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ORIGINAL PAPER

Deinococcus detaillensis sp. nov., isolated from humus soil in Antarctica

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Abstract

A Gram-staining-positive, non-motile, coccus or short-rod-shaped bacterium, designated H1^T, was isolated from a humus soil sample in the Detaille Island of Antarctica. The 16S rRNA gene sequence result indicated that strain H1^T shared the highest 16S rRNA gene sequence identity with the type strain of *Deinococcus alpinitundrae* (96.2%). Growth of strain H1^T occurred at 4–25 °C, pH 6.0–8.0 and in the presence of 0–1.0% NaCl (w/v). The respiratory quinone was MK-8. The major fatty acids were $C_{16:0}$, $C_{17:0}$ cyclo and summed feature 3 ($C_{16:1}$ $\omega 7c$/$C_{16:1}$ $\omega 6c$). The polar lipids were aminoglycophospholipid, aminophospholipid, glycolipid and glycophospholipid. The cell wall peptidoglycan type was A3β. The genomic DNA G+C content was 61.3 mol%. The average nucleotide identity (ANI) between strain H1^T and the closely related *Deinococcus* members was below the cut-off level (95–96%) for species identification. Based on the above results, strain H1^T represents a novel species of the genus *Deinococcus*, for which the name *Deinococcus detaillensis* sp. nov. is proposed. Type strain is H1^T (=CGMCC 1.13938^T=JCM 33291^T).

Keywords Humus soil · Polyphasic taxonomy · *Deinococcus detaillensis*

Abbreviations

ANI Average nucleotide identity
AGPL Aminoglycophospholipid
APL Aminophospholipid
GL Glycolipid
GPL Glycophospholipid

Introduction

The genus *Deinococcus* was first described by Brooks and Murray (1981). They have been isolated from different environments, such as soil (Dong et al. 2015; Joo et al. 2016; Kim et al. 2017), water (Im et al. 2008; Asker et al. 2009), desert (de Groot et al. 2005), hot spring (Ferreira et al. 1997), Antarctic environments (Hirsch et al. 2004), marine flatworm (Lin et al. 2017), car air-conditioning system (Kim et al. 2018), plants (Lai et al. 2006; Li et al. 2018) and even from termite gut (Chen et al. 2012). At the time of writing, the genus includes 78 species (Parte 2018). Members of the

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The 16S rRNA gene sequence of strain H1^T has been deposited in GenBank under the accession number MN116004. The GenBank/EMBL/DDBJ accession numbers for genome sequences of strain H1^T and *Deinococcus alpinitundrae* LMG 24283^T are VKDB00000000 and WXZL00000000, respectively.

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genus *Deinococcus* are aerobic, non-spore-forming, non-motile, coccoid or rod-shaped, pink or red in colour (Brooks and Murray 1981; Dong et al. 2015; Joo et al. 2016; Kim et al. 2017). Most of them have shown remarkable capabilities to resist gamma and UV radiations (Brooks and Murray 1981; de Groot et al. 2005; Hirsch et al. 2004; Zhang et al. 2007). During a study to evaluate the diversity of gamma resistance bacteria, strain designated H1^T, was isolated from a humus soil sample in the Detaille Island of Antarctica. The 16S rRNA gene sequence analysis showed that the strain H1^T shared low sequence identity with the members of the genus *Deinococcus* (96.2%) and as a result, we sought to establish its taxonomic position.

Materials and methods

Strain H1^T isolation and preservation

Strain H1^T was isolated from the humus soil of Detaille Island of Antarctica (66.8667° S, 66.7833° W) by the serial dilution technique. The soil sample was irradiated with 8 kGy of gamma radiation (by a ^{60}Co gamma irradiator) at a dose rate of 2.3831 Gy min^{-1} at room temperature. The sample was serially diluted and an aliquot was spread on 1/5 trypticase soy agar (TSA) medium (Difco). The plates were incubated at 15 °C for 2 weeks. Pink-pigmented Colonies were picked and re-streaked on the same medium until pure colonies were obtained. Strain H1^T was routinely cultivated on 1/5 TSA medium at 15 °C and also stored in glycerol suspensions (30%, v/v) at – 80 °C. Besides, it was preserved in lyophilized form in skimmed milk at room temperature. *Deinococcus alpinitundrae* LMG 24283^T and *Deinococcus radiodurans* DSM 20539^T were obtained from Belgian Co-ordinated Collections of Micro-organisms (BCCM, Belgium) and Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ, Germany), respectively, and were used as a reference strains for comparative studies.

Morphological, physiological and biochemical analysis

Cell morphology and flagella was observed by a light microscope (Olympus, CX22LED) and scanning electron microscope (SEM, Quanta 200; FEI) after 7 days of incubation at 15 °C on 1/5 TSA medium. Gram-staining was performed using the Gram-stain Set S kit (BD Difco) and the Ryunon-staining KOH method (Powers 1995). Growth on tryptone glucose yeast extract (TGY), 1/5 TSA, 1/2 TSA, 1/10 TSA and Reasoner's 2A agar (R2A) was evaluated. Growth at different temperatures (4, 10, 15, 20, 25, 30, 35, 40 and 50 °C) was measured in 1/5 TSA broth after 7 days of incubation. Salt-tolerance was tested at different concentrations of NaCl (0, 0.25, 0.5, 1, 1.5, 2, 4 and 6%, w/v) using 1/5 TSA broth at 15 °C incubated for 7 days. The pH range for growth (pH 4.0–10.0 at intervals of 1.0 pH unit) was determined in 1/5 TSA broth adjusted with the buffer systems as described by Narsing Rao et al. (2020). Catalase activity was determined by assessing the production of bubbles on the addition of a drop of 3% (v/v) H_2O_2 to the bacterial culture. Oxidase activity was determined based on the oxidation of tetramethyl-*p*-phenylenediamine (Kovacs 1956).

Milk coagulation and peptonisation and hydrolysis of starch and Tweens (20, 40, 60 and 80) were determined as described by Gonzalez et al. (1978). Other tests were performed using the API ZYM (BioMerieux) and GEN III Micro Plate (Biolog) assays according to the manufacturer's instructions.

16S rRNA gene amplification and phylogenetic analysis

Strain H1^T genomic DNA extraction and PCR amplification of the 16S rRNA gene sequence was performed as described by Narsing Rao et al. (2020). The obtained 16S rRNA gene sequence was compared with available sequences of cultured species at EZBioCloud server (Yoon et al. 2017). Phylogenetic trees were constructed by three tree-making algorithms, neighbor-joining (Saitou and Nei 1987), maximum-likelihood (Felsenstein 1981), and maximum-parsimony (Fitch 1971), using MEGA version 7.0 (Kumar et al. 2016). Multiple sequences alignments were performed using the CLUSTAL_X (Thompson et al. 1997). Evolutionary distance matrices were calculated according to Kimura's two-parameter model (Kimura 1980) with 1000 bootstrap replications (Felsenstein 1985).

Chemotaxonomic characterization

Biomass for chemotaxonomic studies were harvested from 1/5 TSA broth incubated at 15 °C for 7 days. Cell-wall peptidoglycan was prepared as described by Komagata and Suzuki (1987) and analyzed by using ultra-performance liquid chromatography. Polar lipids were extracted according to the methods described by Minnikin et al. (1979) and analyzed by the two-dimensional thin-layer chromatography (TLC) (Collins and Jones 1980). The fatty acids were saponified, methylated, extracted and analyzed using the standard Microbial Identification system (Sherlock, version 6.2B; MIDI database: TSBA6) (Sasser 1990). Quinones were extracted and purified as described by Collins et al. (1977) and analyzed by HPLC (Kroppenstedt 1982).

Genome sequencing and comparison

The genome sequencing of strain H1^T and *D. alpinitundrae* LMG 24283^T was performed using a paired-end sequencing method with a Hiseq 2000 platform (Illumina). Reads of each data set were filtered, and high-quality reads were assembled using SOAPdenovo2 (Luo et al. 2012) and SPAdes (Bankevich et al. 2012). Genome quality was estimated by CheckM (Parks et al. 2015). Gene prediction was performed using Glimmer (Delcher et al. 1999). The predicted coding sequences translated and searched against COG (Tatusov et al. 2003) and KEGG (Moriya et al. 2007) databases. The rRNAs and tRNAs were predicted using RNAmmer (Lagesen et al. 2007) and tRNAscan-SE, respectively (Lowe et al. 1997). Pan-genome analysis was carried out via the Anvi'o tool (Eren et al. 2015) using NCBI blast and MCL flag (Buchfink et al. 2015, van Dongen et al. 2012). The average nucleotide identity (ANIb) value was determined using pyani (Pritchard et al. 2016).

Detection of gamma and UV radiation tolerance

To detect the gamma and UV radiation tolerance limit of the strain H1^T, it was cultured to exponential growth phase in 1/5 TSA broth. The culture was centrifuged at 12,000 rpm for 10 min at 4 °C. The biomass was collected, washed and re-suspended in saline solution (0.9% NaCl, w/v). The biomass concentration was adjusted to 1×10^7–10^8 CFU ml^{-1}. The gamma radiation doses were set from 0 to 15.0 kGy with a subsequent increase of 2.5 kGy in each step. Treated samples were plated onto 1/5 TSA agar plates and incubated at 15 °C for one week. Similarly, strain H1^T after treatment as above was exposed to a 254 nm UV light for the desired dose and incubated at 15 °C for a week. *D. radiodurans* DSM 20539^T and *E. coli* DH5α were tested simultaneously as positive and negative controls. The final survival results were compared with unirradiated cultures.

Results and discussion

Morphological, physiological and biochemical analysis

Strain H1^T was coccus or short-rod-shape (0.6–0.7 × 1.1–1.4 µm) and non-flagellated (Supplementary Fig. S1). Strain H1^T growth on R2A was negative but the growth of *D. alpinitundrae* LMG 24283^T was positive. Strain H1^T was positive for the hydrolysis of Tween 40 but *D. alpinitundrae* LMG 24283^T was negative. Strain H1^T was positive for lipase (C14) and esterase lipase (C8) but negative for alkaline phosphatase whereas *D. alpinitundrae* LMG 24283^T was negative for lipase (C14) and esterase lipase (C8) but positive for alkaline phosphatase. Detailed differentiating features between strain H1^T and reference strains are shown in Table 1.

16S rRNA gene amplification and phylogenetic analysis

Strain H1^T shared the highest 16S rRNA gene sequence identity with the type strain of *D. alpinitundrae* (96.2%) and less than 95% sequence identity with the other members of the genus *Deinococcus*. In ML tree (Fig. 1), strain H1^T clade with the members of the genus *Deinococcus*. The tree was further found to be stable when reconstructed using NJ (Supplementary Fig. S2) and MP (Supplementary Fig. S3) methods.

Chemotaxonomic characteristics

The cell-wall peptidoglycan of strainH1^T contained lysine, glycine, alanine, aspartic and ornithine, and according to

Table 1 Differential characteristics of strain H1^T and closely related species of the genus *Deinococcus*

Characteristic	1	2
Optimum temperature for growth °C	15	10
Optimum pH for growth	7.0–8.0	6.0–9.0
GEN III micro plate (Biolog)		
Dextrin	+	−
Sucrose	+	−
D-mannitol	+	−
Glucuronamide	−	+
D-Galacturonic acid	−	+
D-fructose-6-PO_4	+	−
D-cellobiose	−	+
Pectin	+	−
D-fructose	+	−
D-galactose	+	−
Glycyl-L-proline	+	−
Acetic acid	+	−
Formic acid	+	−
Tween 40	+	−
Glycerol	−	+
API ZYM		
Alkaline phosphatase	−	+
Esterase lipase (C8)	+	w
Lipase (C14)	+	−
Naphthol-AS-BI-phosphohydrolase	−	+
Trypsin	+	−
α-Galactosidase	+	−

1, H1^T; 2, *D. alpinitundrae* LMG 24283^T

+, positive reaction; −, negative reaction; w, weakly positive

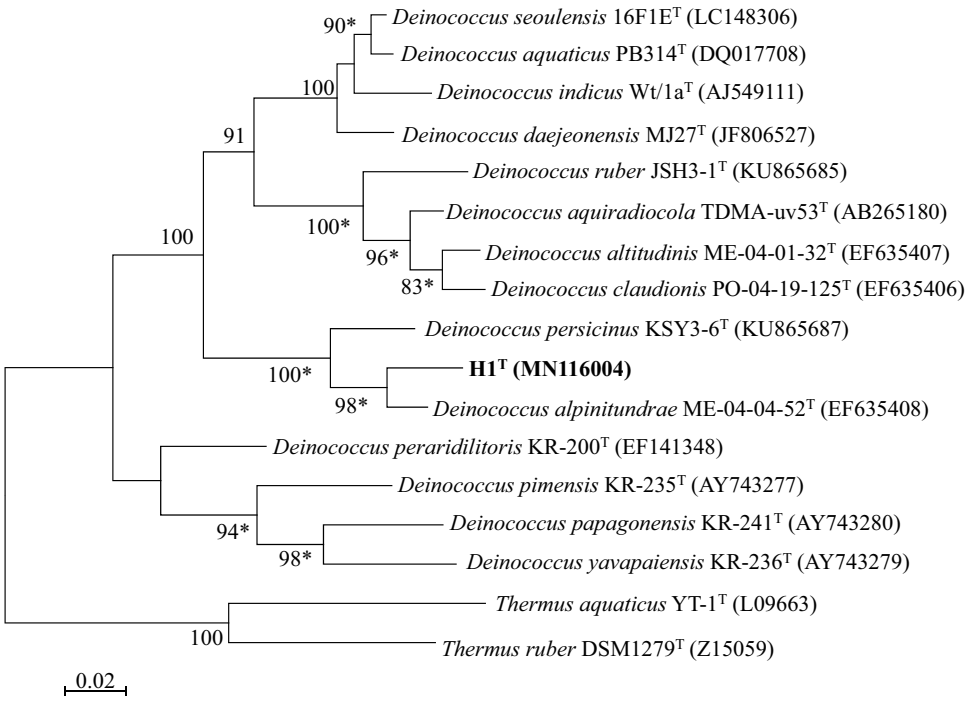

Fig. 1 Maximum-likelihood phylogenetic tree based on 16S rRNA gene sequences showing the relationships of strain H1^T and its closely related species within the genus *Deinococcus*. Bootstrap values of ≥ 70% (percentages of 1000 replications) are shown at branching points. Asterisk indicates the clade retrieved in phylogenetic trees reconstructed with the neighbor-joining and maximum-parsimony algorithms. Bar 0.02 substitutions per nucleotide position. *Thermus aquaticus* YT-1^T and *Thermus ruber* DSM 1279^T were used as an out-group

the classification by Schleifer and Kandler (1972) the peptidoglycan type was A3β. The polar lipids of strain H1^T were aminoglycophospholipid (AGPL), aminophospholipid (APL), glycolipid (GL) and glycophospholipid (GPL) (Supplementary Fig. S4). The polar lipids of *D. alpinitundrae* were GL, APL, APGL and GPL (Calleganet al. 2008). The major cellular fatty acids of strain H1^T were summed feature 3 (composed of $C_{16:1}$ $\omega7c$ / $C_{16:1}$ $\omega6c$, 58.5%), $C_{16:0}$ (20%) and $C_{17:0}$ cyclo (11.9%). The major fatty acids of strain H1^T were consistent with *D. alpinitundrae* LMG 24283^T but their proportions varied (Table S1). The menaquinone of strain H1^T was MK-8 which was similar to that of the other members of the genus *Deinococcus* (Dong et al. 2015; Joo et al. 2016; Calleganet al. 2008).

Genome sequencing and comparison

Assembling of shotgun reads of strain H1^T generated 93 contigs, giving a genome size of 4,007,733 bp. Strain H1^T genome was 97.8% complete and had 1.6% contamination suggesting a good quality genome (Parks et al. 2015). Two rRNAs and 51 tRNAs were predicted. A total of 3883 genes were predicted of which 3491 and 3232 genes could be assigned to the COG and KEGG databases, respectively. The genomic DNA G + C content of strain H1^T was 61.3%. Fig. S5 shows the pangenome analysis result along with total genome length, number of the gene cluster, number of the singleton gene cluster, genomic DNA G + C content, ANI value information, etc. The total number of the gene cluster and singleton gene clusters were higher in strain H1^T when compared with other *Deinococcus* members (Supplementary Fig. S5). The ANIb value between strain H1^T and *D. alpinitundrae* LMG 24283^T was 79.3% while with other *Deinococcus* members the ANIb value was below 79.0% (Table. 2, Supplementary Fig. S5). These values were below the cut-off level (95–96%) recommended as the ANI criterion for interspecies identity (Richter and Rosselló-Móra 2009; Goris et al. 2007).

Gamma and UV radiation resistance

The survival rate of strain H1^T on exposure to increasing doses of gamma and UV radiation was analyzed in comparison with that of *D. radiodurans* DSM 20539^T and *E. coli* DH5α. No growth was observed for *E. coli* DH5α under the gamma radiation dose of 5.0 kGy. However, strain H1^T

Table 2 Average nucleotide identity of strain H1^T and other closely related *Deinococcus* members

ANIb (%)	1	2	3	4	5
D. alpinitundrae	–	73.7	80.4	73.4	79.2
D. deserti	74	–	74.7	73.8	73.2
D. irradiatisoli	80.6	74.7	–	74.3	78.4
D. maricopensis	73.7	73.7	74.3	–	72.8
Strain H1^T	79.3	73.1	78.3	72.5	–

Strains: 1) *D. alpinitundrae* LMG 24283^T (WXZL00000000), 2) *D. deserti* VCD115^T (CP001114), 3) *D. irradiatisoli* 17bor-2^T (CP029494), 4) *D. maricopensis* DSM 21211^T (CP002454) and 5) strain H1^T (VKDB00000000)

and *D. radiodurans* DSM 20539^T grew well under the same condition. At a dose of 15.0 kGy, a few colonies of strain H1^T and *D. radiodurans* DSM 20539^T were observed (Supplementary Fig. S6a). Strain H1^T exhibited a D10 value of 4.8 kGy, similar to the closely related species *D. alpinitundtrae* LMG 24283^T which showed a D10 value of 4.8 kGy (Callegan et al. 2008). The lethal dose of UV radiation for *E. coli* DH5α was 65 J m^{-2}, whereas strain H1^T could grow at the highest dose of 750 J m^{-2} (Supplementary Fig. S6b).

Taxonomic conclusion

Based on phenotypic, phylogenetic, chemotaxonomic and genome analysis strain H1^T represents a novel species of the genus *Deinococcus*, for which the name *Deinococcus detaillensis* sp. nov. is proposed.

Description of *Deinococcus detaillensis* sp. nov

Deinococcus detaillensis (de.tail.len'sis. N.L. masc. adj. *detaillensis* pertaining to Detaille Island, Antarctica).

Cells are Gram-stain positive, non-motile, non-spore-forming and coccus- or short-rod shape (0.6–0.7 × 1.1–1.4 μm). Colonies are pink, circular and smooth on 1/5 TSA at 15 °C for 7 days. Cells grow at 4–25 °C (optimum at 15 °C), pH 6.0–8.0 (optimum at pH 7.0) and in the presence of 0–1.0% NaCl (w/v). Positive for catalase and negative for oxidase. In the Biolog GEN III MicroPlate, positive for D-turanose, sucrose, D-fructose, D-mannitol, D-arabitol, D-galactose, D-fructose-6-PO_4, glycyl-L-proline, pectin, acetic acid, formic acid, acetoacetic acid, Tween 40, dextrin, and D-trehalose. Positive for esterase (C4), esterase lipase (C8), lipase (C14), trypsin, α-galactosidase, *N*-acetyl-glucosidase, α-mannosidase and β-fucosidase. The cell wall peptidoglycan type is A3β. The polar lipids are AGPL, APL, GL, and GPLs. The major fatty acids are $C_{16:0}$, $C_{17:0}$ cyclo and summed feature 3 ($C_{16:1}$ ω7*c*/$C_{16:1}$ ω6*c*). The respiratory quinone is menaquinone 8 (MK-8). The genomic DNA G + C content is 61.3 mol%. The type strain H1^T (= CGMCC 1.13938^T = JCM 33291^T), was isolated from humus soil in the Detaille Island of Antarctica. The GenBank accession numbers for the 16S rRNA gene and the genome sequence are MN116004 and VKDB00000000.

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Compliance with ethical standards

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

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