**Muricauda chongwuensis** sp. nov., isolated from coastal seawater of China

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Received: 16 June 2021 / Revised: 2 September 2021 / Accepted: 21 September 2021 / Published online: 5 October 2021

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### Abstract

In the course of screening for bacterial predators, a Gram-stain-negative, non-flagellated, gliding, long rod-shaped, and yellow-pigmented bacterium, designated strain HICWT, was isolated from coastal seawater of China. Phylogenetic analysis based on 16S rRNA gene sequences indicated that strain HICWT represented a member of the genus *Muricauda* and showed the highest sequence similarity to *M. aquimarina* JCM11811T (98.8%) and *M. ruestringensis* DSM13258T (98.1%). The average nucleotide identity (ANI) and digital DNA–DNA hybridization (dDDH) values between strain HICWT and *M. aquimarina* JCM11811T were 79.2% and 34.1%, respectively. NaCl was required for growth. Optimum growth occurred at 25–30 °C, 2.0–3.0% (w/v) NaCl with pH 7.0. Strain HICWT showed some similar characteristics to the nonobligate bacterial predators, and the cells can attach to the prey cells. Strain HICWT contained MK-6 as the predominant respiratory quinone and had iso-C<sub>15:0</sub> 3-OH as the major cellular fatty acids. The polar lipids contained phosphatidylethanolamine (PE), three unidentified phospholipids (PL1–PL3), one unidentified amino lipids (AL), and three unidentified polar lipids (L1–L3). The genome size of strain HICWT was approximately 3.8 Mbp, with a G+C content of 41.4%. Based on the polyphasic evidence, strain HICWT is proposed as representing a new species of the genus *Muricauda*, for which the name *Muricauda chongwuensis* sp. nov. is proposed. The type strain is HICWT (= JCM 33643T = MCCC 1K03769T).

### Keywords

*Muricauda chongwuensis* · Nonobligate bacterial predator · Polyphasic taxonomy

### Abbreviations

| Abbreviation | Description                   |
|--------------|-------------------------------|
| BALOs        | Bdellovibrio-and-like organisms |
| rRNA         | Ribosomal RNA                  |
| MB           | Marine broth 2216E             |
| MA           | Marine agar 2216E              |
| MCCC         | Marine Culture Collection of China |
| JCM          | Japan Collection of Microorganisms |
| TEM          | Transmission electron microscope |
| gANI         | Genome average nucleotide identity |
| dDDH         | Digital DNA–DNA hybridization  |
| MP           | Maximum parsimony              |
| ML           | Maximum likelihood             |
| NJ           | Neighbor joining               |
| OMVs         | Outer membrane vesicles        |

Communicated by Erko Stackebrandt.

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### Introduction

According to the LPSN (www.bacterio.net/index.html), the family *Flavobacteriaceae* comprises 145 genera, including genus *Muricauda*, which was proposed by Bruns et al. (2001), and subsequently emended by Yoon et al. (2005) and Hwang et al. (2009). Members of the genus *Muricauda* share the characteristics of being Gram-stain-negative, non-motile, strictly or facultatively aerobic, yellow-pigmented rod, and having DNA G+C contents of 41.0–55.0 mol%. At the time of writing, there are 28 valid species in the genus *Muricauda* listed in the LPSN (https://lpsn.dsmz.de/genus/muricauda). These *Muricauda* species were isolated from various saline...
environments, such as intertidal/tidal flat, salt lake, seawater and sediment, sponge, shrimp gill, rhizosphere of marine macroalga and phykosphere of dinoflagellate (Yoon et al. 2005; Yoon et al. 2008; Yoon and Oh 2012; Bae et al. 2007; Dang et al. 2019; Guo et al. 2020; Kim et al. 2020; Park 2019; Liu et al. 2020; Zhang et al. 2020; Chen et al. 2021; Zhu et al. 2021).

Predatory bacteria can be any bacteria that kill or destroy other microbes and consume them as a nutritional resource (Pérez et al. 2016). Most described predatory bacteria except members of Bdellovibrio-and-like organisms (BALOs) (Williams and Chen 2020) are nonobligate predators, such as Ensifer adhaerens (Germida and Casida 1983), Agromyces ramosus and Lysobacter (Jurkevitch and Davidov 2006; Svercel et al. 2011), Pseudobacteriovorax antillogorgicola (Mccauley et al. 2015), Bradymonas sediminis (wang et al. 2015; Mu et al. 2020), Wenzhouxiangella Strain AB-CW3 (Sorokin et al. 2020). In the course of screening for bacte-
rial predators distributed in the coastal waters of China, a yellow-pigmented strain, designated HICWT, was isolated. Strain HICWT showed some similar characteristics to nonobligate bacterial predators, and the results of 16S rRNA gene sequence comparisons indicated that it was phylogenetically related to the genus Muricauda in the family Flavobacteriaceae. The present study determined the taxonomic status of strain HICWT using a polyphasic approach.

Materials and methods

Strain and culture condition

The sample was collected from coastal waters near the town Chongwu in Southeast China (118.545685° E, 24.53178° N). The sample was brought to the laboratory and stored at 4 °C (refrigerator) for 2 days before being processed. Strain HICWT was isolated and purified over five times using the double-layer plate was transferred into a 20 ml tube-
type bottle with 2 ml 1/40 concentration of marine broth 2216E (MB, peptone 5 g, yeast extract 1 g, seawater 1 L, pH 7.2–7.6) and incubated at 28 °C for 2–3 days. Small amounts of cells (each around 1 × 10^5–6 cell ml^-1) of strain HICWT and prey strain LF TCBS 15 were detected in 1/40 (v/v) MB culture. The axenic independent strain HICWT was purified from the 1/40 (v/v) MB co-culture by the standard dilution plating on marine agar 2216E (MA, pH 7.2–7.6) after incubation at 28 °C for 6–7 days. A yellow colony different from the prey strain was picked, checked by light microscopy (CX22RFS1, OLYMPUS) with 1% (w/v) crystal violet staining, then purified by streaking three times on MA. The strain was maintained in MB at 28 °C for 24 h and preserved in MB supplemented with 20% (v/v) glycerol at −20 °C and −80 °C. For long-term storage, the cultures of strain HICWT were lyophilized in 10% (w/v) skim milk and then deposited at the Marine Culture Collection of China (MCCC) and Japan Collection of Microorganisms (JCM). M. aquimarina JCM11811T and M. ruestringensis DSM13258T were obtained from the Marine Culture Collection of China and cultivated under identical conditions.

Phenotypic and biochemical characterization

Cell morphology was observed by light microscopy (CX22RFS1, OLYMPUS) and transmission electron microscopy (TEM, HT7800, Hitachi). For negative stains, cells from 24 h cultures on MA were resuspended with 0.1 mol l^-1 phosphate buffer (pH7.4), then a 400-mesh grid was inverted over a drop of cell suspensions for 1 min. The grid was then washed on two drops of water, and the cells were stained with 2.0% (w/v) uranyl acetate for 10 s.

For predatory characteristic detection, strain HICWT was cultivated either in double-layer agar plates or seawater with washed prey cells (around 1×10^9 cell ml^-1) (Ye et al. 2019). Light microscopy (CX22RFS1, OLYMPUS) and transmission electron microscopy (TEM, HT7800, Hitachi) were used to assess the cell-to-cell contact with attachment to the prey. For negative stains, a 400-mesh grid was inverted over a drop of 24 h co-cultures seawater, washed on one drop of water, and the cells were stained as mentioned above.

Gram staining was performed using a Gram Stain kit (QingDao Hopebio-Technology Co., Ltd) according to the manufacturer’s instructions. Growth temperature and pH values were assessed in MB at different temperatures (15, 20, 25, 28, 30, 35, 37, 40 and 45 °C) and pH values (3.0–10.0 at 1.0 unit intervals) for 42 h. MB with different pH values were prepared using the following biological buffers: citrate/phosphate (pH 3.0–7.0), Tris/HCl (pH 7.0–9.0) and sodium carbonate/sodium bicarbonate (pH 9.0–10.0). Growth at various NaCl concentrations (0, 0.5, 1.0, 2.0, 3.0, 4.0, 5.0, 6.0, 7.0, 8.0, 9.0 and 10.0% (w/v)) was investigated using MB with different NaCl concentrations prepared in the laboratory according to the formula of the medium. Gliding motility was examined on MA with 1.0% agar (w/v) and the hanging-drop method after growing cells in MB broth for 48 h at 28 °C (Bernardet et al. 2002). The aerobic condition of the strain HICWT was determined by a semi-solid (0.5%) stab culture (Dong and Cai 2001). The presence of flexirubin-type pigments was investigated as described by Reichenbach (1989) and Bernardet (2002).
Acetone: methanol (7:2, v/v) mixture was used to extract bacterial carotenoid pigments, and the whole-cell spectrum for carotenoid pigments was detected using the UV–visible spectrophotometer (AOE Instruments (Shanghai) Co., Ltd.) according to Hameed et al. (2011). Oxidase reagent (Hangzhou Microbial Reagent Co., Ltd) was used for testing oxidase activity, and catalase activity was evaluated by the production of oxygen bubbles in 3% (v/v) aqueous hydrogen peroxide solution according to the method of Dong and Cai (2001). Additional enzymic activities and biochemical features of strain HICW^T, M. aquimarina JCM11811^T, and M. ruespringensis DSM13258^T were determined by the API ZYM and API 20NE kits (bioMérieux) according to the manufacturer’s instructions, except that inocula were prepared by suspending cells in artificial seawater (Yang et al. 2013). Antibiotic susceptibility tests were performed using 6 mm filter-paper discs (Hangzhou Microbial Reagent Co., Ltd) with antibiotics added at the following concentrations (µg per disc unless stated otherwise): penicillin (10 U), erythromycin (15), neomycin (30), gentamicin (10), tetracycline (30), doxycycline (30), minocycline (30), kanamycin (30), amikacin (30), oxacillin (1), ampicillin (10), carbenicillin (100), piperaclillin (100), ceftriaxone (30), cefazolin (30), cefuroxime (30), cefotaxime (30), cefoperazone (75).

**Chemotaxonomic characterization**

For analysis of the cell fatty acids, bacteria were cultured in MB at 28 °C for 24 h, and the harvested cells were saponified, methylated, and extracted using the standard MIDI (Sherlock Microbial Identification System, version 6.0B) protocol. The whole-cell fatty acid pattern was then analyzed by gas chromatography (model 6850, Agilent Technologies) and identified using the TSB6.0 database of the Microbial Identification System (Athalye et al. 1985; Sasser 1990). Polar lipids were extracted and examined using two-dimensional thin-layer chromatography according to Kates (1972). Isoprenoid quinones were extracted from freeze-dried cells with chloroform/methanol (2:1, v/v) and analyzed by reversed-phase HPLC (Collins et al. 1984).

**Phylogenetic and genomic analyses**

The genomic DNA of strain HICW^T was extracted using a Rapid Bacterial Genomic DNA Isolation Kit (B518225, Shanghai Sangon Biological Engineering Technology & Services Co., Ltd). The whole genome of strain HICW^T was sequenced by the Guangdong Magigene Biotechnology Co., Ltd., using the Solexa paired-end (150 bp library) sequencing technology protocol. SPAdes software (http://cab.spbu.ru/software/spades/) was used to do genome assembly with multiple-Kmer parameters (Bankevich et al. 2012). The draft genome data of HICW^T has been deposited in GenBank with the accession number WYET000000.0. The G+C contents of the genomic DNA were calculated from the sequenced genome (https://www.ezbiocloud.net/tools/ani). Open Reading Frames (ORFs) were predicted using Prodigal v2.6.3 (Hyatt et al. 2010), and the predicted protein-coding sequences (CDS) were searched against the GenBank, Clusters of Orthologous Groups (COGs), and KEGG databases to analyze gene functions and metabolic pathways.

The partial 16S rRNA gene (around 1400 bp) was amplified from the chromosomal DNA and obtained from plaques of the strain HICW^T on the double-layer agar plate with V. alginolyticus LF TCBS 15 as the prey cells. The universal bacterial primers 27F and 1492R (Delong 1992) were used, and the purified PCR product was sequenced by Xiamen Bioray Biotechnology Co., Ltd. The complete 16S rRNA gene sequence of the strain HICW^T was obtained from its draft genome sequence. The 16S rRNA gene sequence analyses carried out with the online tool EzBioCloud (http://eztaxon-e.ezbiocloud.net) (Kim et al. 2012). 16S rRNA gene sequences of related taxa were selected from the GenBank database. Phylogenetic trees were reconstructed using the MEGA software package version 7.0 (Kumar et al. 2016) with distance options according to the default parameter model and clustering with the neighbor-joining (NJ), maximum-likelihood (ML), and maximum-parsimony (MP) methods, supported using bootstrap values with 1000 replications.

The whole-genome average nucleotide identity (gANI) was calculated using the algorithm as described by Yoon et al. (2017) with the web service of EzBioCloud (https://www.ezbiocloud.net/tools/ani). The digital DNA–DNA hybridizations (dDDH) were determined online at http://ggdc.dsmz.de/ggdc.php# using the Genome-to-Genome Distance Calculation (GGDC) version 2.1 (Meier-Kolthoff et al. 2013). Genomic data of related species were downloaded from the GenBank database.

**Results and discussion**

**Phenotypic and biochemical characteristics**

Cells of strain HICW^T were Gram-stain-negative, slender rods without any flagella, 1.8–3.7 μm in length, 0.3–0.4 μm in width after culturing on MA for 24 h at 28 °C (Table 1, Fig. S1). Outer membrane vesicles (OMVs), the spherical buds of the outer membrane, detached from the bacterial cell surface were detected (Fig. 1). The strain formed small circular yellow colonies on MA for 72 h at 28 °C (Fig. S2a). Colony spreading was observed on MA with 1.0% agar (w/v) (Fig. S2b), and cells glided slowly at the bottom surface of the coverslip. Flexirubin-type pigments were not detected,
but carotenoid pigments with maximal absorption at 454 nm and 480 nm were present (Fig. S3). The carotenoid pigments were yellow and non-diffusible. Nitrate reduction, gelatin hydrolysis, assimilation profile of several substrates, enzymatic activities, and antibiotic susceptibility profiles were the physiological properties differentiating among strain HICWT and closely related species of the genus Muricauda (Table 1, Table S1–S3). Other physiological and biochemical characteristics of strain HICWT are given in Table 1, Fig. S4, and the species description.

Plaques were formed on lawns of V. alginolyticus LF TCBS 15 when strain HICWT was isolated, purified, and cultivated using double-layer agar plates in the first 6 months. Arc-shaped concaves on the plate became visible after a 24 h incubation at 28 °C, then they extended slowly and turned to be clear sunken plaques (Fig. S5). When the plaques were picked and incubated in seawater with prey cells (around 1 × 10^9 cell ml^{-1}) at 28 °C for 48–120 h, strain HICWT showed a poor cell growth, the turbidity of the seawater co-cultured system did not decrease obviously, and the cells of strain HICWT could not be separated from prey cells using the centrifugation or membrane filtration. Subsequently, a 1/40 concentration of MB was used to incubate the plaques, in which the growth of strain HICWT and prey was small and in the same order of magnitude. The method of standard dilution plating on MA was tried to purify the axenic independent

### Table 1 Different characteristics of strain HICWT and related type strains of Muricauda

| Characteristic                  | 1                         | 2                         | 3                         |
|--------------------------------|---------------------------|---------------------------|---------------------------|
| Pigmentation                   | Yellow                    | Orange                    | Yellow                    |
| Cell size (μm)                 | 0.3–0.4 × 1.8–3.7         | 0.2–0.5 × 2.5–6.0         | 0.3–0.6 × 1.1–1.7         |
| Facultative anaerobe           | +                         | –                         | +                         |
| Oxidase activity               | –                         | +                         | –                         |
| Catalase activity              | +                         | +                         | –                         |
| α-Fucosidase                   | +                         | –                         | +                         |
| Ranges (optima) for growth:    |                           |                           |                           |
| Temperature (°C)               | 15–40 (25–30)             | 10–44 (30–37)             | 8–40 (20–30)              |
| NaCl (% w/v)                   | 0.5–8.0 (2.0–3.0)         | 0.5–9.0 (2.0–3.0)         | 0.5–9.0 (2.0–3.0)         |
| pH                             | 6.0–8.0 (7.0)             | 6.0–9.0 (7.0)             | 6.0–9.0 (8.0)             |
| Nitrate reduction              | W                         | –                         | –                         |
| Gelatin hydrolysis             | –                         | –                         | W                         |
| Utilization of:                |                           |                           |                           |
| d-Glucose                      | +                         | –                         | +                         |
| l-Arabinose                    | +                         | –                         | +                         |
| d-Mannose                      | +                         | –                         | +                         |
| N-Acetyl-glucosamine           | –                         | –                         | +                         |
| d-Maltose                      | W                         | –                         | +                         |
| Potassium gluconate            | W                         | –                         | W                         |
| Draft genome size (Mb)         | 3.8                       | 3.4                       | 3.8                       |
| DNA G+C content (mol%)         | 41.4                      | 43.4                      | 41.4                      |
| dDDH values to HICWT (%)       | 100                       | 34.1                      | 34.5                      |
| ANI values to HICWT (%)         | 100                       | 79.2                      | 80.6                      |

Strains: 1, HICWT; 2, M. aquimarina JCM 11811^T; 3, M. ruestringensis DSM 13258^T. The tests for oxidase activities, the API 20NE, and the API ZYM strip were performed on strain HICWT and the related type strains in this study. Genome sequences of the related type strains were taken from GenBank and analyzed in this study. Other data for the related type strains were taken from their original description (Bruns et al. 2001; Yoon et al. 2005).

+ positive, W weakly positive, – negative

### Fig. 1 Transmission electron microscopy image of strain HICWT
cells of strain HICW<sup>T</sup> from the 1/40 MB co-cultured system. Yellow colonies of strain HICW<sup>T</sup> different from the prey strain were detected on 10<sup>-3</sup> diluted plates. Accordingly, the number of strain HICW<sup>T</sup> in the 1/40 MB co-cultured system was estimated at 10<sup>5</sup> CFU ml<sup>-1</sup>, which was consistent with the results of microscope counting (10<sup>5</sup>–6 cell ml<sup>-1</sup>). These results also indicated that strain HICW<sup>T</sup> did not belong to an obligate predator. However, after purification, the axenic independent cells of strain HICW<sup>T</sup> appeared to lose plaque-forming activity against <i>V. alginolyticus</i> LF TCBS 15. The same phenomenon showed on the cells from the early co-cultured systems (preserved with 20% (v/v) glycerol at −20 °C or −80 °C). A similar property was reported on <i>Pseudobacteriovorax antillogorgiicola</i> RKEM611 to lose predatory activity after subsequent transfers on solid media (Mccauley et al. 2015). In a seawater co-cultured system, strain HICW<sup>T</sup> could attach to the prey cells, one cell attached to one or more prey (Figs. 2, and S6). Empty prey cells adjacent to the cell of strain HICW<sup>T</sup> were detected (Fig. 2d). Although strain HICW<sup>T</sup> showed some similar characteristics to the nonobligate bacterial predators, the predation activity was weak in the liquid co-culture system. The predatory mechanism of strain HICW<sup>T</sup> has not yet been elucidated. More conclusive pieces of evidence are needed to prove strain HICW<sup>T</sup> as a bacterial predator. Here, we defined it as a potential predator or quasi-predator.

**Chemotaxonomic characteristics**

The primary fatty acids (>10%) of strain HICW<sup>T</sup> were iso-C<sub>15:0</sub> (31.4%), iso-C<sub>15:1</sub> G (23.5%), and iso-C<sub>17:0</sub> 3-OH (22.5%). These are the three primary fatty acids of the genus <i>Muricauda</i> (Bruns et al. 2001). The differences in fatty acid content between strain HICW<sup>T</sup> and related species in the genus <i>Muricauda</i> are shown in Table S4. The predominant isoprenoid quinone of strain HICW<sup>T</sup> was menaquinone-6 (MK-6), consistent with other <i>Muricauda</i> species for which quinones have been analyzed. Strain HICW<sup>T</sup> contained phosphatidylethanolamine (PE), three unidentified phospholipids (PL1–PL3), one unidentified amino lipids (AL), and three unidentified polar lipids (L1–L3) (Fig. S7). All species with available data of the genus <i>Muricauda</i> contain PE as the significant lipid.

**Phylogenetic and genomic analyses**

Genome features of strain HICW<sup>T</sup> are summarized in Table 2. The draft genome size of strain HICW<sup>T</sup> was determined to be 3,777,431 bp. There were 13 contigs for strain HICW<sup>T</sup>. The coverage values (sequencing depth) of the genome sequences of strain HICW<sup>T</sup> was 428×, whereas the N50 and N90 values were 1,121,114 bp and 125,639 bp, respectively. The G+C content of the genomic DNA of strain HICW<sup>T</sup> was 41.4%, similar to <i>M. aquimarina</i> JCM11811<sup>T</sup> (43.4%) and <i>M. ruestringensis</i> DSM 13258<sup>T</sup> (41.4%) (Table 1). A total of 3569 CDSs with a sequence

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**Fig. 2** Transmission electron microscopy images of strain HICW<sup>T</sup> attach to <i>Vibrio alginolyticus</i> LF TCBS15. Arrow 1, <i>Vibrio alginolyticus</i> LF TCBS15; arrow 2, strain HICW<sup>T</sup>; arrow 3, empty prey cell.
length of 3,434,949 bp were predicted, which account for 90.9% of the genome, and 37 tRNA and five rRNA (one 23S rRNA, one 16S rRNA, and three 5S rRNA) genes were identified. In all, 2896 CDSs were assigned to COG families, and 1714 CDSs were included in 202 pathways.

The partial 16S rRNA gene sequence (800 bp) from the sunken plaques and genomic DNA of strain HICWT showed most closely related to the genus Muricauda (around 83.0% and 97.6% similarity, respectively). The complete 16S rRNA gene sequence from the genome sequence of strain HICWT was 1514 bp in length. Comparisons of the 16S rRNA gene sequence with the corresponding ones in the EzBioCloud databases showed that strain HICWT shared the highest sequence similarity with the 16S rRNA gene of M. aquimarina JCM11811T (98.8%) and M. ruestringensis DSM13258T (98.1%). In the neighbor-joining tree based on 16S rRNA gene sequences of strain HICWT and related-type strains, the new isolate belonged to the family Flavobacteriaceae, fell into the same cluster with the members of the genus Muricauda and was most closely related to M. aquimarina JCM11811T (Fig. 3). The maximum-parsimony and maximum-likelihood trees showed essentially the same topology (Figs. S8 and S9).

The ANI value for comparisons between strain HICWT and M. aquimarina JCM11811T and M. ruestringensis DSM13258T were 79.2% and 80.6% (Table 1), respectively, which were lower than the threshold of 94–96% for bacterial species delineation (Kim et al. 2014; Richter and Roselló-Möra 2009). The dDDH relatedness for strain HICWT with M. aquimarina JCM11811T and M. ruestringensis DSM13258T were 34.1% and 34.5% (Table 1), respectively, which were also clearly below the 70% threshold DDH value generally accepted for the delineation of species (Meier-Kolthoff et al. 2013).

**Taxonomic conclusion**

Based on the results of phenotypic, biochemical, chemotaxonomic, phylogenetic, and genomic analyses, it is clear that strain HICWT is genetically distinct from other strains of the genus Muricauda and represents a new species of the genus Muricauda, for which the name *Muricauda chongwuensis* sp. nov. is proposed.

**Description of *Muricauda chongwuensis* sp. nov.**

*Muricauda chongwuensis* (chong.wu.en'sis. N.L. fem. adj. chongwuensis of Chongwu, the city where the type strain was isolated).

Cells are Gram-stain-negative, facultatively anaerobic, gliding rods (0.3–0.4 × 1.8–3.7 μm) without any flagella. Outer membrane vesicles (OMVs) release from the bacterial cell surface. Colonies are yellow, smooth, convex, circular (1–2 mm in diameter), and semitransparent after growth on MA for 48 h at 28 °C. Non-diffusible yellow carotenoid pigments are produced. Growth occurs...
at 15–40 °C (optimum 25–30 °C). Growth occurs at 0.5–8.0% (w/v, optimum 2.0–3.0%) NaCl, NaCl is necessary for growth. The pH range for growth is 6.0–8.0 with an optimal pH of 7.0. Cells show some similar characteristics to nonobligate bacterial predators, which attach to the prey cells. Catalase is positive, and oxidase is negative.

In the API 20E strip, there are positive results for the reduction of nitrate to nitrite (weakly), d-glucose fermentation, β-glucosidase (Aesculin hydrolysis), beta-galactosidase activities, and the utilization of d-glucose, l-arabinose, d-mannose, d-maltose (weakly), and potassium gluconate (weakly). In API ZYM strip, activities of acid phosphatase, alkaline phosphatase, esterase (C4), esterase lipase (C8), lipase (C14), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, naphthol-AS-BI-phosphohydrolase, α-galactosidase, β-galactosidase, β-glucuronidase (weakly), α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase, and α-fucosidase are present. Resistant to (µg per disc unless stated otherwise): penicillin (10 U), neomycin (30), gentamicin (10), tetacycline (30), doxycycline (30), kanamycin (30), oxacillin (1), ampicillin (10), carbenicillin (100), cefradine (30), cephalaxin (30), cefazoline (30), cefuroxime (30), cetazidime (30), ceftriaxone (30) and cefoperazone (75). The major respiratory quinone is MK-6. The polar lipids contain phosphatidylethanolamine (PE), three unidentified phospholipids (PL1–PL3), one unidentified amino lipids (AL), and three unidentified polar lipids (L1–L3). The predominant fatty acids are iso-C₁₅:₀, iso-C₁₅:₁, G, iso-C₁₇:₀ 3-OH.

The type strain, HICW_T (= JCM 33643_T = MCCC 1K03769⁵), was isolated from coastal waters of Chongwu in Southeast China (118.545685° E, 24.53178° N).

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**Supplementary Information** The online version contains supplementary material available at https://doi.org/10.1007/s00203-021-02591-1.

**Author contributions** M-XC and H-YL conceived the project. M-XC and X-YH experimented and analyzed the data. M-XC wrote the manuscript. All authors have revised the manuscript.

**Funding** This work was supported by the National Natural Science Foundation of China (Grant no. 41506179), National Programme on Global Change and Air-Sea Interaction (Grant no. GASI-03-01-03-01), Natural Science Foundation of Fujian Province (Grant no. 2015J01613), and Fujian Provincial Key Laboratory of Marine Ecological Conservation and Restoration (Grant no. EPR2020002).

**Data availability** The GenBank/EMBL/DDJB accession numbers for the draft genome sequence and the 165 rRNA gene sequence of *Muricauda chongwuensis* HICW_T are WYET00000000 and MK920190, respectively.

**Code availability** Not applicable.

### Declarations

**Conflict of interest** The authors declare that they have no conflict of interest.

**Ethical statement** This article does not contain any studies with human participants or animals performed by any of the authors.

### References

Athalaye M, Noble WC, Minnikin DE (1985) Analysis of cellular fatty acids by gas chromatography as a tool in the identification of medically important coryneform bacteria. J Appl Bacteriol 58:507–512

Bae SS, Kwon KK, Yang SH, Lee HS, Kim SJ, Lee JH (2007) *Flagellimonas eckloniae* gen. nov. sp. nov. a mesophilic marine bacterium of the family *Flavobacteriaceae*, isolated from the rhizosphere of *Ecklonia kurome*. Int J Syst Evol Microbiol 57:1050–1054

Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA (2012) SPAdes: a new genome assembly algorithm and its applications to single cell sequencing. J Comput Biol 19:455–477

Bernardet JF, Nakagawa Y, Holmes B (2002) Proposed minimal standards for describing new taxa of the family *Flavobacteriaceae* and emended description of the family. Int J Syst Evol Microbiol 52:1049–1070

Bruns A, Rohde M, Berthe-Corti L (2001) *Muricauda rustringensis* gen. nov., sp. nov., a facultatively anaerobic, appendaged bacterium from German North Sea intertidal sediment. Int J Syst Evol Microbiol 51:1997–2006

Chen Y, Hu Z, Wang H (2021) *Muricauda amphidinii* sp. nov., a novel marine bacterium isolated from the phycosphere of dinoflagellate *Amphidinium carterae*. Int J Syst Evol Microbiol. https://doi.org/10.1099/ijsem.0.004764

Collins MD, Costas M, Owen RJ (1984) Isoprenoid quinone composition of representatives of the genus *Campylobacter*. Arch Microbiol 137:168–170

Dang YR, Sun YY, Sun LL, Yuan XX, Li Y, Qin QL, Chen XL, Zhang YZ, Shi M, Zhang XY (2019) *Muricauda nanhaiensis* sp. nov., isolated from seawater of the South China Sea. Int J Syst Evol Microbiol 69:2089–2094

Delong EF (1992) Archaea in coastal marine environments. Proc Natl Acad Sci USA 89:5685–5689

Dong XZ, Cai MY (2001) Determinative manual for routine bacteriology. Scientific Press, Beijing (in Chinese)

Germida JJ, Casida LE (1983) *Ensifer adhaerens* predatory activity against other bacteria in soil, as monitored by indirect phase analysis. Appl Environ Microbiol 45:1380–1388

Guo LL, Wu D, Sun C, Cheng H, Xu XW, Wu M, Wu YH (2020) *Muricauda maritima* sp. nov., *Muricauda aequoris* sp. nov., and *Muricauda oceanaensis* sp. nov., three marine bacteria isolated from seawater. Int J Syst Evol Microbiol 70:6240–6250

Hameed A, Arun AB, Ho HP, Chang CMJ, Rekha PD, Lee MR, Singh S, Young CC (2011) Supercritical carbon dioxide micronization of zeaxanthin from moderately thermophilic bacteria *Muricauda lutosaensis* CC-HSB-11°. J Agric Food Chem 59:4119–4124

Hwang CY, Kim MH, Bae GD, Zhang GJ, Kim YH, Cho BC (2009) *Muricauda olearia* sp. nov., isolated from crude-oil-contaminated seawater, and emended description of the genus *Muricauda*. Int J Syst Evol Microbiol 59:1856–1861
