KRD168T and KRD185T, as well as the presence of *meso*-diaminopimelic acid in the cell-wall, MK-8(H2) as the major menaquinone and *iso*-branched hexadecanoic acid as a predominant fatty acid, confirmed the typical physiology of a *Pseudonocardia* species for both strains. The polar lipid profile (Fig. S3) of both strains was characterized by the presence of phosphatidylethanolamine and diphasphatidylglycerol. In addition, two unidentified phospholipids and four unidentified glycolipids were detected in strain KRD168T, whilst strain KRD185T also contained four unidentified phospholipids, two unidentified glycolipids and an unidentified glycoprophospholipid. Moreover, some chemotaxonomic characteristics, such as the metabolic profile and the cellular fatty acid composition, differentiated strains KRD168T and KRD185T from *P. petroleophila* DSM 43193T and *P. broussonetiae* Gen 01T, respectively. In particular, strain KRD168T was negative for α-galactosidase and α-glucosidase activity, while *P. petroleophila* DSM 43193T was positive. Similarly, strain KRD185T was positive for α-glucosidase activity, while *P. broussonetiae* Gen 01T reported no activity. Furthermore, the relatively low proportion of *iso*-branched pentadecanoic acid (11.0% vs 25.2%) and the relatively high proportion of *iso*-branched tetradecanoic acid (7.6% vs 2.0%) distinguished strain KRD168T from *P. petroleophila* DSM 43193T. Likewise, the relatively low proportion of *iso*-branched tetradecanoic acid (1.9% vs 5.6%) and hexadecanoic acid (3.6% vs 9.8%), as well as the relatively high proportion of *iso*-branched pentadecanoic acid (7.7% vs 2.1%) differentiated strain KRD185T from *P. broussonetiae* Gen 01T.

Strains KRD168T, KRD185T and *P. petroleophila* DSM 43193T were cultured on ISP2 agar for 28 days using an inclined coverslip, and their morphology was observed using a Nikon Eclipse TE2000-S Inverted microscope fitted with a 100×/1.3 numerical aperture objective lens (Nikon). Illumination was sourced from a mercury arc lamp with appropriate emission filters for FITC/PI imaging. Fluorescence microscopy was carried out using fluorescein-conjugated wheat germ agglutinin (FITC-WGA) and propidium iodide (PI) to describe structures in the aerial hyphae and apical tip growth [51]. Phase-contrast and fluorescence images were acquired sequentially using an ORCA-100 CCD camera (Hamamatsu).
Table 1. Differential phenotypic characteristics of the analysed strains

Strains: 1, *Pseudonocardia abyssalis* sp. nov. KRD168T; 2, *Pseudonocardia oceani* sp. nov. KRD185T; 3, *Pseudonocardia petroleophila* DSM 43193T (from Zhao *et al.* [53]); 4, *Pseudonocardia hydrocarbonoxydans* DSM 43281T (from Zhang *et al.* [15]); 5, *Pseudonocardia broussonetiae* Gen 01T (from Mo *et al.* [54]).

| Strains                              | 1          | 2          | 3          | 4          | 5          |
|--------------------------------------|------------|------------|------------|------------|------------|
| Morphology on:                       |            |            |            |            |            |
| ISP2                                 | Yellow     | Orange     | Yellow     | Yellow     | Yellow     |
| ISP5                                 | White      | Yellow     | White      | White      | Yellow     |
| Growth at:                           |            |            |            |            |            |
| NaCl (%)                             | 0–3        | 0–3        | 0–4        | 0–2        | 0–8        |
| pH                                   | 6–10       | 6–10       | 6–10       | 6–9        | 5–8        |
| API ZYM                              |            |            |            |            |            |
| Alkaline phosphatase                 | +          | +          | +          | +          | −          |
| Esterase (C4)                        | +          | +          | +          | −          | +          |
| Cystine arylamidase                  | −          | +          | +          | +          | −          |
| Trypsin                              | −          | −          | +          | +          | −          |
| α-Chymotrypsin                       | −          | −          | +          | +          | −          |
| Naphthol-AS-BI-phosphohydrolase      | +          | +          | −          | +          | +          |
| α-Galactosidase                      | −          | −          | +          | +          | −          |
| β-Galactosidase                      | +          | −          | +          | +          | −          |
| α-Glucosidase                        | −          | +          | +          | +          | −          |
| Fatty acids (>1%)                    |            |            |            |            |            |
| C12:0                                | ND         | ND         | ND         | ND         | 1.2        |
| C14:0                                | ND         | ND         | ND         | ND         | 2.9        |
| iso-C14:0                            | 7.6        | 1.9        | 2.0        | 1.5        | 5.6        |
| C15:0ω6c                             | ND         | ND         | ND         | 1.9        | 2.6        |
| iso-C15:0                            | 11.0       | 7.7        | 25.2       | 17.9       | 2.1        |
| iso-C15:1 H                         | 3.2        | 8.9        | 2.6        | 5.8        | 10.7       |
| iso-C16:0                            | 36.3       | 38.5       | 43.2       | 31.7       | 36.1       |
| C16:1 2-OH                          | ND         | ND         | 2.4        | ND         | ND         |
| C16:0                                | 4.7        | 3.6        | 2.0        | 3.6        | 9.8        |
| iso-C17:0                            | 4.2        | 2.0        | 10.2       | 3.2        | ND         |
| anteiso-C17:8                        | 1.1        | 2.4        | ND         | 1.4        | ND         |
| C17:1ω8c                             | 8.0        | 5.1        | ND         | 8.3        | 4.0        |
| C17:0                                | 3.4        | 1.6        | ND         | 1.7        | 1.4        |
| C17:0 10 methyl                      | 2.4        | 2.7        | 1.5        | 1.9        | ND         |
| C18:1ω9c                             | 1.2        | ND         | ND         | ND         | ND         |

*ND,* Not detected.
Image processing and analysis was performed using FIJI [52]. Budding substrate and aerial hyphae with swelling and side branches were observed (Fig. 3). A more filamentous structure was observed for strain KRD185^T than for strain KRD168^T. Spores were rod-like, mostly 0.6–1.4 µm wide and 1.2–1.9 µm long for strain KRD168^T, and 0.7–1.6 µm wide and 1.4–3.9 µm long for strain KRD185^T. Active growth and sporulation were still observed after 28 days.

Based on the phenotypic and chemotaxonomic analysis, strains KRD168^T and KRD185^T exhibit characteristic markers for the genus Pseudonocardia. Furthermore, the phenotypic characterization and genomic relatedness of strains KRD168^T and KRD185^T differentiate them from their closest phylogenetic neighbours. In conclusion, we suggest that the two strains represent two novel species, for which the names Pseudonocardia abyssalis sp. nov. and Pseudonocardia oceani sp. nov. are proposed.

**DESCRIPTION OF PSEUDONOCARDIA ABYSSALIS SP. NOV.**

_Pseudonocardia abyssalis_ (a.bys.sa’lis. L. fem. n. abyssus an abyss, deep sea; L. fem. suff. -alis suffix denoting pertaining to; N.L. fem. adj. abyssalis pertaining to the abyssal depths of the ocean).

Aerobic, Gram-positive, non-motile actinomycetes. Forms yellow aerial and substrate mycelia on ISP2, while white substrate and aerial mycelia are produced on ISP3, ISP4 and ISP5. Growth occurs at 20–30 °C, at pH 6–10 and in the presence of 0–3% (w/v) NaCl. Substrate mycelium is fragmented and rod-shaped spore chains are formed on aerial hyphae and substrate mycelium. The following enzymatic reactions are positive: urease, acetoin production, gelatine hydrolysis, alkaline phosphatase, esterase, esterase lipase, leucine arylamidase and valine arylamidase. The major menaquinone is MK-8(H_4) (91.5%), while MK-8(H_6) (8.5%) is also present. The cell wall contains _meso_-diaminopimelic acid as the diagnostic amino acid, and the major whole-cell sugar is glucose with minor amounts of arabinose and xylose. The polar lipid profile includes phosphatidylethanolamine and diphosphatidylglycerol. The predominant fatty acid is iso-C_{16:0} while iso-C_{15:0} C_{17:1}ω8c and iso-C_{14:0} are also major components.

The type strain, KRD168^T (=DSM 111918^T =NCIMB 15270^T), was isolated from sediments collected from the Southern Ocean at a depth of 4539 m. The genome of the type strain is characterized by a size of 6.31 Mbp and a G+C content of 73.44 mol%.

**DESCRIPTION OF PSEUDONOCARDIA OCEANI SP. NOV.**

_Pseudonocardia oceani_ (o.ce.a’ni. L. gen. n. oceani of the ocean).

Aerobic, Gram-positive, non-motile actinomycetes. Forms yellow substrate mycelium and orange aerial mycelium with white spores formed from the aerial hyphae on ISP2. On ISP3, ISP4 and ISP5 white substrate and aerial mycelia are produced. Growth occurs at 20–30 °C, at pH 6–10 and in the presence of 0–3% (w/v) NaCl. Substrate mycelium is fragmented and rod-shaped spore chains are formed on aerial hyphae and substrate mycelium. The following enzymatic reactions are positive: alkaline phosphatase, esterase,
esterase lipase, leucine arylamidase, valine arylamidase, cystine arylamidase, acid phosphatase, naphthol-AS-BI-phenolphthalein, α-glucosidase and β-glucosidase. The major menaquinone is MK-8(H4) (96.2%), while MK-8(H8) (2.9%) and MK-8(H10) (1.5%) are also present. The cell wall contains meso-diaminopimelic acid as the diagnostic amino acid, and the major whole-cell sugar is glucose with minor amounts of arabinose and xylose. The polar lipid profile includes phosphatidylethanolamine and diphosphatidylglycerol. The predominant fatty acid is iso-C16:0, while iso-C16:1ω7c and C17:0ω6c are also major components.

The type strain, KRD1855 (=DSM 111919t =NCIMB 15269t), was isolated from sediments collected from the Southern Ocean at a depth of 4060 m. The genome of the type strain is characterized by a size of 6.82 Mbp and a G+C content of 73.98 mol%.

Funding information
J.P. is supported by Programa de Innovación y Capital Humano para la Competitividad (PINN) of The Ministry of Science, Technology and Telecommunications of Costa Rica (MICITT) grant 2-1-4-17-037.

Conflicts of interest
The authors declare that there are no conflicts of interest.

References
1. Henssen A. Beiträge zur Morphologie und Systematik der thermophilen Actinomyzeten [Contributions to the morphology and systematics of the thermophilic actinomycetes]. Archiv Mikrobiol 1957;26:373-414.
2. Reichert K, Lipski A, Pradella S, Stackebrandt E, Altwendorf K. Pseudonocardia asaccharolytica sp. nov. and Pseudonocardia sulfatolytica sp. nov., two new dimethyl disulfide-degrading actinomycetes and emended description of the genus Pseudonocardia. Int J Syst Bacteriol 1998;48 Pt 2:441-449.
3. Warwick S, Bowen T, McVeigh H, Embley TM. A phylogenetic analysis of the family Pseudonocardiacae and the genera Actinokineospora and Saccharothrix with 16S rRNA sequences and a proposal to combine the genera Amycolata and Pseudonocardia in an emended genus Pseudonocardia. Int J Syst Bacteriol 1994;44:293-299.
4. Huang Y, Wang L, Lu Z, Hong L, Liu Z, et al. Proposal to combine the genera Actinobispora and Pseudonocardia in an emended genus Pseudonocardia, and description of Pseudonocardia zijinensis sp. nov. Int J Syst Evol Microbiol 2002;52:977-982.
5. Park SW, Park ST, Lee JE, Kim YM. Pseudonocardia carboxydivorsa sp. nov., a carbon monoxide-oxidizing actinomycete, and an emended description of the genus Pseudonocardia. Int J Syst Evol Microbiol 2008;58:2475-2476.
6. Huang Y, Goodfellow M. Pseudonocardia. Trujillo ME, Dedshy S, DeVos P, Hedlund B and Kämpfer P (eds). In: Bergey’s Manual of Systematics of archaea and bacteria. Wiley, 2015. pp. 1–32.
7. Parte AC, Sardà Carbasse J, Meier-Kolthoff JP, Reimer LC, Göker M. List of prokaryotic names with standing in nomenclature (LPSN) moves to the DSMZ. Int J Syst Evol Microbiol 2020;70:5607–5612.
8. LPSN—List of Prokaryotic names with Standing in Nomenclature. Genus Pseudonocardia. https://lpsn.dsmz.de/genus/pseudonocardia
9. Gontang EA, Fenical W, Jensen PR. Phylogenetic diversity of gram-positive bacteria cultured from marine sediments. Appl Environ Microbiol 2007;73:3272-3282.
10. Maldonado LA, Stach JEM, Pathom-aruee W, Ward AC, Bull AT, et al. Diversity of cultivable actinobacteria in geographically widespread marine sediments. Antonie van Leeuwenhoek 2005;87:11–18.
11. Chanama S, Janphen S, Suriyachadkun C, Chanama M. Pseudonocardia mangrovi sp. nov., isolated from soil. Int J Syst Evol Microbiol 2018;68:2949–2955.
12. Liu Z-P, Wu J-F, Liu Z-H, Liu S-J. Pseudonocardia ammoniaoxydans sp. nov., isolated from coastal sediment. Int J Syst Evol Microbiol 2006;56:555–558.
13. Zhang D-F, Jiang Z, Li L, Liu B-B, Zhang X-M, et al. Pseudonocardia sediminis sp. nov., isolated from marine sediment. Int J Syst Evol Microbiol 2014;64:745–750.
14. Tian X-P, Long L-J, Li S-M, Zhang J, Xu Y, et al. Pseudonocardia antitumoralis sp. nov., a deoxyxyboquinone-producing actinomycete isolated from a deep-sea sediment. Int J Syst Evol Microbiol 2013;63:893–899.
15. Zhang G, Wang L, Li J, Zhou Y. Pseudonocardia profundimaris sp. nov., isolated from marine sediment. Int J Syst Evol Microbiol 2017;67:1693–1697.
16. Millán-Aguíñaga N, Soldatou S, Brzosi S, Munnioch JT, Howe J, et al. Awakening ancient polar Actinobacteria: diversity, evolution and specialized metabolite potential. Microbiol 2019;165:1169–1180.
17. Soldatou S, Eldjárn GH, Ramsay A, van der Hooff JJJ, Hughes AH, et al. Comparative metabologenomics analysis of polar actinomycetes. Mar Drugs 2021;19:103.
18. Howe JA, Shimmeld TM, Diaz R. Deep-water sedimentary environments of the Northwestern Weddell Sea and South Sandwich Islands, Antarctica. Deep Res Part II Top Stud Oceanogr 2004;51:1489–1514.
19. Mincer TJ, Jensen PR, Kauffmann CA, Fenical W. Widespread and persistent populations of a major new marine actinomycete taxon in ocean sediments. Appl Environ Microbiol 2002;68:5005–5011.
20. Shirling ET, Gottlieb D. Methods for characterization of Streptomyces species. Int J Syst Bacteriol 1966;16:313–340.
21. Weisburg WG, Barns SM, Pelletier DA, Lane DJ. 16S ribosomal RNA amplification for phylogenetic study. J Bacteriol 1991;173:697–703.
22. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment search tool. J Mol Biol 1990;215:403–410.
23. Yoon S-H, Ha S-M, Kwon S, Lim J, Kim Y, et al. Introducing Ezbiocloud: A taxonomically unified database of 16S rRNA gene sequences and whole-genome assemblies. Int J Syst Evol Microbiol 2017;67:1613–1617.
24. Larkin MA, Blackshields G, Brown NP, Chenna R, McGettigan PA, et al. ClustalW and clustal x version 2.0. Bioinformatics 2007;23:2947–2948.
25. Saitou N, Nei M. The neighbor-joining method: a new method for reconstructing phylogenetic trees. J Mol Biol 1987;165:1060–1085.
26. Tamura K, Nei M. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. Mol Biol Evol 1993;10:512–526.
27. Kumar S, Stecher G, Li M, Knyaz C, Tamura K. MEGA X: Molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol 2018;35:1547–1549.
28. Felsenstein J. Confidence limits on phylogenies: an approach using the bootstrap. Evolution 1985;39:783–791.
29. Marmur J. A procedure for the isolation of deoxyribonucleic acid from micro-organisms. J Mol Biol 1961;3:208–218.
30. Kolmogorov M, Yuan J, Lin Y, Pevzner PA. Assembly of long, error-prone reads using repeat graphs. Nat Biotechnol 2019;37:540–546.
31. Langmead B, Salzberg SL. Fast gapped-read alignment with Bowtie 2. Nat Methods 2012;9:357–359.
32. Walker BJ, Abouelliel A, Soldatou S, Anderson MA, et al. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. PLoS One 2014;9:e112963.
33. Chin C-S, Alexander DH, Marks P, Klammer AA, Drake J, et al. Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. Nat Methods 2013;10:563–569.
34. Koren S, Walenz BP, Berlin K, Miller JR, Bergman NH, et al. Canu: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation. Genome Res 2017;27:722–736.
35. Vaser R, Šikić M. Raven: A de novo genome assembler for long reads. bioRxiv 2020:08.07.242461.
36. Wick RR, Judd LM, Gorrie CL, Holt KE. Unicycler: Resolving bacterial genome assemblies from short and long sequencing reads. *PloS Comput Biol* 2017;13:1–22.
37. Bankievich A, Nurl S, Antipov D, Gurevich AA, Dvorkin M, et al. SPAdes: A new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 2012;19:455–477.
38. Gurevich A, Saveliev V, Vyahhi N, Tesler G. QUAST: Quality assessment tool for genome assemblies. *Bioinformatics* 2013;29:1072–1075.
39. Simão FA, Waterhouse RM, Ioannidis P, Kriventseva EV, Zdobnov EM. BUSCO: Assessing genome assembly and annotation completeness with single-copy orthologs. *Bioinformatics* 2015;31:3210–3212.
40. Meier-Kolthoff JP, Auch AF, Klenk H-P, Göker M. Genome sequence-based species delimitation with confidence intervals and improved distance functions. *BMC Bioinformatics* 2013;14:60.
41. Jain C, Rodriguez-R LM, Phillippy AM, Konstantinidis KT, Aluru S. High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. *Nat Commun* 2018;9:1–8.
42. Richter M, Rosselló-Móra R. Shifting the genomic gold standard for the prokaryotic species definition. *Proc Natl Acad Sci U S A* 2009;106:19126–19131.
43. Meier-Kolthoff JP, Klenk H-P, Göker M. Taxonomic use of DNA G+C content and DNA-DNA hybridization in the genomic age. *Int J Syst Evol Microbiol* 2014;64:352–356.
44. Alanjary M, Steinke K, Ziemert N. AutoMLST: an automated web server for generating multi-locus species trees highlighting natural product potential. *Nucleic Acids Res* 2019;47:276–282.
45. Nolof G, Hirsch P. *Nocardia hydrocarbonoxydans* n. spec., ein oligocarphiler Actinomyctet. *Arch Mikrobiol* 1962;44:266–277.
46. Kuykendall LD, Roy MA, O’Neill JJ, Devine TE. Fatty acids, antibiotic resistance, and deoxyribonucleic acid homology groups of *Bradyrhizobium japonicum*. *Int J Syst Bacteriol* 1988;38:358–361.
47. Miller LT. Single derivatization method for routine analysis of bacterial whole-cell fatty acid methyl esters, including hydroxy acids. *J Clin Microbiol* 1982;16:584–586.
48. Tindall BJ, Sikorski J, Smibert RA, Krieg NR. Phenotypic characterization and the principles of comparative systematics. In: *Methods for General and Molecular Microbiology*. Washington, DC, USA: ASM Press, 2014. pp. 330–393.
49. Rhuland LE, Work E, Denman RF, Hoare DS. The behavior of the isomers of α,γ-diaminopimelic acid on paper chromatograms. *J Am Chem Soc* 1955;77:4844–4846.
50. Stanek JL, Roberts GD. Simplified approach to identification of aerobic actinomycetes by thin-layer chromatography. *Appl Microbiol* 1974;28:226–231.
51. Schwedock J, McCormick JR, Angert ER, Nordwell JR, Losick R. Assembly of the cell division protein FtsZ into ladder-like structures in the aerial hyphae of *Streptomyces coelicolor*. *Mol Microbiol* 1997;25:847–858.
52. Schindelin J, Arganda-Carreras I, Frise E, Kaynig V, Longair M, et al. Fiji: An open-source platform for biological-image analysis. *Nat Methods* 2012;9:676–682.
53. Zhao GZ, Zhu WY, Li J, Xie Q, Xu LH, et al. *Pseudonocardia seriarmatus* sp. nov., a novel actinomycete isolated from the surface-sterilized leaves of *Artemisia annua* L. *Antonie van Leeuwenhoek* 2011;100:521–528.
54. Mo P, Zhao Y, Liu J, Xu Z, Gao J. *Pseudonocardia broussonetiae* sp. nov., an endophytic actinomycete isolated from the roots of *Broussonetia papyrifera*. *Int J Syst Evol Microbiol* 2021;71:004680.