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TAXONOMIC DESCRIPTION

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Marinobacter salinexigens sp. nov., a marine bacterium isolated from hadal seawater of the Mariana Trench

Waqar Ahmad[1], Yanfen Zheng[1], Yuying Li[1], Wen Sun[1], Yuyao Hu[1], Xinxin He[1], Ronghua Liu[1], Chun-Xu Xue[1] and Xiao-Hua Zhang[1,2,3,*]

Abstract

A Gram-stain-negative, strictly aerobic, non-motile and rod-shaped bacterium, designated ZYF650^T, was isolated from the hadal seawater (9600 m) of the Mariana Trench. Results of phylogenetic analysis based on 16S rRNA gene sequences indicated that ZYF650^T formed a lineage within the family *Alteromonadaceae* that was distinct from the most closely related species *Marinobacter mobilis* and *Marinobacter nitratireducens* with 16S rRNA gene sequences similarities of 98.0 and 97.7%, respectively. Strain ZYF650^T showed average nucleotide identity values of 75.7% with *Marinobacter hydrocarbonoclasticus*, 73.3% with *Marinobacter mobilis* and 79.3% with *Marinobacter nitratireducens*, and DNA–DNAhybridization values of 21.5, 21.3 and 22.0% with *M. hydrocarbonoclasticus*, *M. mobilis* and *M. nitratireducens*, respectively, which were lower than the threshold for species delineation. Strain ZYF650^T grew with 0–14% (w/v) NaCl (optimum, 7–8%) at a temperature range of 10–45 °C (optimum, 28 °C) and pH 6.0–9.5 (optimum, pH 7.0–8.0). The sole respiratory quinone was ubiquinone-9 (Q-9). The polar lipids in ZYF650^T comprised phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, three unidentified polar lipids, two unidentified aminolipids and two phospholipids. The predominant fatty acids (more than 10% of total fatty acids) were $C_{18:1}\omega9c$ (21.9%), $C_{16:0}$ (21.7%), $C_{12:0}$ 3-OH (14.0%), $C_{16:1}\omega9c$ (13.2%) and $C_{12:0}$ (12.2%). The DNA G+C content of strain ZYF650^T was 55.6%. On the basis of polyphasic taxonomic analysis, strain ZY650^T is considered to represent a novel specie of the genus *Marinobacter* in the family *Alteromonadaceae*, for which the name *Marinobacter salinexigens* sp. nov. is proposed. The type strain is ZYF650^T (=JCM 33013^T=MCCC 1K03552^T).

The genus *Marinobacter*, within the family *Alteromonadaceae*, class *Gammaproteobacteria*, was first established by Gauthier *et al.* [1] Other members of the family comprise the type genus *Alteromonas* and the genera *Aestuariibacter*, *Agarivorans*, *Agaribacter*, *Alginatibacterium*, *Aliiglaciecola*, *Alkalimarinus*, *Aliagarivorans*, *Alishewanella*, *Bowmanella*, *Catenovulum, Gayadomonas*, *Glaciecola*, *Hydrocarboniclastica*, *Lacimicrobium*, *Mangrovitalea*, *Haliea*, *Neptunicella*, *Marisediminitalea*, *Marinimicrobium*, *Marinobacterium*, *Melitea*, *Microbulbifer*, *Paraglaciecola*, *Planctobacterium*, *Pseudobowmanella*, *Saliniradius*, *Salinimonas* and *Tamilnaduibacter* [2]. The type genus *Alteromonas* was created by Baumann *et al.* [3] According to the DSMZ's PNU database (www.dsmz.de/services/online-tools/prokaryotic-nomenclature-up-to-date/prokaryotic-nomenclature-up-todate/genus/517511), the genus *Marinobacter* includes 50 species at the time of writing. The type species is *Marinobacter hydrocarbonoclasticus* [1]. Bacteria belonging to the genus *Marinobacter* are commonly detected in diverse marine environments such as coastal sediments [1, 2], sea sediments [4], marine aggregates [5], Antarctic environment [6], oil-polluted saline soil [7] and saltern crystalizing pond [8]. The genus comprises many species that could be of great biotechnological interest, as halotolerant and halophilic micro-organisms are well known for their potential biotechnological applications [9]. In this study, we describe a novel, strictly aerobic bacte-

Author affiliations: [1]College of Marine Life Sciences, and Institute of Evolution & Marine Biodiversity, Ocean University of China, Qingdao 266003, PR China; [2]Laboratory for Marine Ecology and Environmental Science, Qingdao National Laboratory for Marine Science and Technology, Qingdao 266071, PR China; [3]Frontiers Science Center for Deep Ocean Multispheres and Earth System, Ocean University of China, Qingdao 266100, PR China.
***Correspondence:** Xiao-Hua Zhang, xhzhang@ouc.edu.cn
Keywords: *Marinobacter salinexigens*; hadal seawater; Mariana Trench.
Abbreviations: ANI, average nucleotide identity; DDH, DNA–DNA hybridization; MA, marine agar; MB, marine broth; ML, maximum-likelihood; MP, maximum-parsimony; NJ, neighbour-joining; Q-9, ubiquinone-9.
The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain ZYF650^T is MN325154. The Whole Genome Shotgun project of strain ZYF650^T has been deposited at DDBJ/ENA/GenBank under the accession VTUU00000000. The version described in this paper is version VTUU01000000.
One supplementary table and four supplementary figures are available with the online version of this article.

rium, ZYF650^T, by using a polyphasic characterization which included the determination of chemotaxonomic and other phenotypic properties and detailed phylogenetic investigation based on 16S rRNA gene sequence.

Strain ZYF650^T was isolated from the hadal seawater at a depth of 9600 m of the Mariana Trench at station L8 (142°11.5′ N 11°20′ E) during the expedition on the R/V *Dong Fang Hong 2* in September 2016 [10, 11]. The Mariana Trench is located in the western Pacific Ocean, an average of 200 km to the east of the Mariana Islands, in the Western Pacific east of Philippines and harbours distinctive micro-organisms in the hadal seawater [10, 11]. The seawater samples were spread on marine agar 2216E (MA; Becton Dickinson) plates and incubated at the room temperature (approximately 22 °C) on board and 28 °C in the laboratory. A circular, smooth and yellowish-white colony, designated strain ZYF650^T, was isolated at 28 °C and subsequently purified three times. Cultures were maintained on MA plates at 28 °C and stocks were preserved in sterile 0.85% (w/v) saline supplemented with glycerol at a final concentration of 15% (v/v) at −80 °C. The type species *M. hydrocarbonoclasticus* ATCC 49840^T, obtained from the American Type Culture Collection (ATCC), as well as two most closely related species *Marinobacter mobilis* CGMCC 1.7059^T, obtained from the China General Microbiological Culture Collection Center (CGMCC), and *Marinobacter nitratireducens* JCM 18428^T, obtained from the Japan Collection of Microorganisms (JCM), were selected as reference strains. Unless stated otherwise, all reference strains were grown under their optimal culture conditions [1, 12, 13].

For 16S rRNA gene sequencing, the DNA of strain ZYF650^T was extracted and purified using standard methods [14]. PCR amplification, cloning and sequencing of the 16S rRNA gene were carried out according to the methods of Zhang *et al.* [15]. The almost-complete 16S rRNA gene sequence (1544 nt) was checked manually and submitted to the GenBank database. Pairwise similarity values between strain ZYF650^T and its closely related type strains were calculated using the EzBioCloud server (www.ezbiocloud.net) [16]. The 16S rRNA gene sequences of the related strains were retrieved from the NCBI database (www.ncbi.nlm.nih.gov) and aligned by using the CLUSTAL X program [17]. Phylogenetic trees were reconstructed based on the neighbour-joining (NJ) [18], maximum-likelihood (ML) [19] and maximum-parsimony (MP) [20] algorithms using MEGA version 7.0 [21]. The Kimura two-parameter model [22] was chosen for both NJ and ML analyses, and the tree-bisection-reconnection (TBR) model was selected for MP analyses. The topologies of phylogenetic trees were evaluated based on the bootstrap resampling method with 1000 replicates.

Pairwise alignment of the 16S rRNA gene sequence of strain ZYF650 showed the highest sequence similarity to *M. mobilis* CGMCC 1.7059^T (98.0%), followed by *M. nitratireducens* JCM 18428^T (97.7%) and *M. xestospongiae* (97.6%) and other species within the genus *Marinobacter*. The 16S rRNA gene sequence similarities indicated that *M. mobilis* and *M. nitratireducens* were the nearest phylogenetic neighbours to the novel isolate. 16S rRNA gene sequence phylogenetic analysis based on the ML (Fig. 1), MP (Fig. S1, available in the online version of this article) and NJ (Fig. S2) algorithms showed that strain ZYF650 formed a deeply rooted lineage within the clade of the genus *Marinobacter* and separated it from the clade composed of the species *M. mobilis*, *M. nitratireducens* and *M. xestospongiae*.

Gram-staining was investigated using the standard method [23]. The cell morphology was observed by transmission electron microscopy (JEM-1200EX, JEOL) after cells had been negatively stained with 1% (w/v) phosphotungstic acid (Fig. S3) following culturing on MA at 28 °C for 24 h [24]. In order to test growth under anaerobic conditions, the strain was cultured on MA with cysteine (0.01%, w/v) as the reducing agent and resazurin (0.02%, w/v) as the anaerobic condition index in an anaerobic jar filled with nitrogen and supplied with a packet of AneroPack-Anaero (Mitsubishi Gas Chemical Co.) and incubated at 28 °C for at least 1 month. Meanwhile, anaerobic growth was also examined on MA supplemented with $NaNO_2$, KNO_3, Na_2SO_4 and $Na_2S_2O_3$ (1.5 g l^{-1}) as terminal electron acceptors, respectively, in the jar mentioned above. The temperature range for growth was determined on MA plates as well as in MB tubes by incubating cultures at 0–50 °C (0, 4, 10, 16, 20, 24, 26, 28, 32, 37, 42, 45 and 50 °C) for 7 days, and at 0 °C and 4 °C for at least 30 days. In the salinity experiment, distilled water was used to prepare synthetic marine ZoBell broth (per litre: 5 g peptone, 1 g yeast extract and 0.01 g $FePO_4$). NaCl concentrations were adjusted to 0, 0.5 and 1–30% (w/v, at intervals of 1%). In the pH range experiment, growth was evaluated at pH 2.0–11.0 (intervals of 1.0 pH unit) in marine broth 2216E (MB; Becton-Dickinson) using the following buffer systems: H_3PO_4/KH_2PO_4 (pH 2.0), sodium ethanoate/ethanoic acid (pH 3.0–5.0), MES (50 mM, pH 5.0–6.0), MOPS (50 mM, pH 7.0), Tricine (50 mM, pH 8.0), TAPS (50 mM, pH 9.0), CAPS (50 mM, pH 10.0) and $Na_2CO_3/NaHCO_3$ (50 mM, pH 11.0). The salinity and pH ranges supporting growth were investigated in MB by measuring the optical densities in test tubes (wavelength 590 nm). The following phenotypic tests, including hydrolysis of starch, casein, gelatin, chitinase cellulose and Tweens 20, 40 and 80, were carried out on strain ZYF650^T and the reference strains according to the standard approaches [25] except that sterile seawater was substituted for distilled water. DNase activity was examined by using DNase agar (Qingdao Hope Bio-technology Co., Ltd) according to the manufacturers' instructions. Amylase, DNAs and gelatinase activities were examined on respective agars with sterile seawater [26]. Activities of constitutive enzymes, fermentation/oxidation profile, acid production, and substrate utilization as sole carbon and energy source of strain ZYF650^T were determined after growth on MA at 28 °C for 24 h by using API 20E, API 50CH and API ZYM strips (bioMérieux) and the GN III MicroPlate (Biolog) according to the manufacturer's instructions except that sterile seawater was used to prepare the inoculum [27]. Antibiotic susceptibility tests were performed using the disc diffusion method [28]. The detailed morphological, physiological and biochemical characteristics of strain ZYF650^T are given in Table 1 and the species description.

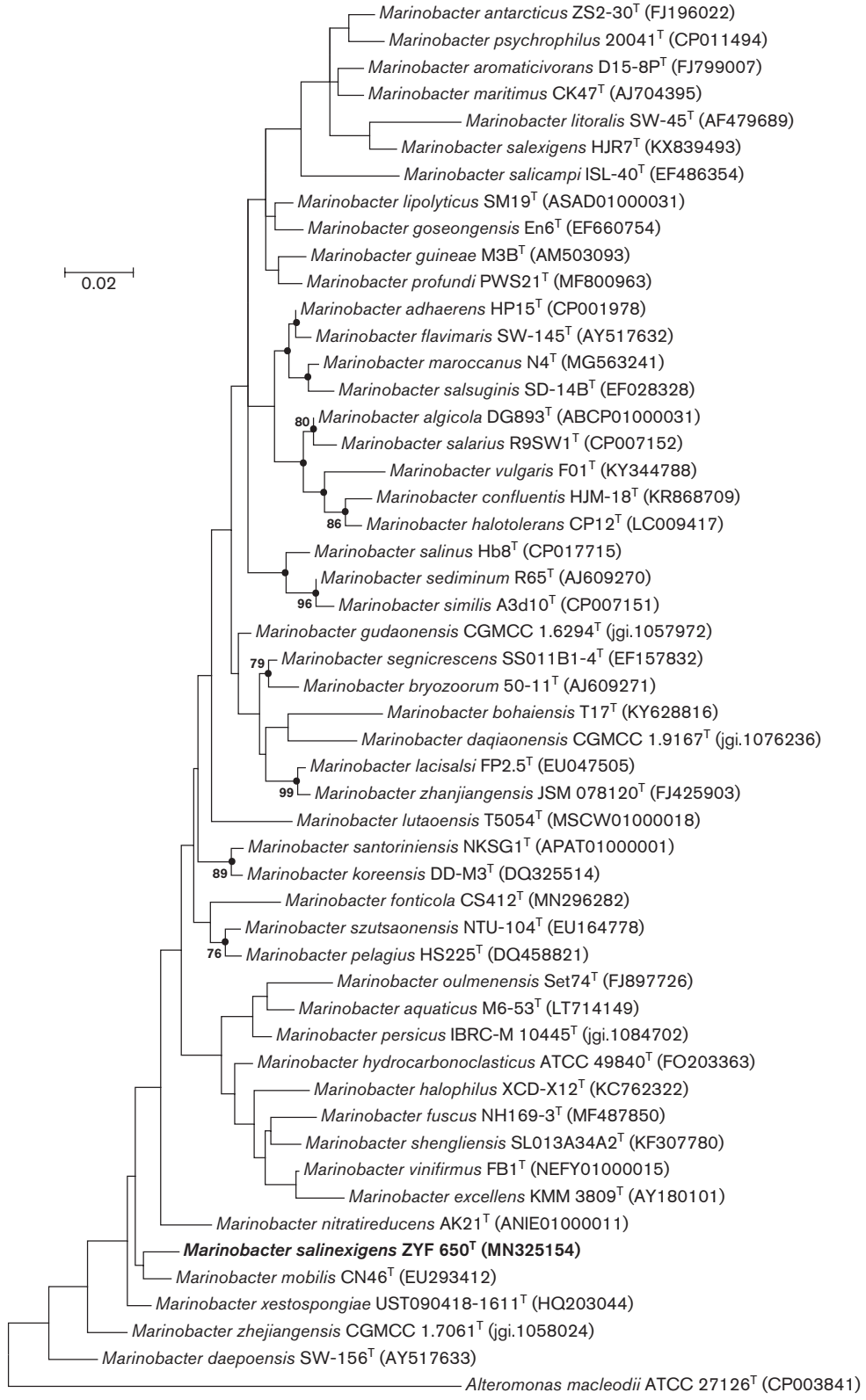

Fig. 1. Maximum-likelihood phylogenetic tree based on 16S rRNA gene sequences (1544 nt) showing the phylogenetic position of strain ZYF650^T and other closely related species. Percentage bootstrap values above 70% (1000 replicates) are shown at branch nodes. Closed circles indicate that the corresponding nodes were also recovered in trees generated with the neighbour-joining and maximum-parsimony algorithms. *Alteromonas macleodii* ATCC 27126^T (GenBank accession no. CP003841) was used as the out-groups. Bar, 0.02 nucleotide substitutions per nucleotide position.

Table 1. Characteristics that differentiate strain ZYF650^T from related species

Strains: 1, YF650^T; 2, *Marinobacter mobilis* CGMCC 1.7059^T; 3, *Marinobacter nitratireducens* JCM 18428^T; 4, *Marinobacter hydrocarbonoclasticus* ATCC 49840^T; 5, *Marinobacter zhejiangensis* CGMCC 1.7061^T; 6, *Marinobacter xestospongiae* JCM 17469^T. Unless otherwise indicated all data from the present study except for the data on cell size and DNA G+C content. +, Positive; –, negative; ND, no data; W, weakly positive reaction.

Characteristics*	**1**	**2**	**3**	**4**	**5**	**6**
Cell shape	Rod	Rod[a]	Rod[b]	Rod[c]	Rod[a]	Rod[d]
Cell size (μm)	0.3–0.4×1.1–1.5	0.5–0.8×1.5–3.1[a]	1.0×2.5[b]	0.6–0.8×2–2.5[c]	1.0–2×0.4–0.8[a]	0.6–0.8×2.0–2.5[d]
NaCl (%, w/v) tolerance range for growth (optimum)	0–14.0 (7.0–8.0)	0.5–10.0 (3.0–5.0)	0.5–6.0 (2.0)	0.5–20.0 (3.0–6.0)	0.5–10.0 (1.0–3.0)[a]	0.5–6.0 (2.0)[d]
pH range for growth (optimum)	6.0–9.5 (7.0–8.0)	6.5–9 (7.0–7.5)	6.0–10.0 (7.0)	6.0–12.0 (7.0–7.5)	6.0–9.5 (7.0–7.5)[a]	5.0–10.0 (7.0–8.5)[d]
Temperature (°C) range for growth (optimum)	10–45 (26–28)	15–42 (30–35)	15–42 (28–35)	10–45 (32)	15–42 (30–35)[a]	15–42 (28–36)[d]
Acid is produced from:						
Lactose	+	–	–	–	–[a]	+[d]
Citrate	–	–	–	+	–[a]	–[d]
D-Xylose	–	–	–	–	–[a]	–[d]
Cellobiose	+	–	–	–	–[a]	–[d]
Acetate	–	+	–	+	+[a]	+[d]
Maltose	W	–	W	–	–[a]	+[d]
Fructose	+	–	+	–	–[a]	+[d]
Glucose	+	–	+	–	–[a]	–[d]
Trehalose	–	–	–	–	–[a]	+[d]
Sucrose	+	–	+	–	–[a]	–[d]
Mannose	–	–	–	–	–[a]	+[d]
Inulin	–	–	+	–	ND[a]	–[d]
Sodium gluconate	–	–	+	–	ND[a]	ND[d]
Succinate	–	+	–	+	+[a]	+[d]
Glycerol	+	–	+	–	–[a]	+[d]
Dulcitol	–	–	–	–	–[a]	+[d]
Inositol	+	+	W	–	–[a]	–[d]
Sorbitol	–	–	+	–	–[a]	–[d]
Mannitol	+	–	+	–	–[a]	+[d]
D-Arabitol	+	W	+	W	ND[a]	–[d]
Methyl α-D-glucoside	–	–	+	–	ND[a]	ND[d]
Rhamnose	–	–	+	–	–[a]	+[d]
Respiratory quinone	Q-9	ND[a]	Q-10[b]	ND[c]	ND[a]	Q-9
Other polar lipids	PL1–PL2, L1, L2–L3	PL3, L2–L5	PL2, L1	PL3, L5–L7	ND[a]	ND[d]
DNA G+C content (mol%)	55.6	58.0–58.9[a]	54.6[b]	52.7[c]	58.4[a]	57.1[d]

*Data taken from: *a*, [13]; *b*, [12]; *c*, [13]; *d*, [43].

For cellular fatty acid analysis, strain ZYF650^T and the reference strains were grown on MA at their respective optimal temperatures for 3 days until the bacterial growth reached the late exponential stage according to the four quadrant streak method [29]. Fatty acid methyl esters were prepared and analysed according to the MIDI standard protocol (Sherlock Microbial Identification System, version 6.10), and identified by the RTSBA 6.0 database of the Microbial Identification System [29]. For respiratory quinone and polar lipid analyses, cell biomass were harvested from MB after shaking at 28 °C for 2 days and freeze-dried. The respiratory quinone of strain ZYF650^T was extracted with chloroform–methanol (2:1, v/v), separated by TLC and identified by HPLC [30]. Polar lipids were extracted [31] and separated by two-dimensional TLC on silica gel 60 F254 plates (Merck) using chloroform–methanol–water (65:25:4, v/v/v) for the first dimension and chloroform–methanol–acetic acid–water (80:12:15:4, v/v/v/v) for the second dimension [32]. Lipids extracted were identified by spraying the plates with appropriate detection reagents [33]. Briefly, all the lipids were detected by using 5% ethanolic molybdophosphoric acid. Ninhydrin spray was applied to determine most of the lipids with free amino groups, while spraying the plate with the lipid phosphate reagent of Dittmer and Lester after the ninhydrin spray could reveal the presence of phospholipids.

The genomic DNA of strain ZYF650^T was extracted according to the procedure of Moore *et al.* [34], and the DNA G+C content was determined by whole genome sequencing. The genome sequencing of strain ZYF650^T was performed on the Illumina HiSeq platform. SOAP*denovo* assembler software was applied to assemble these reads [35] (http://sourceforge.net/projects/soapdenovo2/files/SOAPdenovo2/). Putative coding sequences (CDSs) were identified by Glimmer 3.0 [36]. RNAmmer [37] and tRNAscan [38] were used to predict rRNAs and tRNAs, respectively, and sRNA was identified using the Rfam database [39]. DNA–DNA hybridization (DDH) was performed by method provided by DSMZ (http://ggdc.dsmz.de) [40]. The averagenucleotide identity (ANI; OrthoANI algorithm) and the G+C content were calculated using the software OAT hosted in the EzBioCloud portal [16, 41]. The genome of strain ZYF650^T is 4240922 bp. Among 3899 predicted genes, 3839 genes are protein coding genes and 60 genes are RNAs. A total of nine rRNA genes (five 5S rRNAs, two 16S rRNAs and two 23S rRNAs), 50 tRNAs and one tmRNA genes were identified in the genome. The DNA G+C content of strain ZYF650^T was 55.6%, which was higher than the species *M. hydrocarbonoclasticus* ATCC 49840^T (52.7%) [1] and *M. nitratireducens* JCM 18428^T (54.6%) [6], while lower than the species *M. mobilis* CGMCC 1.7059^T (58.0–58.9%) [7]. The ANI and DDH values between ZYF650^T and its reference species *M. hydrocarbonoclasticus*, *M. mobilis* and *M. nitratireducens* calculated from their genome sequences were 75.7 and 21.5%, 73.3 and 21.3%, and 79.3 and 22.0%, respectively.

The fatty acid profile of strain ZYF650^T was similar to those of *Marinobacter* species described previously. The predominant cellular fatty acids (>10% of total fatty acids) of strain ZYF650^T were $C_{18:1}$ ω9*c* (21.9%), $C_{16:0}$ (21.7%), $C_{12:0}$ 3-OH (14.0%), $C_{16:1}$ ω9*c* (13.2%) and $C_{12:0}$ (12.2%), which are also the most common fatty acids of the phylogenetically most closely related species. The detailed quantitative analysis of the fatty acids of the novel isolate and related species are listed in Table S1.

The polar lipids in ZYF650^T comprised phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, three unidentified polar lipids (L1, L2, L3), two unidentified aminolipids (AL1, AL2) and two phospholipids (PL1, PL2) (Fig. S4). In the reference type strains, similar compositions of phospholipids, phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol and the unidentified polarlipids (L1, L2) were observed. There were some differences between strain ZYF650^T and the three reference strains. The reference strains contain aminophospholipids, while *M. hydrocarbonoclasticus* ATCC 49840^T has a phospholipid (PL4), and *M. nitratireducens* JCM 18428^T contains unidentified polarlipids (L5, L6, L7). All major polar lipids were the same. The sole respiratory quinone detected in strain ZYF650^T was ubiquinone-9 (Q-9), which was different from other three reference strains.

The conclusion drawn from phylogenetic analysis that strain ZYF650^T represents a novel species of the family *Alteromonadaceae* was supported by morphological and physiological characteristics that distinguished it from other species. Phylogenetically, strain ZYF650^T is different from the nearest neighbours within the genus *Marinobactor*. Based on analyses of physiological and chemotaxonomic characteristics, strain ZYF650^T showed significant differences with other species: (i) The predominant respiratory quinone, as an important criterion for differentiating different species, clearly proved that strain ZYF650^T was distinct from reference strains. The sole respiratory quinone of ZYF650^T was quinone-9 (Q-9), which in reference strains was Q-10. (ii) None of the reference strain grow below 0.5% NaCl, however strain ZYF650^T was able to grow at 0% NaCl, a feature that differentiated this strain from its relatives within the genus. (iii) Strain ZYF650^T showed ANI values of 75.7% with *M. hydrocarbonoclasticus*, 73.3% with *M. mobilis* and 79.3% with *M. nitratireducens* and DDH values of 21.5, 21.3 and 22.0% with *M. hydrocarbonoclasticus*, *M. mobilis* and *M. nitratireducens*, respectively. As species boundaries for ANI values are 95–96 and DDH values are 70%, genome comparison results proved that strain ZYF650^T establish a novel *Marinobacter* species [42]. (iv) Relatively high contents of $C_{18:1}$ *ω9c* (21.9%) in ZYF650^T also differentiate the species from type strains *M. mobilis* and *M. nitratireducens* which contain 3.7 and 16.7%, respectively. (v) The optimal temperature range of ZYF650^T is relatively lower than all the other listed species. (vi) ZYF650^T contains PL1 and L3 as other polar lipids and none of the type species contain them. (vii) The DNA G+C content of strain ZYF650^T lies within the range of genus *Marinobacter* but is different from all other close relatives.

More detailed phylogenetic and chemotaxonomic characteristics are given in the species description and Table 1. By

combining phenotypic, phylogenetic and genetic data, strain ZYF650^T was assigned as the novel type species of the genus *Marinobacter*, for which the name *Marinobacter salinexigens* sp. nov. is proposed.

DESCRIPTION OF *MARINOBACTER SALINEXIGENS* SP. NOV.

Marinobacter salinexigens (sal.in.e'xi.gens. L. masc. n. *sal* salt; L. pref. *in-* not; L. pres. part. *exigens* requiring; N.L. part. adj. *salinexigens* not requiring salt).

Displays the following characteristics in addition to those given in the species description. Cells are approximately 0.3–0.4 µm wide and 1.1–1.5 µm long after cultured on MA for 24 h at 28 °C. Colonies on MA are circular, smooth and white yellowish with an entire margin of 1–2 mm in diameter after incubation for 24 h at 28 °C. The pH range for growth is pH 6.0–9.5 (optimum, pH 7.0). Growth occurs at 10–45 °C (optimum, 26–28 °C) and at NaCl concentrations (w/v) of 0–14% (optimum, 7–8%). Starch, gelatin and DNA are hydrolysed. In the API 20E strips, there are positive results for sodium pyruvate and gelatin, and negative ones for all the other characteristics.

According to the results of API ZYM strip, enzymatic activities are detected for esterase (C4), esterase lipase (C8), lipase (C14), leucine arylamidase, cystine arylamidase, and naphthol-AS-BI-phosphohydrolase, but not for alkaline phosphatase, valine arylamidase, trypsin, α -chymotrypsin, acid phosphatase, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, α-mannosidase, *N*-acetyl-β-glucosaminidase and α-fucosidase. According to the results of API 50CH strip, acid is produced from glycerol, L-arabinose, D-ribose, L-xylose, *N*-acetyl-glucosamine, arbutin, aesculin, salicin, amygladin, cellobiose, lactose (bovine origin), melibiose, D-lyxose and D-tagatose. In the Biolog GN III MicroPlate system, there are positive results for cellobiose, gelatin, L-glutamic acid, L-pyroglutamic acid, pectin, D-galactoronic acid, tetrazolium violet, tetrazolium blue, 1% Nacl 4% Nacl, 8% Nacl, sodium lactate, D-fructose, D-fructose PO_4, D-gluconic acid, glucuronamide, L-lactic acid, L-malic acid, β-hydroxy-D-L-butryric acid, propionic acid, formic acid, pH 6, acetic acid and lithium chloride. The sole respiratory quinone is ubiquinone-9 (Q-9). The polar lipids in ZYF650^T comprise phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, three unidentified polar lipids two unidentified aminolipids and two phospholipids. The predominant fatty acids (more than 10% of total fatty acids) are $C_{18:1}$ ω9*c*, $C_{16:0}$, $C_{12:0}$ 3-OH, $C_{16:1}$ ω9*c* and $C_{12:0}$. The DNA G+C content of strain ZYF650^T is 55.6%.

Resistant to antibiotics chlortetracycline, novobiocin and cephahydroxil, but sensitive to neomycin, ceftazidime, amoxicillin, polymyxin B and ampicillin, while toward chloramphenicol strain ZYF650^T showed intermediate sensitivity.

The type strain, ZYF650^T (=JCM 33013^T=MCCC 1K03552^T), was isolated from the seawater of the Mariana Trench. The genomic DNA G+C content of the type strain is 55.6mol%. The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain ZYF650^T is MN325154. The Whole Genome Shotgun project of strain ZYF650^T has been deposited at DDBJ/ENA/GenBank under the accession VTUU00000000. The version described in this paper is version VTUU01000000.

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

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