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A new species of crayfish of the genus *Cherax* from Indonesian New Guinea (Crustacea, Decapoda, Parastacidae)

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https://zoobank.org/3D6F5C84-3E90-482E-9FF9-8599D4D99EDC

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Abstract

A new species of the genus *Cherax* is described and illustrated. *Cherax wagenknechtae* **sp. nov.**, endemic to the Beraur and Klasabun River drainages in the western part of the Kepala Burung (Vogelkop) peninsula, West Papua, Indonesia, is described, figured and compared with its closest relatives, *Cherax pulcher* Lukhaup, 2015. The new species may be easily distinguished from *Cherax pulcher* by the shape of the chelae, rostrum and body, and coloration.

Key Words

freshwater, molecular phylogeny, morphology New Guinea, taxonomy

Introduction

The crayfish of the island of New Guinea were extensively studied by Holthuis (1949, 1956, 1958, 1982, 1986, 1996), with additions by Lukhaup and Pekny (2006, 2008), Lukhaup and Herbert (2008), Lukhaup (2015), Lukhaup et al. (2015), Patoka et al. (2015), Lukhaup et al. (2017) and Lukhaup et al. (2018).

In January 2016, the first author visited Sorong Regency and South Sorong Regency, West Papua, Indonesia, to clarify the distribution of some crayfish species present in the pet trade. During our stay in Sorong we also had the chance to visit a creek about 50 km south of the city where our guide, Irianto Wahid, and a local collector, showed us the location of *Cherax* species that is in the pet trade under the name *Cherax boesemani* "Red Brick''. In the present contribution, this species is described as new to science. *Cherax wagenknechtae* sp. nov. is genetically and morphologically most similar to *Cherax pulcher* Lukhaup, 2015 from Hoa Creek, close to the village of Teminabuan in the southern-central part of the Kepala Burung (Vogelkop) Peninsula.

Cherax wagenknechtae sp. nov. may be easily distinguished from *Cherax pulcher* by coloration and pattern of live individuals, by the shape of the chelae, shape of rostrum and by using sequence divergence.

Materials and methods

Samples of *Cherax wagenknechtae* sp. nov. and *C. pulcher* were collected from creeks in West Papua and Papua provinces (Table 1). Holotypes and allotypes were photographed and kept alive in indoor tanks until samples were obtained for DNA analysis. After this procedure the animals were preserved in 70% ethanol. Morphometric parameters of all individuals were taken using an electronic digital caliper with an accuracy of 0.1 mm. For the molecular analyses, sequences from an additional ten species of *Cherax* and from two other parastacid genera used as outgroups were downloaded from GenBank (see Table 1).

Material has been deposited at the Museum Zoologicum Bogoriense (= Bidang Zoologi) Research Centre for Biosystematics and Evolution (= Pusat Riset Biosistematika dan Evolusi), National Research and Innovation

Table 1. Material studied with GenBank accession numbers. Sequences of species represented by more than one sequence are listed consecutively as labelled in Fig. 9.

Species/sample	Location	GenBank acc. nos	
		COI	16S
C. boesemani	Ajamara Lake, Papua Barat; 1°17'19.97"S, 132°14'49.14"E; January 23, 2016	KY654084	KY654089
		KY654085	KY654090
C. alyciae	Creek, Boven Digoel Regency, West Papua,	MH457597	MH457588
	Indonesia; December 7, 2016	MH457599	MH457590
		MH457598	MH457589
C. communis	Lake Paniai	-	MH457602
C. gherardiae	Pet trade	KU821417	KU821417
C. holthuisi	Papua Barat	KU821419	KU821433
C. miscolicus	Tomolol Misool	#	#
		#	#
		#	#
		#	#
		-	#
C. monticola	Baliem River, Wamena, Papua	KF649851	KF649851
		-	KJ920818
C. mosessalossa	Klademak Creek, Sorong City 0°52'23.59"S, 131°16'24.40"E; January 26, 2016	MH457602	MH457594
		MH457602	MH457595
C. paniaicus	Lake Tage, Papua (Field collection)	KJ950528	KJ920830
C. peknyi	Unnamed Creek, tributary of Fly River, Papua New Guinea	MH457600	MH457591
		MH457601	MH457592
		MH457604	MH457596
C. pulcher	Hoa Creek (Teminabuan), Papua Barat; 1°28'32.73"S, 132°3'54.94"E; January 23, 2016	KY654083	KY654088
C. snowden	Oinsok (Ainsok River Drainage), Papua Barat; 1°11'40.07"S, 131°50'1.14"E; January 24, 2016	KY654082	KY654087
C. wagenknechtae sp. nov.	Unnamed creek / Tributary to the Beraur River / Klamono	#	#
		#	#
C. warsamsonicus	Small tributary to Warsamson River 0°49'16.62"S, 131°23'3.34"E; January 20, 2016 Papua Barat	KY654086	KY654091
		KU821424	KU821438
		KU821426	KU821437
Engaeus strictifrons	Crawford River, Victoria, Australia	AF493633	AF492812
Euastacus bispinosus	Crawford River, Victoria, Australia	AF493634	AF492813

= GenBank accession number pending.

Agency (= **BRIN**), Jalan Raya Jakarta-Bogor Km 46 Cibinong 16911, Indonesia (**MZB**); and the Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Berlin (**ZMB**).

DNA was purified from about 2 mm^3 of muscle tissue with a Qiagen BioSprint 96 using the manufacturer's protocol. Polymerase chain reaction (PCR) was used to amplify two mitochondrial gene fragments, a ~535 bp region of the 16S ribosomal RNA gene (16S) using primers 1471 and 1472 (Crandall and Fitzpatrick 1996) and a 710 bp fragment of the Cytochrome Oxidase subunit I gene (COI) using primers LCO1490 and HCO2198 (Folmer et al. 1994).

PCR was performed in 25 µl volumes containing 1× Taq buffer, 1.5 mM $MgCl_2$, 200 µM each dNTP, 1 U Taq polymerase, ca. 50–100 ng DNA and ddH_2O. After an initial denaturation step of 3 min at 94 °C, cycling conditions were 35 cycles at 94 °C for 35 s, 45 °C (COI) or 50 °C (16S) for 60 s, and 72 °C for 1 min (COI) or 90 s (16S), with a final elongation step of 5 min at 72 °C. The same primers were used in PCR and sequencing. PCR products were sent to Macrogen Europe for purification and cycle sequencing of both strands of each gene.

Sequences were aligned by eye (COI) and with MAFFT (16S) using the G-INS-i strategy suitable for thorough alignments of sequences with global homology (Katoh et al. 2002). The resulting alignments had a length of 658 bp (COI) and 542 bp (16S), respectively. To determine the best substitution model for Bayesian Inference and Maximum Likelihood analyses (see below), hierarchical likelihood ratio tests were carried out with jModelTest (Posada 2008) on both sequence sets (24 models tested). Based on the Akaike Information Criterion and the Bayesian Inference Criterion, the GTR + I + G (COI) and the GTR + G (16S) models (BIC: HKY + I + G and HKY + G; more complex models chosen) were selected. The two sequence datasets were subsequently analyzed both separately and combined.

Phylogenetic trees were reconstructed by maximum parsimony (MP) using the heuristic search algorithm as implemented in PAUP* (Swofford 2002), with gaps treated as fifth base. Support for nodes was estimated by bootstrap analysis (1,000 bootstrap replicates with 10 random addition sequence replicates each). Maximum Likelihood (ML) analyses were conducted with RAxML (Stamatakis et al. 2008; RAxML BlackBox; 100 bootstrap replicates). In addition, Bayesian inference was employed to infer phylogeny by using MrBayes 3.2.7 (Ronquist and Huelsenbeck 2003). The MCMCMC-algorithm was run with four independent chains for 10,000,000 generations, samplefreq=500, and burnin=10,001) using the models specified above. The combined dataset was subjected to a partitioned analysis (ML and BI) using the different models for the two genes in the BI analyses. Genetic distances were calculated using MEGA 7.0 (Kumar et al. 2016). All new sequences have been deposited in GenBank (see Table 1).

Systematics

Parastacidae Huxley, 1879
Genus *Cherax* Erichson, 1846

Cherax wagenknechtae sp. nov.

https://zoobank.org/D2375BD1-E2C0-4CC0-B6AC-E86B3ACE8603

Figs 1–5

Material examined. *Holotype*: male (MZB Cru 5359), under rocks and among roots and in debris along banks of unnamed creek of the Klasabun River drainage, West Papua, Indonesia. Coll. Irianto Wahid and local people. January, 2016. GPS (1°15'59.91"S, 131°18'21.29"E) Crayfish were exported by KKCrayfish Farm in Jakarta for the pet business. ***Allotype*:** female (MZB Cru 5361), same data as holotype. ***Paratypes*:** (MZB Cru 5360), same data as

holotype. Additional material (n=3) one male and two females are deposited at the Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Berlin (ZMB 33781). The additional non-type material deposited in Berlin comes from local crayfish collectors who collect for the pet trade. No exact data is available on this material.

Diagnosis. Carapace surface covered with scattered small tubercles, three spines posterior to cervical groove on lateral carapace present. Eyes large, pigmented. Cornea as broad as eyestalk. Rostrum lance shaped with elevated, thickened margins, non-setose. Rostral margins with three prominent teeth. Posterior extensions of the rostral margins prominent. Postorbital ridges prominent with one acute spine at anterior terminus. Uncalcified patch on lateral margin of chelae of adult male, white, translucent. Propodal cutting edge with a few short setae in posterior part and one large tubercle. Chelae pinkish red, becoming dark red to black in the lateral and anterior part. Fixed finger and dayctyl with hooked yellow tips anteriorly. Dorsolateral margins of chelae slightly elevated, usually pink or creamy. Other walking legs blue-gray. Carapace and pleon pinkish red dorsally, becoming reddish gray laterally.

Description of male holotype. (Figs 2, 3) Body and eyes pigmented. Eyes not reduced, rather large; cornea globular, darkly pigmented, nearly as long as eyestalk; eyestalk slightly narrower than cornea. Body subovate, slightly compressed laterally. Pleon narrower than cephalothorax (width 26.7 mm and 31.3 mm respectively). Rostrum (Fig. 3A) broad in shape, reaching the end of ultimate antennular peduncle and about three times as long than wide (width 5.9 mm at base, length 17.5 mm). Margins slightly elevated continuing in rostral carinae on carapace, almost straight in basal part, distally tapering towards apex. Lateral rostral margin bearing three prominent teeth in distal half, pointing upwards at angle of approximately 45°. A few short hairs present between the distal teeth and the acumen. Acumen with anteriorly orientated spine.

Rostral carinae extending as slight elevation posteriorly on carapace terminating at ending of postorbital ridges. Postorbital ridges well-developed, terminating in spiniform tubercle anteriorly, fading at three-fourth of occipital carapace length, posteriorly. Postorbital ridges about 1/4 of CL. Cervical and branchiocardiac grooves distinct, non-setose, three prominent and well- developed spines present behind cervical groove on lateral sides of carapace. Carapace surface smooth, ventrolateral margins rounded, slightly elevated.

Areola length 20.9 mm, narrowest width 11.1 mm. Length of areola 34.7% of total length of carapace (66.3 mm). Sparsely pitted.

Scaphocerite (Fig. 3D), broadest at posterior third, convex in distal part, becoming narrower in basal part; thickened lateral margin terminating in corneous spine, slightly overreaching ultimate segment of antennular peduncle. Right scaphocerite 17.5 mm long and 6.4 mm wide. Rounded inner margin strongly covered by setae. Antennulae and antennae typical for genus. Antennae slightly longer than body. Antennular peduncle slightly overreaching acumen, antennal peduncle slightly overreaching tip of apex of scaphocerite. Antennal protopodite smooth, no spine, row of hairs on inner margin; basicerite with one lateral and one ventral spine.

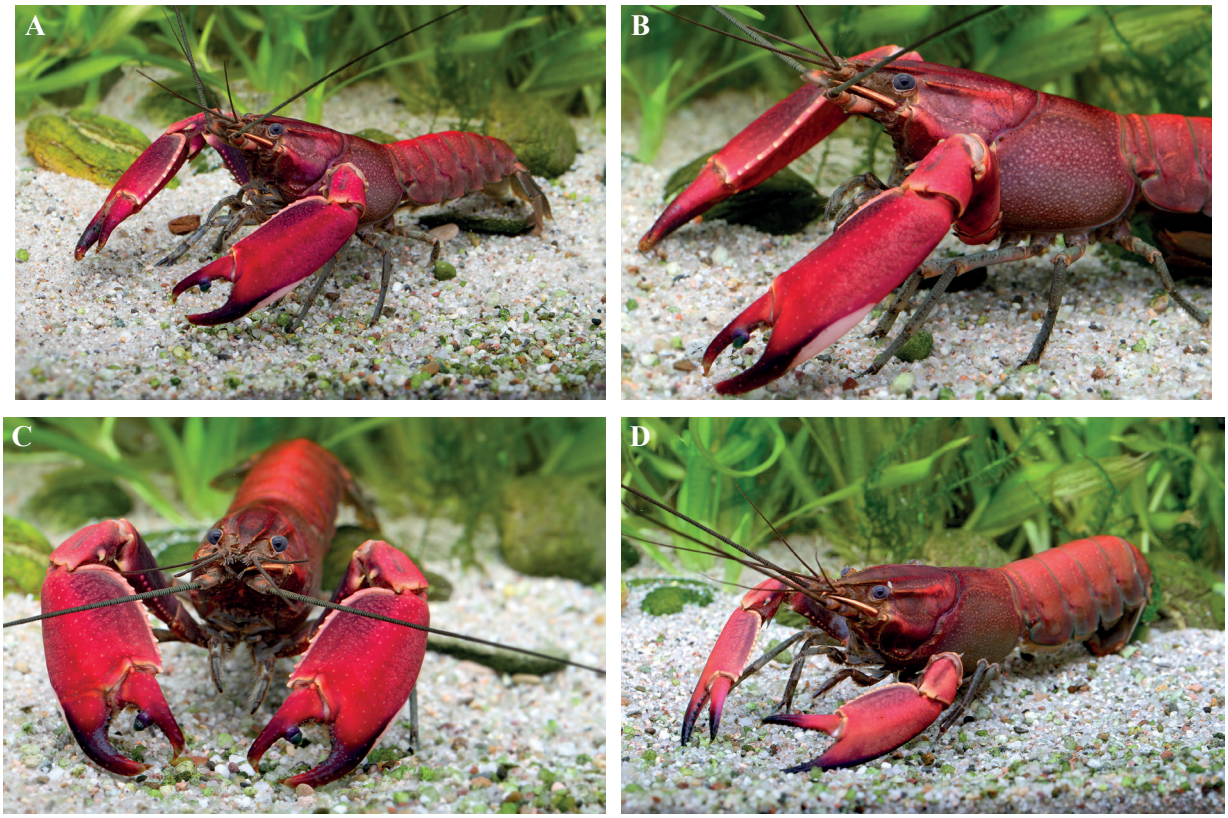

Figure 1. *Cherax wagenknechtae* sp. nov. **A.** Paratype male (MZB Cru 5360) Beraur River drainage; **B.** Idem, side view; **C.** Idem frontal view; **D.** Allotype female (MZB Cru 5361).

Figure 2. *Cherax wagenknechtae* sp. nov. holotype male (MZB Cru 5359). Scale bar: 10 mm.

Mouthparts typical for the genus. Epistome with subcordiform cephalic lobe anteriorly bearing lanceolate cephalomedian projection constricted at base. Lateral margins of lobe not thickened; each lateral margin with two groups of 10–12 tubercles separated by the smooth central part. Central part smooth, not pitted, excavate.

First pereopod equal in form, chela gaping. Right chela 63.7 mm long, 11.9 mm deep, 24.5 mm wide. Left chelae (Fig. 3B, C) 65.6 mm long and 11.8 mm high, 24.4 mm wide, strongly compressed. Fingers shorter than palm (right dactylus 24.4 mm long). Dactylus broad at base (9.6 mm), tapering slightly towards tip.

Tip of dactylus with sharp, corneous, hooked tooth pointing outwards at an angle slightly larger than a right angle to the dacty. Cutting edge of dactyl with continuous row of small granular teeth posteriorly and one prominent larger tooth at middle of cutting edge. Ventral and dorsal surface of movable finger smooth with scattered punctuation. Ventral posterior half of cutting edge with scattered short setae reaching from base to prominent larger tooth. Fixed finger smooth, scattered punctuation, triangular, merging gradually into palm, ending in sharp, corneous. Tips of fingers slightly crossing when fingers clasp. Upper surface of palm practically smooth, slightly pitted, more densely pitted at margins. Fixed finger slightly broader as dactyl at base (11.4 mm). Dense, short setae present in posterior ventral part of fixed finger, reaching from base to about one third of dactyl and fixed finger. Cutting edge of fixed finger with row of 5 rather small granular teeth at posterior half and one prominent larger one at mid-length. Outer lateral margin of chelae with swollen soft and uncalcified patch (21.7 mm on the right chelae and 21.7 on the left chelae) which extends from about middle of palm slightly overreaching base of dactylus. Row of 12–13 mesial granules at dorsolateral margin. Dorsolateral margins elevated.

Dorsal surface of carpus (18.4 mm) smooth, with slight excavation in middle part and with a well-developed mesial carpal spine. Ventral carpal surface distal margins slightly elevated, non-setose and with fovea; proxilateral margin with well-developed ventral carpal spine and a prominent ventromesial carpal spine oriented at an angle of approximately 45°.

Merus (29.5 mm) laterally depressed in basal part; surface smooth; small dorsal meral spine present. Inner ventrolateral margin densely covered with small granules, three ventral meral spines present, one at mid-length other in middle of anterior part, third on distal ventrolateral inner margin.

Ischium (19.5 mm) smooth with two small spines at ventrolateral inner margin.

Second pereopod reaching anteriorly to approximately corneus spine of scaphocerite. Finger (8.5 mm) slightly longer than palm (6.0 mm), of same dept. A few scattered short setae present on dactyl and fixed finger. Cutting edge of fixed finger and carpus with row of dense, short setae. Carpus (12.3 mm), smooth, slightly pitted, longer than palm. Merus (20.1 mm) 1.6 times longer than carpus. Ischium (9.2 mm) about as half as long as merus.

Third pereopod overreaching second by length of finger of second pereopods. Fingers shorter than palm.

Fourth pereopod reaching distal margin of scaphocerite. Dactylus with corneous tip. Short scattered setae present. Propodus more than twice as long as dactylus, nearly 1.5 times as long as carpus; somewhat flattened, with many stiff setae on lower margin. Merus just slightly longer than propodus.

Fifth pereopod similar to fourth, slightly shorter.

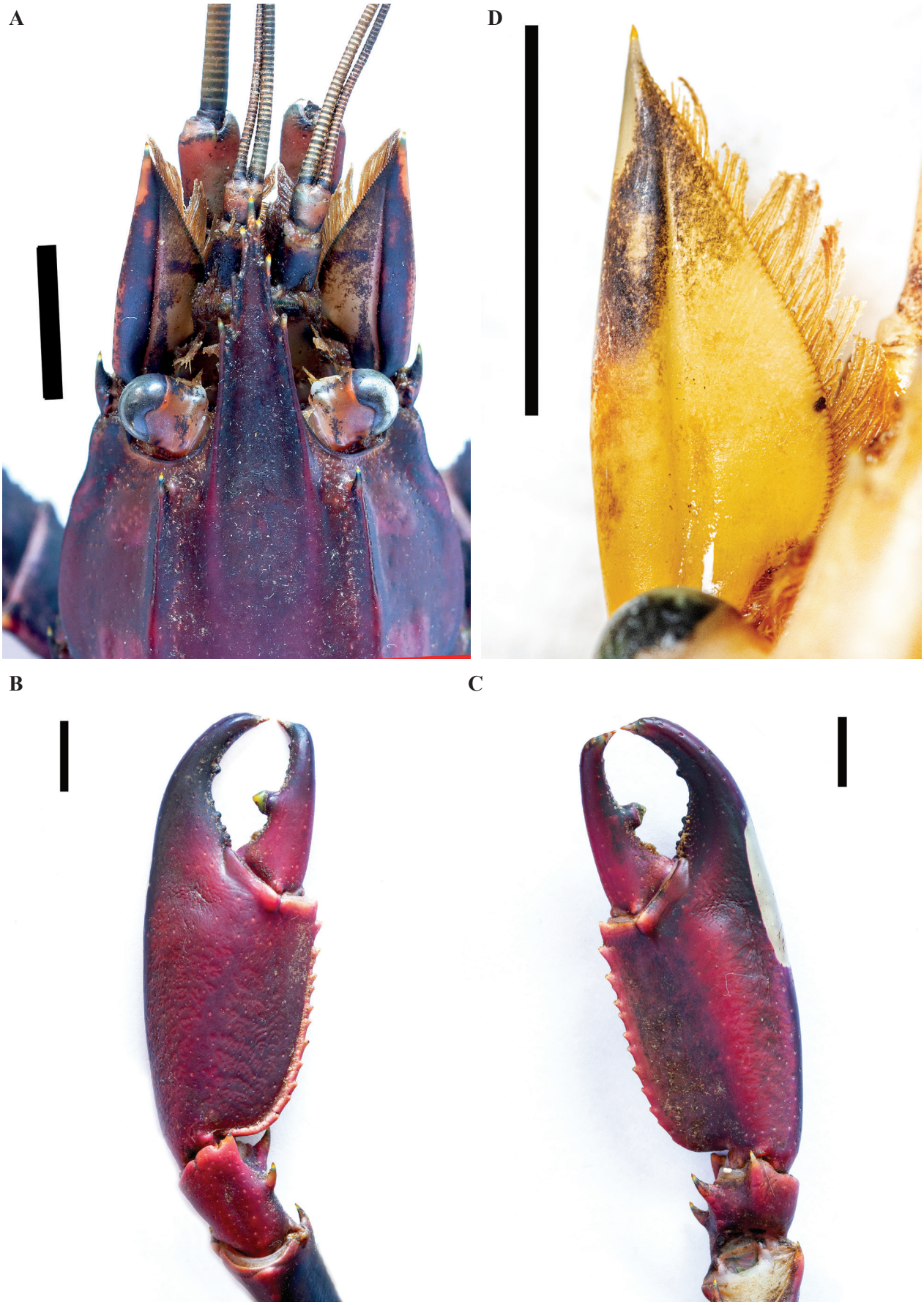

Figure 3. *Cherax wagenknechtae* sp. nov. holotype male (MZB Cru 5359). **A.** Dorsal view of carapace; **B.** Dorsal view of left chelae; **C.** Ventral view of left chelae; **D.** Scaphocerite dorsal view. Scale bars: 10 mm (**A, B, C, D**).

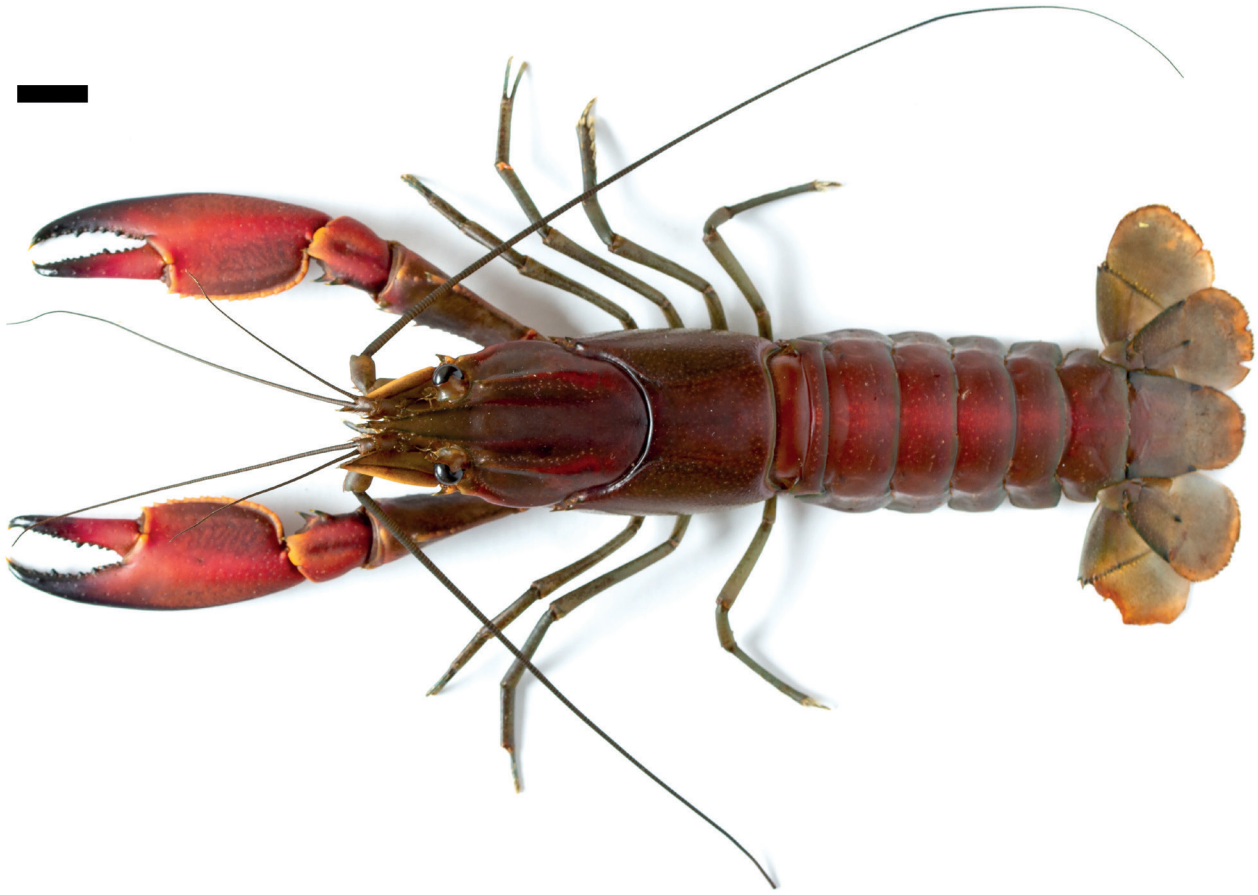

Figure 4. *Cherax wagenknechtae* sp. nov., allotype female (MZB Cru 5361).

Dorsal surface of pleon smooth, with scattered pits; abdominal segments (3–5) with short setae present on caudal margins of segment.

Telson with posterolateral spines, dense short setae present in posterior third. Posterior margins setose. Uropodal protopod with two distal spines on mesial lobe. Exopod of uropod with transverse row of posteriorly directed diminutive spines ending in one more prominent spine, posteriorly directed on outer margin of mesial lobe. Terminal half of exopod with small spines and short hairs, slightly corrugated. Endopod of uropod smooth. Short scattered hairs present on posterior third of dorsal exopod. Posterolateral spine on outer margin present. Second spine on medial dorsal surface present, directed posteriorly.

Description of allotype female (Fig. 4). Chela of first pereopods equal, 2.7 times as long as broad (43.9 mm and 15.7 mm respectively). No soft patch in distal lateral margin of the chelae of females observed (n=112). Mesial margin of palm slightly elevated, forming slender serrated ridge with row of 15–16 small granular teeth. Cutting edge of dactylus with 15–16 rather small granular teeth. Cutting edge of fixed finger with 10–11 small granules. Small scattered short setae visible along ventral cutting edges of chelae, denser and longer in ventral posterior area. Tips of fingers slightly crossing when fingers clasp, not gaping. Cervical groove distinct, non-setose. Pleon just slightly wider than cephalothorax (widths 25.9 mm and 25.6 mm respectively). Same color pattern as in males.

Size. The biggest male examined has a carapace length of 71.5 mm, and a total length of 153 mm, the holotype male has a total length of 143 mm and the other males have a total length between 94 mm and 152 mm; the allotype has a carapace length of 56.6 mm and a total length of 127 mm (n=9).

Color. The living animals (Fig. 8A–B) are colored as follows. Males from Klasabun River Drainage: Chelae light to dark red with pink or creamy dorsolateral margins and white patch. Anterior part usually dark blue or black, more intense colored. Corneous tooth on tip of fingers orange. Cephalothorax bright red to dark red to black, dorsally more intense, fading ventrally to light red or creamy. Segments of pleon dark red to bright red, lateral pleura lighter becoming creamy red. Walking legs blue or gray blue. Distal margin of tail-fan brownish red to orange. Animals from the village of Klamono (Beraur River Drainage) differ in the coloration of chelae. Chelae dark blue to black, sometimes creamy blue. Dorsolateral margins light creamy. These males have usually also orange or yellow rostral margins. Females: same color as males, sometimes less intense.

Molecular phylogenetic results. *Cherax wagenknechtae* sp. nov. is sister species to *Cherax pulcher* (Fig. 10), both are, in turn, sister group to *C. warsamsonicus*. *Cherax wagenknechtae* sp. nov. is well isolated from *C. pulcher* with a sequence divergence (p-distance)

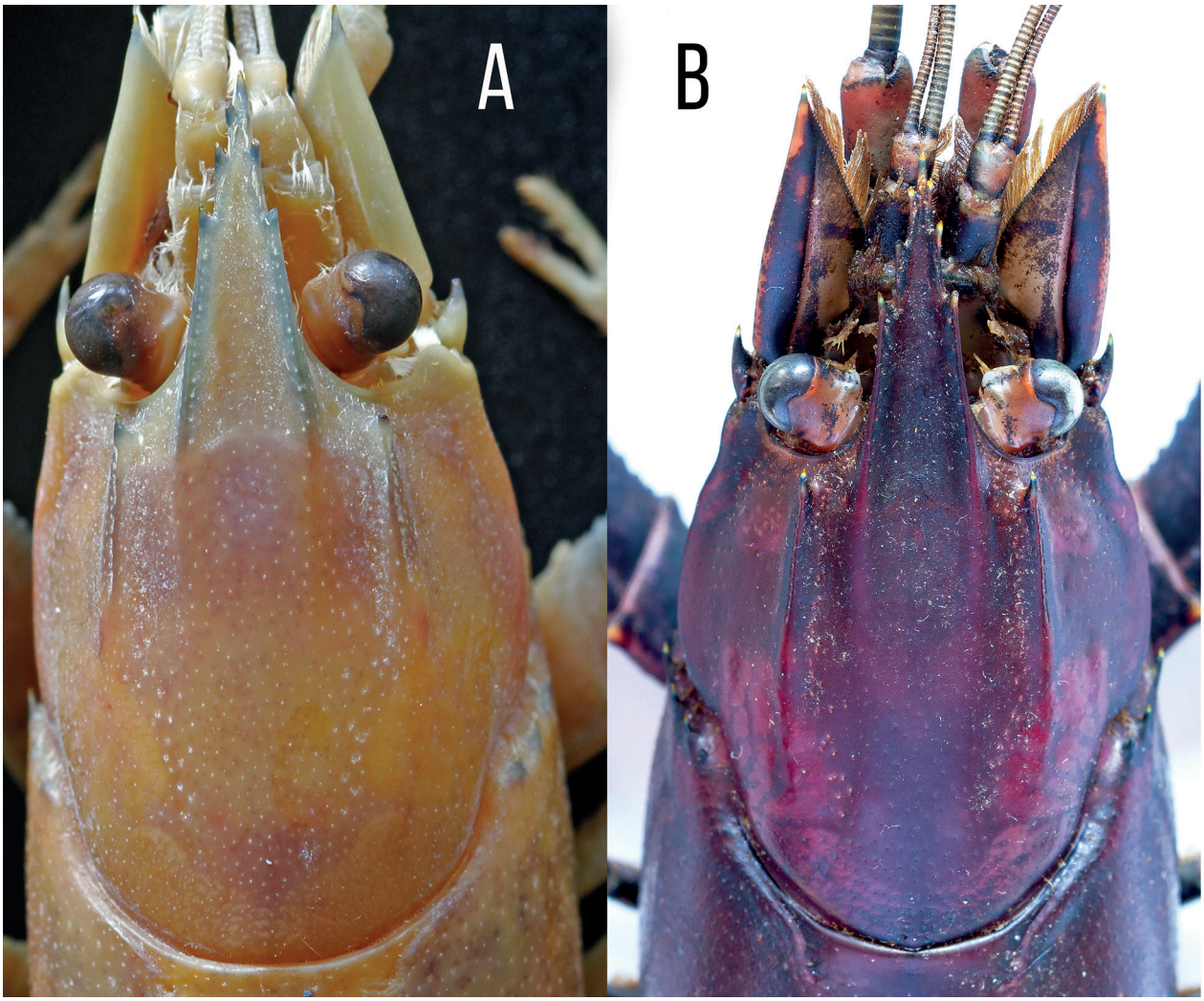

Figure 5. Rostrum dorsal view. **A.** *Cherax pulcher* holotype male (RMNH. CRUS. D. 57217) **B.** *Cherax wagenknechtae* sp. nov. holotype male (MZB Cru 5359).

of 3.2% (16S, Fig. 11) and 6.8% (COI, Fig. 12), respectively, supporting the morphology-based description of *C. wagenknechtae* as a new species.

Deposition of types. The holotype (MZB Cru 5359), allotype (MZB Cru 5361) and paratypes (MZB Cru 5360) are deposited at the *Museum Zoologicum Bogoriense* (= *Bidang Zoologi*) Reseach Centre for Biosystematics and Evolution (= *Pusat Riset Biosistematika dan Evolusi*), National Research and Innovation Agency (= BRIN), Jalan Raya Jakarta-Bogor Km 46 Cibinong 16911, Indonesia. Additional paratypes are deposited at the Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Berlin (ZMB 33781).

Systematic position. Munasinghe et al. (2004a, b), Austin (1996); and Austin and Knott (1996) however, identified three lineages with different geographic ranges within *Cherax* based on molecular genetics and phylogenetic studies. These consist of a southwestern group, an eastern group and a northern group. Support for the latter group, however, was based on only very limited sampling (e.g. single samples of *C. quadricarinatus*, *C. rhynchotus* and *C. peknyi* in Munasinghe et al. (2003) study. Munasinghe et al. (2004b) indicate that the division of *Cherax* into two subgenera, as conceived by Holthuis and subsequent authors dealing with New Guinea crayfish has to be reconsidered. Based on Munasinghe et al. (2004a, b), Austin (1996), and Austin and Knott (1996). *Cherax wagenknechtae* sp.nov. belong to the northern species group lineage now consisting of 26 species:

Cherax acherontis Patoka, Bláha & Kouba, 2017, *Cherax albertisii* (Nobili, 1899), *Cherax alyciae* Lukhaup, Eprilurahman & von Rintelen, 2017, *Cherax boesemani* Lukhaup & Pekny, 2008, *Cherax boschmai* Holthuis, 1949, *Cherax buitendijkae* Holthuis, 1949, *Cherax communis* Holthuis, 1949, *Cherax gherardii* Patoka, Bláha & Kouba, 2015, *Cherax holthuisi* Lukhaup & Pekny, 2006, *Cherax lorentzi aruanus* (Roux, 1911), *Cherax lorentzi lorentzi* (Roux, 1911), *Cherax longipes* Holthuis, 1949, *Cherax misolicus* Holthuis, 1949, *Cherax murido* Holthuis, 1949, *Cherax monticola* Holthuis, 1950, *Cherax mosessalossa* Lukhaup, Eprilurahman & von Rintelen, 2017, *Cherax minor* Holthuis, 1996,

Cherax peknyi Lukhaup & Herbert, 2008, *Cherax pallidus* Holthuis, 1949, *Cherax papuanus* Holthuis, 1949, *Cherax paniaicus* Holthuis, 1949, *Cherax pulcher* Lukhaup, 2015, *Cherax solus* Holthuis, 1949, *Cherax snowden* Lukhaup, Panteleit & Schrimpf, 2015, *Cherax wagenknechtae* sp. nov. (this study), and *Cherax warsamsonicus* Lukhaup, Eprilurahman & von Rintelen, 2017.

Systematic remarks

In comparison to all species of the northern group the new species, *C. wagenknechtae* sp. nov. is most similar to *C. pulcher*, a species that is known from the Hoa Creek drainage, close to the City of Teminabuan, Papua New Guinea. *Cherax wagenknechtae* sp. nov. is known to be endemic in the drainage of Beraur and Klasabun River in Western part of the Kepala Burung (Vogelkop) peninsula, while *C. pulcher* is found in Hoa creek and some other nameless creeks in and around Teminabuan, South Sorong in the eastern part of the type location of *C. wagenknechtae* sp. nov. separated by a straight distance of approximately 55.73 km measured using Google earth software.

Cherax wagenknechtae sp. nov. differs from *C. pulcher* in the following characters: shape of the chelae (Fig. 9A–D), shape of the rostrum (Fig. 5A, B) and in coloration (Fig. 8A–C). The middle prominent tooth in the cutting edge of the dactyl of *C wagenknechtae* is larger than *C. pulcher*. *Cherax wagenknechtae* has a bright color of the inner lateral ridge of the propodus compare to *C. pulcher*. The rostrum of *Cherax wagenknechtae* sp. nov. is slightly broader and longer compared to *C. pulcher.* Postorbital ridges of *C. wagenknechtae* fading at three-fourth of occipital carapace length, posteriorly while *C. pulcher* fading at two-thirds of occipital carapace length, posteriorly. Morphometric measurements comparison for *C. wagenknechtae* sp. nov. and *C. pulcher* is provided in Table 2.

Cherax wagenknechtae sp. nov. chelae has usually light to dark red with pink or creamy dorsolateral margins and white patch. Anterior part usually dark blue or black, more intense colored. Corneous tooth on tip of fingers orange while *C. pulcher* chelae has light blue to dark blue, decalcified swollen area in distal part of the lower margin white or cream coloration. Individuals of *Cherax wagenknechtae* from the Beraur River drainage usually have a wine red to blackish red chelae with black fingertips, the carapace is red to brownish red as well as the pleon. The elevated dorsolateral margins of the chelae are pinkish to creamy. Individuals from the Klasabun River drainage have a similar body coloration that often changes in the rostrum and scaphocerite to creamy with some slightly bluish or gray. Chelae are creamy with blue becoming bluish gray to the outer lateral margin. Fingertips dark blue to black. The elevated dorsolateral margins are creamy.

The coloration of *Cherax pulcher* is as follows. Chelae light blue to dark blue, becoming white on the outer lateral margins. The elevated dorsolateral margins are blue. Anterior part of the cephalothorax pinkish to striking pink fading laterally to a greenish-gray. Dorsal pleon dark blue to black becoming pinkish gray and pinkish to the margins. Older individual usually darker blue in coloration.

Etymology. *Cherax wagenknechtae* sp. nov. is named after Sahra Wagenknecht, an outstanding German left-wing politician, economist, author and publicist. She inspired the first author to fight determinedly for a better and fairer future for us all. This is the best way we know to thank her for her much appreciated service and effort to represent the socially disadvantaged, her fight for freedom, peace and a rare talent to unite morals and politics.

Ecology. Endemic to the Beraur and Klasabun River drainages in the western part of the Kepala Burung (Vogelkop) peninsula (Fig. 6). One of the creeks harboring these crayfish is shallow (20–100 cm) with a moderate flow and had a pH of approximately 5.5. The temperature is around 25–26 °C. In most parts no water plants are present. The substrate of the creek is silt or sand and soil mostly covered with silt and detritus. (Fig. 7). Crayfish hide in short burrows in the riverbank, under larger rocks or in detritus that is present in all the parts of the creek. Big males have been observed as active during the day. In some villages these crayfish are harvested for food by locals but it seems that even if they are collected for the pet trade and for some villages for human consumption, the population is stable. The creek is surrounded by dense forest. To improve the knowledge of the distribution of the species more field surveys will be necessary.

Common name. As a common name for this crayfish we propose Red Brick Crayfish as it is already available under this name in the pet trade.

Table 2. Morphometric measurements comparison for *C. wagenknechtae* sp. nov. and *C. pulcher* examined in the present study showing means, standard deviation, minimum and maximum. All measurements are in millimeters (mm).

Characters	*C. wagenknechtae*		*C. pulcher*	
	male	female	male	female
Chela lenght	53.3±8.5 (43.2–65.7)	40.7±7.3 (28.6–48.1)	49.7±17.9 (24.3–73)	n/a
Chela broad	21.2±2.9 (17.6–25.1)	15. 1±2.2 (11.7–17.9)	20.9±7.7 (10.3–28.6)	n/a
Chela high	9.4±1.2 (8.2–11.2)	7.3±1.3 (5.1–8.2)	10.7±2.1 (7.8–12.8)	n/a
Ratio Chela	2.6±0.3 (2.4–3.1)	2.7±0.2 (2.4–2.9)	2.4±0.1 (2.3–2.5)	n/a
Rostrum lenght	14.2±5.8 (11.6–15.3)	13.7±1.9 (12.3–15.1)	13.3±2.9 (8.7–16.6)	n/a
Rostrum broad	5.9±0.5 (5.2–6.5)	5.3±1.1 (3.8–7.1)	4.9±1.3 (2.9–7.1)	n/a
Ratio rostrum	2.25±0.9 (1.9–2.6)	2.6±0.3 (2.3–2.9)	2.7±0.4 (2.2–3.3)	n/a
Areola broad middle	10.6±1.7 (8–13.2)	11.4±1.9 (8.7–14.3)	8.6±2.7 (5–12.4)	n/a
Pleon	67.7±8.3 (56–77.5)	67.4±7.3 (57.1–77.8)	59.1±7.0 (51–70)	n/a
Carapace broad	25.6±3.7 (20–31.2)	24.9±3.7 (19.1–29.5)	23.8±7.2 (14.8–34)	n/a
Carapace lenght	59.8±4.7 (53.1–65.2	52.7±6.6 (43.5–58.7)	59.1±10.5 (46–71.7)	n/a
Ratio Carapace / Pleon	1.2±0.5 (1.15–1.17)	1.2±0.1 (1.16–1.19)	1.05+0.1 (1–1.1)	n/a

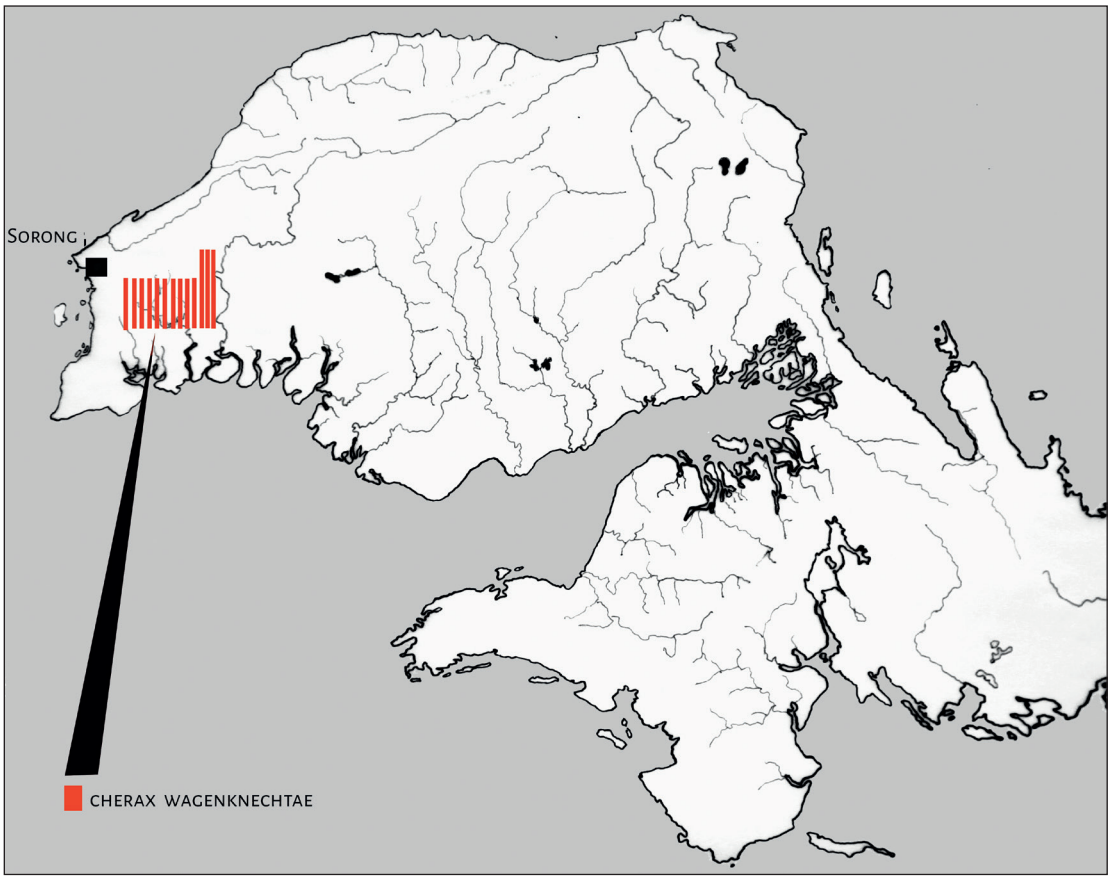

Figure 6. The Bird's Head Peninsula, West Papua, Indonesia with the drainage of Beraur and Klasabun River drainages, indicated. Red bars = distribution area.

Figure 7. Unnamed Creek in the Beraur River drainage, habitat of the new species.

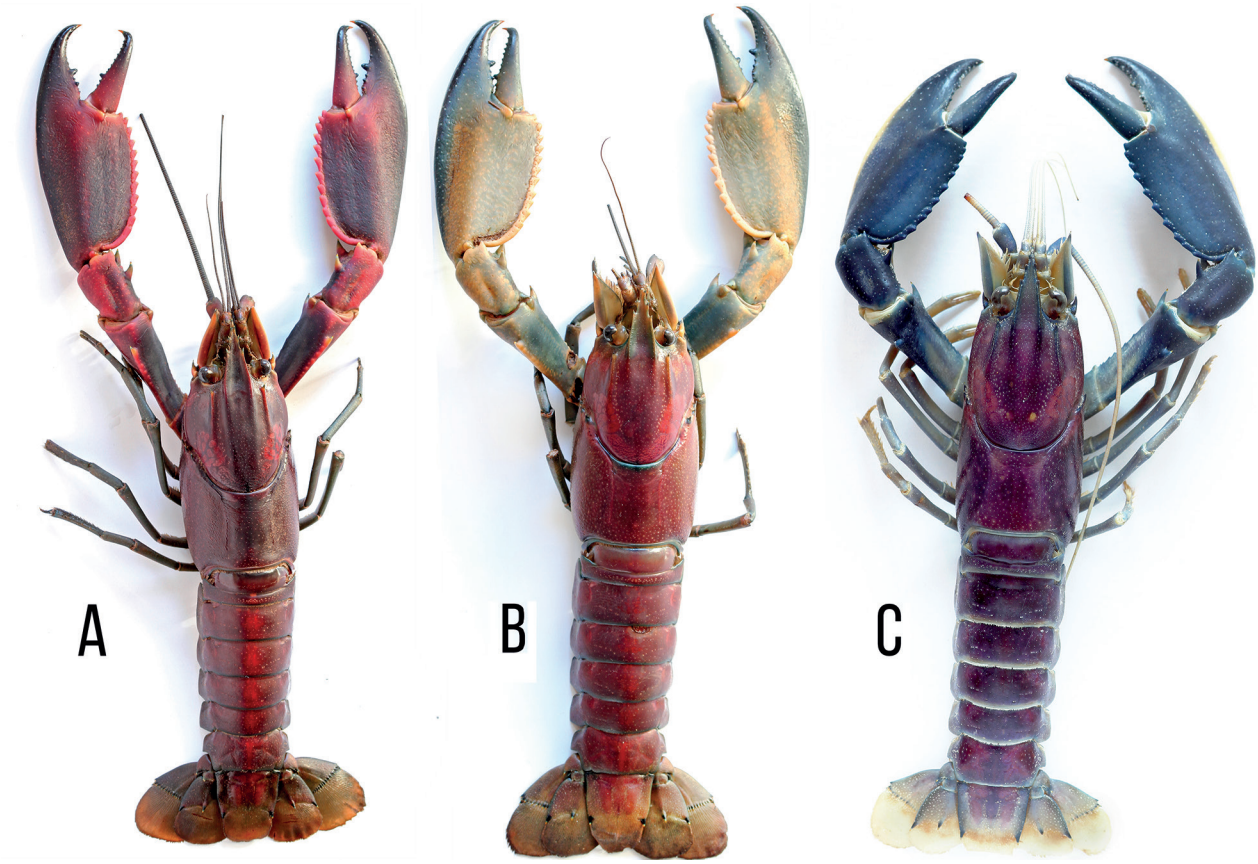

Figure 8. Coloration comparison *Cherax wagenknechtae* sp. nov. with *Cherax pulcher*. **A.** *Cherax wagenknechtae* sp. nov. from Beraur River drainage; **B.** *Cherax wagenknechtae* sp. nov. from Klasabun river drainage; **C.** *Cherax pulcher* from Hoa Creek in Teminabuan.

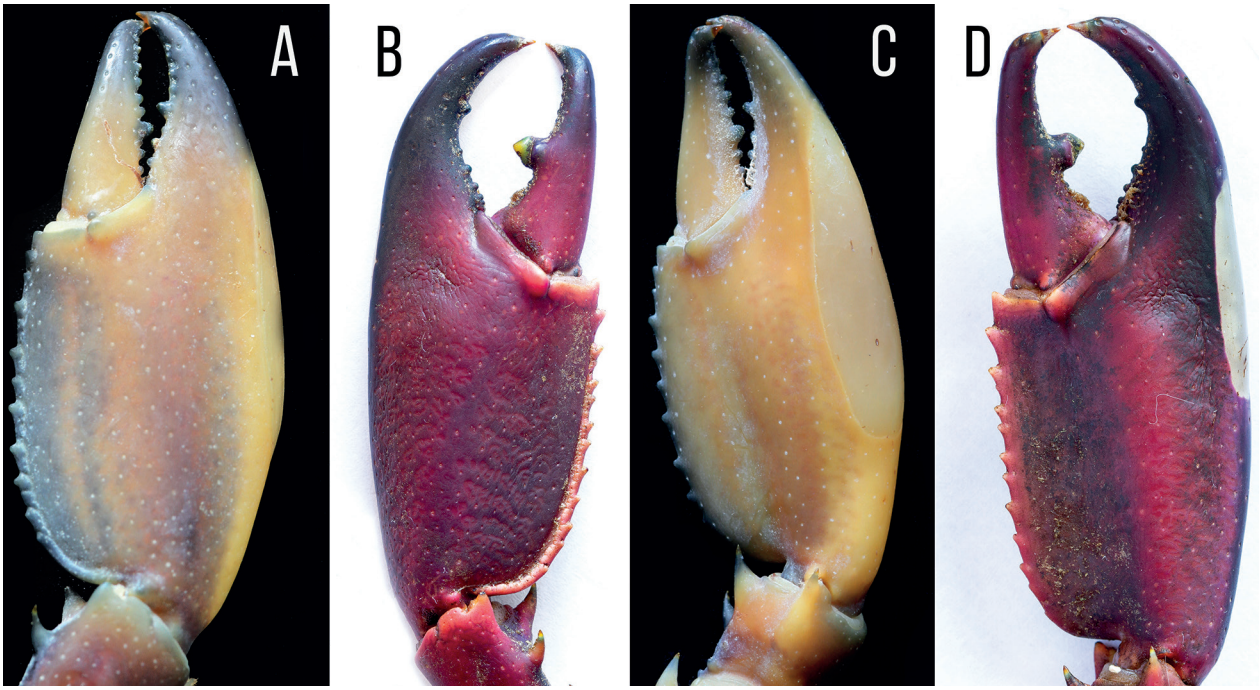

Figure 9. Chelae comparison Cherax pulcher and Cherax *Cherax wagenknechtae* sp. nov. **A.** Dorsal view of right chelae of *Cherax pulcher*; **B.** Dorsal view of left chelae of *Cherax wagenknechtae* sp. nov.; **C.** Ventral view of right chelae of *Cherax pulcher*; **D.** Ventral view of left chelae of *Cherax wagenknechtae* sp. nov.

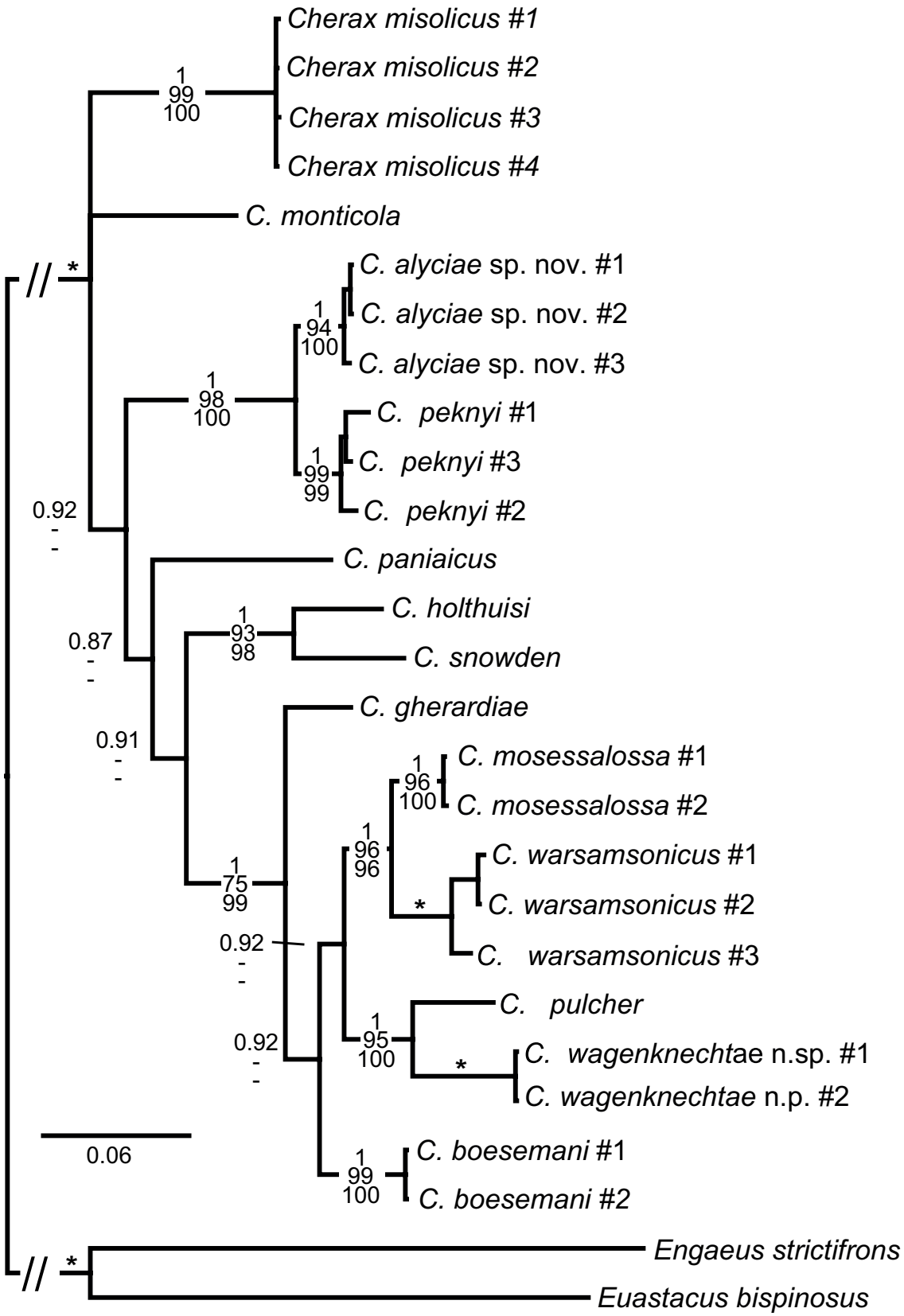

Figure 10. Phylogenetic relationships of *Cherax wagenknechtae* sp. nov. within the northern New Guinea *Cherax* lineage, reconstructed by BI analyses of two mitochondrial gene fragments. Number on branches show, from top, Bayesian posterior probabilities (>0.9) and ML/MP bootstrap values (>70). An asterisk indicates nodes with full support (1/100/100) in all analyses. The scale bar indicates the substitution rate. See Table 1 for information on the sequenced specimens.

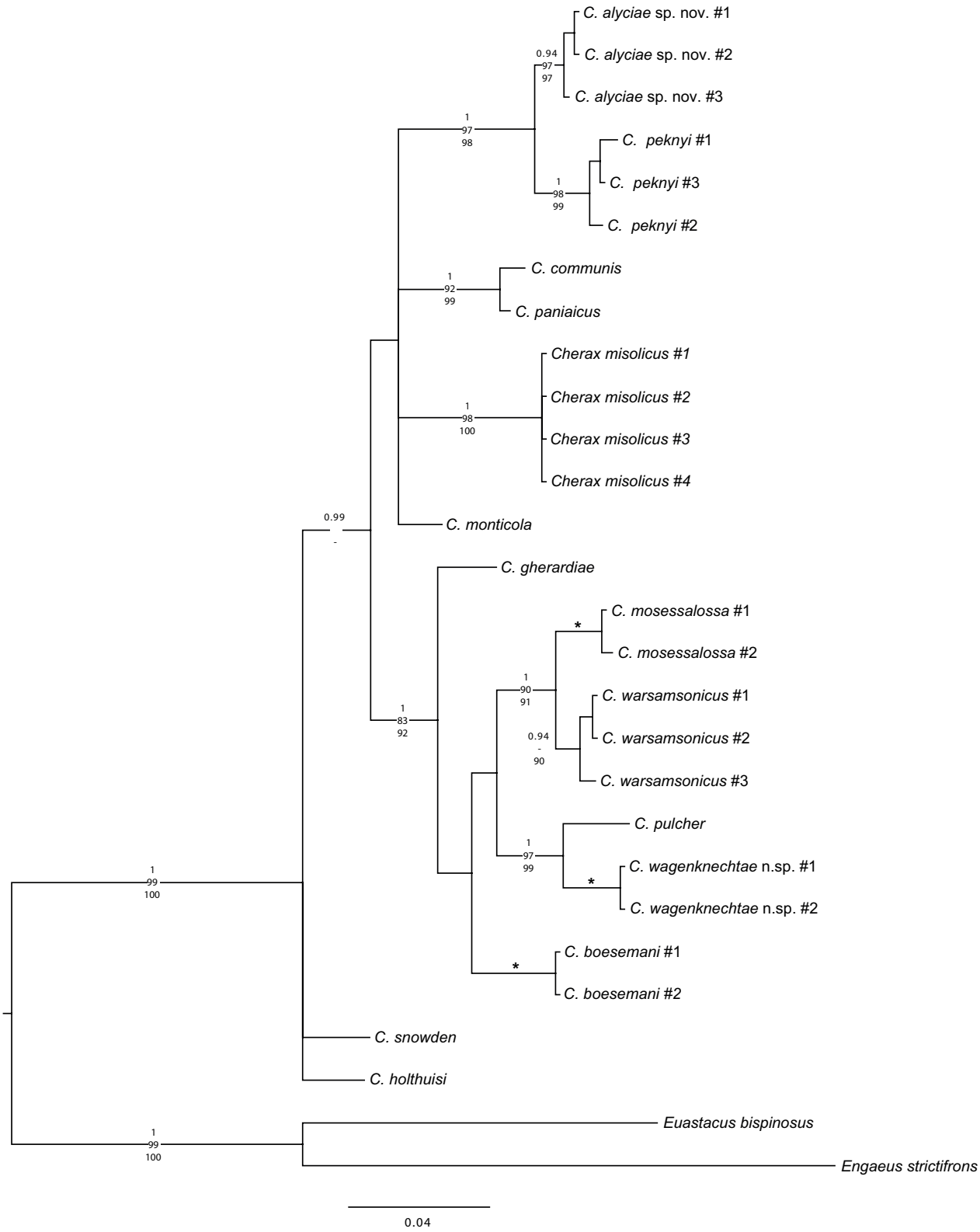

Figure 11. Phylogenetic relationships of *Cherax wagenknechtae* sp. nov. within the northern New Guinea *Cherax* lineage, reconstructed by BI analyses of a fragment of the mitochondrial 16S rRNA gene. Number on branches show, from top, Bayesian posterior probabilities (>0.9) and ML/MP bootstrap values (>70). An asterisk indicates nodes with full support (1/100/100) in all analyses. The scale bar indicates the substitution rate. See Table 1 for information on the sequenced specimens.

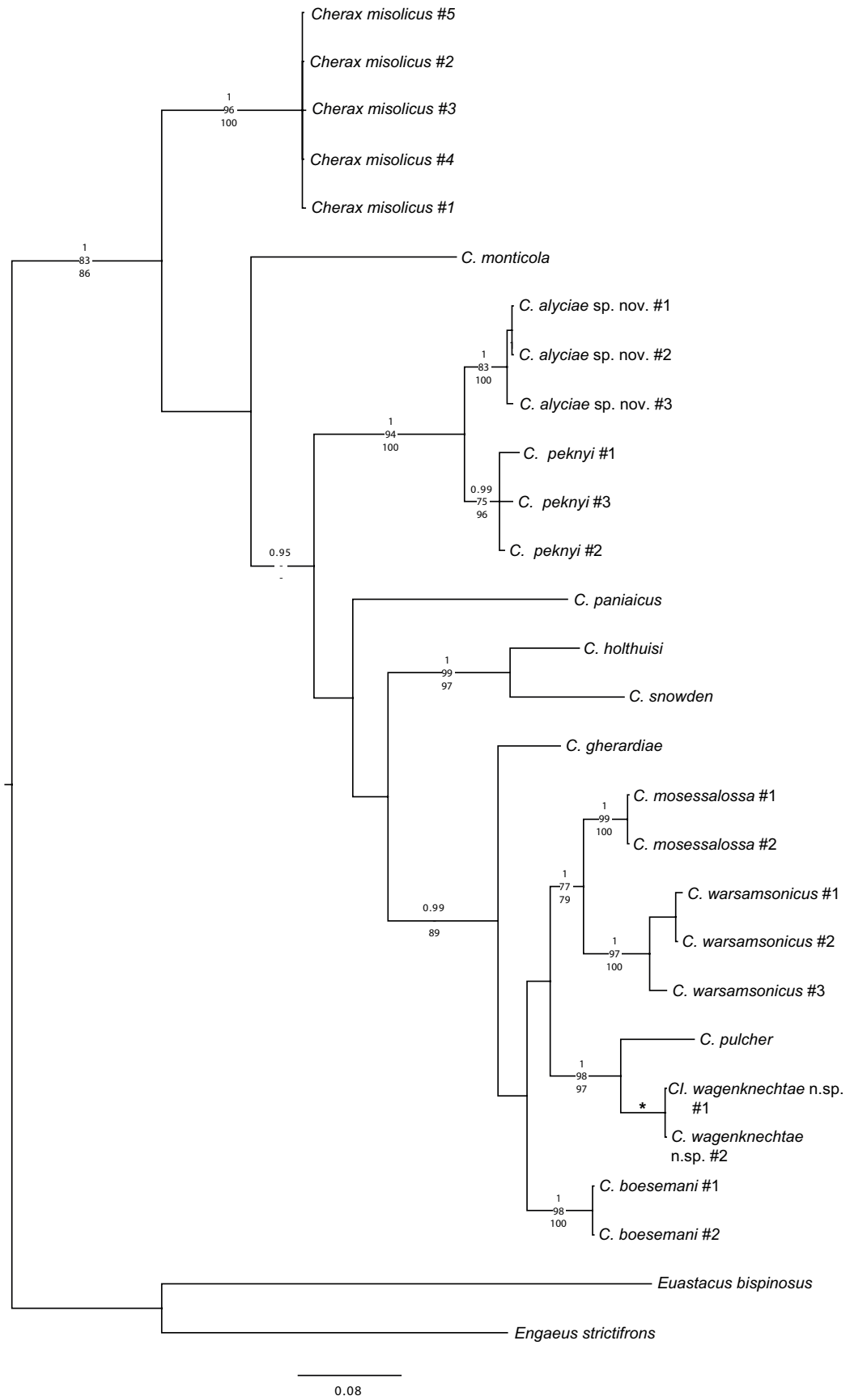

Figure 12. Phylogenetic relationships of *Cherax wagenknechtae* sp. nov. within the northern New Guinea *Cherax* lineage, reconstructed by BI analyses of a fragment of the mitochondrial cytochrome oxidase subunit 1 gene. Number on branches show, from top, Bayesian posterior probabilities (>0.9) and ML/MP bootstrap values (>70). An asterisk indicates nodes with full support (1/100/100) in all analyses. The scale bar indicates the substitution rate. See Table 1 for information on the sequenced specimens.

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