

Two New Sympatric Aquatic Freshwater Crab Species, *Megapleonium taishanense* sp. nov. and *Cantopotamon chixiense* sp. nov. (Crustacea: Brachyura: Potamidae), from Taishan, Guangdong, China

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Two new species of freshwater crabs are described from a hillstream in Chixi Town, Taishan City, Guangdong Province, China: *Megapleonium taishanense* sp. nov. and *Cantopotamon chixiense* sp. nov. The two new species are sympatric and are similar in size, colour and superficial appearance in the field. Inspection of key morphological characters sets them apart as undescribed species from two different genera. *Megapleonium taishanense* sp. nov. and *Cantopotamon chixiense* sp. nov. can immediately be separated from their respective congeners by their unique G1 morphology but also their combination of carapace, maxilliped 3 and male pleon characters. A phylogeny constructed using the mitochondrial COI gene places *Cantopotamon chixiense* sp. nov. in its own clade as sister to *C. yangxiense* Huang, Ah Yong & Shih 2017 and a previous 16S rRNA gene study has already shown that *Megapleonium taishanense* sp. nov. represents an independent clade within *Megapleonium* Huang, Shih & Ah Yong 2018, supporting the current taxonomic treatment of both new species.

Keywords: China, COI, Freshwater crab, Hillstream, New species, Systematics

BACKGROUND

Taishan City lies in the coastal south of sub-tropical Guangdong and is historically known as the ‘First Home of Overseas Chinese’ owing to the large number of emigrants who left from there, especially during the 19th and early 20th centuries. The region remains poorly sampled for freshwater crabs with only one species, *Cantopotamon shangchuanense* Huang, Ah Yong & Shih, 2017, being formally reported

from there. A September 2019 survey of a hillstream in Chixi yielded several specimens of small aquatic freshwater crabs. Initial morphological examination suggested they belonged to an undescribed species of *Cantopotamon* Huang, Ah Yong & Shih, 2017, and tissue from one female was used for 16S rRNA gene sequencing. To our surprise, the sequence clustered with *Megapleonium* Huang, Shih & Ah Yong 2018. Upon re-examination and sequencing of additional specimens, it was determined that the single sequenced female indeed

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belongs to *Megapleonum* and differs from all the other *Cantopotamon* specimens in the relative length of the pereiopod 5 dactylus and vulva size. It became clear that we were dealing with two similar looking sympatric species and further collection efforts to find males of the species of *Megapleonum* were needed. In September of 2024, the first and second authors revisited the same locality and successfully collected one male and one female *Megapleonum* amongst the much more numerous new species of *Cantopotamon*. With this, the two new species are described herein.

MATERIALS AND METHODS

Specimens were collected by hand, preserved in 75–95% ethanol, and deposited in the collections of the Sun Yat-sen Museum of Biology, Sun Yat-sen University, Guangzhou, China (SYSBM), and College of Life Sciences, Nanjing Normal University, Nanjing, China (NNU). The terminology used primarily follows that of Dai (1999) and Davie et al. (2015). Carapace length (CL) is measured along the dorsal midline. Carapace width (CW) is the greatest width, measured across the branchial margins. The male gonopods 1 and 2 are abbreviated as G1 and G2, respectively. Measurements (mm) are of the carapace width and length, respectively.

We sequenced the *COI* gene of two specimens of the new species of *Cantopotamon* from Chixi, Taishan (GenBank accession numbers: PX400621, PX400622), and two additional samples from Yangchun and Hailing Island, Yangjiang identified as *Cantopotamon yangxiense* Huang, Ahyong & Shih, 2017 (GenBank accession numbers: PX400619, PX400620). Sequences of *Cantopotamon yangxiense* were obtained following Shih et al. (2016). The sequence of *Cantopotamon chixiense* sp. nov. SYSBM 002165 was extracted using the TIANamp Genomic DNA Kit (Tiangen, Beijing, China). A 658 basepair (bp) fragment of the *COI* gene was amplified using the primers LCO1490, HCO2198 (Folmer et al. 1994). The PCR conditions for the above primers included an initial denaturation for 3 minutes at

94°C, followed by 5 cycles of denaturation for 30 s at 94°C, annealing for 45 s at 42°C, and extension for 60 s at 68°C, followed by 35 cycles of denaturation for 30 s at 94°C, annealing for 60 s at 46°C, and extension for 60 s at 72°C, followed by a final extension for 3 minutes at 72°C. The sequence of *Cantopotamon chixiense* sp. nov. SYSBM 002194 was extracted using the EasyPure Genomic DNA Kit (Transgen Biotech, Beijing, China). A 658 basepair (bp) fragment of the *COI* gene was amplified using the primers LCO1490, HCO2198 (Folmer et al. 1994). The PCR conditions for the above primers were an initial denaturation for 3 minutes at 94°C, followed by 35 cycles of denaturation for 30 s at 94°C, annealing for 45 s at 45°C, and extension for 60 s at 72°C, followed by a final extension for 3 minutes at 72°C. All sequences were then obtained through a commercial sequencing company.

We also used all additional *COI* sequences of *Cantopotamon* species available on NCBI (Huang et al. 2017, Table 1). We aligned these sequences with MUSCLE v5.1.0 (Edgar 2022), setting 100 replicates with varying random seeds and extracted the alignment with the highest column confidence score. We opted for running both Bayesian Inference (BI) and Maximum Likelihood (ML) phylogenetic reconstructions using MrBayes v3.2.7a (Ronquist et al. 2012) and IQ-TREE v2.4.0 (Minh et al. 2020), respectively, to compare results from two different lines of evidence. For the BI analysis, we sampled the substitution model space while running the MCMC, therefore, setting a model a priori was not necessary. After running the analysis, the model with the highest posterior probability was A-C = A-G = A-T /= C-G /= C-T /= G-T (model code: 111234). We conducted five independent runs of 5,000,000 generations with three chains each, sampling every 1000 generations after discarding the first 25% as burn-in. We assessed convergence by checking whether the standard deviation of split frequency values fell below 0.01 (Ronquist et al. 2005). We then extracted the Maximum Clade Credibility (MCC) tree from the distribution of 18,755 sampled trees with the maxCladeCred from the phangorn package (Schliep 2011) in R (R Core Team 2013) and computed median branch length based on the

Table 1. GenBank accession numbers of sequences used in the phylogenetic analysis

Species	GenBank Accession	Museum Voucher
<i>Cantopotamon shangchuanense</i>	LC342055.1	SYSBM:1429
<i>Cantopotamon shangchuanense</i>	LC342054.1	SYSBM:1428
<i>Cantopotamon hengqinense</i>	LC342053.1	SYSBM:1561
<i>Cantopotamon hengqinense</i>	LC342052.1	SYSBM:1559
<i>Cantopotamon zhuhaiense</i>	LC342051.1	SYSBM:1439
<i>Cantopotamon yangxiense</i>	LC342056.1	SYSBM:1564

distribution of trees with the `add_edge_length` function from the same package. For the ML analysis, we used the same muscle alignment as input and selected the best-fitting substitution model with ModelFinder (Kalyaanamoorthy et al. 2017) as implemented in IQ-TREE2. The Model with the best support according to the Bayesian Information Criterion was TIM2+F+I. We conducted five independent runs, each with 20,000 ultrafast bootstrap replicates, 1000 initial parsimony trees, 200 initial top trees and 25 best trees retained. Finally, we extracted the consensus tree for comparison with the BI analysis. We then plotted and annotated the tree retrieved from BI, using `ggtree` (Yu et al. 2017). Additionally, we computed pairwise absolute basepair differences between haplotypes with `ape` (Paradis et al. 2004) as implemented in R (R Core Team 2013). Kimura-2-parameter (K2P; Kimura 1980) distances were also calculated for comparative purposes, as this metric remains widely used in DNA barcoding studies, despite its known limitations (Srivathsana and Meier 2011). Lastly, we created a haplotype network with PopART v1.7 (Leigh and Bryant 2015), applying the Integer NJ Network algorithm, to visualize divergence and possible connections between haplotypes in the genus *Cantopotamon*.

RESULTS

TAXONOMY

Family Potamidae Ortmann, 1896
Subfamily Potamiscinae Bott, 1970
***Cantopotamon* Huang, Shih & Ah Yong, 2017**

***Cantopotamon chixiense* sp. nov.**

(Figs. 1–3, 6H–I, 8B)

urn:lsid:zoobank.org:act:CC6E6934-32DB-44B3-A60C-C3749B98842B

Material examined: Holotype: SYSBM 002158, male (19.7 × 16.7 mm), Longtan Forest, Chixi Town, Taishan City, Guangdong Province, China, 21.96°N, 112.99°E, hillstream under rock, coll. Chao Huang & Bernhard Bein, September 2019. Paratypes: SYSBM 002159–002160, 2 males (17.0 × 14.3 mm, 13.9 × 11.5 mm) same data as holotype. SYSBM 002161–002162, 2 females (28.0 × 23.3 mm, 12.4 × 10.2 mm) same data as holotype. SYSBM 002163–002164, 2 males (17.8 × 15 mm, 16.9 × 14.2 mm), SYSBM 002165, 1 female (28.1 × 22 mm), NNU 16C-202408CT, 2 males (18.1 × 14.9 mm, 16.4 × 13.3 mm), Longtan Forest, Chixi Town, Taishan City, Guangdong Province, China, 21.96°N, 112.99°E,

hillstream under rock, coll. Chao Huang & Bernhard Bein, September 2024.

Others: SYSBM 002166–002167, 1 male (17.9 × 14.5 mm), 1 female (20.8 × 16.1 mm), Dashikeng, Chixi Town, Taishan City, Guangdong Province, China, 21.98°N, 112.97°E, hillstream under rock, coll. Chao Huang & Bernhard Bein, September 2024. SYSBM 002193–002194, 2 males (14.4 × 11.9 mm, 10.6 × 9 mm), Tonggu, Taishan City, Guangdong Province, China, 21.874178°N, 112.903947°E, hillstream under rock, coll. Chao Huang, October 2024.

Etymology: This species is named after the type locality Chixi Town, Taishan.

Diagnosis: Carapace broader than long, dorsal surface slightly convex, epigastric cristae low, not confluent with postorbital cristae (Fig. 1). Maxilliped 3 merus width about 1.2 × length; ischium width about 0.7 × length; exopod reaching proximal one-third of merus; flagellum very long (Fig. 3A). Male anterior thoracic sternum broad, width about 1.8 × length (Fig. 2B). Male pleon narrowly triangular, pleonite 6 width approximately 2.2 × length; telson width 1.3 × length (Fig. 2C). G1 long, slender, tip exceeding suture between thoracic sternites 4/5 *in situ* (Fig. 2D); subterminal article straight, slender, about 2.6 × length of terminal article (Fig. 2C–E); terminal article relatively short, sinistrally twisted on the left G1, bifurcated, tip pronounced, pointing meso-anteriorly; inner margin with pronounced projection similar in shape and size to the tip (Figs. 6H, I). G2 subterminal article slender, flagelliform terminal article thin, around 2.1 × length of subterminal article (Fig. 2B).

Description: Carapace broader than long, about 1.2–1.3 times as wide as long ($n = 14$); regions visible, dorsal surface slightly convex; surface pitted (Fig. 1). Frontal margin flat (Figs. 1, 2A). Epigastric cristae low, not confluent with postorbital cristae; bifurcated shallow groove between epigastric cristae (Fig. 1). Anterolateral regions strongly rugose (Fig. 1). Branchial region not distinctly swollen (Fig. 1). Cervical and H-groove obvious (Fig. 1). Mesogastric region flat (Fig. 4). External orbital angle relatively prominent, triangular with convex outer margin, tip slight pointing inward, separated from anterolateral margin by gap (Figs. 1, 2A). Epibranchial tooth granular (Figs. 1, 2A). Anterolateral margin lined with 15–19 granules; posterolateral margin posteriorly convergent (Fig. 1); posterolateral margin with striae (Fig. 1). Orbits regular; supraorbital margins cristate, infraorbital margins lined with fused granules (Fig. 2A). Eye normal (Figs. 1, 2). Sub-orbital, pterygostomial and sub-hepatic regions rugose (Fig. 2A). Median lobe of epistome buccal margin triangular, lateral margins straight (Fig. 2A).

Maxilliped 3 merus subtrapezoidal, with slight

median depression, width about $1.2 \times$ length; ischium subtrapezoidal with very shallow median sulcus, distomesial margin rounded, width about $0.7 \times$ length. Exopod reaching proximal one-third of merus; flagellum very long, almost as long as exopod (Fig. 3A).

Chelipeds (pereopod 1) equal (Figs. 3F–I). Merus trigonal in cross section, surface pitted; outer dorsal margin slightly crenulated, inner and ventral margin lined with granules (Figs. 1, 2A). Carpus dorsal surface rugose, with spine at inner-distal angle, spinule at base (Fig. 1). Major cheliped palm length about $1.3\text{--}1.5 \times$ height in male ($n = 5$) and females ($n = 2$); dactylus $1.0\text{--}1.2 \times$ palm length in males ($n = 5$) and $1.0\text{--}1.3$ in females ($n = 2$) (Fig. 3F–I). Palm surface pitted, occlusal margin of fingers lined with 23–29 small, relatively fine, blunt teeth, with almost no gap when closed (Fig. 3F–I).

Ambulatory legs (pereopods 2–5) relatively long, slender with very short setae on propodus and dactylus margins, relatively denser on inner margin of P5

propodus (Fig. 1). Pereiopod 3 merus $0.7 \times$ CL in males ($n = 5$), $0.7\text{--}0.8$ in females ($n = 3$) (Fig. 1). Pereiopod 5 propodus length $2.0\text{--}2.2 \times$ height in males ($n = 5$), $2.2\text{--}2.3$ in females ($n = 3$), about as long as dactylus (Fig. 1).

Male thoracic sternum pitted; sternites 1–4 width about $1.8 \times$ length; sternites 1 and 2 fused to form broad triangle; fused sternites 1 and 2 demarcated from sternite 3 by slightly sinuous sulcus; sternites 3, 4 fused without distinct sulcus (Fig. 2B). Male sterno-pleonal cavity barely reaches mid-length of cheliped coxa (Fig. 2B). Male pleonal locking tubercle positioned at low half of sternite 5 (Fig. 2D). Female vulva subovate, large, lower margin reaching the suture of sternites 6/7, relatively closely positioned (Fig. 2F).

Male pleon narrowly triangular; pleonites 3–6 progressively narrower; pleonite 6 width approximately $2.2 \times$ length; telson width $1.3 \times$ length; lateral margins almost straight, telson subtriangular (Fig. 2C). Female

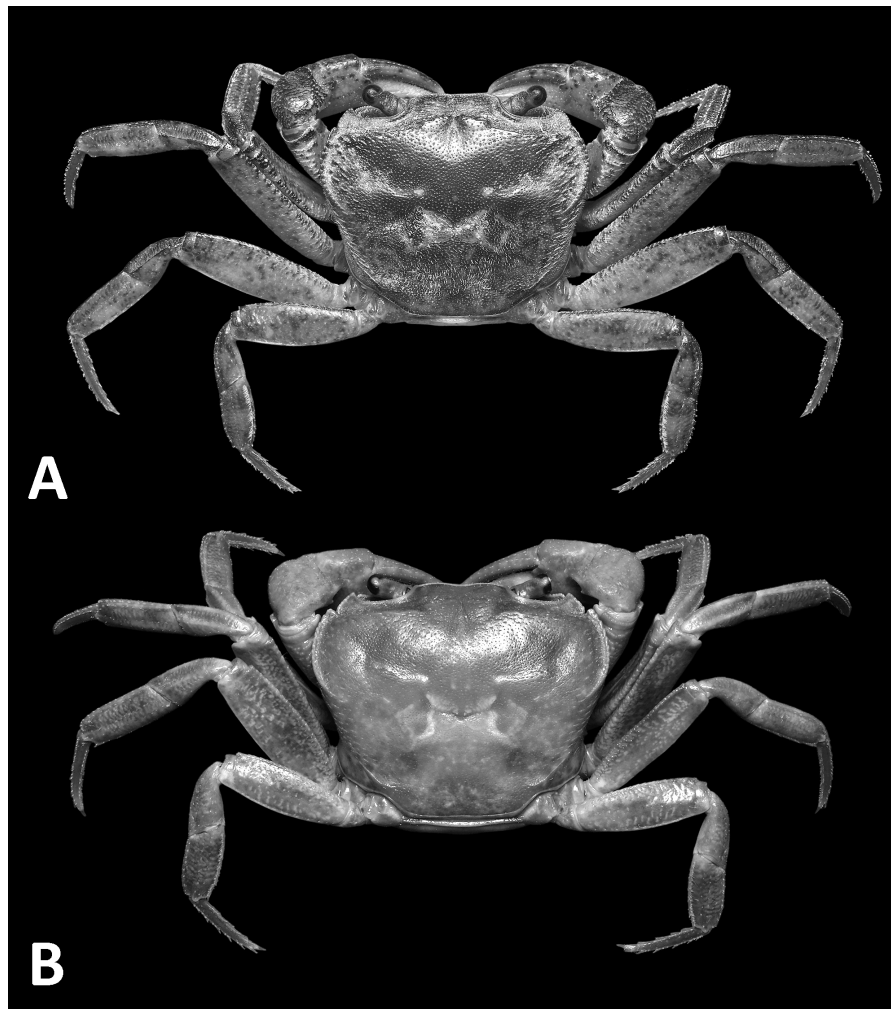


Fig. 1. A: Dorsal habitus. *Cantopotamon chixiense* sp. nov., male holotype (19.7×16.7 mm), SYSBM 002158; B: female paratype (28.0×23.3 mm), SYSBM 002161.

pleon sub-ovate (Fig. 2E).

G1 long, slender, tip exceeding suture between thoracic sternites 4/5 *in situ* (Fig. 2D); subterminal article straight, slender, about $2.6 \times$ length of terminal article (Fig. 2C–E); terminal article relatively short, sinistrally twisted on the left G1, bifurcated, tip pronounced, pointing meso-anteriorly; inner margin with pronounced projection similar in shape and size to the tip (Fig. 6H, I). G2 subterminal article slender,

flagelliform terminal article thin, around $2.1 \times$ length of subterminal article (Fig. 2B).

Colour in life: Generally camouflage brown all over (Fig. 8).

Habitat: *Cantopotamon chixiense* is a typical aquatic lowland hillstream species that shares the same hillstream with the rarer *Megaplemonum taishanense* sp. nov.

Distribution: Chixi Town, Taishan City,

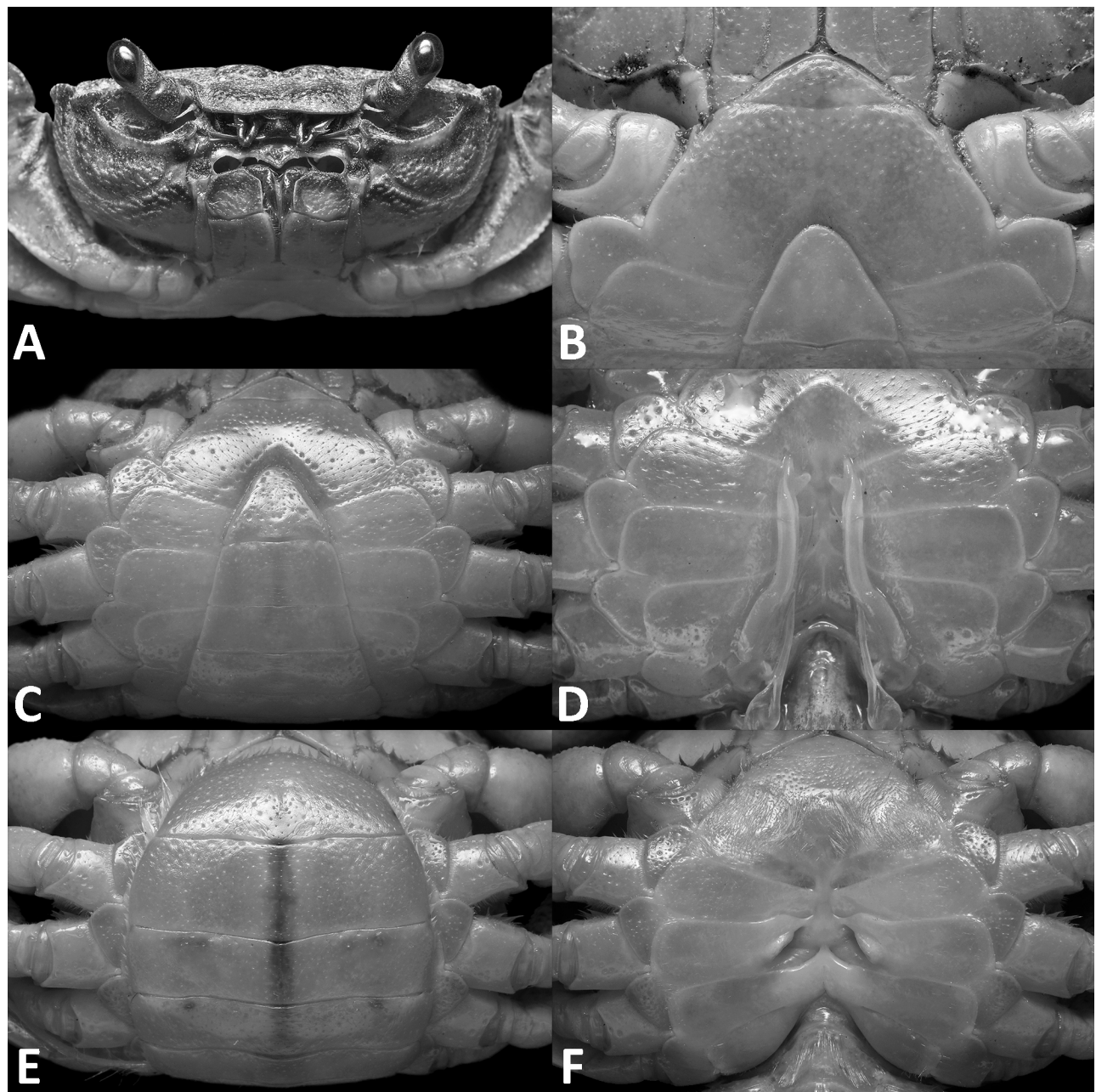


Fig. 2. A–D: *Cantopotamon chixiense* sp. nov., male holotype (19.7 × 16.7 mm), SYSBM 002158; E, F: female paratype (28.0 × 23.3 mm), SYSBM 002161. A: Cephalothorax, anterior view; B: anterior thoracic sternum; C: anterior thoracic sternum and pleon, ventral view; D: sterno-pleonal cavity with G1 *in situ*, ventral view; E: pleon, ventral view; F: vulvae, ventral view.

Guangdong Province, China (Fig. 9).

Remarks: All known species of the genus *Cantopotamon* share the same ecotype and are very conserved in external morphology. While some subtle differences of the male pleon were observed between species, it is mostly the G1 morphology that sets them apart (Huang et al. 2017). The same holds for *C. chixiense*, which is most similar to *C. yangxiense* in the G1 shape. However, in *C. chixiense*, the G1 terminal article is bifurcated, with a pronounced tip, pointing

meso-anteriorly and the inner margin has pronounced projection similar in shape and size to the tip (vs. pointing anteriorly, inner margin with sub-distal blunt projection, tip blunt in *C. yangxiense*, Huang et al. 2017: figs. 8B, C, 9G, H). *Cantopotamon chixiense* also differs from *C. shangchuanense* Huang, Ahyong & Shih, 2017, which also occurs in Taishan (with G1 curved inwards and pointing anteriorly, inner distal margin strongly convex, tip blunt; Huang et al. 2017: figs. 4B, C, 9C, D). *Cantopotamon chixiense* sp. nov. can further be

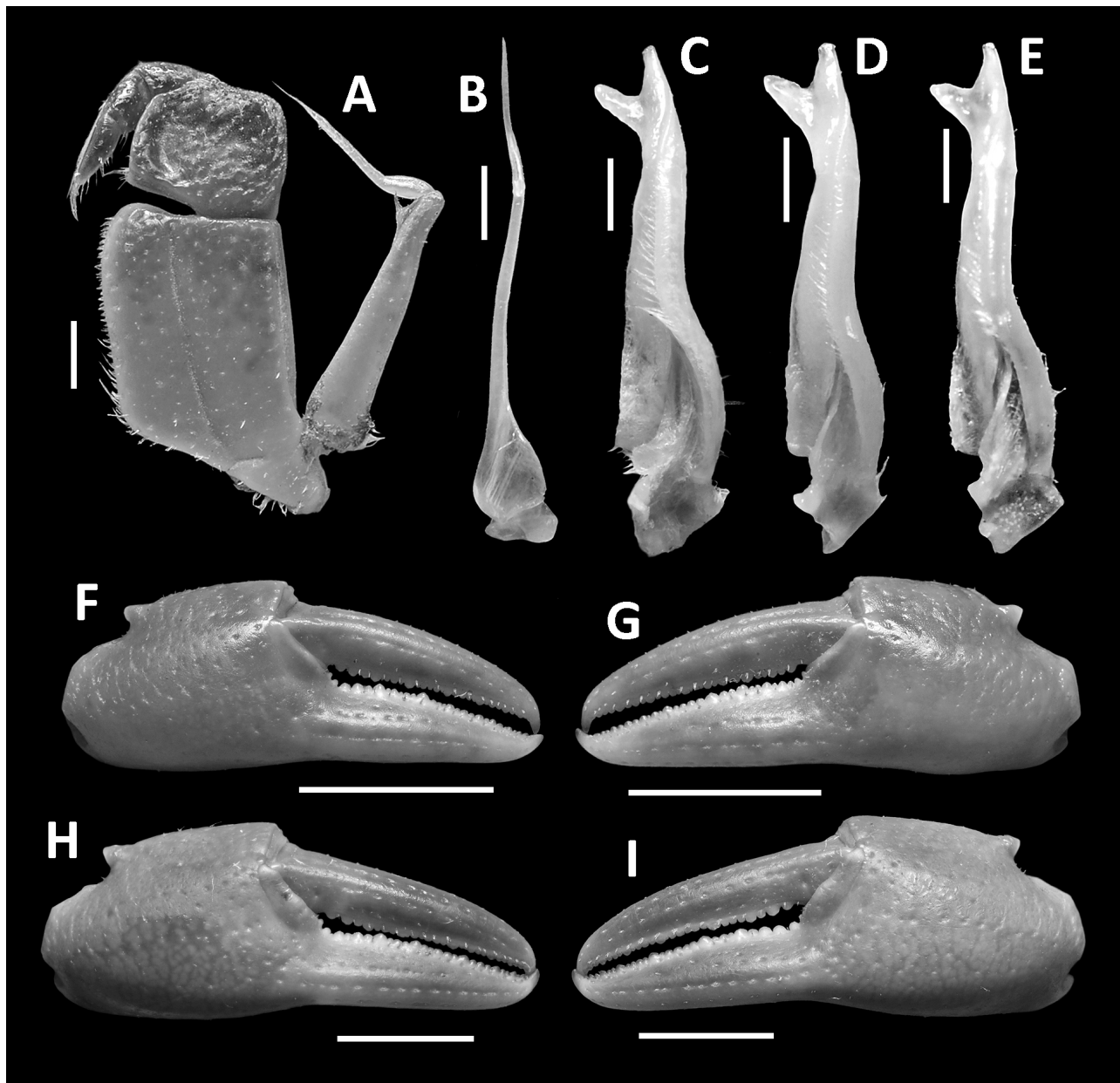


Fig. 3. A–C, F–G: *Cantopotamon chixiense* sp. nov., male holotype (19.7 × 16.7 mm), SYSBM 002158; D: male paratype (17.0 × 14.3 mm), SYSBM 002159; E: male paratype (17.8 × 15.0 mm), SYSBM 002163; H, I: female paratype (28.0 × 23.3 mm), SYSBM 002161. A: Left maxilliped 3; B: left G2, pleonal view; C–E: left G1, ventral view; F, H: major cheliped; G, I: minor cheliped. Scale bars: A–E = 1.0 mm, F–I = 5.0 mm.

separated from these two species in subtle differences of the male pleon, with its pleonite 6 width approximately $2.2 \times$ length and telson width $1.3 \times$ length (vs. 2.0 and 1.4 respectively in *C. yangxiense*, Huang et al. 2017: fig. 7C, and 2.3 and 1.4 respectively in *C. shangchuanense*, Huang et al. 2017: fig. 3C).

Additionally, the epigastric cristae are not obviously confluent with the postorbital cristae in *Cantopotamon chixiense* sp. nov. whereas that of all other congeners are more or less confluent. On closer inspection, however, this character is sometimes not clear cut and there can be slight variations between individuals. The diagnosis of this character of *Cantopotamon* would have to be corrected to “epigastric cristae confluent or not confluent with the postorbital cristae” accordingly.

Megapleonum Huang, Shih & Ah Yong, 2018

***Megapleonum taishanense* sp. nov.**

(Figs. 4–5, 6A–G, J, K, 8B)

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Material examined: Holotype: SYSBM 002168, male (17.9×14.2 mm), Longtan Forest, Chixi Town, Taishan City, Guangdong Province, China, 21.96°N , 112.99°E , hillstream under rock, coll. Chao Huang & Bernhard Bein, September 2024. Paratypes: SYSBM 002169, 1 female (21.2×17.0 mm), Longtan Forest, Chixi Town, Taishan City, Guangdong Province, China, 21.96°N , 112.99°E , hillstream under rock, coll. Chao Huang & Bernhard Bein, September 2019. SYSBM 002170, 1 female (11.7×8.9 mm), same data as

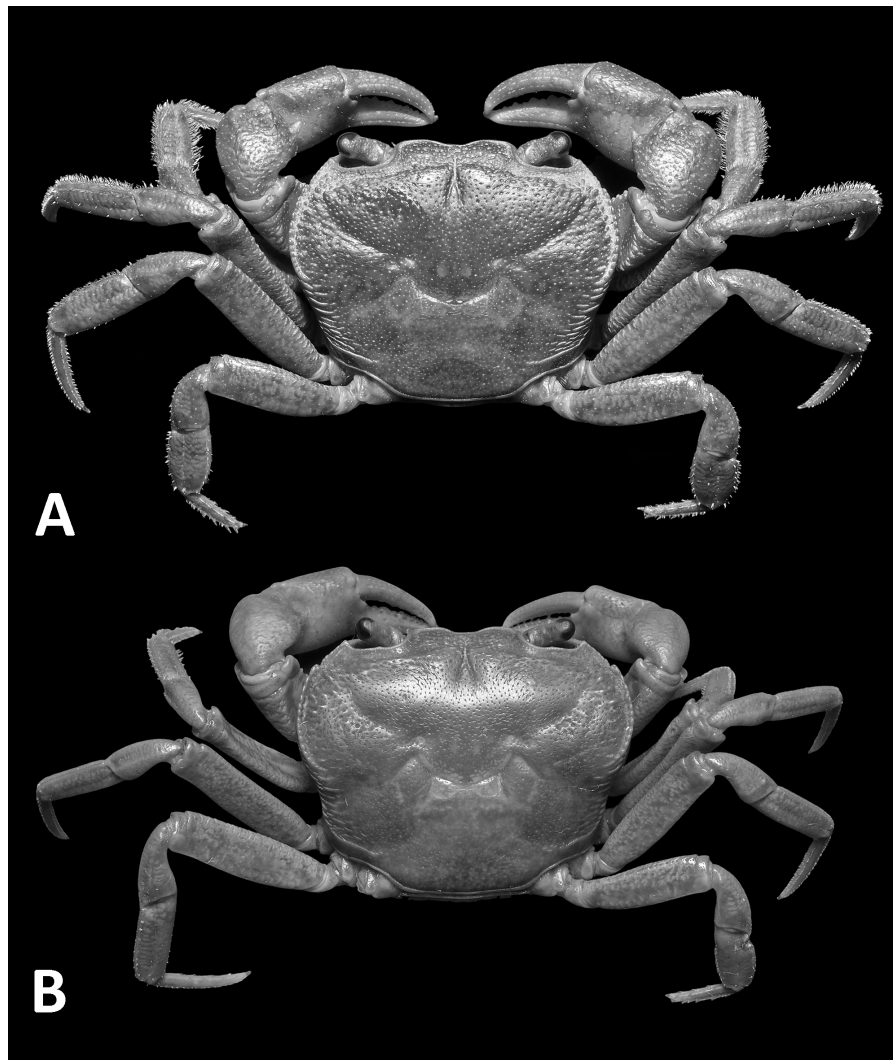


Fig. 4. Dorsal habitus. A: *Megapleonum taishanense* sp. nov., male holotype (17.9×14.2 mm), SYSBM 002168; B: female paratype (21.2×17.0 mm), SYSBM 002169.

holotype.

Etymology: This species is named after the type locality Taishan City.

Diagnosis: Carapace broader than long, dorsal surface slightly convex, postorbital, epigastric cristae confluent (Fig. 4). Maxilliped 3 merus width about $1.4 \times$ length; ischium width about $0.7 \times$ length; exopod reaching slightly beyond anterior edge of ischium; flagellum vestigial to short, as long as dactylus (Fig. 6A). Ambulatory legs without long setae, P5 dactylus

shorter than propodus (Fig. 4). Male anterior thoracic sternum very broad, width about $1.8 \times$ length (Fig. 5B). Male pleon large, broadly triangular, pleonite 6 width about $2.5 \times$ length, telson width around $1.8 \times$ length (Fig. 5C). G1 large, sinuous, tip well exceeding suture between thoracic sternites 4/5 *in situ* (Fig. 5D); subterminal article length about $1.9 \times$ length of terminal article (Fig. 6C); subterminal article thick, outer margin strongly concave, distal end slanted with outer-distal section highest; terminal article short, sinuous, bent

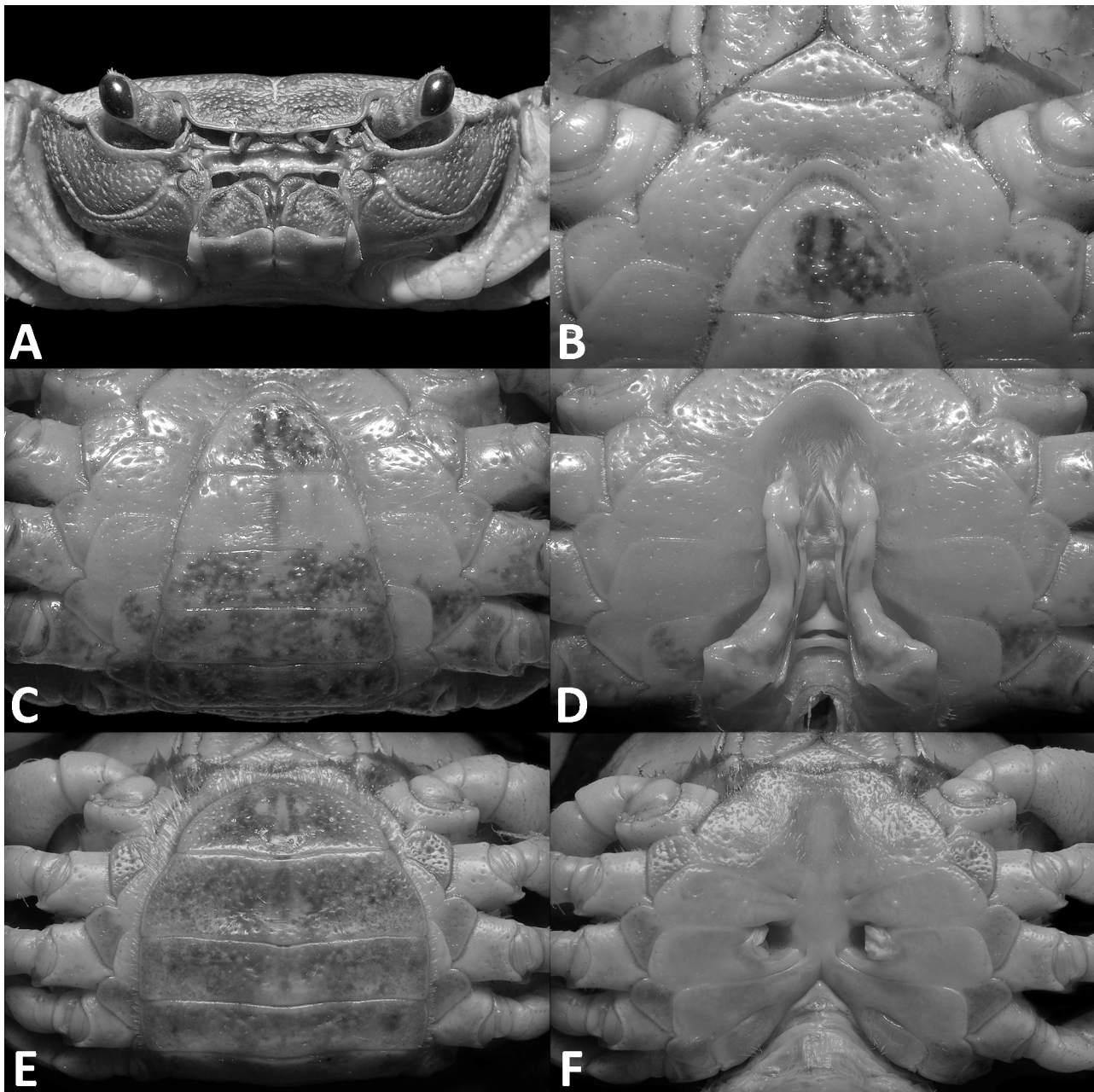


Fig. 5. A–D: *Megapleum taishanense* sp. nov., male holotype (17.9 × 14.2 mm), SYSBM 002168; E, F: female paratype (21.2 × 17.0 mm), SYSBM 002169. A: Cephalothorax, anterior view; B: anterior thoracic sternum; C: anterior thoracic sternum and pleon, ventral view; D: sternopleonal cavity with G1 *in situ*, ventral view; E: pleon, ventral view; F: vulvae, ventral view.

inwards then outwards and strongly tapering towards tip, base with swollen bulge on ventral side (Fig. 6J, K). G2 subterminal article thick, slightly bent outwards distally, flagelliform terminal article thin, around $2.0 \times$ length of subterminal article (Fig. 6B).

Description: Carapace broader than long, about 1.2–1.3 times as wide as long ($n = 3$); regions visible, dorsal surface slightly convex; surface pitted (Fig. 4). Frontal margin sinuous, deflexed (Figs. 4, 5A). Epigastric cristae and postorbital cristae confluent; bifurcated shallow groove between epigastric cristae (Fig. 4). Anterolateral regions slightly rugose (Fig. 4). Branchial regions not distinctly swollen (Fig. 4). Cervical and H-groove obvious (Fig. 4). Mesogastric region flat (Fig. 4). External orbital angle triangular, outer margin slightly convex, separated from anterolateral margin by small gap (Figs. 4, 5A). Epibranchial tooth granular, indistinct (Figs. 4, 5A). Anterolateral margin lined with 13–16 granules; posterolateral margin posteriorly convergent (Fig. 4);

posterolateral margin with striae (Fig. 4). Orbits regular; supraorbital margins cristate, infraorbital margins lined with fused granules (Fig. 5A). Eyes normal (Figs. 4, 5A). Sub-orbital, pterygostomial and sub-hepatic regions slightly rugose, pitted (Fig. 5A). Antennules large, folded within broad fossae; antennae very short (Fig. 5A). Median lobe of epistome buccal margin triangular, lateral margins straight (Fig. 5A).

Maxilliped 3 merus subtrapezoidal, with slight median depression, width about $1.4 \times$ length; ischium subtrapezoidal with very shallow median sulcus, distomesial margin rounded, width about $0.7 \times$ length. Exopod reaching proximal one-third of merus; flagellum vestigial to short, as long as dactylus (Fig. 6A).

Chelipeds (pereiopod 1) subequal (Fig. 6D–G). Merus trigonal in cross section, surfaces pitted; outer dorsal margin slightly crenulated, inner and ventral margin lined with large granules (Figs. 4, 5A). Carpus dorsal surface slightly rugose, with small blunt spine at inner-distal angle, two granular spinules at base (Fig. 4).

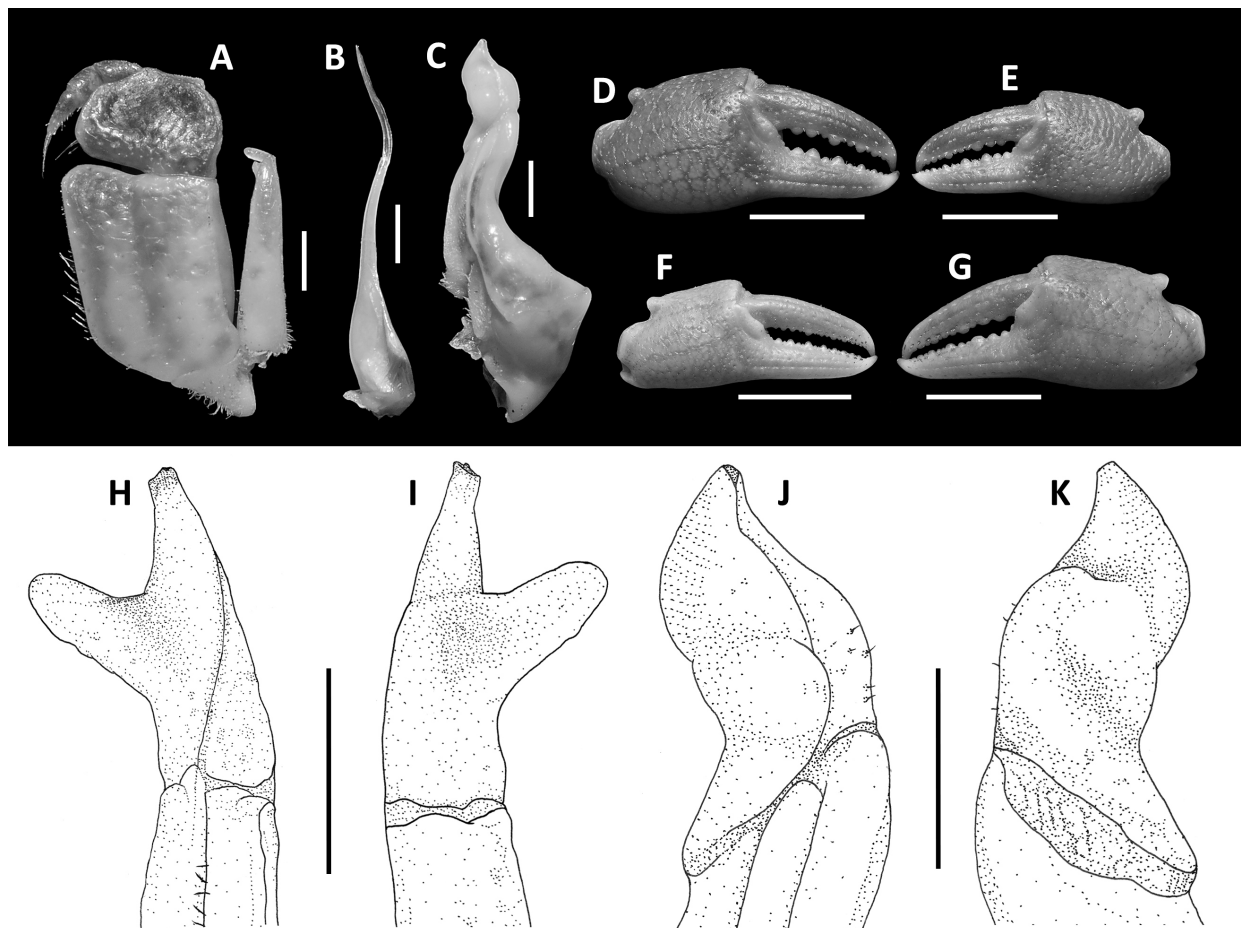


Fig. 6. A–C, D–E, J, K: *Megapleionum taishanense* sp. nov., male holotype (17.9 × 14.2 mm), SYSBM 002168; F, G: female paratype (21.2 × 17.0 mm), SYSBM 002169; H, I: *Cantopotamon chixiense* sp. nov., male holotype (19.7 × 16.7 mm), SYSBM 002158. A: Left maxilliped 3; B: left G2, pleonal view; C: left G1, ventral view; D, G: major cheliped; E, F: minor cheliped; H, J: G1 terminal article, ventral view; I, K: G1 terminal article, dorsal view. Scale bars: A–C, H–K = 1.0 mm, D–G = 5.0 mm.

Major cheliped palm length about $1.4 \times$ height in male ($n = 1$), 1.5 in female ($n = 1$); dactylus $0.9 \times$ palm length in both male ($n = 1$) and female ($n = 1$) (Fig. 6D–G). Palm surface pitted, occlusal margin of fingers with 11–16 irregular blunt teeth, with very small gape when closed (Fig. 6D–G).

Ambulatory legs typical (pereiopods 2–5), with very short setae on margins, male hairier than female (Fig. 4). Pereiopod 3 merus $0.7 \times$ CL in male ($n = 1$), 0.6 in female ($n = 1$) (Fig. 4). Pereiopod 5 propodus length $1.9 \times$ height in males ($n = 1$), 2.2 in female ($n = 1$), longer than dactylus (Fig. 4).

Male thoracic sternum pitted; sternites 1–4 width about $1.8 \times$ length; sternites 1 and 2 fused to form broad triangle; fused sternites 1 and 2 demarcated from sternite 3 by slightly sinuous sulcus; sternites 3, 4 fused with distinct sulcus (Fig. 5B). Male sterno-pleonal cavity reaching anteriorly slightly beyond mid-length of cheliped coxa (Fig. 5B). Male pleonal locking tubercle positioned at mid-length of sternite 5 (Fig. 5D). Female vulvae ovate, large, reaching the suture of sternites 5/6, relatively widely separated (Fig. 5F).

Male pleon large, broadly triangular; pleonites 3–6 progressively narrower; pleonite 6 width approximately $2.5 \times$ length; telson width $1.8 \times$ length; lateral margins almost straight, apex rounded (Fig. 5C). Female pleon sub-ovate (Fig. 5E).

G1 large, sinuous, tip well exceeding suture between thoracic sternites 4/5 *in situ* (Fig. 5D); subterminal article length about $1.9 \times$ length of terminal article (Fig. 6C); subterminal article thick, outer margin strongly concave, distal end slanted with outer-distal section highest; terminal article short, sinuous, bent inwards then outwards and strongly tapering towards tip, base with swollen bulge on ventral side (Fig. 6J, K). G2 subterminal article thick, slightly bent outwards distally, flagelliform terminal article thin, around $2.0 \times$ length of subterminal article (Fig. 6B).

Colour in life: Generally camouflage brown all over (Fig. 8).

Habitat: *Megapleonium taishanense* is a typical aquatic lowland hillstream species that is found in low abundance at the type locality. It shares the same hillstream with the much more abundant *Cantopotamon chixiense* sp. nov.

Distribution: Chixi Town, Taishan City, Guangdong Province, China (Fig. 9).

Remarks: *Megapleonium taishanense* is most similar to *Megapleonium shenzhen* Huang & Mao, 2021 and *Megapleonium yangdongense* Huang, Shih & Ah Yong, 2025 in general external appearance and G1 shape; they are also closely related as can be seen in their deep-rooted clustering in the phylogenetic tree in Huang et al. (2025, fig. 12). *Megapleonium taishanense*

sp. nov. differs from *M. shenzhen* by its proportionally narrower carapace (about 1.2–1.3 times as wide as long (Fig. 4) vs. 1.3–1.4 in *M. shenzhen*, Huang et al. 2021: fig. 2); proportionally narrower male pleon with almost straight lateral margins (pleonite 6 width approximately $2.5 \times$ length (Fig. 5C) vs. lateral margins slightly convex and pleonite 6 width approximately $2.6 \times$ length in *M. shenzhen*, Huang et al. 2021: fig. 2C); and the G1 terminal article (short, sinuous, bent inwards then outwards and strongly tapering towards tip, base with swollen bulge on ventral side (Fig. 6J, K) vs. terminal article stout, goose-head-shaped, tip pointed, pointing inner-upwards, distal part forming lobe, ventral side with large bulging curved flap in *M. shenzhen*, Huang et al. 2021: figs. 3C–E, 4G). *Megapleonium taishanense* sp. nov. differs from *M. yangdongense* by its wider male pleon (vs. $2.4 \times$ in *M. yangdongense*, Huang et al. 2025: fig. 9C); and G1 terminal article (short, sinuous, bent inwards then outwards and strongly tapering towards tip, base with swollen bulge on ventral side (Fig. 6J, K) vs. short, both lateral margins slightly convex, bifurcated with one point being the opening tip and other a smaller projection on the outer margin, both pointing upwards in *M. yangdongense*, Huang et al. 2025: figs. 10C–E, 11C, D). In addition, the new species has two granular spinules at the base of the cheliped carpus spine at inner-distal angle, whereas both *M. shenzhen* and *M. yangdongense* only have one. It is worth mentioning that while this character can be useful in separating the above species, it is not so effective other species. For example, the base spinule in *Megapleonium falx* Huang, Shih & Ah Yong, 2025, and *Megapleonium ferrumequinum* Huang, Shih & Ah Yong, 2025, actually consists of two fused spinules with a visible demarcation between them and the one in *M. wangjiani* Huang, Shih & Ah Yong, 2025, is low and hard to discern.

In the field, *Megapleonium taishanense* sp. nov. may be confused with the sympatric *Cantopotamon chixiense* sp. nov., especially when comparing females and small males. In this instance, *Megapleonium taishanense* sp. nov. can be distinguished by having a shorter pereopod 5 dactylus relative to the propodus (Fig. 4 vs. about same length in *Cantopotamon chixiense* sp. nov., Fig. 1), and the epigastric cristae and postorbital cristae being confluent (Fig. 4 vs. not confluent in *Cantopotamon chixiense* sp. nov., Fig. 1).

Genetic analysis

The recovered BI tree for the genus *Cantopotamon* is generally very well supported with only the node between *C. yangxiense* and *Cantopotamon chixiense* sp. nov. with low support. Species within this genus form

two major clades, one consisting of *C. zhuhaiense* and *C. hengqinense*, and the other including the rest (Fig. 7A). *Cantopotamon shangchuanense* is outgroup to *C. yangxiense* and *Cantopotamon chixiense* sp. nov. The haplotype network reveals clear structuring among the five species: haplotypes of the same species are clustered in groups separated by multiple steps. *Cantopotamon yangxiense* exhibits the most interspecific haplotype divergence within the genus (Fig. 7B). For pairwise K2P distances of the *COI* gene, the minimum is 7.73% (between *C. zhuhaiense* and *C. hengqinense*) and maximum is 14.35% (between *C. hengqinense* and *C. yangxiense*). There is higher divergence between *C. shangchuanense* and *C. yangxiense* (11.24%–11.26%) than between *C. shangchuanense* and *C. chixiense* (10.96%–11.22%) (Fig. 7C).

DISCUSSION

The phylogenetic positions and placement in the haplotype network of the analysed specimens of *Cantopotamon* reflect their geographic distributions (Fig. 7A, B). As reported by Huang et al. (2017), species from the eastern part of the range in Zhuhai (*Cantopotamon hengqinense* Huang, Ahyong & Shih, 2017 and *Cantopotamon zhuhaiense* Huang, Ahyong & Shih, 2017) and from the western part of the range in Taishan and Yangjiang form two monophyletic clades with high bootstrap and posterior probability support (Fig. 7A). Regarding the western clade, the specimens from Yangchun and Hailing Island, Yangjiang identified as *C. yangxiense* form a clade with a previously sequenced specimen from that species (Huang et al. 2017) collected in Yangxi, Yangjiang. The new species forms a sister clade to *C. yangxiense*, and occurs to the east of it in Chixi, Taishan. The interspecific *COI* K2P distance range of *Cantopotamon* is similar or higher than that of other freshwater crab genera from East Asia, e.g., *Candidiopotamon* (min: 10.72%, max: 13.65%, Shih et al. 2023) or *Nanhaipotamon* (min: 1.02%, max: 13.53%, Shih et al. 2011).

Interestingly, *C. shangchuanense* from an inshore island close to where the new species was found is recovered as an outgroup to both mainland species and it is likewise recovered in the haplotype network (Fig. 7B). Huang et al. (2017) suggest vicariant speciation in the case of *C. shangchuanense*, possibly caused by isolation from the mainland when existing land bridges disappeared. According to this hypothesis, and in accordance with our phylogeny and haplotype network, ancestral *C. shangchuanense* split from a common mainland ancestor of *C. chixiense* and *C. yangxiense*. The two mainland species subsequently then diverged

from each other, potentially caused by expansion towards the west or geographic barriers appearing between previously interconnected populations. Additionally, we find a potential case of incipient speciation caused by mainland-island isolation in the specimen of *C. yangxiense* from Hailing (Yangjiang) island, located just two kilometers off the mainland. The specimen we sequenced clusters as an outgroup to the mainland specimens from the same species in both tree and haplotype network, reflecting the pattern we saw between *C. shangchuanense* and its mainland relatives. Moreover, this species shows by far the highest intraspecific K2P distance (6.12–6.29%) in our dataset, just below the minimum interspecific K2P distance observed (7.73%) and well above genetic distances measured between congeneric freshwater crab species, for example 1.02% between *N. wenzhouense* and *N. dongyinense* (Shih et al. 2011). Morphologically, however, there are no observable significant differences between the mainland and island specimens, not even in the G1. The island population possibly represents a separate species, but without sufficient data, we treat them as conspecific for the time being. Further collections and population genomic investigations are needed to elucidate the biogeographic and phylogenetic history of *C. yangxiense* and its allies.

Megapleonum taishanense sp. nov. was referred to as *M. sp.* “Taishan” in the 16S rRNA gene based phylogenetic analysis in Huang et al. (2025, fig. 12). It is sister to *M. shenzhen*, and together with *M. yangdongense*, the three form a deeply nested clade within the genus. The current study adds morphological evidence to support the formal recognition of this new taxon. *Megapleonum taishanense* sp. nov. is currently known from only one hillstream, the real distribution of this species remains unclear though it is most likely highly endemic. The type locality lies upstream of a man-made reservoir, and a man-made channel diverts part of the stream flow. Aside from these modifications, the habitat is presently minimally disturbed and does not appear to face immediate threats.

CONCLUSIONS

In our study, two new species of potamid crabs are described based on the integrative evidence from morphology and molecular phylogeny inferred from the *COI* gene. The sympatric species pair *Megapleonum taishanense* sp. nov. and *Cantopotamon chixiense* sp. nov. from Chixi, Taishan, Guangdong, are superficially similar but can be separated from each other by distinct morphological characters. The former species is much rarer than the latter and is only found from one single

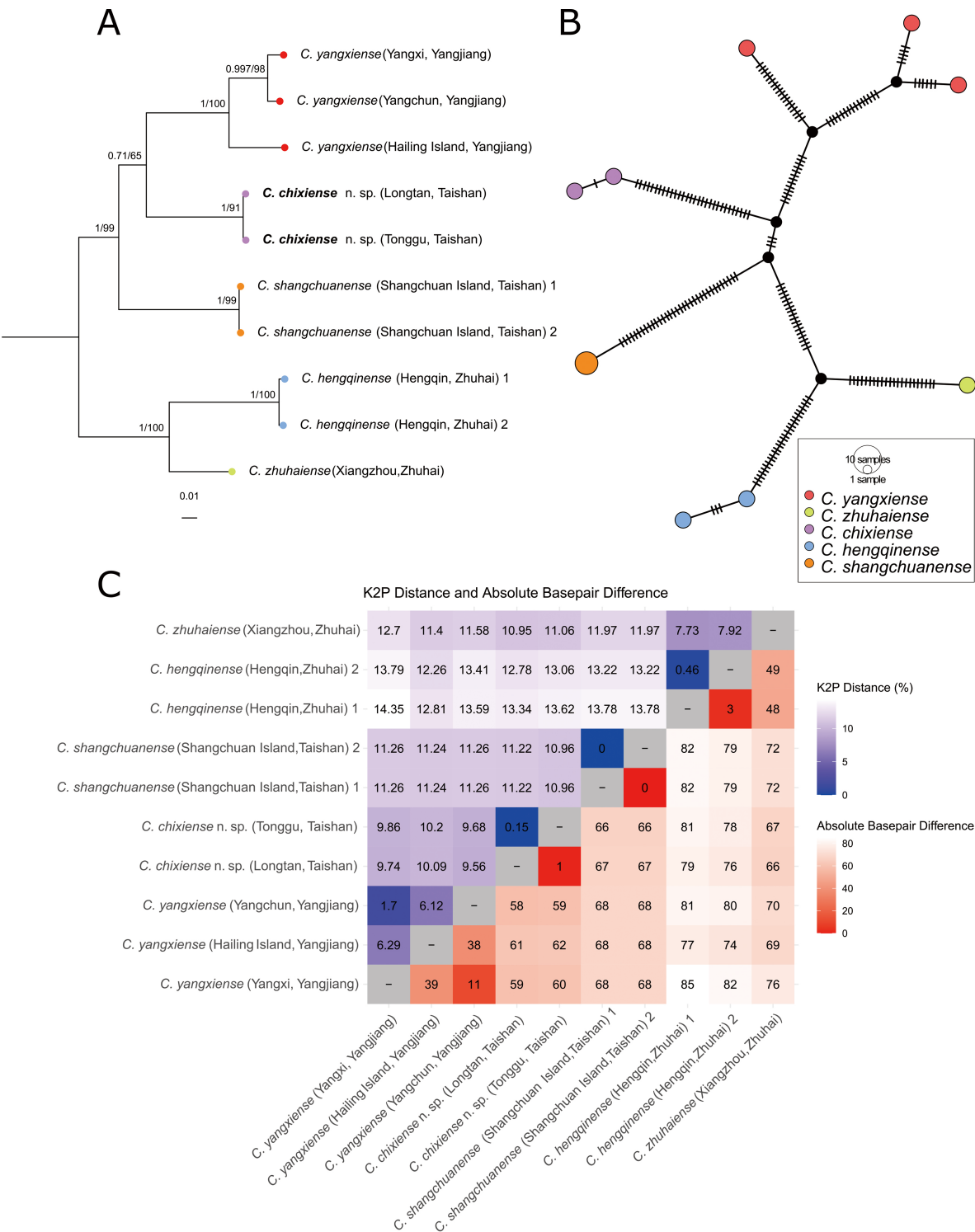


Fig. 7. Phylogenetic relationships and genetic distance of the genus *Cantopotamon* based on *COI* sequences. A: Midpoint-rooted Maximum Clade Credibility tree based on Bayesian Inference (BI). Posterior probabilities (BI) and maximum likelihood (ML) ultrafast bootstrap values are shown at each node, scale at the bottom indicates substitutions per site. Colours at tips represent species assignments as in A, single dashes between circles signify putative nucleotide substitutions, black circles are unobserved haplotypes. B: Haplotype network computed with integer Neighbor Joining. Each circle is a single haplotype, colours refer to species assignments as in A, single dashes between circles signify putative nucleotide substitutions, black circles are unobserved haplotypes. C: Kimura-2-Parameter (K2P) distance and Absolute Basepair Difference matrix between and within *Cantopotamon* species. Upper left half of matrix shows K2P distance percentage (blue shades), lower bottom half shows absolute basepair difference between haplotypes (red shades). Higher distance and more basepair differences are depicted in lighter, lower distance and fewer basepair differences in darker shades.

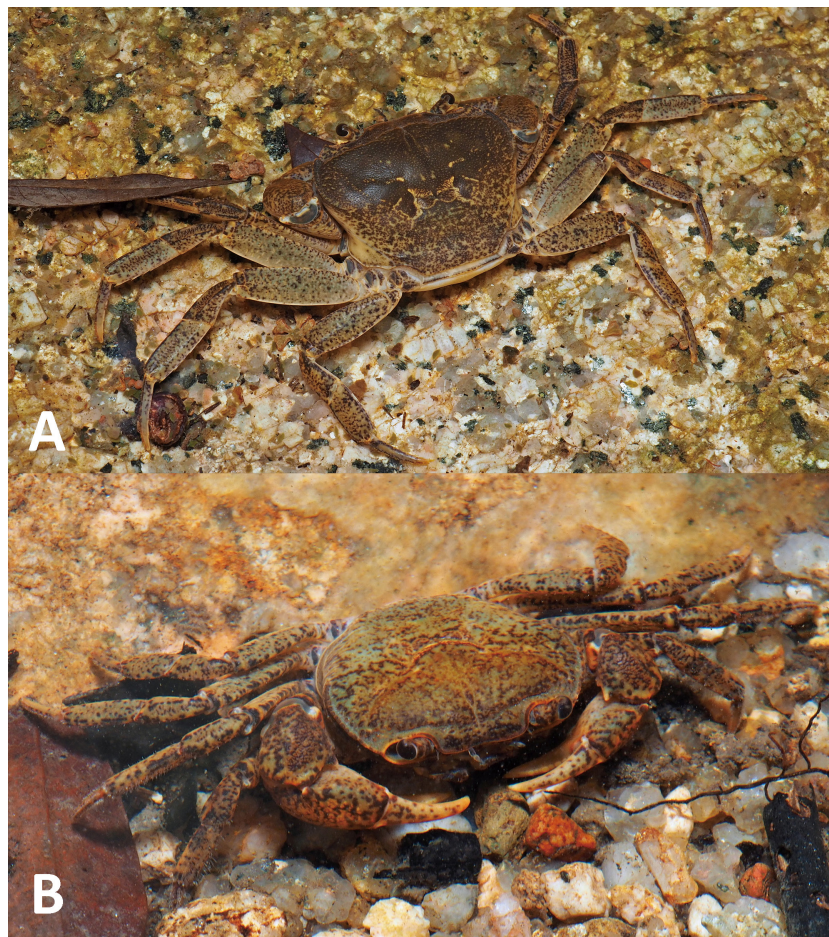


Fig. 8. Colour in life. A: *Cantopotamon chixiense* sp. nov., male; B: *Megapleonium taishanense* sp. nov., male.

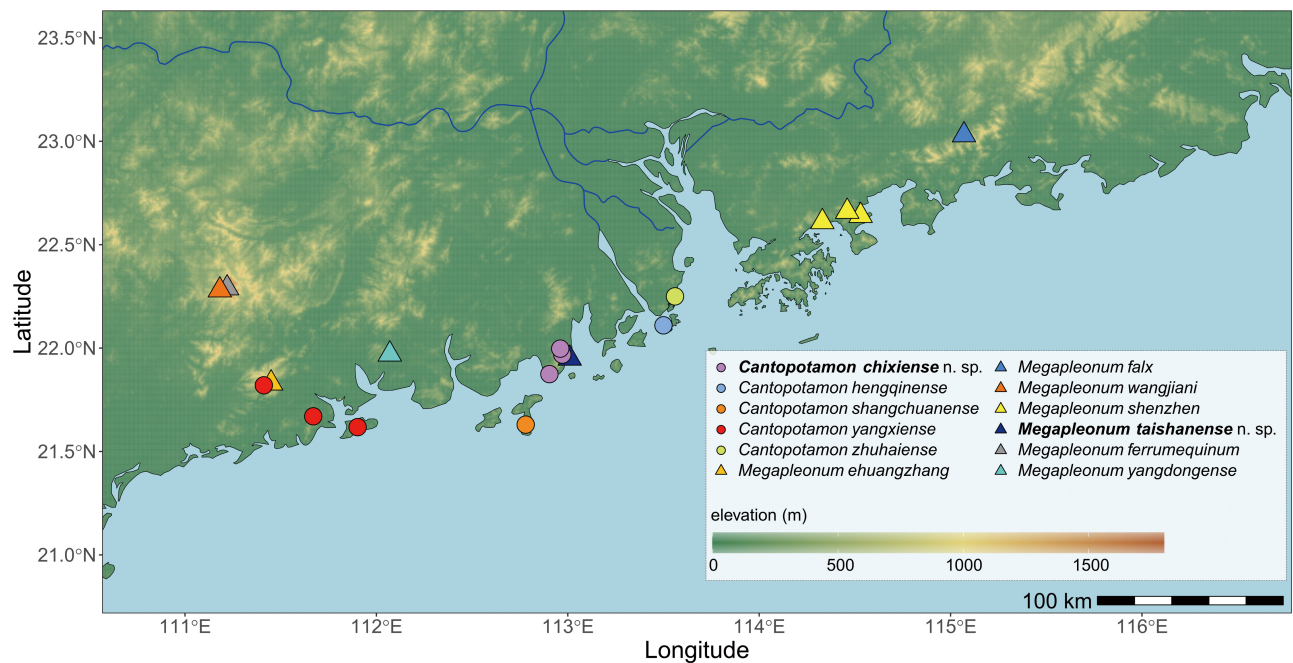


Fig. 9. Distribution map with the Pearl River (Guangdong) mouth at its centre of known *Cantopotamon* spp. and *Megapleonium* spp.

hillstream, making it currently a point endemic. These findings underscore the still largely unknown diversity of freshwater crabs in Guangdong, China.

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Authors' contributions: CH conceptualized the study, and drafted the manuscript; BB performed the molecular analysis and drafted the discussion; JZ drafted the description of *Cantopotamon chixiense* sp. nov.

Competing interests: CH, BB and JZ declare that they have no conflict of interests.

Availability of data and materials: Sequences generated in the study have been deposited in GenBank database (accession numbers: PX400619, PX400620, PX400621, PX400622).

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