A new species of freshwater crab of the genus *Nanhaipotamon* Bott, 1968 (Crustacea, Decapoda, Brachyura, Potamidae) from Longhai, Fujian Province, China

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Abstract
A new species of freshwater crab of the genus *Nanhaipotamon* Bott, 1968 is described from Xiaye Village, Chengxiang Town, Longhai County, Zhangzhou City, Fujian Province, China. The new species is distinguished from congeners by the combination of characters of its carapace, third maxilliped, unequal chelipeds, triangular male abdomen and unique male first gonopod. Molecular evidence derived from partial mitochondrial 16S rRNA and COI genes also support the species as new.

Keywords
freshwater crab, new species, Oriental region, taxonomy

Introduction

The genus *Nanhaipotamon* Bott, 1968 was originally established by Bott (1968), with several species from Taiwan, Philippines, and the Ryukyus (Japan). Dai (1997) revised the genus and described nine species from China. The latest research on *Nanhaipotamon*
described a new species from Macau, *N. macau* Huang, Wong & Ahyong, 2018 (Huang et al. 2018a). Currently, *Nanhaiapotamon* is only known from Guangdong, Fujian, Zhejiang, Taiwan, Hong Kong, and Macau (Shih et al. 2011; Huang et al. 2018a). Prior to the present study, *Nanhaiapotamon* contained 18 species (Dai 1999; Cheng et al. 2003; Shih et al. 2005; Cheng et al. 2009; Huang et al. 2012, 2018a; Lin et al. 2012; Lin et al. 2013).

In 2019, during a survey of freshwater crab resources in Longhai, Fujian Province, the first author collected several specimens of the genus *Nanhaiapotamon*. In August 2020, we made another collection trip to obtain additional samples. After morphological comparison, we found the Longhai specimens to be distinct from known species of *Nanhaiapotamon*. Molecular evidence based on the 16S rRNA and COI genes also support it as new. Therefore, we herein describe a new species, *Nanhaiapotamon longhaiense* sp. nov.

**Materials and methods**

Specimens were collected from Longhai, Fujian Province by Mao-Rong Cai and preserved in 95% ethanol. The holotype and allotype were deposited at the Department of Parasitology of the Medical College of Nanchang University, Jiangxi, China (NCU MCP). Other examined materials were deposited at the Center for Disease Control and Prevention of Zhangzhou City, Zhangzhou, China (ZZCDC) and the National Tropical Disease Research Center, Shanghai, China (TDRC). Carapace width and length were measured in millimeters. The abbreviations G1 and G2 refer to the first and second gonopod. The terminology used herein primarily follows that of Dai (1999) and Davie et al. (2015).

We compared the new species with type materials of other nine species of *Nanhaiapotamon* deposited in Chinese Academy of Sciences, Beijing, China (CAS CB). Comparative materials are as follows: *Nanhaiapotamon guangdongense* Dai, 1997: holotype, 1♂, Guangdong Province, CAS CB 05141. *Nanhaiapotamon hepingense* Dai, 1997: holotype, 1♂, Guangdong Province, Heping County, 7 May 1965, CAS CB 05106. *Nanhaiapotamon hongkongense* Shen, 1940: holotype, 1♂, Hongkong, Jun. 1991, CAS CB 05107. *Nanhaiapotamon nanriense* Dai, 1997: holotype, 1♂, Fujian Province, Putian County, Nanri Island, 15 Nov. 1975, CAS CB 05103. *Nanhaiapotamon pinghense* Dai, 1997: holotype, 1♂, Guangdong Province, Heping County, 7 May 1965, CAS CB 05132. *Nanhaiapotamon pingyuanense* Dai, 1997: holotype, 1♂, Pingyuan County, Guangdong Province, Sep. 1983, CAS CB 05131. *Nanhaiapotamon wenzhouense* Dai, 1997: holotype, 1♂, Wenzhou City, Zhejiang Province, 1979, CAS CB 05143. *Nanhaiapotamon yongchuense* Dai, 1997: holotype, 1♂, Fujian Province, Yongchun County, 29 Jun. 1977, CAS CB 05104. *Nanhaiapotamon huaanense* Dai, 1997: holotype, 1♂, Huaan County, Fujian Province, 15 Jun. 1984, CAS CB 05105.

Institutional abbreviations used in the paper are as follows: CAS CB, Chinese Academy of Sciences, Beijing, China; NCHUZOO, Zoological Collections of the Department of Life Science, National Chung Hsing University, Taichung, Taiwan; NCU MCP, Department of Parasitology of the Medical College of Nanchang Univer-
Approximately 50 mg of muscle tissue was excised from ambulatory legs and chelipeds. Total genomic DNA was extracted from the tissues using the DP1902 Tissue Kit (BioTeKe Inc., Beijing, China) following the manufacturer’s protocol. Then, the 16S rRNA gene was amplified using polymerase chain reaction (PCR) with the primers 1471 (5’-CCTGTTTANCAAAAACAT-3’) and 1472 (5’-AGATAGAAACCAACCTGG-3’) (Crandall and Fitzpatrick 1996). The COI gene was amplified with primers LCO1490 and HCO2198 (Folmer et al. 1994). The PCR conditions were as follows: denaturation for 50 s at 94 °C, annealing for 40 s at 52 °C and extension for 1 min at 72 °C (33 cycles), followed by a final extension for 10 min at 72 °C. The PCR products were purified and sequenced using an ABI 3730 automatic sequencer. We performed molecular analysis with the partial mitochondrial 16S rRNA and COI genes fragment. In total, 59 sequences were used to construct phylogenetic trees (Table 1). Sequences were aligned using MAFFT v. 7.215 (Katoh and Standley 2013) based on the G-INS-I method, and the conserved regions were selected with Gblocks 0.91b (Castresana 2000) using the default settings. The best-fitting model for Bayesian Inference (BI) analysis was determined by MrModeltest v. 2.3 (Nylander 2004), selected by the Akaike information criterion (AIC). The obtained model was GTR+G+I for both genes. MrBayes v. 3.2.6 (Ronquist et al. 2012) was employed to perform BI analysis, and four Monte Carlo Markov Chains of 2,000,000 generations were run with sampling every 1,000 generations. The first 500,000 generations were discarded as burn-in. The best evolutionary model for maximum likelihood (ML) analysis was HKY+I+G for 16S rRNA and GTR+G+I for COI, determined by MEGA X (Kumar et al. 2018) based on the Bayesian information criterion (BIC). An ML tree was built based on 1000 bootstrap replicates in MEGA X (Kumar et al. 2018). The pairwise distance based on the K2P (Kimura 2-Parameter) model was calculated by MEGA X (Kumar et al. 2018).

Results

Systematics

Family Potamidae Ortmann, 1896

*Nanhaipotamon* Bott, 1968

*Nanhaipotamon longhaiense* sp. nov.

http://zoobank.org/E25133A7-AB4A-4CAA-8DF8-2DC9957384D9

Figs 1–4, 5A, 6, 7

**Type material.** *Holotype:* ♂ (25.2 × 21.5 mm), CHINA, Fujian Province, Longhai County, Chengxiang Town, Xiaye Village, 24°23′02″N, 117°34′76″E, alt. 55 m, 27
Aug. 2019, Mao-Rong Cai leg, NCU MCP 417701. \textbf{Paratypes}: 1 ♀ (allotype) (26.5 × 22.5 mm), same data as holotype, NCU MCP 428601; 2 ♂♂ (27.1 × 22.0 mm, 29.0 × 23.3 mm), same data as for holotype, ZZCDC 613201, ZZCDC 613203.

\textbf{Other specimens examined}. 9 ♂♂ (28.1 × 22.6 mm, 25.3 × 20.8 mm, 22.9 × 18.9 mm, 22.8 × 18.9 mm, 22.8 × 18.9 mm, 22.3 × 18.8 mm, 22.3 × 18.8 mm, 21.4 × 17.4 mm, 21.4 × 17.1 mm), same locality data as for holotype, 10 Aug. 2020, Mao-Rong Cai and Jie-Xin Zou leg, ZZCDC 613204 to 613208, TDRC 002101 to 002104; 6 ♀♀ (26.4 × 22.2 mm, 23.4 × 18.9 mm, 21.6 × 17.7 mm, 21.2 × 16.8 mm, 21.2 × 16.2 mm, 18.4 × 15.2 mm), same locality data as for preceding, ZZCDC 613213 to 613215, TDRC 002105 to 002107.

\textbf{Diagnosis}. Carapace subquadrat, regions indistinct, anterolateral regions slightly rugose; cervical groove shallow and wide, H-shaped groove shallow; postorbital cristae sharp, almost fused with epigastric cristae (Figs 1A, 3A). External orbital angle triangular, separated from anterolateral margin by wide, concave notch; epibranchial teeth small, granular; anterolateral margin lined with conspicuous granules (Figs 1A, 3A). Third maxilliped merus with shallow median depression, exopod flagellum slightly longer than 1/3 exopod length (Fig. 2D). Chelipeds strongly unequal; fingers with small gap when closed (Figs 1A, 3A). G1 slender, inner distal angle semicircular, inner margin of terminal segment convex, distal margin flat, outer distal angle blunt, laterally bent outwards at angle of about 60° (Figs 4A–D, 5A). Female vulvae ovate, medium-sized, wholly within sternite 6, opening directed inward (Fig. 3B).

\textbf{Description}. Carapace subquadrat, broader than long; dorsal surface smooth, distinctly convex longitudinally, with tiny pits; anterolateral region rugose. Branchial regions swollen (Figs 1A, 3A). Cervical groove shallow and wide; H-shaped groove between gastric and cardiac regions shallow (Figs 1A, 3A). Epigastric cristae conspicuous, separated by narrow gap; postorbital cristae sharp, almost fused with epigastric cristae (Figs 1A, 3A). Front distinctly deflexed, margin ridged in dorsal view. External orbital angle triangular, separated from anterolateral margin by wide, concave notch. Epibranchial tooth small, granular. Anterolateral margin distinctly cristate, lined with approximately 20 granules (Figs 1A, 3A). Posterolateral surface smooth, with inconspicuous oblique striae, converging towards posterior carapace margin (Figs 1A, 3A). Orbits large; supraorbital, infraorbital margins cristate. Sub-orbital regions covered with granules (Fig. 1B); pterygostomial regions covered with large rounded granules; sub-hepatic regions covered with striae (Fig. 1B). Posterior margin of epistome with median triangle, lateral margin sinuous (Fig. 1B).

Third maxilliped merus about 1.2 times as broad as long, trapezoidal, with median depression; ischium about 1.3 times as long as broad, rectangular, with distinct median sulcus; exopod reaching approximately 1/4 of merus length, exopod flagellum slightly longer than 1/3 exopod length (Fig. 2D).

Chelipeds strongly unequal. Merus cross-section trigonal, inner-lower margin crenulated. Carpus surface weakly wrinkled, with longitudinal depression and sharp
Table 1. GenBank accession number of the species used for phylogenetic analysis.

| Species                        | Museum number | Locality          | GenBank number       | Reference                   |
|--------------------------------|---------------|-------------------|----------------------|-----------------------------|
| Amamiku amamensis Minei, 1973 | NCHUZOOL 13125 | Kagoshima, Japan  | 16S rRNA, AB428457   | Shih et al. 2009            |
| Apotamonastes hainanensis Parisi, 1916 | NCHUZOOL | Hainan, China     | 16S rRNA, AB428459   | Shih et al. 2009            |
| Candidiopotamon rathbunae De Man, 1914 | NCHUZOOL | Taiwan            | 16S rRNA, AB208598   | Shih et al. 2006            |
| Cryptopotamon anaconolathon Kemp, 1918 | NCHUZOOL 13123 | Taiwan            | 16S rRNA, AB428455   | Shih et al. 2009            |
| C. hainanense Huang, Ahyong & Shih, 2017 | SYSBM 1559 | Guangdong, China  | 16S rRNA, AB428451   | Huang et al. 2017a          |
| Chinapotamon maolanense Zou, Bai & Zhou, 1980 | NCHUZOOL | Guangxi, China    | 16S rRNA, MH183299   | Shih et al. 2009            |
| Chinapotamon giberreum Dai, Song, Li & Liang, 1980 | NCHUZOOL | Guizhou, China    | 16S rRNA, AB428455   | Shih et al. 2009            |
| Diapoton cereum Huang, Shih & Ng, 2017 | SYSBM 1555 | Guizhou, China    | 16S rRNA, LC199519   | Huang et al. 2017b          |
| D. cereum Huang, Shih & Ng, 2017 | SYSBM 1556 | Guizhou, China    | 16S rRNA, LC199520   | Huang et al. 2017b          |
| Gentothelphusa albogilva Shy, Ng & Yu, 1994 | NCHUZOOL | Taiwan            | 16S rRNA, AB127366   | Shih et al. 2004            |
| G. marginata fulva Naruse, Shokita & Shy, 2004 | NCHUZOOL 13124 | Okinawa, Japan   | 16S rRNA, AB428456   | Shih et al. 2009            |
| G. olee Shy, Ng & Yu, 1994 | NCHUZOOL 13123 | Taiwan            | 16S rRNA, AB428455   | Shih et al. 2009            |
| Hainanapotamon fuchengense Dai, 1995 | NCHUZOOL 13128 | Hainan, China     | 16S rRNA, AB428461   | Shih et al. 2009            |
| Huanapotamon angulatum Dai, Chen, Song, Fan, Lin & Zeng, 1979 | NCHUZOOL | Fujian, China     | 16S rRNA, AB428454   | Shih et al. 2009            |
| Luteomon spinaledum Huang, Shih & Ahyong, 2018 | SYSBM 001609 | Guangdong, China  | 16S rRNA, LC383796   | Huang et al. 2018a          |
| Minapotamon nasicum Dai, Chen, Song, Fan, Lin & Zeng, 1979 | NCHUZOOL 13121 | Fujian, China     | 16S rRNA, AB428450   | Shih et al. 2009            |
| Neociuropotamon jianfengense Dai & Naiyanetr, 1994 | NCHUZOOL 13127 | Hainan, China     | 16S rRNA, AB428460   | Shih et al. 2009            |
| Nanhaiapotamon wupingense Cheng, Yang, Zhang & Li, 2003 | NCHUZOOL 13125 | Fujian, China     | 16S rRNA, AB433548   | Shih et al. 2011            |
| N. wupingense Cheng, Yang, Zhang & Li, 2003 | NCHUZOOL | Fujian, China     | 16S rRNA, AB470496   | Shih et al. 2011            |
| N. pingyuanense Dai, 1997 | CAS CB 05131 | Guangdong, China  | 16S rRNA, AB265237   | Shih et al. 2007            |
| N. huaanense Dai, 1997 | CAS CB 05105 | Fujian, China     | 16S rRNA, AB212870   | Shih et al. 2005            |
| N. pinghense Dai, 1997 | CAS CB 05132 | Guangdong, China  | 16S rRNA, AB433553   | Shih et al. 2011            |
| N. hepingense Dai, 1997 | CAS CB 05106 | Guangdong, China  | 16S rRNA, AB433552   | Shih et al. 2011            |
| N. hongkongense Shen, 1940 | NCHUZOOL | Hongkong           | 16S rRNA, AB212869   | Shih et al. 2005            |
| N. formosanum Parisi, 1916 | NCHUZOOL | Taiwan            | 16S rRNA, AB212867   | Shih et al. 2005            |
| Species                        | Museum number   | Locality          | GenBank number       | Reference          |
|-------------------------------|-----------------|-------------------|----------------------|--------------------|
| *N. yongchuense* Dai, 1997    | CAS CB 05104    | Fujian, China     | 16S rRNA, AB433546   | Shih et al. 2011   |
| *N. nanriense* Dai, 1997      | NCHUZOOL        | Fujian, China     | 16S rRNA, AB212868   | Shih et al. 2005   |
| *N. wenzhouense* Dai, 1997    | NCHUZOOL 13132  | Zhejiang, China   | 16S rRNA, AB433543   | Shih et al. 2011   |
| *N. dongyinense* Shih, Chen & Wang, 2005 | NCHUZOOL        | Dongyin, Taiwan   | 16S rRNA, AB212863   | Shih et al. 2005   |
| *Quanzimon aflagellum* Dai, Song, Li & Liang, 1980 | SYSBM 001404  | Guangxi, China    | 16S rRNA, MG709239   | Huang 2018.        |
| *Ryukyum yaeyamense* Minei, 1973 | NCHUZOOL 13126  | Okinawa, Japan    | 16S rRNA, AB428458   | Shih et al. 2009   |
| *Socotrapotamon nojidense* Apel & Brandis, 2000 | ZRC 2000.2232  | Socota, Yemen      | 16S rRNA, AB428493   | Shih et al. 2009   |
| *Yarepotamon gracilipa* Dai, Song, Li & Liang, 1980 | ZRC         | Guangxi, China    | 16S rRNA, AB428452   | Shih et al. 2009   |
| *N. longhaini sp. nov.*      | NCU MCP 417701  | Fujian, China     | 16S rRNA, MT809486   | This study         |
| *N. longhaini sp. nov.*      | NCU MCP 417702  | Fujian, China     | 16S rRNA, MT809487   | This study         |
| *N. longhaini sp. nov.*      | NCU MCP 417703  | Fujian, China     | 16S rRNA, MT809488   | This study         |
| *N. longhaini sp. nov.*      | NCU MCP 417704  | Fujian, China     | 16S rRNA, MT809489   | This study         |
| *Huanaapotamon nanchengense* Dai, Zhou & Peng, 1995 | NCHUZOOL      | Jiangxi, China    | COI, AB511392        | Shih et al. 2011   |
| *N. huanaense* Dai, 1997      | CAS CB 05105    | Fujian, China     | COI, AB433572        | Shih et al. 2011   |
| *N. pingyuancense* Dai, 1997  | CAS CB 05131    | Guangdong, China  | COI, AB265249        | Shih et al. 2011   |
| *N. wupingense* Cheng, Yang, Zhang & Li, 2003 | NCHUZOOL 13125 | Fujian, China     | COI, AB433569        | Shih et al. 2011   |
| *N. longkongense* Shen, 1940  | NCHUZOOL        | Hongkong          | COI, AB433574        | Shih et al. 2011   |
| *N. yongchuense* Dai, 1997    | CAS CB 05104    | Fujian, China     | COI, AB433567        | Shih et al. 2011   |
| *N. nanriense* Dai, 1997      | NCHUZOOL        | Fujian, China     | COI, AB433565        | Shih et al. 2011   |
| *N. wenzhouense* Dai, 1997    | NCHUZOOL 13132  | Zhejiang, China   | COI, AB433564        | Shih et al. 2011   |
| *N. dongyinense* Shih, Chen & Wang, 2005 | NCHUZOOL        | Dongyin, Taiwan   | COI, AB433562        | Shih et al. 2011   |
| *N. formosanum* Parisi, 1916  | NCHUZOOL        | Taiwan            | COI, AB433557        | Shih et al. 2011   |
| *N. guangdongense* Dai, 1997  | –               | Guangdong, China  | COI, MK226145        | Huang et al. 2018a |
| *N. maceu* Huang, Wong & Ah Yong, 2018 | –               | Macau             | COI, MK226142        | Huang et al. 2018a |
| *N. longhaini sp. nov.*      | NCU MCP 417701  | Fujian, China     | COI, MW703830        | This study         |
| *N. longhaini sp. nov.*      | NCU MCP 417702  | Fujian, China     | COI, MW729699        | This study         |
| *N. longhaini sp. nov.*      | NCU MCP 417703  | Fujian, China     | COI, MW729700        | This study         |
| *N. longhaini sp. nov.*      | NCU MCP 417704  | Fujian, China     | COI, MW729701        | This study         |
| *N. longhaini sp. nov.*      | NCU MCP 417705  | Fujian, China     | COI, MW729702        | This study         |
| *N. longhaini sp. nov.*      | NCU MCP 417706  | Fujian, China     | COI, MW729703        | This study         |
| *N. longhaini sp. nov.*      | NCU MCP 417707  | Fujian, China     | COI, MW729704        | This study         |

Spine at inner-distal angle with spinule at base. Palm of larger chela about 1.3 times as long as high. Movable finger (dactylus) slightly shorter than the immovable finger (pollex). Inner margin of fingers with rounded, blunt teeth; fingers forming small gap when closed (Figs 1A, 3A).
Ambulatory legs slender, second leg longest, merus 0.5–0.6 times as long as carapace length; last leg with propodus 2.1 times as long as broad, slightly shorter than dactylus. Dactylus gently curved, with sharp spines on the surface (Figs 2C, 3A).

Male thoracic sternum smooth, pitted (Fig. 2A). Sternites 1, 2 completely fused to form triangular structure; sternites 2,3 separated by visible suture; sternites 3, 4 fused without obvious suture (Fig. 2A). Male sterno-pleonal cavity relatively deep, exceeding imaginary line connecting posterior edges of cheliped coxae (Fig. 2B). Median longitudinal suture of sternites 7, 8 deep and long. Tubercle of abdominal lock positioned at mid-length of sternite 5 (Fig. 2B). Female vulvae ovate, medium-sized, wholly within sternite 6, opening directed inward (Fig. 3B).

Male abdomen triangular; somites 4–6 gradually narrowed longitudinally, lateral margins slightly convex; somite 6 about 2.2 times as wide as long; telson about 1.4 times as wide as long (Fig. 2A).

G1 slender, tip of terminal segment reaches beyond pleonal locking tubercle (Fig. 2B), subterminal segment about 2.4 times as long as terminal segment (Fig. 4A). Inner distal angle semicircular, inner margin of terminal segment convex, distal margin flat, outer distal angle blunt, bent outwards at angle of about 60° (Figs 4A–D, 5A). G2 subterminal segment about 1.9 times length of distal segment (Fig. 4E).

**Etymology.** The new species is named after the county where is located, Longhai County, Zhangzhou City, Fujian Province, China.

**Distribution.** Longhai County, Zhangzhou City, Fujian Province, China.

**Ecology.** The new species occurs in the wetlands of low-elevation hills and mountains, amongst dense vegetation where there is little to no water flow year-round (Fig. 7B). During the day, the crabs usually hide in mud burrows close to the water source (Fig. 7A) or hide under rocks under water. We observed a berried female in August, suggesting the time around this month to be a part of the breeding season (Fig. 3C).

**Remarks.** With a convex carapace dorsal surface, unequal chelipeds and triangular male abdomen, *Nanhaipotamon longhaiense* sp. nov. fits the diagnosis of *Nanhaipotamon*. Like some species within this genus, *N. longhaiense* sp. nov. shows intraspecific variation in G1 morphology, the distal margin of the G1 terminal segment is flat to oblique (Fig. 6A–C). In the holotype, the distal margin is flat (Fig. 6A), whereas in some adult specimens, the distal margin is oblique (Fig. 6B, C), and the inner margin of the G1 terminal segment is slightly convex to distinctly convex (Fig. 6A–C).

We make comparisons between the new species and seven species of *Nanhaipotamon*, among which *N. wuping* and *N. macau* are morphologically similar to this new species, *N. yongchuense*, *N. huaanense* and *N. nanriense* are geographically close (Dai 1999), and *N. guangdongense* and *N. hepingense* are from Guangdong near Fujian (Dai 1999). *Nanhaipotamon longhaiense* sp. nov. can be differentiated from its congeners by its unique G1 (Fig. 5A). Compared to *N. longhaiense* sp. nov., which has a semicircular G1 terminal segment inner distal angle, *N. guangdongense*, *N. hepingense*, *N. yongchuense*, *N. nanriense*, and *N. huaanense* differ in having instead a bluntly triangular G1 terminal segment inner distal angle (Fig. 5B–F). The G1 terminal segment inner distal angle is also semicircular in both *N. wupingense* and *N. macau* (Huang et al. 2018a); however,
the terminal segments in these two species are proportionately larger. In *N. macau*, the G1 terminal segment distal margin is sinuous to V-shaped (cf. Huang et al. 2018a: fig. 5D, E). In *N. wupingense*, the G1 terminal segment distal margin is sinuous to an inverte V-shaped (cf. Cheng et al. 2003: fig. 7; Huang et al. 2018a: fig. 6D). In *N. longhaiense* sp. nov., however, the G1 terminal segment distal margin is flat to oblique (Fig. 6A–C). The detailed differences between the new species and congeners are presented in Table 2.
New species of *Nanhaipotamon* from Fujian

Figure 2. *Nanhaipotamon longhaiense* sp. nov. holotype male (25.2 × 21.5 mm) (NCU MCP 417701)

A ventral view of anterior thoracic sternum, telson, and male pleonal somites 4–6

B ventral view of sterno-pleonal cavity with G1 *in situ*

C the fourth ambulatory leg

D left third maxilliped. Scale bars: 5 mm.
Figure 3. *Nanhaipotamon longhaiense* sp. nov. Paratype female (26.5 × 22.5 mm) (NCU MCP 428601).
A overall habitus B female vulvae C female holding eggs. Scale bars: 1 cm.
Phylogenetic analyses

In this study, we obtained the partial mitochondrial 16S rRNA and COI genes from specimens of *Nanhaipotamon* collected from Xiaye Village, Chengxiang Town, Longhai County, Fujian Province, China. A total of 37,546 bp 16S rRNA gene sequences and 22,658 bp COI gene sequences were used to construct the BI and ML trees. The topological structures of the 16S rRNA and COI trees are similar. Both trees show that *N. longhaiense* sp. nov. and 11 other species of *Nanhaipotamon* are clustered into one clade (Figs 8, 9). In the 16S rRNA tree, four sequences of *N. longhaiense* sp. nov. form a small branch within *Nanhaipotamon*, while in the COI tree, the *N. longhaiense* sp. nov. clade and *N. wupingense* are sister to each other, indicating a close phylogenetic relationship between *N. longhaiense* sp. nov. and *N. wupingense*. The pairwise distances between the 12 species of *Nanhaipotamon* were calculated based on the COI gene. The result shows that the pairwise genetic distances between *Nanhaipotamon* range from 0.0239 to 0.1552 (Table 3), while distances between *N. longhaiense* sp. nov. and its congeners are from 0.0880 to 0.1423. Therefore, the genetic distance is large enough to support *N. longhaiense* sp. nov. as new. Both the phylogenetic position and genetic divergences provide evidence supporting the recognition of *N. longhaiense* sp. nov. as a new species.

Discussion

*Nanhaipotamon* is endemic to China and mainly distributed in the low-elevation coastal areas or islands in southeastern China. Due to the isolating effect of mountain
Figure 5. G1s of six species of *Nanhaipotamon*. A *N. longhaiense* sp. nov., NCU MCP 417701 B *N. guangdongense*, Dai, 1997, CB 05141 C *N. hepingense*, Dai, 1997, CB 05106 D *N. yongchuense*, Dai, 1997, CB 05104 E *N. nanriense*, Dai, 1997, CB 05103 F *N. huaanense*, Dai, 1997, CB 05105.

Figure 6. G1s of *N. longhaiense* sp. nov. A holotype, NCU MCP 417701 B paratype, ZZCDC 613201 C paratype, ZZCDC 613203.
New species of *Nanhaipotamon* from Fujian

ranges, *Nanhaipotamon* is restricted to an area east of the Wuyishan Range and south of the Nanling Range (Shih et al. 2011). With 18 species, including *N. longhaiense* sp. nov., species diversity in *Nanhaipotamon* is the highest among sympatric genera (*Longpotamon*, *Somanniathelphusa*, *Huananpotamon*, *Bottapotamon*, *Minpotamon*, *Heterochelamon*, *Cantopotamon*, *Cryptopotamon*, *Eurusamon*, *Yarepotamon*, *Yuebeipotamon*) except *Geothelphusa*. *Huananpotamon* is followed by *Nanhaipotamon*, with 15 species distributed on both sides of the Wuyishan Range (Fujian and Jiangxi Provinces) (Shih et al. 2011; Chu et al. 2018). While all the other sympatric genera consist

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**Figure 7.** Habitat environment. **A** burrow inhabited by the new species (indicated by circle) **B** habitat environment.
of fewer than 10 species. Therefore, *Nanhaipotamon* has important value as part of the regional biodiversity.

In the morphological classification of freshwater crabs, the G1 character provides important morphological identification features (Dai 1999). Intraspecific variation in G1 morphology has been reported in some species of *Nanhaipotamon*, such as *N. guangdongense* from different localities (Huang et al. 2012; Huang et al. 2018a). In *N. longhaiense* sp. nov., intraspecific variation of G1 morphology was also found. Several questions have arisen due to G1 intraspecific variation: Dai (1997) described *N. hepingense* and *N. pinghense*, both from Heping County, Guangdong Province. Shih et al. (2011) provided molecular evidence that they are synonymous and many scholars agree with this (Huang et al. 2012; Chu et al. 2018). Huang et al. (2012) described *N. zhuhaiense* in Zhuhai, Guangdong Province, where *N. guangdongense* is also found. Later, Huang et al. (2018a) indicated that *N. zhuhaiense* and *N. guangdongense* are probably conspecific, but they did not have sufficient material on which to take taxonomic action. These problems were caused by intraspecific variation, which makes it difficult to classify species based

### Table 2. Morphological difference among eight species of *Nanhaipotamon*.

| Species/character | Ratio of flagellum length to exopod length | G1 in situ | Inner margin of G1 terminal segment | Inner distal angle of G1 terminal segment | Outer distal angle of G1 terminal segment |
|-------------------|-------------------------------------------|-----------|-------------------------------------|------------------------------------------|-----------------------------------------|
| *N. longhaiense* sp. nov. | 0.4 (Fig. 2D) | Exceeding pleonal locking tubercle (Fig. 2B) | Convex (Fig. 5A) | Semicircular (Fig. 5A) | Relatively stout; bent outwards at angle of about 60° (Fig. 5A) |
| *N. nanriense* (cf. Dai 1999: fig. 53) | 0.4 | Exceeding pleonal locking tubercle | Gently convex (Fig. 5E) | Blunt; triangular (Fig. 5E) | Relatively stout; bent outwards at angle of about 45° (Fig. 5E) |
| *N. yongchuense* (cf. Dai 1999: fig. 54) | 0.1 | Exceeding pleonal locking tubercle | Gently convex (Fig. 5D) | Blunt; triangular (Fig. 5D) | Relatively stout; bent outwards at angle of about 45° (Fig. 5D) |
| *N. huaanense* (cf. Dai 1999: fig. 55) | 0.1 | Reaching pleonal locking tubercle | Gently convex | Blunt; triangular | Relatively slender; bent outwards at angle of about 60° |
| *N. wupingense* | 0.1 (cf. Cheng et al. 2003: fig. 5) | Exceeding pleonal locking tubercle (cf. Cheng et al. 2003: fig. 3) | Gently convex (cf. Cheng et al. 2003: fig. 7) | Distinctly expanded; semicircular (cf. Cheng et al. 2003: fig. 7) | Relatively stout; bent outwards >60° (cf. Cheng et al. 2003: fig. 7) |
| *N. macau* | 0.2 (cf. Huang et al. 2018a: fig. 5A) | Exceeding pleonal locking tubercle (cf. Huang et al. 2018a: fig. 3D) | Gently convex (cf. Huang et al. 2018a: fig. 5D, E) | Distinctly expanded; semicircular (cf. Huang et al. 2018a: fig. 5D, E) | Relatively stout; bent outwards at angle of about 90° (cf. Huang et al. 2018a: fig. 5D, E) |
| *N. hepinglese* (cf. Dai 1999: fig. 59) | 0.5 | Exceeding suture 4/5 | Gently convex (Fig. 5C) | Blunt; triangular (Fig. 5C) | Relatively stout; bent outwards >60° (Fig. 5C) |
| *N. guangdongense* (cf. Dai 1999: fig. 60) | 0.5 | Not reaching pleonal locking tubercle | Distinctly convex (Fig. 5B) | Triangular (Fig. 5B) | Relatively stout; bent outwards >60° (Fig. 5B) |
Figure 8. Phylogenetic tree based on 16S rRNA. Topologies and branch lengths were obtained from BI analysis. Support values represented at the nodes were from BI and ML.

Table 3. Pairwise genetic distances between 12 species of *Nanhaipotamon*.

| Species                  | 1   | 2   | 3   | 4   | 5   | 6   | 7   | 8   | 9   | 10  | 11  | 12  |
|--------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| *N. formosanum*          |     |     |     |     |     |     |     |     |     |     |     | 0.0269 |
| *N. dongyinense*         | 0.0269 |     |     |     |     |     |     |     |     |     |     |     |
| *N. wenzhouense*         | 0.0319 |     |     |     |     |     |     |     |     |     |     |     |
| *N. nanriense*           | 0.0303 | 0.0255 | 0.0306 |     |     |     |     |     |     |     |     |     |
| *N. yongchunense*        | 0.0458 | 0.0408 | 0.0425 | 0.0305 |     |     |     |     |     |     |     |     |
| *N. hongkongense*        | 0.1088 | 0.1009 | 0.1031 | 0.0928 | 0.0991 |     |     |     |     |     |     |     |
| *N. wupingense*          | 0.0312 | 0.1272 | 0.1340 | 0.1437 | 0.1390 | 0.1444 |     |     |     |     |     |     |
| *N. huaanense*           | 0.1503 | 0.1227 | 0.1317 | 0.1437 | 0.1366 | 0.1444 | 0.0239 |     |     |     |     |     |
| *N. guangdongense*       | 0.1243 | 0.1140 | 0.1207 | 0.1098 | 0.1302 | 0.0985 | 0.1373 | 0.1420 |     |     |     |     |
| *N. macau*               | 0.1060 | 0.1246 | 0.1275 | 0.1159 | 0.1342 | 0.1066 | 0.1437 | 0.1461 | 0.0409 |     |     |     |
| *N. wupingense*          | 0.1116 | 0.0975 | 0.1058 | 0.1039 | 0.1141 | 0.1018 | 0.1529 | 0.1529 | 0.1366 | 0.1534 |     |     |
| *N. longhaiense* n.sp.   | 0.0976 | 0.0880 | 0.0920 | 0.0922 | 0.0902 | 0.1031 | 0.1423 | 0.1329 | 0.1184 | 0.1252 | 0.1033 |     |
| *N. guangdongense*       | 0.1026 | 0.0875 | 0.1058 | 0.1039 | 0.1141 | 0.1018 | 0.1529 | 0.1529 | 0.1366 | 0.1534 |     |     |
| *N. macau*               | 0.1060 | 0.1246 | 0.1275 | 0.1159 | 0.1342 | 0.1066 | 0.1437 | 0.1461 | 0.0409 |     |     |     |
| *N. wupingense*          | 0.1116 | 0.0975 | 0.1058 | 0.1039 | 0.1141 | 0.1018 | 0.1529 | 0.1529 | 0.1366 | 0.1534 |     |     |
| *N. longhaiense* n.sp.   | 0.0976 | 0.0880 | 0.0920 | 0.0922 | 0.0902 | 0.1031 | 0.1423 | 0.1329 | 0.1184 | 0.1252 | 0.1033 |     |
| *N. guangdongense*       | 0.1026 | 0.0875 | 0.1058 | 0.1039 | 0.1141 | 0.1018 | 0.1529 | 0.1529 | 0.1366 | 0.1534 |     |     |
Figure 9. Phylogenetic tree based on COI. Topologies and branch lengths were obtained from BI analysis. Support values represented at the nodes were from BI and ML.

on morphology alone. Therefore, when describing a new species of this genus, it is recommended that morphological classification be combined with molecular analysis. There are likely other problems with some species in this genus, and therefore a revision is necessary.

Conclusion

In this article, we report a new species of *Nanhaipotamon* collected from Xiaye Village, Chengxiang Town, Longhai County, Fujian Province, China. *Nanhaipotamon longhaiense* sp. nov. can be distinguished from congeners by the combination of carapace, third maxilliped, and male first gonopod characters. Molecular evidence based on the mitochondrial 16S rRNA and COI genes also support it as a new species of the genus *Nanhaipotamon*. 
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**Supplementary material 1**

**BI phylogenetic tree based on 16S gene**

Authors: Mao-Rong Cai, Qi-Hong Tan, Jie-Xin Zou

Data type: phylogenetic

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**Supplementary material 2**

**ML phylogenetic tree based on 16S gene**

Authors: Mao-Rong Cai, Qi-Hong Tan, Jie-Xin Zou

Data type: phylogenetic

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Supplementary material 3

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Supplementary material 4

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