Marinobacter maroccanus sp. nov., a moderately halophilic bacterium isolated from a saline soil

Nadia Boujida,[1†] Montserrat Palau,[2†] Saoulajan Charfi,[1] Àngels Manresa,[2] Nadia Skali Senhaji,[1] Jamal Abrini,[1] David Miñana-Galbis[2*]

Author affiliations: [1]Biotechnology and Applied Microbiology Research Group, Department of Biology, Faculty of Sciences, University Abdelmalek Essaâdi, BP2121, 93002 Tetouan, Morocco; [2]Secció de Microbiologia, Dept. Biologia, Sanitat i Medi Ambient, Facultat de Farmàcia i Ciències de l'Alimentació, Universitat de Barcelona, Av. Joan XXIII, 27-31, 08028 Barcelona, Catalonia, Spain.

[†]These authors contributed equally to this work.

***Correspondence:** David Miñana-Galbis, davidminyana@ub.edu

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The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA and *rpoD* gene sequences and the whole genome shotgun project of strain N4[T] are MG563241, MG551593, and PSSX01000000, respectively.

Abstract

During the taxonomic investigation of exopolymer producing halophilic bacteria, a rod-shaped, motile, Gram-stain-negative, aerobic, halophilic bacterium, designated strain N4^T, was isolated from a natural saline soil located in the northern Morocco. The optimal growth of the isolate was at 30–37 ºC and at pH 6.0–9.0, in the presence of 5–7% (w/v) NaCl. Useful tests for the phenotypic differentiation of strain N4^T from other *Marinobacter* species included α-chymotrypsin and α-glucosidase activities and the carbohydrate assimilation profile. The major fatty acids detected in strain N4^T were $C_{18:1}$ *ω9c*, $C_{16:0}$, and $C_{16:1}$ *ω7c*/$C_{15:0}$ iso 2-OH. Sequence analysis of the 16S rRNA indicated that strain N4^T belonged to the genus *Marinobacter* and was closely related to *Marinobacter adhaerens* NC17506^T (99.04%), *Marinobacter salsuginis* SD-14B^T (98.97%), and *Marinobacter flavimaris* SW-145^T (98.36%). Phylogenetic analysis of the *rpoD* gene sequence also showed that the nearest neighbours of strain N4^T were *M. adhaerens* (90.63%) and *M. salsuginis* (91.13%). Strain N4^T showed 87.98% similarity in the average nucleotide identity (ANI) with *M. flavimaris* and *M. salsuginis*, and 87.47% with *M. adhaerens*. In the in-silico genome-to-genome distance (GGD), strain N4^T showed DNA-DNA hybridization (DDH) values of 33.30% with *M. adhaerens*, 34.60% with *M. flavimaris* and 34.70% with *M. salsuginis*. DNA G+C content of N4^T was 57.3 mol%. Based on the results of phenotypic characterization, phylogenetic analysis and genome comparison, strain N4^T represents a novel species of the genus *Marinobacter*, for which the name *Marinobacter maroccanus* sp. nov. is proposed. The type strain is N4^T (=CECT 9525^T=LMG 30466^T).

The genus *Marinobacter* Gauthier *et al*. 1992 [1], with *Marinobacter hydrocarbonoclasticus* as its type species and 42 species with validly published names described until now, belongs to the family *Alteromonadaceae* within the *Gammaproteobacteria* [2]. Members of the genus *Marinobacter* are Gram negative, rod shaped, motile, mesophilic, halophilic, aerobic, oxidase- and catalase- positive, and can grow anaerobically by denitrification [3]. Most of them have been isolated from saline environments like seawater [4], sea sediments [5], marine aggregates [6], Antarctic environment [7], oil polluted saline soil [8] and saltern crystalizing pond [9]. This genus comprises many species that could be of great biotechnological interest since halotolerant and halophilic microorganisms are well known for their potential biotechnological applications [10].

During a search of exopolymer producing halophilic bacteria, strain N4^T was isolated from a natural saline soil of a wetland located in Douar Hjar Melaghi, in the Ouezzane province (34° 44' 33.006" N 5° 11' 19.803"W). The sample was diluted in 5% w/v sea salt solution, transferred to plates containing MY agar medium [11] supplemented with a 10% w/v of sea salt solution [12] and incubated at 37ºC for 7 days. Isolated colony of strain N4^T was selected and transferred to fresh plates of the same medium and maintained aerobically at 4ºC and in MY broth containing 5% sea salt solution with 20% (v/v) glycerol at –80ºC.

Growth conditions, Gram staining, and motility were observed by light microscopy while morphology, cell size and shape of cells were determined by transmission electron microscopy. Growth at 0, 0.5, 1, 2, 3, 5, 7.5, 10, 15, 20, 25 and 30% (w/v) NaCl was assessed in MY agar at pH 7.0 and incubated at 30ºC. Temperature and pH ranges were studied on solid MY supplemented with 5 % w/v sea salts solution. For temperature range, the plates were incubated at temperatures varying from 4 to 45°C. For pH range, the pH of the medium was adjusted to 5, 5.5, 6, 7, 8, 9 and 10. The plates were incubated for 7 days for all the tests. Growth on MacConkey agar and Cetrimide agar both supplemented with 5% sea salt solution was tested. Oxidase and catalase activities and hydrolysis of starch, casein, gelatin, lecithin, DNA, tyrosine and Tween 20 and 80 were determined according to Barrow and Feltham (1993) [13]. API 20NE, API 50CH and API ZYM strips

(bioMérieux, France) were used to study the utilization of carbohydrates and enzymes activities. The inoculum was prepared by suspending colonies of strain N4^T in a 5% (w/v) sea salt solution and transferred to the API strips following the recommendations of the manufacturer. In the case of API 50CH, the media was supplemented with a 5% (w/v) sea salt solution. The API 20NE, API CH50 and API ZYM tests were also done for reference strains *Marinobacter flavimaris* LMG 23834^T and *Marinobacter guineae* M3B^T. Susceptibility to antibiotics was tested according to the method described by Bauer *et al*. (1966) [14] using the following antibiotics: amoxicyllin /clavulanic acid (30 µg), ampicillin (10 µg), ceftriaxone (30 µg), doxycycline hydrochloride (30 µg), nalidixic acid (30 µg), norfloxacin (10 µg), ofloxacin (5 µg), oxacillin (5 µg), penicillin G (6 µg), polymixin B (300 µg), rifampicin (30 µg), spectinomycin (100 µg), sulphamethoxazole (25 µg) (Oxoid), cefuroxime (30 µg) (Bio-Rad), chloromphenicol (30 µg), ciprofloxacin (5 µg), gentamycin (30 µg), pristinomycin (15 µg) (Himedia) and vancomycin (30 µg) (Bioanalyse).

For fatty acids analysis, strain N4^T was cultivated on solid MY medium supplemented with 5% sea salt solution for 2 days at 37ºC. Fatty acids were extracted according to the protocol of the Microbial Identification System (Microbial ID; MIDI), and profiles were determined using the Sherlock Microbial Identification system (MIDI, database TSBA 40, version 4.10) [15].

Genomic DNA was extracted using a genomic DNA extraction kit (REAL, Durviz S. L., València, Spain). 16S rRNA gene was amplified by PCR using primers 16F27 [16] and 16S15R [17]. Partial amplification of the gene *rpoD* with primers 70Fs and 70Rs [18] was also performed. The amplified products were purified using the ExoSAP-IT® (Affymetrix, Santa Clara, CA, USA). Purified PCR products were later sequenced by the Genomics Unit of Scientific and Technological Centers from University of Barcelona (CCiTUB) using the same primers as for the PCRs plus 16S11F and 16S5R primers [17] in the case of the gene 16S rRNA. Pairwise sequence similarity values between the obtained 16S rRNA sequences and reference sequences were calculated by the Identify tool included in the EzBioCloud portal (http://www.ezbiocloud.net/) [19]. Multiple sequence alignments and phylogenetic analysis of 16S rRNA and *rpoD* gene sequences from strain N4^T (GenBank

accession nos. MG563241 and MG551593, respectively) and related species (taken from the GenBank database, www.ncbi.nlm.nih.gov) were performed using MEGA version 7 [20]. Phylogenetic trees were constructed using the neighbour-joining method and their topological robustness was evaluated by bootstrap analysis based on 1,000 replicates.

The whole genome of the strain N4^T was sequenced by the Centre for Genomic Regulation (CRG, Barcelona) using Illumina Hi-seq platform (2 x 125 bp reads and 501.49x coverage). Assembly of the contigs was performed with the program a5-assembler [21], Prokka [22] was used for the annotation of the genes and Mauve [23] for genome sequence alignment and reordering contigs according to the reference genome of *Marinobacter adhaerens* HP15^T (NC_017506). Genome annotation was also acquired from NCBI Prokaryotic Genomes Annotation Pipeline (PGAP) [24]. The whole genome shotgun project of strain N4^T was deposited in GenBank under the accession no. PSSX01000000. The in-silico genome-to-genome distance (GGD) between genomes was calculated using the genome-to-genome calculator 2.0 (GGDC), a digital DNA-DNA hybridization (dDDH) method provided by DSMZ (http://ggdc.dsmz.de) [25]. The average nucleotide identity (ANI) and the GC content were calculated using the software OAT hosted in the EzBioCloud portal [19, 26].

Cells of strain N4^T were rod-shaped, Gram-negative and motile. The strain grows optimally in the media that contains 5-7% NaCl (w/v) at pH 7-8 and 30-37ºC. N4^T was catalase- and oxidase-positive and able to hydrolyze lecithin and Tween 20 and 80. Many phenotypic characteristics differentiated strain N4^T from other *Marinobacter* species, mainly for the *α*-chymotrypsin and *α*-glucosidase activities and the carbohydrate assimilation profile (Table 1). The API ZYM system revealed that the strain was positive for acid phosphatase, alkaline phosphatase, esterase (C4), esterase (C8), lipase (C14), cystine arylamidase, leucine arylamidase, valine arylamidase, naphtol-AS-BI-phosphohydrolase, *α*-chymotrypsin, *α*-glucosidase and N-acethyl-*β*-glucosaminidase. The API 20NE system showed that the strain was positive for the reduction of nitrates to nitrites and the assimilation of D-maltose, malate and trisodium citrate. Using the API

50CH system, the strain was able to oxidize D-glucose, D-fructose, D-maltose, D-sucrose and glycerol.

The fatty acid profile of strain N4^T was similar to those of *Marinobacter* species previously described. The major fatty acids detected in strain N4^T were $C_{18:1}$ *ω9c* (22.84%), $C_{16:0}$ (22.43%), $C_{16:1}$ *ω7c*/$C_{15:0}$ iso 2-OH (15.93 %), $C_{12:0}$ 3-OH (7.97%), $C_{12:0}$ (6.99%) and $C_{16:1}$ *ω9c* (4.86%) which are the most common fatty acids of the most phylogenetically closely related species (Table 2).

Phylogenetic analysis based on 16S rRNA and *rpoD* gene sequences revealed that strain N4^T belongs to the genus *Marinobacter* (Figs 1 and 2). Strain N4^T showed the highest 16S rRNA gene sequence similarities with *Marinobacter adhaerens* HP15^T (99.04%), *M. salsuginis* SD-14B^T (98.97%), *M. flavimaris* SW-145^T (98.36%), *M. similis* A3d10^T (98.22%), *M. salinus* Hb8^T (98.15%), *M. sediminum* R65^T (98.15%) and *M. lipolyticus* SM19^T (98.02%). Strain N4^T could not be discriminated from *M. adhaerens* and *M. salsuginis* since 16S rRNA gene sequence similarities were >98.65%, the threshold for species delineation [27]. On the basis of *rpoD* gene sequences, the nearest neighbours of strain N4^T were again the type strains of *M. adhaerens* and *M. salsuginis* (Fig. 2), with sequence similarities of 90.63 and 91.13%, respectively. These similarity values are below the species cut-off value (>97%) described for other genera as *Aeromonas* and *Pseudomonas* [28, 29], suggesting that this strain could represent a novel *Marinobacter* species.

A total genome length of 4,340,695 bp was obtained from 61 contigs, with an N_{50} of 166,663 and a GC content of 57.3%. Genome annotation from PGAP revealed 4,007 genes, with 3,899 coding genes, 3 complete rRNAs (5S, 16S, and 23S), 45 tRNAs, and 4 ncRNAs. Based on 16S rRNA gene sequence similarities and phylogenetic positions, genomic sequences of the type strains of *M. adhaerens* (NC_017506), *M. salsuginis* (PRJNA187995) and *M. flavimaris* (PSSW00000000) were selected for genome comparison. Strain N4^T showed ANI values of 87.98% with *M. flavimaris* and *M. salsuginis*, and 87.47% with *M. adhaerens*, and DDH values of 34.70%, 34.60% and

33.30% with *M. salsuginis*, *M. flavimaris*, and *M. adhaerens*, respectively. As species boundary for ANI and DDH values are 95~96 and 70 %, respectively, genome comparison results confirmed that strain N4^T constitutes a novel *Marinobacter* species [30].

Based on the results of phenotypic characterization, phylogenetic analysis (16S rRNA and *rpoD* genes) and genome comparison (ANI and DDH), strain N4^T represents a novel species of the genus *Marinobacter*, for which the name *Marinobacter maroccanus* sp. nov. is proposed.

DESCRIPTION OF *MARINOBACTER MAROCCANUS* SP. NOV.

Marinobacter maroccanus (ma.roc.ca'nus. L. masc. adj. *maroccanus*, from the L. *Maroccanum Regnus*, Morocco, where the type strain was isolated).

Cells are rod-shaped (0.5×1.6–2 µm), Gram-stain-negative, aerobic, motile and non-spore-forming. After 2 days of incubation at 30ºC, colonies on solid MY medium supplemented with 5% sea salt solution are circular (1.5–2 mm in diameter), smooth and brownish that darkens over incubation time. Temperature, salt and pH ranges for growth are 4–40ºC, 2–15% NaCl and pH 6–9 respectively. Optimal growth occurs at 5–7% NaCl, 30–37ºC and pH 7–8. Not able to growth on MacConkey agar and Cetrimide agar. Cells are oxidase- and catalase-positive, reduce nitrate to nitrite. Indole, arginine dihydrolase and acid from glucose are not produced. Lecithin and Tween 20 and 80 are hydrolyzed but not casein, DNA, esculin, gelatin, starch, tyrosine or urea. Positive for the utilization of D-fructose, D-glucose, D-maltose, D-sucrose, glycerol, malate, trissodium citrate, but negative for adipic acid, amygdaline, arbutine, capric acid, D-adonitol, D- or L-arabinose, D- or L-arabitol, D-cellobiose, D-fucose, D-galactose, D-lactose, D-lyxose, D-mannitol, D-mannose, D-melezitose, D-melibiose, D-raffinose, D-ribose, D-sorbitol, D-tagatose, D-trehalose, D-turanose, D- or L-xylose, dulcitol, erythritol, esculine ferric citrate, gentiobiose, glycogen, inositol, inulin, L-rhamnose, L-sorbose, methyl αD-glucopyranoside, methyl αD-mannopyranoside, methyl-βD-xylopyranoside, N-acetylglucosamine, phenilacetic acid, potassium gluconate, potassium 2-ketogluconate, potassium 5-ketogluconate, salicin, starch or xylitol. Enzymatic activities are observed for

acid phosphatase, alkaline phosphatase, *α*-chymotrypsin, cysteine arylamidase, esterase (C4), esterase (C8), *α*-glucosidase, leucine arylamidase, lipase (C14), N-acethyl-*β*-glucosaminidase, naphtol-AS-BI-phosphohydrolase, valine arylamidase, but not for *α*-fucosidase, *α*-galactosidase, *β*-galactosidase, *β*-glucuronidase, *β*-glucosidase, *α*-mannosidase or trypsin. Resistant to cefuroxime (30 µg), ofloxacin (5 µg), oxacillin (5 µg), vancomycin (30 µg), but susceptible to amoxicillin/clavulanic acid (30 µg), ampicillin (10 µg), ceftriaxone (30 µg), chloramphenicol (30 µg), ciprofloxacin (5 µg), doxycycline hydrochloride (30 µg), gentamycin (30 µg), nalidixic acid (30 µg), norfloxacin (10 µg), penicillin G (6 µg), polymixin B (300 µg), pristinomycin (15 µg), rifampicin (30 µg), spectinomycin (100 µg) and sulphamethoxazole (25 µg). The predominant cellular fatty acids are $C_{18:1}$ *ω9c* (22.84%), $C_{16:0}$ (22.43%), $C_{16:1}$ *ω7c*/$C_{15:0}$ iso 2-OH (15.93 %), $C_{12:0}$ 3-OH (7.97%), $C_{12:0}$ (6.99%) and $C_{16:1}$ *ω 9c* (4.86%).

The type strain, N4^T (=CECT 9525^T=LMG 30466^T), was isolated from a hypersaline environment in Douar Hjar Melaghi, Ouezzane province, Morocco. The DNA G+C content of the type strain is 57.3 mol%.

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316 **Table 1.** Differential phenotypic characteristics of strain N4^T and other species of the
317 genus *Marinobacter*
318 Strains: 1, N4^T; 2, *M. adhaerens* HP15^T [6]; 3, *M. flavimaris* SW-145^T [31]; 4, *M. lipolyticus*
319 SM19^T [32]; 5, *M. salinus* Hb8^T [33]; 6, *M. salsuginis* SD-14B^T [34]; 7, *M. sediminum* KMM
320 3657^T [35]; 8, *M. similis* A3d10^T [4]. +, Positive; –, negative; ND, no data available.

Characteristic	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**
NaCl range for growth (%)	2-15	0.5-20	1-20	1-15	0.5-15	1-20	0.5-18	0.5-20
Temperature range for growth (ºC)	4-40	4-45	4-45	15-40	10-37	10-45	4-42	4-40
Nitrate reduction to nitrite	+	−	+	−	+	+	ND	+
Nitrite reduction to N_2	−	−	−	−	−	+	−	−
Hydrolysis of:								
Casein	−	ND	−	ND	ND	+	−	ND
Gelatin	−	−	−	−	+	+	−	−
API ZYM test:								
α-Chymotrypsin	+	ND	−	ND	+	−	−	−
α-Glucosidase	+	ND	−	ND	−	−	−	−
Utilization of:								
D-Cellobiose	−	−	−	−	−	−	+	−
D-Fructose	+	−	+	+	−	−	−	−
D-Glucose	+	−	−	+	+	+	+	−
D-Maltose	+	−	−	+	+	−	−	−
D-Mannose	−	−	−	−	+	−	+	−
D-Sucrose	+	−	−	−	−	−	+	−
Citrate	+	−	−	−	+	−	−	−
Glycerol	+	−	−	−	ND	+	+	−
Malate	+	+	+	ND	+	+	−	ND
Mannitol	−	−	−	+	+	−	−	−
Phenylacetic acid	−	+	−	−	+	−	−	−
DNA G+C content (mol%)	57.3	56.90	58.00	57.00	54.51	55.90	56.50	57.60

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Table 2. Fatty acid compositions (%) of strain N4^T and other species of the genus *Marinobacter*.

Strains: 1, N4^T; 2, *M. adhaerens* HP15^T [6]; 3, *M. flavimaris* SW-145^T [31]; 4, *M. lipolyticus* SM19^T [32]; 5, *M. salinus* Hb8^T [33]; 6, *M. salsuginis* SD-14B^T [34]; 7, *M. sediminum* KMM 3657^T [35]; 8, *M. similis* A3d10^T [4]. –, Not detected.

Fatty acid	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**
$C_{10:0}$	0.37	0.2	0.5	1.5	–	–	–	–
$C_{12:0}$	6.99	6.00	9.1	8.3	6.6	7.3	4.15	0.60
$C_{13:0}$	0.05	–	–	–	–	–	–	–
$C_{14:0}$	1.29	1.2	1.1	–	0.9	1.1	0.92	1.00
$C_{15:0}$	0.15	–	0.7	1.0	–	–	–	0.3
$C_{16:0}$	22.43	21.7	26.7	28.5	19.8	22.9	21.78	15.20
$C_{17:0}$	0.63	1.1	3.7	3.6	0.9	0.5	1.31	2.00
$C_{18:0}$	2.03	3.4	3.3	2.7	1.1	2.90	2.20	4.90
$C_{14:1}$ *ω7c*	–	–	–	–	–	–	–	2.20
$C_{16:1}$ *ω9c*	4.86	9.0	10.2	10.5	12.8	10.5	13.28	8.10
$C_{16:1}$ *ω7c*	–	–	–	–	–	–	15.87	20.90
$C_{16:1}$ *ω5c*	0.17	–	–	–	–	–	–	–
$C_{17:1}$ *ω8c*	0.85	2.00	3.8	2.9	2.1	3.8	2.79	4.9
$C_{18:1}$ *ω9c*	22.84	21.6	17.4	13.9	11.7	17.2	16.12	21.20
$C_{18:1}$ *ω7c*	2.84	3.70	1.2	2.3	–	–	2.91	14.30
$C_{18:3}$ *ω6c* (6,9,12)	0.72	1.65	–	–	–	–	1.88	–
$C_{19:0}$ *ω8c* cyclo	–	–	1.7	–	–	–	–	–
$C_{16:1}$ *ω6c*/$C_{16:1}$ *ω7c*	–	–	–	–	13.6	13.10	–	–
$C_{18:1}$ *ω6c*/$C_{18:1}$ *ω7c*	–	–	–	–	2.1	3.00	–	–
$C_{13:0}$ iso	0.08	0.13	–	–	–	–	–	–
$C_{15:0}$ iso	0.06	–	–	–	–	–	–	–
$C_{17:0}$ iso	0.16	0.32	–	–	–	–	–	–
$C_{10:0}$ 3-OH	0.12	–	–	–	–	–	–	–
$C_{11:0}$ 3-OH	0.10	0.2		–	–	0.5	–	–
$C_{12:0}$ 2-OH	0.14	–	–	–	–	–	–	–
$C_{12:0}$ 3-OH	7.97	7.9	10.5	–	5.5	9.3	8.04	2.80
$C_{12:1}$ 3-OH	0.07	–	–	11.3	–	–	–	–

$C_{15:0}$ iso 3-OH	0.74	–	–	–	–	–	–	–
$C_{16:1}$ 2-OH	0.39	–	–	–	–	–	–	–
$C_{18:0}$ 3-OH	–	–	–	–	15.7	–	–	–
$C_{14:0}$ 3-OH/$C_{16:1}$ iso I	0.05	–	–	–	–	–	–	–
$C_{16:1}$ *ω7c*/$C_{15:0}$ iso 2-OH	15.93	14.6	6.8	–	–	–	–	–
$C_{17:1}$ iso *ω9c*/$C_{16:0}$10 methyl	–	–	–	–	4.5	–	–	–
$C_{16:0}$ N alcohol	2.40	3.19	–	–	–	–	–	–
$C_{16:1}$ *ω7c* alcohol	0.65	–	–	–	–	–	–	–
$C_{16:0}$ 10 methyl	3.56	0.6	0.2	4.0	–	2.6	–	–
$C_{17:0}$ 10 methyl	0.87	1.09	–	–	–	–	–	–

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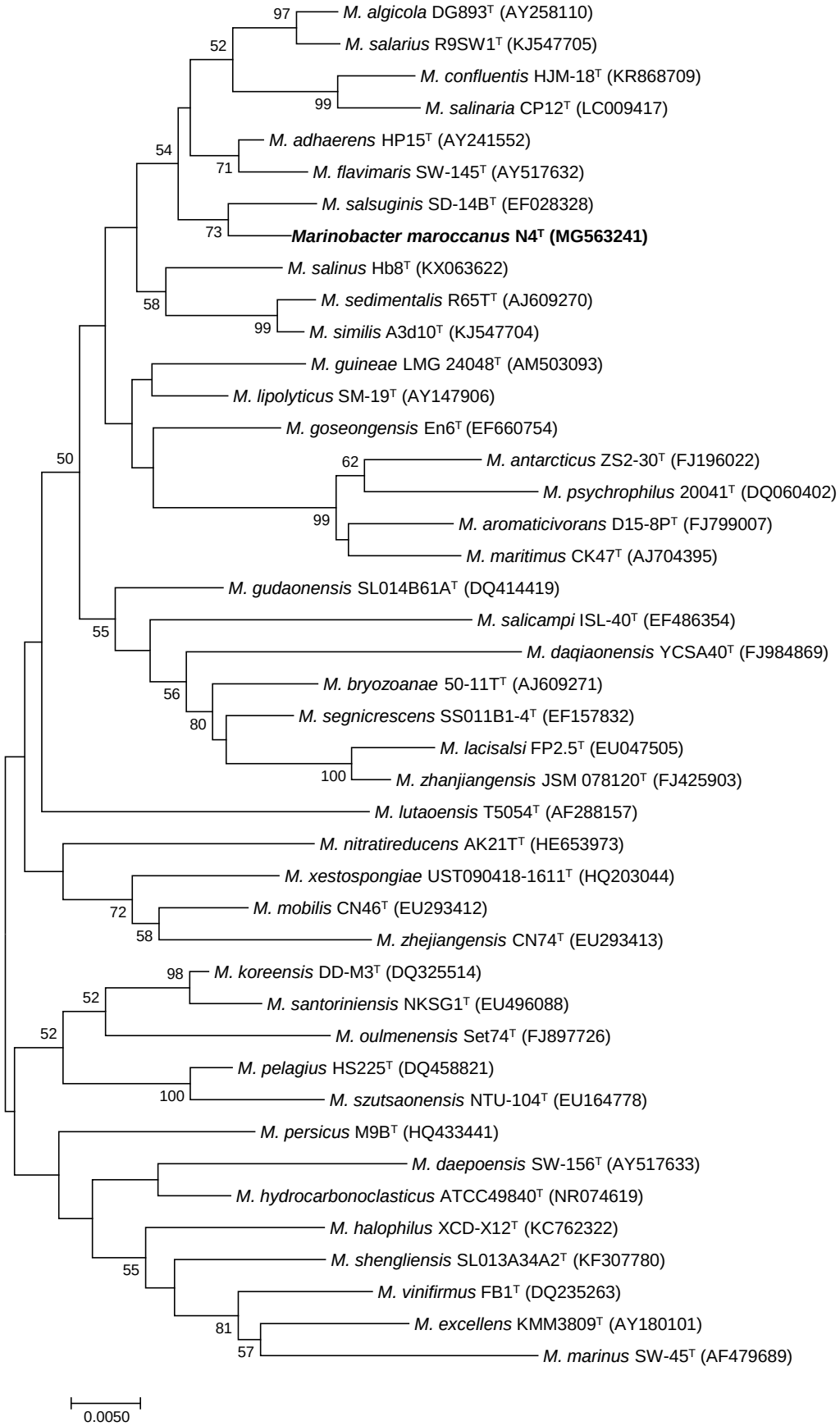
FIGURE LEGENDS

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences, showing the position of strain N4^T with respect to other members of the genus *Marinobacter*. GenBank accession numbers are indicated in parentheses. Bar, distance of 0.005 substitutions per nucleotide position as calculated by MEGA. Bootstrap values (>50 %) after 1,000 replicates are shown.

Fig 2. Neighbour-joining phylogenetic tree based on *rpoD* gene sequences, showing the position of strain N4^T with respect to other members of the genus *Marinobacter*. GenBank accession numbers are indicated in parentheses. Bar, distance of 0.02 substitutions per nucleotide position as calculated by MEGA. Bootstrap values (>50 %) after 1,000 replicates are shown.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M. salinaria CP12T (LC009417)
M. adhaerens HP15T (AY241552)
M. flavimaris SW-145T (AY517632)
M. salsuginis SD-14BT (EF028328)
Marinobacter maroccanus N4T (MG563241)
M. salinus Hb8T (KX063622)
M. sedimentalis R65TT (AJ609270)
M. similis A3d10T (KJ547704)
M. guineae LMG 24048T (AM503093)
M. lipolyticus SM-19T (AY147906)
M. goseongensis En6T (EF660754)
M. antarcticus ZS2-30T (FJ196022)
M. psychrophilus 20041T (DQ060402)
M. aromaticivorans D15-8PT (FJ799007)
M. maritimus CK47T (AJ704395)
M. gudaonensis SL014B61AT (DQ414419)
M. salicampi ISL-40T (EF486354)
M. daqiaonensis YCSA40T (FJ984869)
M. bryozoanae 50-11TT (AJ609271)
M. segnicrescens SS011B1-4T (EF157832)
M. lacisalsi FP2.5T (EU047505)
M. zhanjiangensis JSM 078120T (FJ425903)
M. lutaoensis T5054T (AF288157)
M. nitratireducens AK21TT (HE653973)
M. xestospongiae UST090418-1611T (HQ203044)
M. mobilis CN46T (EU293412)
M. zhejiangensis CN74T (EU293413)
M. koreensis DD-M3T (DQ325514)
M. santoriniensis NKSG1T (EU496088)
M. oulmenensis Set74T (FJ897726)
M. pelagius HS225T (DQ458821)
M. szutsaonensis NTU-104T (EU164778)
M. persicus M9BT (HQ433441)
M. daepoensis SW-156T (AY517633)
M. hydrocarbonoclasticus ATCC49840T (NR074619)
M. halophilus XCD-X12T (KC762322)
M. shengliensis SL013A34A2T (KF307780)
M. vinifirmus FB1T (DQ235263)
M. excellens KMM3809T (AY180101)
M. marinus SW-45T (AF479689)
97
52
99
54
71
73
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72
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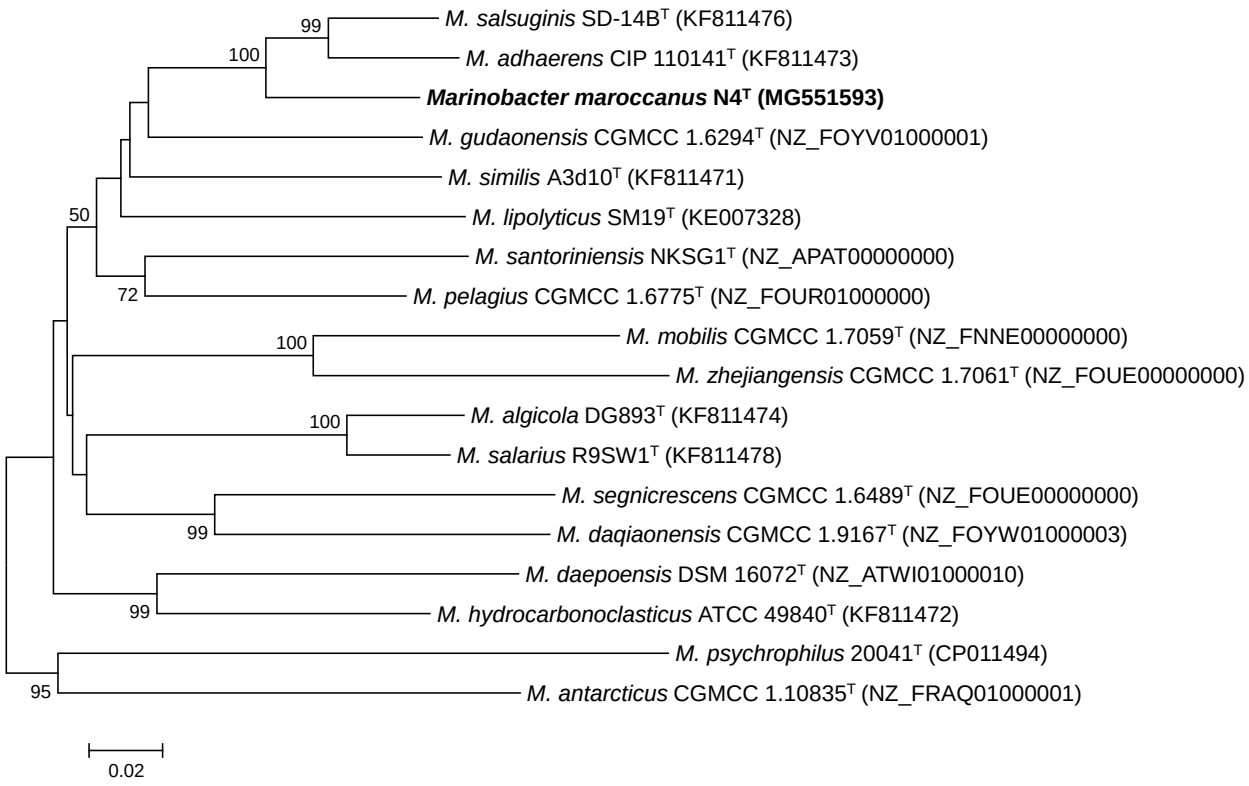
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Marinobacter maroccanus N4T (MG551593)
M. gudaonensis CGMCC 1.6294T (NZ_FOYV01000001)
M. similis A3d10T (KF811471)
M. lipolyticus SM19T (KE007328)
M. santoriniensis NKSG1T (NZ_APAT00000000)
M. pelagius CGMCC 1.6775T (NZ_FOUR01000000)
M. mobilis CGMCC 1.7059T (NZ_FNNE00000000)
M. zhejiangensis CGMCC 1.7061T (NZ_FOUE00000000)
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