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Idiomarina mangrovi sp. nov., isolated from rhizosphere soil of a mangrove *Avicennia marina* forest

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Abstract

A Gram-staining negative, aerobic, motile and rod-shaped bacterium, designated ZQ330^T, was isolated from rhizosphere soil of a mangrove (*Avicennia marina*) forest of Zhangzhou, Fujian Province, China. The growth range of NaCl concentration was 0.5–10.0 % (w/v), with an optimum at 2.5–3.0 % (w/v), the temperature range for growth was 10–40 °C, with an optimum at 28–30 °C, the pH range for growth was pH 6.0–9.5, with an optimum at pH 7.5. Phylogenetic analysis based on 16S rRNA gene sequences revealed that strain ZQ330^T exhibited less than 97.0 % sequence similarity to all type strains with validly published names and revealed that strain ZQ330^T formed a distinct lineage in the genus *Idiomarina*. The average nucleotide identity, and *in silico* DNA–DNA hybridization values between strain ZQ330^T and the reference strains were 64.8–69.9 % and 27.5–28.4 %, respectively. Chemotaxonomic analysis indicated that the main respiratory quinone was Q-8, the predominant cellular fatty acids were iso-$C_{15:0}$, iso-$C_{17:0}$, summed feature 9 ($C_{16:0}$ 10-methyl and/or iso-$C_{17:1}\omega 9c$), iso-$C_{15:1}$F, $C_{16:0}$, $C_{18:0}$, summed feature 3 ($C_{16:1}\omega 8c$ and/or iso-$C_{16:1}$ 2-OH) and summed feature 8 ($C_{18:1}\omega 6c$ and/or $C_{18:1}\omega 7c$). The polar lipid profile was composed of diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylglycerol, an unidentified glycolipid, an unidentified aminolipid, an unidentified phospholipid and two unidentified lipids. Based on the genotypic, phenotypic, chemotaxonomic and phylogenetic features, strain ZQ330^T is considered to represent a novel species, for which the name *Idiomarina mangrovi* sp. nov. is proposed. The type strain is ZQ330^T (=MCCC 1K03495^T=KCTC 62455^T).

The genus *Idiomarina* is the type genus of the family *Idiomarinaceae* within the class *Alteromonadales* and the type species, *Idiomarina abyssalis*, was originally proposed by Ivanova *et al.* in 2000 [1]. The genus *Pseudidiomarina* belongs to the family *Idiomarinaceae*, which was established by Jean *et al.* in 2006 [2]. Taborda *et al.* [3] proposed the transfer of the species classified in the genus *Pseudidiomarina* to the genus *Idiomarina* in 2009. Hence, the family *Idiomarinaceae* contained 28 species with validly published named (www.bacterio.net/idiomarina.html) at the time of writing [4]. Most species of the genus *Idiomarina* have been isolated from high salinity habitats and marine environments, such as seawater [5–10], hypersaline water [3, 11–15], marine organism [16, 17] and marine sediment [18, 19]. Various characteristics of the genus *Idiomarina* include being Gram-stain-negative, aerobic, catalase-positive and oxidase-positive, requiring NaCl for growth, have major fatty acids primarily containing iso-branched fatty acids. Q-8 is the predominant ubiquinone. The DNA G+C content ranges from 45 to 54 mol% [10, 14, 15].

A soil sample was collected from rhizosphere soil of a mangrove (*Avicennia marina*) forest of Zhangzhou (24° 20′, 117° 45′), Fujian Province, China, in the spring of 2016 and stored at 4 °C until used. Samples were suspended and diluted by sterile water, using the tenfold dilution series method, then spread onto modified ZoBell 2216E agar plates which were incubated at 28 °C [20]. The modified ZoBell 2216E medium contained (per litre distilled water): 0.5 g yeast extract, 0.1 g peptone, 0.1 g ferric citrate, 19.45 g NaCl, 8.8 g $MgCl_2{\cdot}6H_2O$, 1.8 g $CaCl_2{\cdot}2H_2O$, 0.55 g KCl, 0.16 g $NaHCO_3$, 3.24 g Na_2SO_4, 0.08 g KBr, 34 mg $SrCl_2$, 22 mg H_3BO_4, 4 mg $NaSiO_4$, 2.4 mg NaF, 1.6 mg NH_4NO_3, 8 mg Na_2HPO_4, pH 7.4 adjusted with NaOH. After 5 days

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Abbreviations: AAAI, average amino acid identity; ANI, average nucleotide identity; DDH, DNA–DNA hybridization; MA, marine 2216 agar; MB, marine 2216 broth; ML, maximum-likelihood; MP, maximum-parsimony; NJ, neighbour-joining.
The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain ZQ330^T is MK131388, and Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number RJLC00000000. The version described in this paper is version RJLC01000000.
One supplementary table and four supplementary figures are available with the online version of this article.

of incubation, a white-coloured colony was selected and purified by repeated streaking onto marine agar 2216 (MA; Difco) plates, and named strain ZQ330^T. To data, strain ZQ330^T may be the first *Idiomarina* strain isolated from a mangrove environment. Strain ZQ330^T was routinely cultured on MA and preserved at −80 °C in marine broth 2216 (MB; Difco) supplemented with 20 % (v/v) glycerol for further study.

The genomic DNA of strain ZQ330^T was extracted and purified using a Wizard Genomic DNA purification kit (Promega) by following the manufacturer's instructions. The 16S rRNA gene of strain ZQ330^T was amplified with universal primers 27F (5′-AGAGTTTGATCMTGGCTCAG-3′) and 1492R (5′-TACGGYTACCTTGTTACGACTT-3′). PCR products were purified by PCR clean-up kit (Sigma) and cloned into pMD 19 T vector (TaKaRa) for sequencing. The 16S rRNA gene sequence (1397 bp) obtained in this study was compared with closely related sequences of reference organisms via BLAST analysis (http://bioinfo.unice.fr/blast) [21] and the EzBioCloud (www.ezbiocloud.net/) [22]. The sequence was subjected to multiple alignments with the sequences of closely related bacteria using CLUSTAL_X 2.1 [23]. Phylogenetic trees were reconstructed using MEGA version 7.0 [24] by neighbour-joining (NJ; Fig. 1), maximum-parsimony (MP; Fig. S1, available in the online version of this article) and maximum-likelihood (ML; Fig. S2) methods. Strain ZQ330^T showed 96.9–92.9 % sequence similarity to the type strains of other species of the genus *Idiomarina*, and 93.8–93.4 % to the four type strains of genus *Aliidiomarina*. *Idiomarina aestuarii* JCM 16344^T showed highest sequence similarity (96.9 %) to strain ZQ330^T. Similarity values between the 16S rRNA gene sequences of strain ZQ330^T and the type strains of other genera were lower than 90 %. All the topological structures of NJ, ML and MP trees were highly similar, illustrating that strain ZQ330^T coherently clustered into the clade of genus *Idiomarina* by forming a distinct lineage among the most closely related species including *Idiomarina taiwanensis* JCM 13360^T (96.4 %) and *Idiomarina indica* JCM 18138^T (94.7 %). Hence, *I.diomarina aestuarii* JCM 16344^T (96.9 %), *Idiomarina taiwanensis* JCM 13360^T (96.4 %), *I. diomarina indica* JCM 18138^T (94.7 %) and *Idiomarina abyssalis* DSM 15222^T (93.8 %) (type species of the genus *Idiomarina*) were selected as reference strains in this study, and obtained from the Japan Collection of Microorganisms (JCM) and Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ). Unless otherwise stated, all strains were incubated in MA or MB at 28 °C.

Salt tolerance for growth was tested at 28 °C in MB prepared according to the formula of the standard medium supplemented with NaCl with 0–12.0 % (w/v) NaCl (at 0.5 % intervals, pH 7.0). The temperature range for growth was tested at 4, 10, 15, 20, 25, 28, 30, 35, 37, 40, 45 and 50 °C in MB (pH 7.0). The pH range for growth was determined at 0.5 pH intervals by supplementing 30 mM buffering agents in MB at 28 °C, including sodium 4-morpholin-1-ylethylsulphonate (MES; pH 5.5–6.4), 3-(4-Morpholino) propanesulfonic acid sodium salt (MOPS; pH 6.5–7.9), Tricine (pH 8.0–8.9) and Bis-Tris propane (pH 9.0–9.5) [25]. The optimal growth results were monitored by measuring OD_{590} in a UV/visible spectrophotometer (Ultrospec 6300 pro, Amersham Biosciences) and measured after 5 days of incubation. The growth limits were tested after 14 days of incubation [26]. Cell morphology of strain ZQ330^T was studied by transmission electron microscopy (JEM-1230, Jeol) after uranyl acetate (0.5 %, w/v) staining and paraffin sectioning methods under 80 KV (Fig. S3). Gram staining was performed with a commercial Gram-stain kit (BD) following the manufacturer's protocol and observed by optical microscopy (BX40, Olympus), after growth on MA for 3 days at 28 °C.

The whole genome of strain ZQ330^T was extracted by using a modified CTAB method [27] and sequenced by Solexa PE150 sequencing technology with the HiSeq platform (Beijing Genomics Institute). The sequencing generated 1.146 Gb of clean data (approximate 500-fold genome coverage). The *de novo* assembly of the reads was performed using ABySS 1.5.2 [28]. The assembly k-value was tested from 32 to 64 to find the optimal k-value using abyss-pe script. The quality of microbial genomes was assessed using the bioinformatic tool Check M [29]. The data of G+C content and the genome sequences of *I. indica* JCM 18138^T (FMXN00000000), *I. aesturaii* JCM 16344^T (PYVG00000000), and *I. abyssalis* DSM 15222^T (LGOW00000000) were retrieved from the GenBank database. The analysis and description methods were used and matched the standard of genome data for the taxonomy of prokaryote according to Chun *et al.* [30]. The G+C content of strain ZQ330^T was analysed by using the RAST server (http://rast.nmpdr.org/rast.cgi) using the draft genome sequence [31]. The average nucleotide identity (ANI) value was calculated using the OrthoANIu algorithm of the Chunlab's online ANI calculator [32]. The ANI value based on the BLAST alignment algorithm (ANIb) [33] and the MUMmer algorithm (ANIm) [34] were performed using JSpecies software [35]. *In silico* DNA–DNA hybridization (DDH) values were calculated by using the Genome-to-Genome Distance Calculator (GGDC) [36].

The genome completeness of strain ZQ330^T was 97.8 % with 0.17 % contamination. The genome sequences considered as good reference genomes for deeper analyses ($\geq$95 % completeness,$\leq$5 % contamination) [29]. The genome sequence of strain ZQ330^T consists of 17 scaffolds, 2 469 236 bp in total (N50=264 727 bp). The genome has a total of 2343 genes, including 2294 protein-coding genes, 46 tRNA and 3 rRNA genes (a 5S, a 16S and a 23S). The DNA G+C content of strain ZQ330^T was 50.9 mol%, which similar to the genus *Idiomarina* (45–54 mol%) as described by Hameed *et al.* [37] and distinct from *I. taiwanensis* JCM 13360^T (49.3 %) [2], *I. indica* JCM 18138^T (49.3 %), *I. aestuarii* JCM 16344^T (49.0 %) and *I. abyssalis* DSM 15222^T (46.9 %). The *in silico* DDH value between strain ZQ330^T

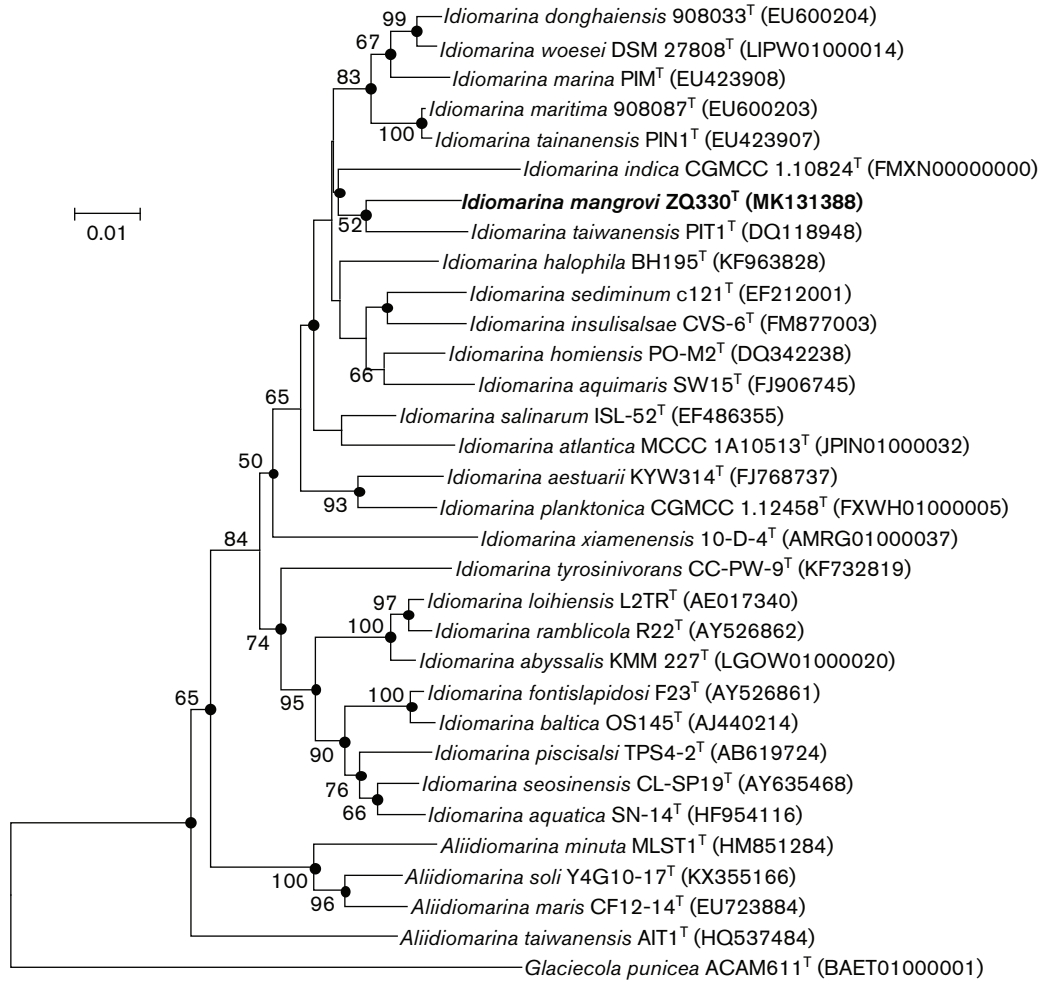

Fig. 1. Neighbour-joining phylogenetic tree based on the 16S rRNA gene sequences of strain ZQ330^T and representatives of related taxa. Bootstrap values were expressed as a percentage of 1000 replicates and only those higher than 50 % are given at the branch points. Bar, 0.01 substitutions per nucleotide position. *Glaciecola punicea* ACAM 611^T (BAET01000001) was selected as an outgroup. Filled circles indicate branches that were also formed by using the maximum-likelihood and maximum-parsimony methods.

and the reference strains of *I. indica* JCM 18138^T, *I. aestuarii* JCM 16344^T and *I. abyssalis* DSM 15222^T were 28.4 %, 28.1 and 27.5 %, respectively, which were below the 70 % threshold value for GGDC proposed for the delineation of bacterial species [33]. The ANI values between strain ZQ330^T and *I. indica* JCM 18138^T (69.8 % OrthoANI, 69.4 % ANIb, 83.6 % ANIm), *I. aesturaii* JCM 16344^T (64.8 % OrthoANI, 65.0 % ANIb, 82.9 % ANIm) and *I. abyssalis* DSM 15222^T (67.7 % OrthoANI, 66.9 % ANIb, 83.5 % ANIm) were all below the species circumscriptions threshold (95 %) [38], which supported the analysis of *in silico* DDH. In addition, DDH analysis was performed with genomic DNA from strain ZQ330^T and *I. taiwanensis* JCM 13360^T using the method described by Coram and Rawlings [39] and Tonjum *et al.* [40]. Strain ZQ330^T possessed low DNA–DNA relatedness to *I. taiwanensis* JCM 13360^T (40.4±1.8 %), which was lower than the 70 % cutoff to define a bacterial species [33].

Anaerobic growth for strain ZQ330^T was determined with a microaerobic system (AnaeroPack-MicroAero, 2.5 l; MGC) using MA, to which 20 mM sodium thiosulfate, 5 mM sodium sulfite, 20 mM sodium sulfate, 5 mM sodium nitrite and 20 mM sodium nitrate were respectively added as potential electron acceptors [25]. Oxidase activity was tested by oxidation of 1.0 % (w/v) tetramethyl-*p*-phenylenediamine reagent and catalase activity was evaluated by production of oxygen bubbles in a 3.0 % (v/v) aqueous hydrogen peroxide solution. The cell motility was studied by the hanging-drop technique and the development of turbidity throughout a tube of semi-solid MB medium. Utilization of carbon substrates was tested at concentration of 0.5 % (w/v) using whole components of soluble material of MB, yeast extract (0.01 %, w/v) was added as growth factors. Tests for indole and H_2S production, methyl red and Voges–Proskauer reactions, hydrolysis of casein, starch, gelatin, tyrosine, aesculin, Tweens (20, 40, 60, 80),

Table 1. Differential phenotypic characteristics of strain ZQ330^T and its most closely related species

Strains: 1, ZQ330^T; 2, *Idiomarina taiwanensis* JCM 13360^T; 3, *Idiomarina indica* JCM 18138^T; 4, *Idiomarina aestuarii* JCM 16344^T; 5, *Idiomarina abyssalis* DSM 15222^T.

All strains are positive for catalase, alkaline phosphatase, leucine arylamidase, trypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase; and assimilation of D-glucose, L-glutamic acid and L-proline. Aerobic and motile, requires Na+ or sea water for growth. All strains are negative for agarase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, *N*-acetyl-β-glucosaminidase, α-mannosidase, α-fucosidase; Indole production, methyl red, Voges–Proskauer reaction, degradation of L-arginine filter paper or CM-cellulose, reduction of nitrates to nitrogen, assimilation of D-fructose and trehalose, acid production from most substrates except for D-glucose, amygdalin, arbulin, aesculin and salicin in the API 50CH system. +, Positive; –, negative. ND, not detected.

Characteristic	1	2	3	4	5
Growth in/at:					
NaCl (%)	1.0–10.0	0.5–11.0*	0.5–10.0†	1.0–10.0‡	0.6–15.0§
Optimum NaCl (%)	2.5–3.0	1.0–4.0*	1.5–3.0†	3.0‡	ND
Temperature (°C)	10–40	15–42*	12-50†	10–37‡	4–30§
Optimum temperature (°C)	28–30	30–35*	35-37δ	30‡	20–22§
pH	6.0–9.5	6.5–9.0*	6.0–9.0†	5.0–10.0‡	5.5–9.5§
Optimum pH	7.5	8.0*	7.0–7.5†	7.0‡	7.5–8.0§
Cell diameter (μm)	0.2	0.4–0.5*	0.6–0.8†	0.3‡	0.7–0.9§
G+C content (%)	50.9	49.3*	49.3	49.0	46.9
H_2S production	+	–	–	–	–
Oxidase	–	+	+	+	+
Amylase	+	–	–	–	–
Degradation of:					
Casein	+	–	–	+	–
Starch	+	–	–	–	–
Tween 20	+	+	–	+	+
Tween 40	+	+	–	+	+
Tween 60	+	+	–	+	+
Tween 80	–	+	–	+	+
Gelatin	+	+	–	–	+
Tyrosine	–	+	+	+	+
DNA	–	–	+	+	+
Tests of API ZYM:					
Esterase (C4)	+	+	+	–	+
Esterase lipase (C8)	+	+	+	–	+
Lipase (C14)	–	+	–	–	–
Valine arylamidase	+	+	–	–	+
Cystine arylamidase	+	+	–	–	–
α-Chymotrypsin	+	+	–	+	+
Tests of API 20NE:					
Reduction of nitrates to nitrites	–	+	+	–	–
Fermentation of glucose	–	–	+	–	–
Urease	–	+	–	–	–
Aesculin ferric citrate	+	–	–	+	–
Tests of API 50CH:					
D-Glucose	+	+	–	–	–
Amygdalin	+	–	–	–	–
Arbulin	+	–	–	–	–
Aesculin	+	+	–	+	–
Salicin	+	–	–	–	–
Utilized as sole carbon sources:					
D-Mannose	+	–	+	+	–
Citric acid	+	–	–	+	+
Cellobiose	+	–	–	–	–

Table 1. cont.

Characteristic	1	2	3	4	5
Melibiose	+	−	−	−	−
maltose	+	+	+	−	−
Lactose	+	−	−	+	+
L-arabinose	−	−	+	−	−
Sucrose	−	−	+	−	+
D-Sorbitol	−	−	+	+	+
myo-Inositol	−	−	+	+	−
Succinic acid	−	+	−	−	−
i-Erythritol	−	−	−	+	−
D-Galactose	−	−	−	+	+
L-Rhamnose	−	−	+	+	−

*Data from Jean *et al.* [2].

†Data from Song *et al.* [8].

‡Data from Park *et al.* [7].

§Data from Ivanova *et al.* [1].

carboxymethyl cellulose (CMC), filter paper and gelatin were performed as described previously [26]. Acid production was tested using API 50CH systems with marine oxidation-fermentation (MOF) medium. Enzymatic activities and other physiological and biochemical traits were tested using API ZYM and API 20NE stripes (bioMérieux) according to the manufacturer's instructions. The reference strains were tested simultaneously with strain ZQ330^T under the same conditions.

The phenotypic characteristics (Table 1) revealed that there are many common traits between strain ZQ330^T and reference strains. All strains were isolated from marine environments, aerobic and motile, positive for catalase, alkaline phosphatase, leucine arylamidase, trypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase; and assimilation of D-glucose, L-glutamic acid and L-proline. All strains are negative for agarase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, *N*-acetyl-β-glucosaminidase, α-mannosidase, α-fucosidase, indole production, Voges–Proskauer reaction, degradation of L-arginine filter paper or CM-cellulose, and reduction of nitrates to nitrogen; and assimilation of D-fructose and trehalose. Acid production data were not obtained from most substrates except for D-glucose, amygdalin, arbulin, aesculin and salicin in the API 50CH system. Consequently, many phenotypic features could distinguish strain ZQ330^T from the reference strains. Such as, strain ZQ330^T was positive for H_2S production, degradation of casein and starch, acid production from amygadlin, arbulin and aslicin, utilization of cellobiose, and having melibiose as a sole carbon source, but the reference strains were all negative for these features. However, all references strains were able to degraded tyrosine, but strain ZQ330^T was not. In addition, large distinct phenotypic features enabled strain ZQ330^T to be distinguished from the reference strains (Table 1).

For analysis of the whole-cell fatty acid profile, strain ZQ330^T and the four reference strains were harvested during the third quadrants, grown on MA at 28 °C for 3 days. Whole cell fatty acids were analysed according to the instructions of the Microbial Identification System (MIDI; Microbial ID) with the standard MIS Library Generation Software version 4.5 [41]. Strain ZQ330^{T}was grown on MB at 28 °C for 3 days, and cells were collected from 300 ml culture broth by filtration. Polar lipids were extracted with chloroform/methanol (1 : 2; v/v) and identified by two-dimensional TLC on silica gel 60 F_{254} (Merck) plates (10 cm×10 cm) as described by Tindall [42]. Chromatography in the first direction, was performed by using chloroform/methanol/water (65 : 25 : 3.8, v/v) and chloroform/methanol/acetic acid/water (40 : 7.5 : 6 : 1.8, v/v) in the second direction as developing solvents. The lipids were visualized on the plates, after being developed in the development solvent. For visualization and detection of total polar lipids, aminolipids, phospholipids and glycolipids, TLC plates were sprayed with molybdophosphoric acid, ninhydrin reagent, molybdenum blue and α-naphthol/H_2SO_4 reagent, respectively [42]. To determine respiratory quinones, strain ZQ330^T was cultured on MB for 3 days at 28 °C, and then cells were harvested and freeze-dried. Then respiratory quinones were extracted from freeze-dried cells (500 mg) using chloroform/methanol (2 : 1, v/v) and analysed by LC-MS [43].

The predominant respiratory quinone in strain ZQ330^T was ubiquinone 8 (Q-8; 97 %) which was in agreement with all members of the genus *Idiomarina* [14]. A minor amount of Q-7 (3 %) was also present. The major cellular fatty acids (>10 %) of strain ZQ330^T were iso-$C_{15:0}$, iso-$C_{17:0}$ and summed feature 9 ($C_{16:0}$ 10-methyl and/or iso-$C_{17:1}\omega 9c$). iso-$C_{15:1}$F, $C_{16:0}$, $C_{18:0}$, summed feature 3 ($C_{16:1}\omega 8c$ and/or iso-$C_{16:1}$ 2-OH) and summed feature 8 ($C_{18:1}\omega 6c$ and/or $C_{18:1}\omega 7c$) were also obtained from strain ZQ330^T which the

component ratios are over 5 %. A comparison of the fatty acid profiles is shown in Table S1, the results of the fatty acid analyses of reference strains in this study were also consistent with original descriptions, revealed that the data were similar in terms of the major fatty acids [1, 2, 7, 8] and major differences only in contents of iso-$C_{15:0}$, iso-$C_{15:1}$F, $C_{16:0}$, $C_{18:0}$, summed feature 8 ($C_{18:1}\omega6c$ and/or $C_{18:1}\omega7c$) and summed feature 9 ($C_{16:0}$ 10-methyl and/or iso-$C_{17:1}$ $\omega9c$) between strain ZQ330^T and the reference strains. As shown in Fig. S4, the polar lipids of strain ZQ330^T comprised diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylglycerol, an unidentified glycolipid, an unidentified aminolipid, an unidentified phospholipid and two unidentified lipids.

In conclusion, on the basis of the phylogenetic analysis, genotypic, phylogenetic and phenotypic characteristics, strain ZQ330^T was clearly distinguished from other species within the genus *Idiomarina*. A novel species, *Idiomarina mangrovi* sp. nov., with the type strain ZQ330^T, is proposed.

DESCRIPTION OF *IDIOMARINA MANGROVI* SP. NOV.

Idiomarina mangrovi (man.gro′vi. N.L. gen. n. *mangrovi* of a mangrove, referring to the isolation of the type strain from mangrove soil).

Cells are Gram-stain-negative and motile by means of lateral flagellum. Colonies on MA medium are circular, convex, smooth, opaque, non-pigmented and approximately 1.0–2.0 mm in diameter after 3 day at 28 °C. Cells are rod-shaped, about 0.2 µm wide and 0.8–1.4 µm long. Growth occurs at 10–40 °C (optimum, 28–30 °C), pH 6.0–9.5 (pH 7.5) and in 0.5–10.0 % (w/v) NaCl (2.5–3.0 %). Positive for catalase and amylase activities, H_2S production, degradation of casein, gelatin, starch and Tweens (20, 40, 60), and assimilation of D-glucose, L-glutamic acid, L-proline, D-mannose, citric acid, cellobiose, melibiose, maltose and lactose. Negative for oxidase, agarase, DNase, indole production, methyl red test, Voges–Proskauer reaction, reduction of nitrates to nitrogen, and degradation of L-arginine, Tween 80, tyrosine, filter paper and CM-cellulose. The activities of alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, aesculin freeic citrate, α-chymotrypsin, acid phosphatase and naphthol-AS-BI-phosphohydrolase are present. Acid production from D-glucose, amygdalin, arbulin, aesculin and salicin. The principal fatty acids are iso-$C_{15:0}$, iso-$C_{17:0}$ and summed feature 9 ($C_{16:0}$ 10-methyl and/or iso-$C_{17:1}$ $\omega9c$). iso-$C_{15:1}$F, $C_{16:0}$, $C_{18:0}$, summed feature 3 ($C_{16:1}\omega8c$ and/or iso-$C_{16:1}$ 2-OH) and summed feature 8 ($C_{18:1}\omega6c$ and/or $C_{18:1}\omega7c$). The respiratory quinone is Q-8. The polar lipid profile is composed of diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylglycerol, an unidentified glycolipid, an unidentified aminolipid, an unidentified phospholipid and two unidentified lipids.

The type strain, ZQ330^T (=MCCC 1K03495^T=KCTC 62455^T), was isolated from rhizosphere soil of mangrove *Avicennia marina* forest of Zhangzhou (24° 20′, 117° 45′), Fujian Province, China. The GenBank accession numbers for the 16S rRNA gene sequence and the whole genome sequence of strain ZQ330^T are MK131388 and RJLC00000000, respectively. The DNA G+C content of the type strain is 50.9 mol% (calculated from the genome sequence).

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

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