Halomonas jincaotanensis sp. nov., isolated from the Pamir Plateau degrading polycyclic aromatic hydrocarbon

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Abstract
A Gram-strain-negative, rod-shaped, aerobic bacterium, designated strain TRM 85114T, was isolated from the Jincaotan wetland in the Pamir Plateau of China. This strain grew optimally at 30 °C and pH 6.0 in the presence of 3% (w/v) NaCl. Phylogenetic analysis of 16S rRNA gene sequences revealed that strain TRM 85114T was affiliated with the genus Halomonas, and shared high sequence similarity with Halomonas korlensis XK1T (97.3%) and Halomonas tibetensis pyc13T (96.4%). Strain TRM 85114T contained C16:0 and C19:0 cyclo ω8c as primary cellular fatty acids, Q-9 as predominate respiratory quinone, diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine, phospholipids of unknown structure containing glucosamine, unidentified aminophospholipids, unidentified lipids and three unidentified phospholipids as the major polar lipids. The complete genome of TRM 85114T comprised 3,902 putative genes with a total of 4,126,476 bp and a G+C content of 61.6%. The average nucleotide identity and digital DNA–DNA hybridization values between strain TRM 85114T and related type Halomonas strains of H. korlensis XK1T, H. tibetensis pyc13T, Chromohalobacter salexigens DSM 6768T, and Halomonas urumqiensis BZ-SX-JJ27T were 75.4–88.9% and 22.9–39.2%, respectively. Based on phenotypic, chemotaxonomic, and molecular features, strain TRM 85114T represents a novel species of the genus Halomonas, for which the name is proposed as Halomonas jincaotanensis sp. nov.. The type strain is TRM 85114T (CCTCC AB 2021006T = LMG 32311T). The amount of 1-naphthylamine degradation by strain TRM 85114T reached up to 32.0 mg/L in 14 days.

Keywords Halomonas jincaotanensis · Polyphasic taxonomy · Pamir Plateau · Halophilic · 1-Naphthylamine · Degradation

Introduction
Halophilic microorganisms, particularly Halomonas spp., usually accumulate polyphosphate (Nguyen et al. 2012), produce biodegradable polyhydroxyalkanoates (Jiang et al. 2018; Tuma et al. 2020) and various metabolic chemicals (Du et al. 2020; Jiang et al. 2021). Based on the advantages of energy-saving, water-saving, time-saving, less investment in equipment, high concentration of final product, and simplification of separation process, Halomonas spp. have been used as platform strains in the field of synthetic biology to produce multiple products in Next Generation Industrial Biotechnology (NGIB) (Yu et al. 2019). The genus Halomonas initially proposed by Vreeland et al. (1980) belongs to the family Halomonadaceae of the phylum Proteobacteria. At present, this genus contains more than 160 validly named species. Members of the genus Halomonas have been isolated from diverse terrestrial and aquatic habitats, such as lake water (Kazemi et al. 2021), saline-alkali land (Dou et al. 2015), tidal flat (Koh et al. 2017), Arctic marine (Williamson et al. 2016), deep-sea sediment (Xu et al. 2013), and hypersaline wetlands (Ramezani et al. 2020). The Jincaotan wetland in Pamir Plateau is an environment characterised with saline and high altitude, in which extremophiles could be abundant.

Polycyclic aromatic hydrocarbon (PAH) is one of the most common pollutants in the soil and/or water environment and have become a matter of urgency due to their negative impacts on human health (Premnath et al. 2021). 1-Naphthylamine is a derivative of PAHs, as one of the top...
priority contaminants and carcinogens (Hu et al. 2011), significant accumulation in the soil and subsequent migration into the aquatic system have led to chronic exposure, which is associated with cancerous diseases in humans and aquatic animals and enhanced mutagenicity of soil and/or sediments. The genus of Halomonas has shown an eminent capacity to degrade polycyclic aromatic hydrocarbons (Al Farraj et al. 2020; Govarthanan et al. 2020), such as anthracene, phenanthrene, pyrene, naphthalene, and benzo[a]pyrene, and therefore have tremendous potential for environmental remediation. In this study, we obtained a novel species of Halomonas from the Pamir Plateau, designated TRM 85114<sup>T</sup>, explored its taxonomic characterisation and ability to degrade 1-naphthylamine, which has yet to be reported.

**Materials and methods**

**Sample collection, isolation, and preservation**

A soil sample was collected from the Jincaotan wetland (37° 47′ N, 75° 16′ E) in the Pamir Plateau, 3100 m above sea level. During the isolation process, 100 μL of mixed water and soil sample was spread onto 12% modified growth medium (MGM) agar plates (Dyall-Smith 2015), and incubated at 15 °C for 2 weeks. Colonies showing different morphologies were picked and purified, among which strain TRM 85114<sup>T</sup> was routinely grown on 12% MGM plates with inoculated strain TRM 85114<sup>T</sup>, and motility was tested in triplicate and included only results of colonies showing O<sub>2</sub> on 12% MGM agar plates, and motility was tested by filter paper discs containing the following antimicrobial compounds (content per disc): ampicillin (10 μg), vancomycin (30 μg), carbenicillin (100 μg), penicillin (1 μg), oxacillin (1 μg), piperacillin (100 μg), cefalexin (30 μg), cefadroxil (30 μg), ceftriaxone (30 μg), minocycline (30 μg), erythromycin (15 μg), norfloxacin (10 μg), ofloxacin (5 μg), ciprofloxacin (5 μg), polymyxin B (300 μg), Bactrim (25 μg), or clindamycin (2 μg) on 12% MGM plates at 30 °C for 3 days. In addition, the temperature tolerance of 3, 2, and 1 °C, and NaCl tolerance of 11, 12, 13, and 14 w/v% for growth were tested of strain TRM 85114<sup>T</sup>. In particular, tolerance to different NaCl concentrations were tested in basic 12% MGM liquid medium without NaCl. Growth requirements of Mg<sup>2+</sup>, SO<sub>4</sub><sup>2-</sup>, K<sup>+</sup> as well as production of exopolysaccharide and polyhydroxyalkanoate (PHA) were determined as described previously (Poli et al. 2013). Physiological tests of oxidation/fermentation of D-glucose, respiration of nitrate and nitrite, production of H<sub>2</sub>S from L-cysteine, reduction of nitrate to nitrite, hydrolysis of gelatin, casein, starch, Tween (20, 40, 60, and 80), aesculin, and DNA, production of indole, test of methyl red and Voges-Proskauer, activity of catalase, oxidase, urease, phenylalanine deaminase, lysine and ornithine decarboxylases, and o-nitrophenyl-β-D-galactopyranosidase were performed according to the ways proposed previously (Mata et al. 2002; Arahal et al. 2007). Rapid identification systems, including API 20E, API 20NE, and API 50CH (bioMérieux), were applied to detect acid production and substrate utilization in three replicates at 30 °C for 72 h, in accordance with the manufacturer’s instructions. Antibiotic susceptibility was detected by filter paper discs containing the following antimiobial compounds (content per disc): ampicillin (10 μg), vancomycin (30 μg), carbenicillin (100 μg), penicillin (1 μg), oxacillin (1 μg), piperacillin (100 μg), cefalexin (30 μg), cefadroxil (30 μg), ceftriaxone (30 μg), minocycline (30 μg), erythromycin (15 μg), norfloxacin (10 μg), ofloxacin (5 μg), ciprofloxacin (5 μg), polymyxin B (300 μg), Bactrim (25 μg), or clindamycin (2 μg) on 12% MGM agar plates with inoculated strain TRM 85114<sup>T</sup>. The inhibition zones were measured as described previously by Zhong et al. (2016), after incubation at 30 °C for 2 days. The test was conducted in triplicate and included only results exhibiting the same resistant pattern in all the plates.

**Chemotaxonomic characterization**

The respiratory quinones of strain TRM 85114<sup>T</sup> was extracted from freeze-dried biomass (Collins et al. 1977), and subsequently confirmed using HPLC (Collins and Jones 1981). For the analysis of cellular fatty acids, strain TRM 85114<sup>T</sup> and four reference strains were cultured on 12% MGM plates at 30 °C and the microbial cells were harvested at the 4th day. The fatty acids were extracted from fresh cells (Athalye et al. 1985), and analyzed by gas chromatography referred to the Microbial Identification System (Sherlock version 6.1; MIDI database: RTSBA6). The compositions of polar lipids were extracted, separated using two-dimensional TLC (Parsons and Patton 1967) and determined by spraying with four dyes of 10% ethanolic molybdatophosphoric acid
(for total lipids), ninhydrin (for aminolipids), molybdenum blue (for phospholipids), and anisaldehyde (for glycolipids), respectively.

Sequence similarity and phylogenetic analysis

Genomic DNA of strain TRM 85114T was extracted by using a TIANGEN (Beijing, China) bacterial DNA extraction kit. The 16S rRNA gene of strain TRM 85114T was amplified and sequenced using primers 27F (5′-AGAGTT TGATCMTGGCTCAG-3′) and 1492R (5′-TACGGYTAC CTTGTTACGACTT-3′) (Ramezani et al. 2020). Primers gyrB119F (5′-GARGTBATCATGACSGTGCT-3′) and gyrB1419R (5′-GCRTCSGTC- ATGGATGATSAY-3′), rpoD88F (5′-ATGATYAACGACATGGGYAT-3′) and rpoD1321R (5′-TTSAKCTTR- TTGATGGTCTC-3′) (de la Haba et al. 2012) were applied to amplified and sequenced the housekeeping genes gyrB and rpoD, respectively. The 16S rRNA gene sequence was then compared with the available sequences using EzBioCloud database (https://www.ezbiocloud.net/identify) (Yoon et al. 2017) and the NCBI database (https://blast.ncbi.nlm.nih.gov) (Altschul et al. 1990). Phylogenetic trees based on neighbor-joining (NJ) (Saitou and Nei 1987), maximum-likelihood (ML) (Felsenstein 1981), and maximum-parsimony (MP) (Czelusniak et al. 1990) algorithms with bootstrap values (1,000 replications) (Felsenstein 1981), and based on Kimura two-parameter model (Kimura 1980) to calculate evolutionary distance, were constructed using MEGA version 7.0 software (Kumar et al. 2016). The 16S rRNA, gyrB, and rpoD gene sequences of strain TRM 85114T and the most closely species were constructed using MEGA version 7.0 software (Kumar et al. 2016). The resuspension was (1 mL) inoculated into 250-mL Erlenmeyer flasks containing 100 mL of 12% MGM medium. Fifty mg/L of 1-naphthylamine was added into the culture flasks and incubated in dark at 180 rpm for 14 days at 30 °C. Samples (1 mL) were withdrawn at days 0, 2, 4, 6, 8, 10, 12 and 14, and 1-naphthylamine was detected at 222 nm. Furthermore, the degradation content of 1-naphthylamine was calculated based on a standard curve, which was constructed according to different contents of 1-naphthylamine solutions (20, 40, 60, 80, 100, and 120 mg/L). The isolates were treated without 1-naphthylamine degradation efficiency of the culture was determined using HPLC. The methanol solution was used for gradient elution, the concentration lasted from 10 to 100% for 40 min, and the absorption peak of 1-naphthylamine was detected at 222 nm. Furthermore, the degradation content of 1-naphthylamine was calculated based on a standard curve, which was constructed according to different contents of 1-naphthylamine solutions (20, 40, 60, 80, 100, and 120 mg/L). The isolates were treated without 1-naphthylamine were used as control. All experiments were performed in triplicate, and mean values after subtracted blank controls (10.2 mg/L) were reported.

Detection of 1-naphthylamine degradation capacity

Batch experiments were performed to study the ability of TRM 85114T on 1-naphthylamine biodegradation (Govart-han et al. 2020). The isolate grown in 12% MGM medium for 4 days were harvested, washed, and resuspended in 12% MGM medium (A600, 0.6). The resuspension was (1 mL) inoculated into 250-mL Erlenmeyer flasks containing 100 mL of 12% MGM medium. Fifty mg/L of 1-naphthylamine was added into the culture flasks and incubated in dark at 180 rpm for 14 days at 30 °C. Samples (1 mL) were withdrawn at days 0, 2, 4, 6, 8, 10, 12 and 14, and 1-naphthylamine degradation efficiency of the culture was determined using HPLC. The methanol solution was used for gradient elution, the concentration lasted from 10 to 100% for 40 min, and the absorption peak of 1-naphthylamine was detected at 222 nm. Furthermore, the degradation content of 1-naphthylamine was calculated based on a standard curve, which was constructed according to different contents of 1-naphthylamine solutions (20, 40, 60, 80, 100, and 120 mg/L). The isolates were treated without 1-naphthylamine were used as control. All experiments were performed in triplicate, and mean values after subtracted blank controls (10.2 mg/L) were reported.

Results and discussion

Phenotypic and physiological characterization

The cells of strain TRM 85114T was Gram-stain-negative, short rod-shaped, aerobic, and non-motile bacteria
showed that strain TRM 85114T clustered tightly with C10:0 (0.8%), C11:0 3-OH (0.3%), and C20:2. Table 1, the primary cellular fatty acids in strain TRM were C16:0 (18.0%) and C19:0 cyclo.

Chemotaxonomic characteristics

The predominant respiratory quinone identified in strain TRM 85114T was Q-9 (34.8%), followed by Q-8 (15.2%), and Q-6 (4.7%), which were coincident to members detected in other strains of the genus Halomonas (Qu et al. 2011; Zhang et al. 2016; Lu et al. 2018). As shown in Supplementary Table 1, the primary cellular fatty acids in strain TRM 85114T were C16:0 (18.0%) and C19:0 cyclo (10.3%), in that C10:0 (0.8%), C11:0 3-OH (0.3%), and C20:2 6,9c (0.3%) were generally similar to those detected in other closely related strains. Moreover, strain TRM 85114T was different from the four reference strains in terms of the types of polar lipids present, including diphosphatidylglycerol (DPG), phosphatidylglycerol (PG), phosphatidylethanolamine (PE), phospholipids of unknown structure containing glucosamine (NPG), unidentified aminophospholipids, unidentified lipids, and three unidentified phospholipids (Supplementary Fig. S2). Two components of PG and PE were detected in most Halomonas spp., but NPG were evidently different from other strains of the genus Halomonas (Zhong et al. 2016; Lu et al. 2018; Ramezani et al. 2020). Based on the information of genome annotation, a process of UDP-N-acetylg glucosamine biosynthetic was searched, which suggests that the presence of NPG in strain TRM 85114T.

Phylogenetic and phylogenomic analyses

Based on EzBioCloud analysis, the 16S rRNA gene sequence of strain TRM 85114T (GenBank accession no. MWS84241) has highly similar with members of the genus Halomonas. The highest similarity was shown with the type strain of Halomonas XK1T (97.3%), followed by H. tibetensis pyc13T (96.4%), Chromohalobacter israelensis ATCC 43985T (96.2%), C. salexigens DSM 3043T (96.1%), H. urumqiensis BZ-SZ-XJ27T (96.1%), and H. daqiaonensis CGMCC 1.9150T (96.0%). However, the sequence similarity was less than 96.0% with other species of genera within the family Halomonadaceae. The results suggested that strain TRM 85114T constitutes a possible novel species in the genus Halomonas.

A NJ tree based on 16S rRNA gene (1504 bp) (Fig. 1) showed that strain TRM 85114T clustered tightly with H. korlensis XK1T with strong bootstrap support (> 99%) forming an independent sub-cluster with the members of the genus Halomonas, which was in good agreement with the results of the ML and MP trees (Supplementary Fig. S3 and S4). A NJ tree based on the concatenated gene sequences (16S rRNA; gyrB 472 bp; rpoD 1243 bp) phylogenetic tree (Supplementary Fig. S5) showed that strain TRM 85114T forming an independent cluster separating from other group members. To further elucidate the phylogenetic relationship of strain TRM 85114T, we compared its proteome with 19 related species to investigate evolutionary specialization. A total of 8,805 orthologous gene families consisting of 71,909 genes were identified across these species, including a core set of 1140 genes shared among them. The ML tree based on these core gene sequences revealed the position of strain TRM 85114T (Fig. 2), which was grouped into a new clade comprising H. korlensis XK1T, which was consistent with the MLSA phylogenetic trees, supporting the view that strain TRM 85114T represent a novel member of the genus Halomonas.

Genomic features and analysis

The obtained draft genome of TRM 85114T (accession no. JAHCLU000000000) was 4,126,476 bp in length with G+C content of 61.6%, comprising of 60 contigs (N50 = 190,960 bp) and 52 scaffolds (N50 = 208,915 bp). The annotated genome encodes 3,902 genes, including 1,666 CDSs, 57 tRNAs and 3 rRNAs (one copy of 5S, one copy of 16S, and one copy of 23S rRNA gene). The completeness and contamination of the genome were 99.9% and 0.01%, respectively. The general features of the genome for strain TRM 85114T was similar with its closely related reference strains (Table 2). The ANI and dDDH values between strain TRM 85114T and the type strains of H. korlensis XK1T (88.9%, 39.2%), C. salexigens DSM 6768T (75.4%, 22.9%), and H. urumqiensis BZ-SZ-XJ27T (78.6%, 25.7%) were significantly lower than the criteria for prokaryotic species delineation thresholds [ANI (95–96%) (Kim et al. 2014); dDDH (70%) (Wayne et al. 1987)] (Table 2), confirms that strain TRM 85114T represents a novel species of the genus Halomonas.

To survive and compete in diverse environmental habitats, Halomonas species evolved a variety of metabolic pathways. Based on the KEGG orthology-based annotation, 3544 genes (90.8%) were annotated and assigned to putative functions, of which 1389 genes were related to metabolism associated pathways, and 249 genes belonged to environmental information processing pathways. What’s more, 44 ORFs were detected for aromatic hydrocarbon degradation (Supplementary Table S2), in which contig15_2804 (frmA, ADH5, adhC) were comment as naphthalene degradation.
Table 1  Differential characteristics of strain TRM 85114\textsuperscript{T} and related species of the genus *Halomonas*

| Characteristic                  | 1          | 2          | 3          | 4          | 5          |
|--------------------------------|------------|------------|------------|------------|------------|
| Colony pigmentation            | Cream–white| Brown      | Brown      | Cream–yellow| Cream–yellow|
| Cell morphology                | Short rods | Rods or short rods\textsuperscript{a} | Rods\textsuperscript{b} | Short rod\textsuperscript{c} | Rods\textsuperscript{d} |
| Cell size (μm)                 | 0.4–0.5×0.9–1.0 | 0.8–1.0×1.3–1.7\textsuperscript{a} | 0.4×0.6–1.2\textsuperscript{b} | 1.0×1.5–2.0\textsuperscript{c} | 0.3–0.6×1.2–2.2\textsuperscript{d} |
| Mobility                       | –          | –          | –          | +          | +          |
| Temperature range (°C)          | 4–35 (30)  | 4–37 (30)  | 8–37 (30)  | 4–40 (37)  | 4–40 (37)  |
| Salinity range (% w/v)         | 1–13 (3)   | 1–20 (7)   | 1–15 (6)   | 1–25 (8)   | 1–15 (8)   |
| pH range                       | 6–9 (7)    | 6–9 (7)    | 6–10 (8)   | 6–9 (8)    | 6–9 (8)    |
| Hydrolysis of:                 |            |            |            |            |            |
| Starch                         | +          | +          | –          | –          | –          |
| Tween 40                       | +          | –          | –          | –          | –          |
| Tween 60                       | +          | –          | –          | –          | –          |
| H\textsubscript{2}S production | +          | +          | –          | –          | –          |
| Nitrate reduction              | –          | +          | –          | +          | +          |
| Voges-Proskauer test           | +          | +          | +          | +          | –          |
| Urease activity                | –          | +          | –          | –          | –          |
| Phenylalanine deaminase activity | +        | –          | –          | –          | +          |
| Exopolysaccharides             | –          | +          | +          | –          | –          |
| Acid from (API 20E)            |            |            |            |            |            |
| d-Glucose                      | +          | +          | –          | +          | –          |
| Sucrose                        | –          | +          | –          | +          | –          |
| Rhamnose                       | +          | –          | –          | +          | –          |
| Arabinose                      | +          | +          | –          | –          | –          |
| Melibiose                      | –          | +          | –          | –          | –          |
| Assimilation of (API 20NE)     |            |            |            |            |            |
| d-Glucose                      | –          | –          | –          | +          | –          |
| d-Mannose                      | +          | +          | –          | +          | –          |
| Mannitol                       | –          | –          | –          | +          | –          |
| Maltose                        | –          | –          | –          | +          | –          |
| Gluconate                      | –          | +          | –          | +          | –          |
| Citric acid                    | –          | +          | –          | +          | –          |
| Adipic acid                    | –          | +          | –          | –          | –          |
| Malic acid                     | +          | +          | –          | +          | –          |
| Utilization as sole carbon source (API 50CH) |            |            |            |            |            |
| d-Galactose                    | +          | +          | –          | –          | +          |
| d-Lactose                      | –          | +          | +          | +          | –          |
| d-Mannose                      | +          | +          | –          | +          | –          |
| d-Arabinose                    | +          | +          | +          | +          | –          |
| d-Ribose                       | +          | +          | +          | +          | –          |
| d-Xylose                       | –          | +          | –          | +          | –          |
| d-Melibiose                    | –          | +          | –          | –          | –          |
| d-Gentiose                     | –          | +          | –          | –          | –          |
| d-Fucose                       | –          | +          | –          | –          | –          |
| Sensitivity to:                |            |            |            |            |            |
| Ampicillin                     | –          | +          | +          | –          | +          |
| Vancomycin                     | +          | –          | –          | –          | +          |
| Carbenicillin                  | –          | –          | +          | –          | +          |
| Cefalexin                      | –          | +          | +          | +          | +          |
| Tetracycline                   | –          | –          | –          | –          | +          |
| Erythromycin                   | +          | +          | +          | –          | –          |
| Neomycin                       | +          | –          | +          | –          | –          |
The biodegradation efficiency of 1-naphthylamine by strain TRM 85114T was verified and confirmed in this study. Results indicated that the retention time of 1-naphthylamine was at the 26th min, and the absorption peak area of it decreased significantly over time (Supplementary Fig. S6). According to the standard curve of 1-naphthylamine (Supplementary Fig. S7), the amount of 1-naphthylamine degradation by strain TRM 85114T on days 4 and 14 were calculated for 21.6 mg/L and 32.0 mg/L, respectively (Supplementary Fig. S8). The result indicated that strain TRM 85114T was capable of degrading 1-naphthylamine. Thus, strain TRM 85114T could be of potential value in the bioremediation of water and/or soil systems contained with 1-naphthylamine.

**1-Naphthylamine degradation rate**

The biodegradation efficiency of 1-naphthylamine by strain TRM 85114T was verified and confirmed in this study. Results indicated that the retention time of 1-naphthylamine was at the 26th min, and the absorption peak area of it decreased significantly over time (Supplementary Fig. S6). According to the standard curve of 1-naphthylamine (Supplementary Fig. S7), the amount of 1-naphthylamine degradation by strain TRM 85114T on days 4 and 14 were calculated for 21.6 mg/L and 32.0 mg/L, respectively (Supplementary Fig. S8). The result indicated that strain TRM 85114T was capable of degrading 1-naphthylamine. Thus, strain TRM 85114T could be of potential value in the bioremediation of water and/or soil systems contained with 1-naphthylamine.
Fig. 2 Maximum-likelihood tree constructed based on 1140 core genes of TRM 85114T and related type strains. Bootstrap values over 50% are shown on the nodes as percentages of 1,000 replicates

Table 2 Genomic characteristics of strain TRM 85114T and closely related species

| Attribute                  | 1            | 2            | 3            | 4            | 5            |
|----------------------------|--------------|--------------|--------------|--------------|--------------|
| Genome size (Mb)           | 4.1          | 3.6          | 3.7          | 3.9          | 3.72         |
| DNA G+C content (%)        | 61.6         | 62.6         | 63.9         | 61.7 ± 0.8   | 63.7         |
| Contig                     | 60           | 108          | 36           | 22           | 49           |
| Total genes                | 3892         | 3795         | 3410         | 3597         | 3512         |
| Protein coding genes       | 3738         | 3346         | 3301         | 3504         | 3351         |
| RNA genes                  | 137          | 79           | 88           | 65           | 71           |
| rRNA genes (5S/16S/23S)    | 3            | 7            | 15           | 6            | 13           |
| tRNA genes                 | 57           | 54           | 69           | 55           | 54           |
| Other RNAs                 | 77           | 18           | 4            | 4            | 4            |
| GenBank accession number   | JAHCLU00000000000 | FPBP000000000 | AAHZ010000000 | PYUD000000000 | FOBC000000000 |

ANI value (%)  
1 2 3 4 5  
100 88.9 75.4 79.6 80.5  
2 3 4 5  
100 100 100 100 100  

Taxa: 1, strain TRM 85114T; 2, H. korlensis XK1T; 3, C. salexigens DSM 6768T; 4, H. urumqiensis BZ-SZ-XJ27T; 5, H. daqiaonensis CGMCC 1.9150T
The bioinformatic analysis of the genomes was carried out using the NCBI prokaryotic genome annotation pipeline (www.ncbi.nlm.nih.gov/genome/annotation_prok/).
ANI average nucleotide identity
Halomonas jincaotanensis (jin.cao.tan.en’sis. N.L fem. adj. jincaotanensis, pertaining to Jincaotan, Pamir Plateau, Xinjiang, China, from where the type strain was isolated).

Cells are Gram-strain-negative, short rod-shaped, non-motile, and aerobic (0.9–1.0 × 0.4–0.5 μm in size). Colonies are circular, cream-white, convex, and smooth. It grows between 4 and 35 °C (optimum, 30 °C), tolerate for 1–3% (w/v) NaCl (optimum, 3%), and pH of 6.0–9.0 (optimum, pH 7.0). This strain has the ability to hydrolyze starch, aesculin, Tween 20, 40, and 60, but not Tween 80, casein, DNA, gelatin, and urea. Positive for catalase, oxidase, phenylalanine deaminase, reduce nitrate to nitrite, ferment d-glucose to produce acid, respire on nitrate and nitrite, produce H₂S from l-cysteine, produce poly-β-hydroxyalkanoate, and methyl red test, but negative for lysine and ornithine decarboxylases, ω-Nitrophenyl-β-lysine and ornithine decarboxylases, β-hydroxyalkanoate, and methyl red test, but negative for lysine and ornithine decarboxylases, ω-Nitrophenyl-β-lysine and ornithine decarboxylases.

Non-motile, and aerobic (0.9–1.0 × 0.4–0.5 μm in size). The type strain, TRM 85114T (= CCTCC AB 2021006T = LMG 32311T), was isolated from the wetland soil of Jincaotan in the Pamir Plateau.

The GenBank accession numbers for the 16S rRNA gene and the draft genome sequences of strain TRM 85114T are MW584241 and JAHCLU000000000, respectively.

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Author contributions XB performed the experiments, analyzed the data, and drafted the manuscript. ZL conducted the degradation test of 1-naphthylamine. ZX, CW, and MR critically revised the manuscript. LZ contributed to the creation. All authors read and approved the manuscript. We thank HC and PX for finding and providing Halomonas tibetensis pyc13T.

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Declarations

Conflict of interest All authors declare no conflict of interest.

Ethical approval No specific ethical or institutional permission was required for sampling, and our experimental studies did not involve endangered or protected species.

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