



A new species of freshwater crab of the genus *Himalayapotamon* Pretzmann 1966 (Decapoda: Brachyura: Potamidae) from Jammu and Kashmir, Northern India

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Abstract

A new species of potamid freshwater crab of the genus *Himalayapotamon* Pretzmann 1966 is described here on the basis of several specimens collected from different localities in Poonch district, in Jammu province of Jammu and Kashmir, India. The new species *Himalayapotamon jammuense* can be differentiated from its congeners by a suite of carapace (i.e., postorbital cristae) and gonopod (first and second) characters. In addition, molecular evidences derived from two mitochondrial gene (*16s* rRNA and *cox1*) and one nuclear gene (*28s* rRNA) supported the morphological findings. Genetically, *H. jammuense* is sister to clade containing *H. robertsonianum* (Pakistan) and *H. koolooense* (Punjab) which are found in close proximity to Jammu and Kashmir. Moreover, genetic distance inferred for the gene *16s* rRNA significantly support the species described in the study as a new species.

Keywords *Himalayapotamon jammuense* · Postorbital cristae · Gonopod · Potaminae · *16s* rRNA · *cox1* · *28s* rRNA

Introduction

The potamid crab genus *Himalayapotamon* Pretzmann 1966, is indigenous to the foot hills of India, Pakistan, Nepal and Bhutan. *Himalayapotamon* was previously established as a subgenus of *Potamon* by Pretzmann (1966), with Brandis (2001) later treating it as a full genus describing both its morphology and zoogeography. *Himalayapotamon* can be distinguished from *Potamon* by the cervical groove being deep, precisely S-shaped, posterior part joining cardiac groove, terminal segment of male first gonopod being covered by long and stiff setae (versus cervical groove superficial and almost straight and male first gonopod terminal segment having setae of shorter length in *Potamon*). Geographically,

Potamon is more widely distributed throughout Near East Asia to the Mediterranean Europe (Brandis et al. 1999); on the other hand, *Himalayapotamon* is mainly restricted to the Himalayan region (Brandis 2001).

Himalayapotamon is currently represented by 13 species (Brandis and Sharma 2005; Ng et al. 2008; Mitra and Valarmathi 2017; Pati and Singh 2017; Klaus and Brandis 2018): viz. *H. atkinsonianum* Wood-Mason 1871, *H. koolooense* Rathbun 1904, *H. ambivium* Alcock 1909, *H. bifarium* Alcock 1909, *H. emphyseteum* Alcock 1909, *H. monticola* Alcock 1910, *H. babaulti* Bouvier 1918, *H. marinellii* Pretzmann 1963, *H. kasaulis* Pretzmann 1966, *H. sunkoshiense* Brandis & Sharma 2005, *H. chambaensis* Mitra & Valarmathi 2017, *H. garhwalense* Pati & Singh 2017 and *H. robertsonianum* Klaus & Brandis 2018. From Jammu and Kashmir, only one species *H. emphyseteum* has been recorded (Alcock 1909). During a field survey of the area, many specimens of the genus *Himalayapotamon* from Poonch district (Fig. 1) were collected. After comparison with allied species, differences in the male first gonopod and carapace characters in these specimens distinguished them from all known congeners and, they are hereby described as a new species of *Himalayapotamon*.

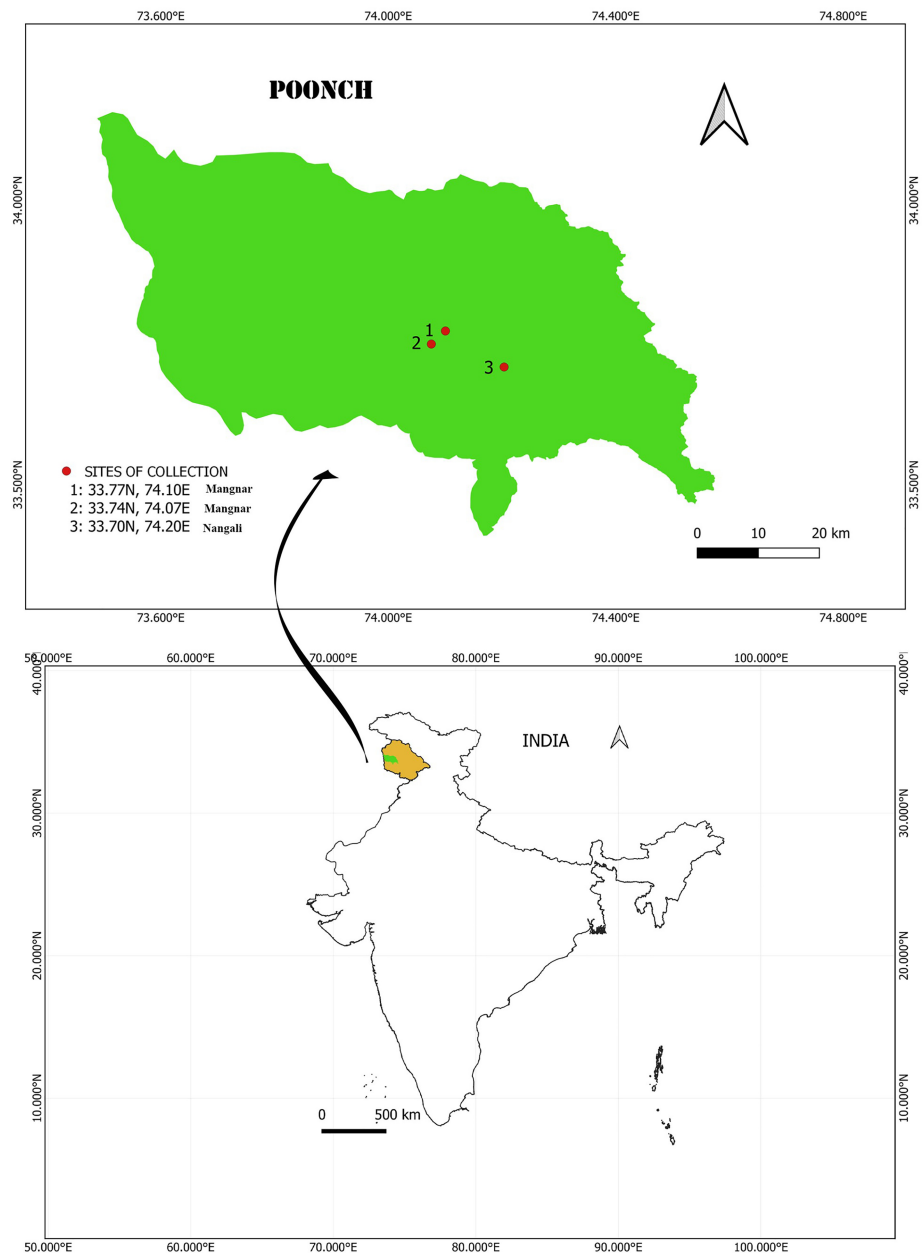
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Fig.1 Collection site of *Himalayapotamon jammuense* (Source Map has been created using QGIS version 3.34.2-Prizren)



Materials and methods

Specimens examined were deposited in the National Zoological Collection (NZC) of Zoological Survey of India (ZSI), Solan, India (ZSI C-110, ZSI C-111 and ZSI C-112). Terminologies for carapace measurement and morphology are followed after Bahir and Yeo (2007), with changes recommended by Davie et al. (2015). The following abbreviations have been used: cl, carapace length; cw, carapace width; ch, carapace height; fw, frontal width; p2–p5, pereopods 2–5; s1–s8, thoracic sternite 1–8; G1, first male gonopod; G2 second male gonopod.

Measurements of the specimens were carried out using digital vernier caliper and morphological characters specific to the identification of species were subsequently compared with congeners. Gonopod measurements and structural variations were studied in stereomicroscope. All measurements are in millimeters.

Material examined

India (Poonch district, J&K): Holotype adult male (cw 47.59 mm, cl 37.34 mm, ch 19.99 mm, fw 14.52 mm), Mangnar, 4 km from Poonch (33.77° N 74.1° E) (Fig. 1), 12 Oct. 2017, collected by: H. Kour (ZSI C-110). Paratypes,

4 paratypes (Largest cw 53.31 mm, cl 40.35 mm, ch 21.63 mm, fw 16.60 mm; smallest cw 32.63 mm, cl 25.34 mm, ch 13.43 mm, fw 9.94 mm), Mangnar, 4 km from Poonch (33.74° N 74.07° E), 10 Oct. 2017, collected by: H. Kour (ZSI C-111); 1 adult female (cw 44.11 mm, cl 34.53 mm, 17.68 mm, fw 12.78 mm), Nangali, 6 km from Poonch (33.70° N 74.20° N), 22 Oct. 2017, collected by: H. Kour (ZSI C-112). Other material: 2 males (largest cw 47.92 mm, cl 36.25 mm, ch 19.43 mm, fw 17.27 mm; smallest cw 27.28 mm, cl 20.87 mm, ch 10.77 mm, fw 9.01 mm), 3 females (largest cw 40.65 mm, cl 31.30 mm, ch 17.20 mm, fw 12.04 mm; smallest cw 28.95 mm, cl 22.89 mm, ch 11.22 mm, fw 9.45 mm), Khari, 10 km from Poonch (33.75° N 74.02° N).

Molecular analysis

Muscle tissue was excised from chelipeds, total genomic DNA was extracted from the tissue using QIAamp DNA Mini Kit (250) following the manufacturer's protocol. Then *16s* rRNA, *cox1* and *28s* rRNA genes were amplified using polymerase chain reaction. *16s* rRNA gene was amplified by using primer 16L29 (5'-YGC CTG TTT ATC AAA AAC AT-3') and 16H37 (5'-CCG GTY TGA ACT CAA ATC ATG T-3') Klaus et al. (2009). *cox1* gene was amplified using primer pair LCOI-1490 (5'-GGT CAA CAAA TCA TAAA GAT ATTG-3') and HCOI-2198 (5'-TAAA CTT CAG GGT GAC CAAA AAA TCA-3') Folmer et al. (1994). The *28s* rRNA gene was amplified using primer pair TSD2 (5'-GTA CCG TGA GGG AAA GTT G-3') and D4AR (5'-GTC CGT GTT TCA AGA CGG G-3') Littlewood and Johnston (1995). Each PCR was carried out in a total volume of 25 µl containing 2 µl of genomic DNA, 12.5 µl of GoTaq G2 Hot Start colorless Master Mix (Promega), 8.5 µl of nuclease-free water and 1 µl each of forward and reverse primer. For *16s* rRNA the PCR amplifications were performed by following cycling conditions: 36 cycles of 95 °C for 30 s, 50 °C for 40 s and 72 °C for 1 min; for *cox1*: 35 cycles of 95 °C for 30 s, 42 °C for 1 min and 72 °C for 2 min; for *28s* rRNA 31 cycles of 94 °C for 30 s, 50 °C for 30 s and 72 °C for 1 min. An initial denaturation of 95 °C for 10 min and final extension of 72 °C for 7 min was common for all the genes.

PCR product was purified using Krishgen biosystems PCR purification kit according to manufacturer's protocol. The purified product was cycle sequenced using ABI Big-Dye v 3.1 chemistry. All samples were run on a 16 capillary 3130xl automated sequencer (Applied Biosystems, Hitachi, Japan) at the Regional Medical Research Centre, Dibrugarh, Assam. The cycle sequencing reactions were run in both directions using PCR primers as sequencing primers.

Eight new sequences of *16s* (3), *cox1* (3) and *28s* (2) obtained were deposited in GenBank™ with following accession numbers for *16s*: OR041661-OR041663, *cox1*:

OR038164-OR038166 and *28s*: OR083335-OR083336. Sequences were aligned with previously published corresponding sequences of *Himalayapotamon* and other related genera (Table 1) in sequence editor program Geneious Prime v2023.1.2 (Kearse et al. 2012). Bayesian Inference and Maximum Likelihood phylogenetic analysis of sequence data were performed using MrBayes (Huelsenbeck and Ronquist 2001) and PhyML (Guindon et al. 2010) as implemented in Geneious Prime. Best fit model was determined using jModelTest (Posada 2008), selected by Akaike information criterion (AIC). The General Time Reversible (GTR) was best fit model for *28s*, while for *cox1* and *16s*, Hasegawa–Kishino–Yano (HKY) was best substitution model for corresponding data set. The rate variations among sites included by these models corresponds to only Gamma Distributed rates (+ G). For construction of Bayesian tree, up to 5 million iterations were employed for each alignment and states sampled every 1000 cycles. Convergence of the run was considered complete if the average standard deviation of split frequency was < 0.01. Burn in was 10% of iterations. Maximum likelihood analysis was performed using nearest neighbor interchanges (NNI). To quantify the stability of the clades bootstrap analysis of 1000 replicates was used. The pairwise estimates of Kimura-2-parameter (K2P) distance (Kimura 1980) among the various species of interest was calculated using MEGA v11.0.9 (Tamura et al. 2021).

Results

Taxonomy

The new species belongs to family Potamidae Ortmann 1896; subfamily Potaminae Ortmann 1896; genus *Himalayapotamon* Pretzmann 1966 and species *H. jammuense* (Figs. 2–6).

Diagnosis

Carapace broader than long; dorsal surface setose, almost flat, slightly convex longitudinally; epigastric cristae oblique; postorbital cristae distinctly cut by cervical groove at a point just below an imaginary line drawn perpendicularly across external orbital tooth to postorbital cristae (Figs. 2A, 4A); front bilobed; mesogastric groove inverted Y-shaped; cervical groove S-shaped; G1 terminal segment conical, stout, short, distally curved outwardly, flexible zone broadly U-shaped, ca 0.28 times combined length of subterminal joint and flexible zone (Fig. 3A–C); G2 longer than G1, almost straight (Fig. 3D).



Table 1 GenBank accession Numbers of the species used for phylogenetic analysis

Species	GenBank Accession No	Site	References
16S rRNA gene			
<i>Himalayapotamon jammuense</i>	OR041661	Poonch, Jammu & Kashmir, India	Present Study
<i>Himalayapotamon jammuense</i>	OR041662	Poonch, Jammu & Kashmir, India	Present Study
<i>Himalayapotamon jammuense</i>	OR041663	Poonch, Jammu & Kashmir, India	Present Study
<i>Himalayapotamon robertsonianum</i>	LR131129	Murree Hills, Pakistan	Klaus and Brandis (2018)
<i>Himalayapotamon koolooense</i>	LR131128	Bhin valley, Kumasa, India	Klaus and Brandis (2018)
<i>Himalayapotamon sunkoshiense</i>	LR131130	Bhagmati, tributary of Cha-Khola, Nepal	Klaus and Brandis (2018)
<i>Himalayapotamon sunkoshiense</i>	LR131131	Bhagmati, tributary of Cha-Khola, Nepal	Klaus and Brandis (2018)
<i>Himalayapotamon atkinsonianum</i>	AB290632	Mahananda River, India	Yeo et al. (2007)
<i>Himalayapotamon atkinsonianum</i>	AB428510	Nepal	Shih et al. (2009)
<i>Himalayapotamon atkinsonianum</i>	LR131125	Mabandra Gupha Parkhara, Nepal	Klaus and Brandis (2018)
<i>Himalayapotamon emphysetum</i>	LR131126	Central, Daune Khola, Daune, Nawalparsi dist., Nepal	Klaus and Brandis (2018)
<i>Himalayapotamon emphysetum</i>	LR131127	Central, Daune Khola, Daune, Nawalparsi dist., Nepal	Klaus and Brandis (2018)
<i>Himalayapotamon sp.</i>	AB428511	Uttaranchal, India	Shih et al. (2009)
<i>Acanthopotamon martensi</i>	LR131132	Bengal, Terai, India	Klaus and Brandis (2018)
<i>Potamon ruttneri</i>	LR131133	Sistan-Baluchestan Prov., Iran	Klaus and Brandis (2018)
COX1 gene			
<i>Himalayapotamon jammuense</i>	OR038164	Poonch, Jammu & Kashmir, India	Present Study
<i>Himalayapotamon jammuense</i>	OR038165	Poonch, Jammu & Kashmir, India	Present Study
<i>Himalayapotamon jammuense</i>	OR038166	Poonch, Jammu & Kashmir, India	Present Study
<i>Potamon persicum</i>	MZ506899	Bisotum, Kermanshah Prov., Iran	Rezaei Tavabe et al. (2022)
<i>Potamon rhodium</i>	MZ506924	Greece	Rezaei Tavabe et al. (2022)
<i>Potamon bilobatum</i>	MG729766	Southern Caspian Sea Region	Parvizi et al. (2018)
<i>Potamon ibericum</i>	MK570621	Iran	Parvizi et al. (2018)
<i>Potamon ruttneri</i>	MZ506918	Abgarm, Razavi Khorasan Prov, Iran	Rezaei Tavabe et al. (2022)
<i>Chiromantes haematocheir</i>	OL877138	–	Unpublished
28S rRNA gene			
<i>Himalayapotamon jammuense</i>	OR083335	Poonch, Jammu & Kashmir, India	Present study
<i>Himalayapotamon jammuense</i>	OR083336	Poonch, Jammu & Kashmir, India	Present Study
<i>Longpotamon mindongense</i>	KT586367	China	Ji et al. (2016)
<i>Longpotamon chekiangense</i>	KT586306	China	Ji et al. (2016)
<i>Paratelpusa sp.</i>	MZ338295	China	Pan et al. (2022)
<i>Paratelpusa gibbosa</i>	MZ338296	China	Pan et al. (2022)

Description of male holotype

Carapace broader than long, cw 1.27 times cl. Dorsal surface setose, almost flat, slightly convex longitudinally (Fig. 2A, B); regions demarcated by deep grooves, rows of granules in epibranchial region; epigastric cristae oblique, rugose; postorbital cristae sharp, separated from postorbital tooth; postorbital cristae distinctly cut by cervical groove at a point just below the imaginary line of external orbital tooth (Fig. 4A); anterolateral border serrated, well convex, slightly shorter than posterolateral border; anterolateral region with many oblique ridges; posterolateral border convergent posteriorly; posterolateral region with some oblique striae. Front width 0.30 times cw, bilobed, granulated; mesogastric groove

inverted Y-shaped; cervical groove S-shaped, anterior part deep, broad, posterior part not distinct; cardiac groove prominent; H-shaped groove distinct; external orbital angle broadly triangular, short, acute, outer margin nearly twice as inner margin (Figs. 2A, 4A). Orbital margin triangular, a small notch on the middle of the upper orbital margin, a distinct triangular notch just below the external orbital tooth on the lower orbital margin; pterygostomial region granulated. Epistomal median tooth acutely triangular (Figs. 2B).

Third maxilliped ischium longer than broad, with deep median sulcus, merus almost quadrangular, slightly broader than long, exopod sinuous, reaching about half length of merus (Fig. 4B). Antennular fossae slit like. Eyes with large cornea.

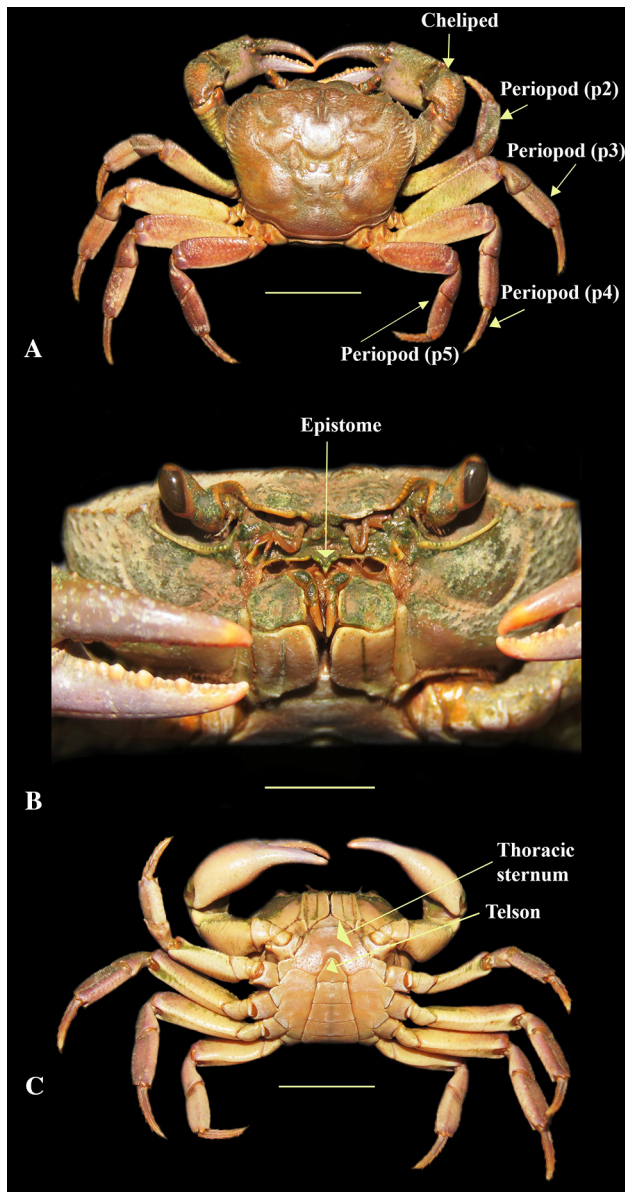


Fig. 2 *Himalayapotamon jammuense*, holotype male (cw 47.59 mm, cl 37.34 mm) (ZSI C-110). **A**, dorsal view, **B** frontal view, **C**, ventral view. Scale Bar = 30 mm

Cheliped subequal, right cheliped stouter than left, propodus, merus and carpus of cheliped rugose, inner angle of carpus with short sub-median tooth, followed posteriorly by one or two smaller teeth. Fingers of chela slightly shorter than palm, cutting edge aligned with sharp conical teeth, four broad molar teeth on cutting edge of movable finger and three broad molar teeth on cutting edge of immovable finger (Fig. 4C). P2 as long as major cheliped, ambulatory legs strong, dactylus stout, slightly longer than propodus, width of propodus p4 and p3 about half of their length.

Thoracic sternum smooth sparsely pitted, glabrous. Suture s2/s3 distinct as deep, narrow groove, reaching lateral

margins, suture s3/s4 only represented as a small groove laterally (Fig. 2C). Sterno-abdominal cavity deep (Fig. 6A), long, reaching up to imaginary line joining median part of coxae of cheliped.

Pleon (abdomen) smooth, triangular. First somite very short, second to sixth gradually increasing in length; sixth somite broader than long, trapezoidal, median length slightly greater than half of its maximum width, lateral margin almost straight, convergent distally, telson broader than long, with slightly concave lateral margin, distally rounded.

G1 sinuous, terminal segment conical, stout, short, ca.0.28 times than subterminal joint and flexible zone, flexible zone U-shape, terminal segment curved outwardly, subterminal segment broad, groove for G2 marginal (Figs. 3A–C, 4D–E); G2 longer than G1, almost straight, terminal segment 0.66 times longer than subterminal segment (Figs. 3D, 4F).

Live color

The dorsal surface of the carapace is brownish; the ambulatory legs are pale brown with a violet patch on the carpus and propodus; the upper parts of the cheliped are olive and brown; the dactylus is violet, and the teeth, dentary edge and tips of fingers are deep orange.

Variations

The male paratypes (Fig. 5A–C) are similar to the holotype in overall physiognomy, yet cw 1.29 times cl. The postorbital cristae are nevertheless more distinctly serrate in paratypes than in holotype. External orbital tooth is more acute in paratypes than in holotype.

Female paratypes (Fig. 5D–F) resemble the holotype in nearly all non-sexual characters, yet cw 1.3 times cl. The abdomen in female is broad, ovate, and almost conceals the sternum except for small tip of anterior thoracic sternite. Their vulvae are ovate, very large, occupying nearly most of thoracic sternite 6 and situated adjacent to margin with thoracic sternite 5 (Fig. 6B).

Habit and habitat

Some individuals dug nest hole under the rock bed in fast flowing streams, while others can be seen on muddy or gravel bottom in slow moving streams. In the day time, they mostly hide themselves in the small hole openings. The new species is only known from Poonch district of Jammu and Kashmir (Fig. 1). The temperature of water ranged from 15 to 25 °C.





Fig. 3 *Himalayapotamon jammuense*, holotype male (ZSI C-110). **A** dorsal view of right G1, **B** ventral view of right G1, **C** dorsal view of tip of right G1, **D** right G2. Scale Bar = 2 mm

Etymology

The specific epithet refers to the type locality, Jammu province of Jammu and Kashmir state.

Phylogenetic analysis

In this study we examined three genes of three specimens collected from Poonch district of Jammu and Kashmir. The final length of the aligned sequences was 630–680 bp, 519–522 bp and 300–307 bp for *cox1*, *16s* rRNA and *28s* rRNA respectively. Table 2 gives an overview of genetic differences between the different species based on *16s* rRNA gene as it is the only gene with much submissions of related genera to compare with, based on p-distance. Phylogenetic trees based on Bayesian inference and maximum likelihood (Fig. 7A–F) differ somewhat in arrangement of forms within the genus *Himalayapotamon*. The three fragments of *16s* rRNA gene can be seen very close genetically, indicating they are members of same species and are consistent with the results of morphological study. Despite having differences in the arrangement of various members of *Himalayapotamon* in ML and BI tree as shown by *16s* rRNA (Fig. 7A and B), yet the new species can be seen clustered

with *Himalayapotamon robertsonianum* and *Himalayapotamon koolooense*. Where as in case of *cox1* and *28s* rRNA (Fig. 7C–F) a lack of GenBank submissions of other members of genera *Himalayapotamon* comparison and relative relationship of the members of the genera cannot be well demonstrated. These genes, specifically *cox1* are known to exhibit a conserved level of variation that make it more preferable for discrimination of taxa at a very significant level.

Discussion

Himalayapotamon jammuense can be easily distinguished from its congeners by following suit of characters: postorbital cristae distinctly cut by cervical groove at a point just below an imaginary line drawn perpendicularly across external orbital tooth to postorbital cristae; G1 terminal segment conical, stout, short, distally curved outwardly, flexible zone broadly U-shaped, ca 0.28 times combined length of sub-terminal joint and flexible zone (Fig. 3A–D). *H. jammuense* superficially resembles *H. emphysetum* Alcock 1910 where anterolateral border is rugose, carapace wider than long, telson longer than broad, G1 terminal segment being short, yet the former differs from the latter in following characters:

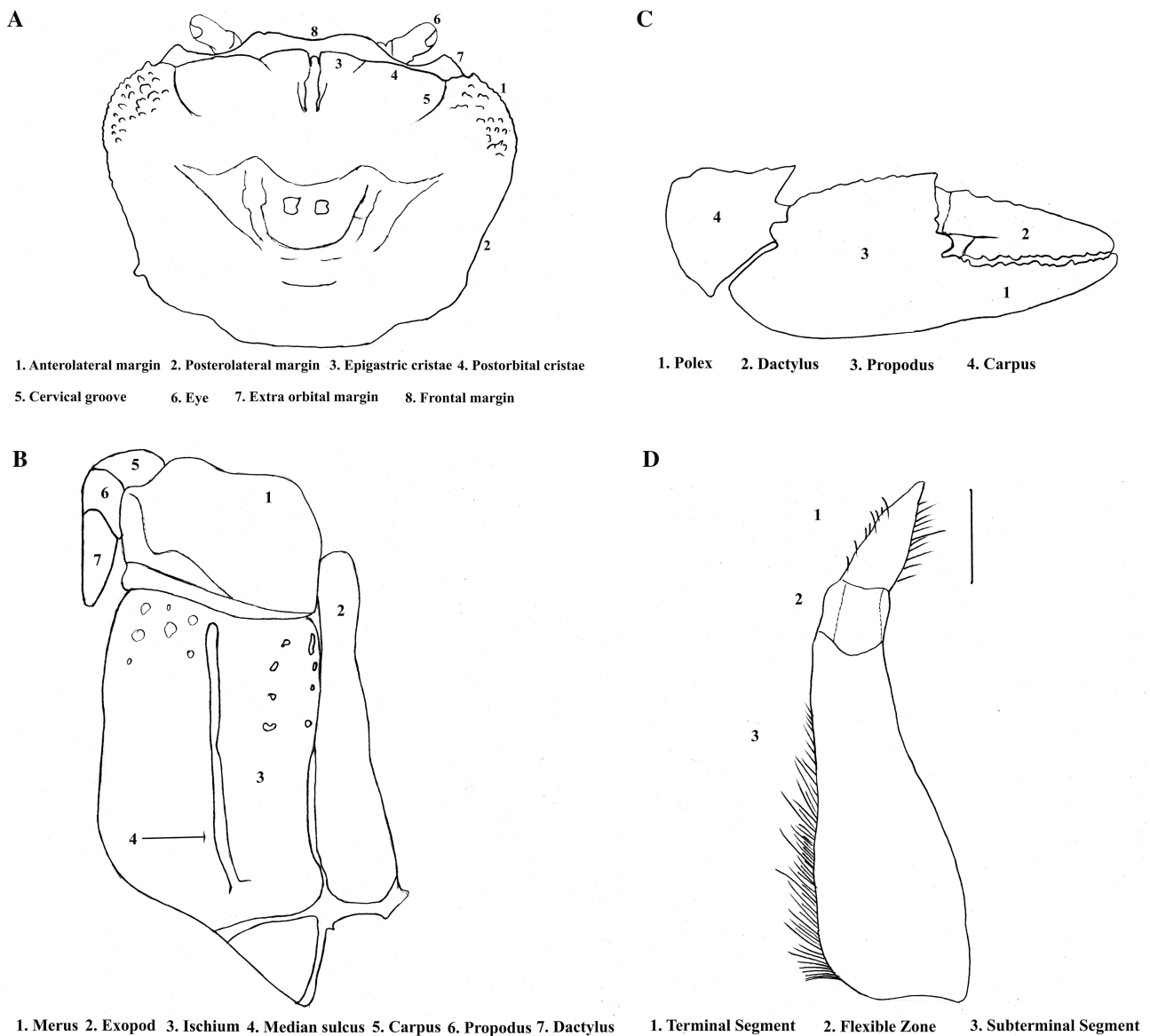


Fig. 4 *Himalayapotamon jammuense*, holotype male (cw 47.59 mm, cl 37.34 mm) (ZSI C-110). Line Diagrams: **A** dorsal carapace, **B** third maxilliped, **C** right major cheliped, **D** dorsal view of right G1, **E** ventral view of right G1, **F** right G2

comparatively low carapace convexity (carapace strongly convex in *H. emphysetum*; see Alcock 1910: Fig. 2); posterolateral border slightly convergent posteriorly (strongly convergent in *H. emphysetum*, see Brandis 2001: Fig. 4a); G1 terminal segment slightly bent outward (G1 terminal segment straight in *H. emphysetum*, see Alcock 1910: pl. 1, Fig. 2a; Brandis & Sharma 2005: Fig. 4B, C; Bott 1970: pl 37, Fig. 17).

The new species also superficially resembles *H. atkinsonianum* Wood-Manson 1871 in having large and nearly flat carapace, but is distinguished by several features from the latter i.e., cervical groove not so prominent all along the length, disrupted in between (cervical groove cut deep

throughout the length in *H. atkinsonianum*). G1 terminal segment more or less conical (typically S-shaped, tip is dorsally elongated and crosses over ventral part, spoon shaped in *H. atkinsonianum*, see Bott 1970: Figs. 14, 15, pl 37; Brandis 2001: Figs. 2B, C); flexible zone of G1 is symmetrically U-shaped (flexible zone asymmetrical in *H. atkinsonianum*, see Brandis 2001: Fig. 3B, C).

The new species is similar to *H. garhwalense* Pati & Singh 2017, in characters as carapace structure broader than long, epigastric and postorbital cristae separated from each other by a distinct groove, sixth abdominal somite broader than long, G1 terminal segment comparatively short, conical. It differs from *H. garhwalense* in following characters



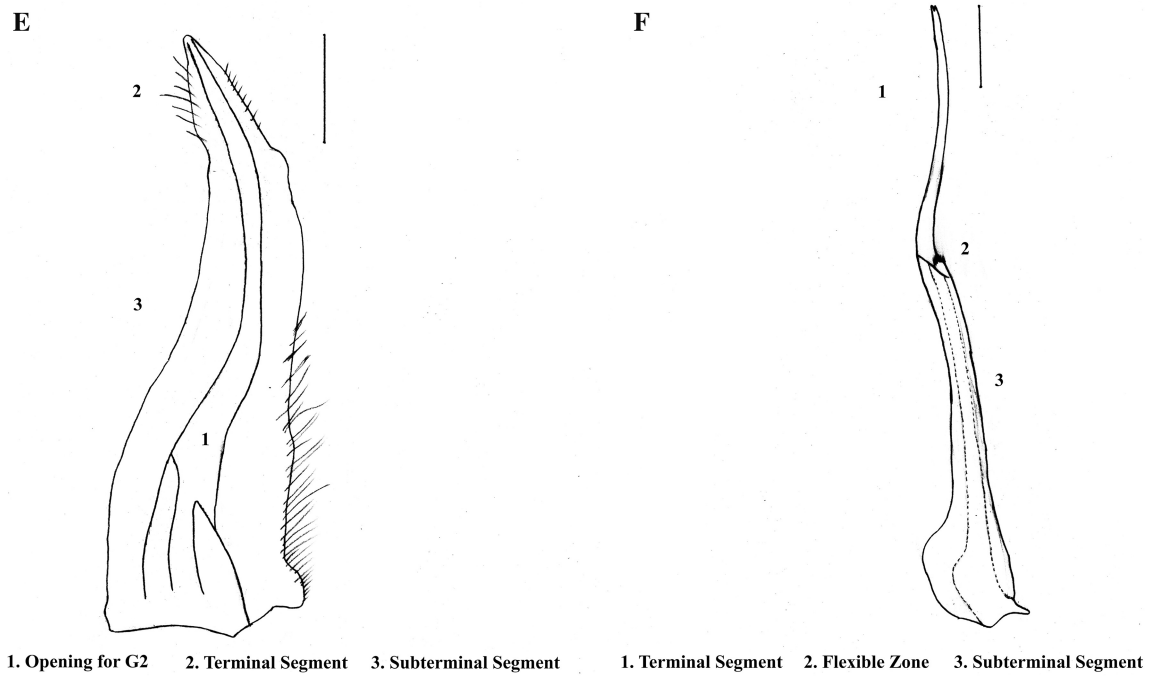


Fig. 4 (continued)

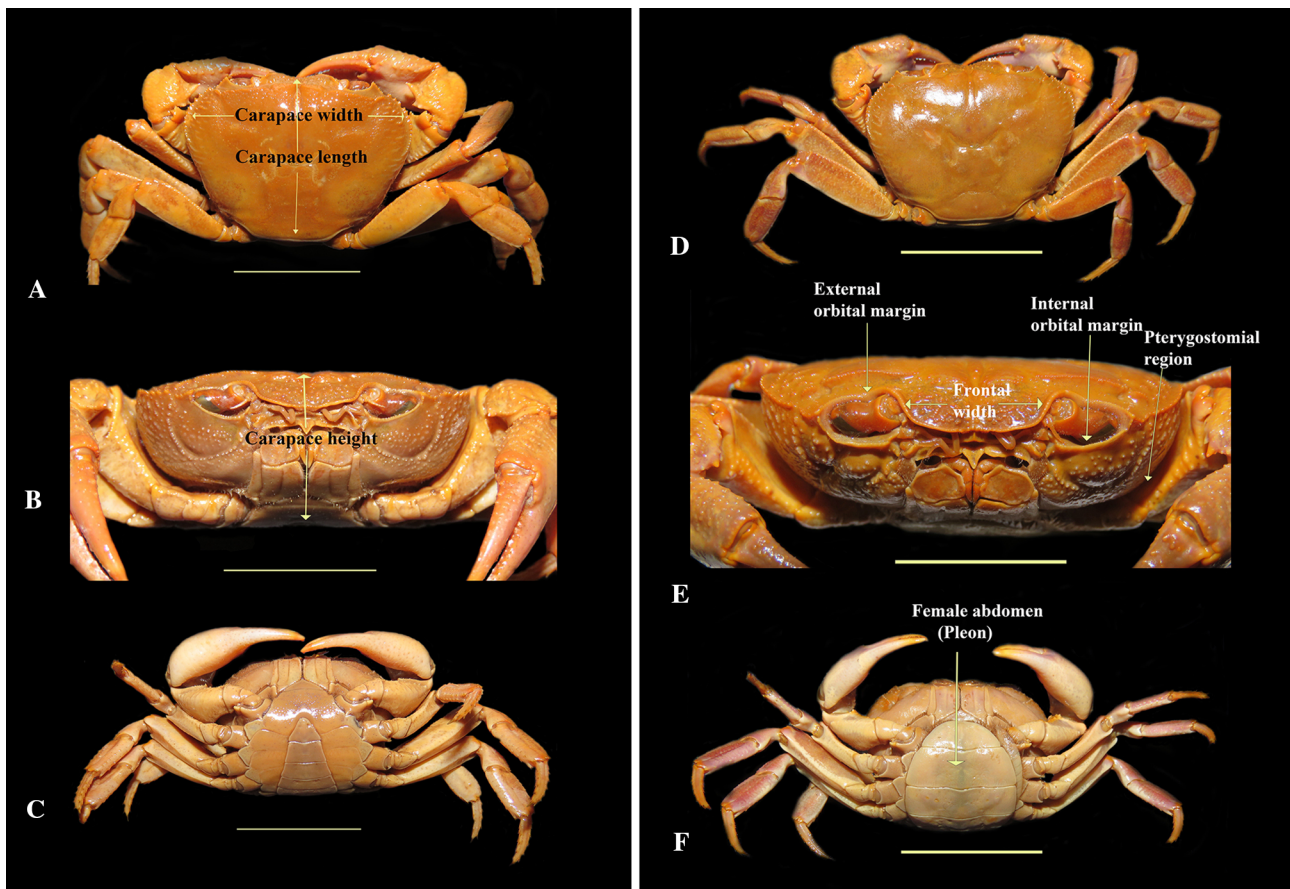


Fig. 5 *Himalayapotamon jammuense*, paratype male (cw 53.31 mm, cl 40.35 mm) (ZSI C-111) **A** dorsal view, **B** frontal view, **C** ventral view, paratype female (cw 47.92 mm, cl 36.25) (ZSI C-112) **D** dorsal view, **E** frontal view, **F** ventral view. Scale Bar = 30 mm



Fig. 6 *Himalayapotamon jammuense*, **A** sternopleonal cavity of male holotype with G1 and G2; **B** sternopleonal cavity of female paratypes. Scale Bar = 10 mm

as: postorbital cristae slightly concave in *H. jammuense* (postorbital cristae distinctly curved in *H. garhwalense* Pati & Singh 2017: Fig. 2A, B), G1 terminal segment outwardly bent in new species (G1 terminal segment stout in *H. garhwalense*; Pati & Singh 2017: Fig. 3 A–C); G2 terminal part is long and stout (G2 terminal part relatively short, curved, hook like in *H. garhwalense* Pati & Singh 2017: Fig. 3D).

The new species is similar to *H. chambaensis* in features as: carapace broader than long, sixth abdominal somite broader than long, epigastric and postorbital cristae separated distinctly, but is different from the above mentioned in following features: G1 terminal segment conical and stout in *H. jammuense* (G1 terminal segment relatively long, sub cylindrical in *H. chambaensis*) G2 terminal part is long and stout (G2 terminal part relatively long, rolled back as a full coil, Mitra & Valarmathi 2017: Fig. 3A–D).

On ground of morphological characters *H. jammuense* can be well distinguished from its congeners. On close analysis of phylogenetic analysis and measurement of genetic distance on basis of *16s* rRNA gene it is well evident that the species show marked difference and can be described as a new species. By analysis of BL and

Table 2 Pairwise genetic distance of *Himalayapotamon jammuense* based on 16S rRNA gene

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
<i>Potamon_rutneri_LR131133</i>															
<i>Acanthopotamon_martensi_LR131132</i>	0.13229														
<i>H.jammuense_OR041661</i>	0.11033	0.15739													
<i>H.jammuense_OR041662</i>	0.10602	0.15188	0.00195												
<i>H.jammuense_OR041663</i>	0.09977	0.14290	0.00000	0.00000											
<i>H.sp_LR131129</i>	0.10255	0.14760	0.00394	0.00194	0.00245										
<i>H.enphysetum_LR131127</i>	0.08028	0.12543	0.08354	0.07979	0.06687	0.07667									
<i>H.enphysetum_LR131126</i>	0.08028	0.12543	0.08354	0.07979	0.06687	0.07667	0.00000								
<i>H.kooloense_LR131128</i>	0.09782	0.14795	0.07923	0.07554	0.05551	0.07246	0.08121	0.08121							
<i>H.sp_HMsI_AB428511</i>	0.08166	0.13046	0.07962	0.07733	0.06687	0.07554	0.00584	0.00584	0.07765						
<i>H.atkinsonianum_LR131125</i>	0.12725	0.14356	0.11558	0.11099	0.10128	0.10731	0.07217	0.07217	0.08638	0.06854					
<i>H.atkinsonianum_AB428510</i>	0.12679	0.14335	0.11074	0.10828	0.09797	0.10654	0.07098	0.07098	0.08537	0.06479	0.00195				
<i>H.atkinsonianum_AB290632</i>	0.12487	0.14732	0.11147	0.11175	0.10958	0.11009	0.07970	0.07970	0.08957	0.07753	0.05741	0.05429			
<i>H.sunkoshiense_LR131131</i>	0.12523	0.14450	0.111370	0.10926	0.10645	0.10568	0.08299	0.08299	0.09299	0.08198	0.05645	0.05741	0.00589		
<i>H.sunkoshiense_LR131130</i>	0.12523	0.14450	0.111370	0.10926	0.10645	0.10568	0.08299	0.08299	0.09299	0.08198	0.05645	0.05741	0.00589	0.00000	



Fig. 7 Phylogenetic relationship of *Himalayapotamon jammuense* with other related species. **A** Maximum likelihood tree based on *16s* rRNA gene fragment, **B** Bayesian Inference tree based on *16s* rRNA gene fragment, **C** Maximum likelihood tree based on *cox1* gene fragment, **D** Bayesian Inference tree based on *cox1* gene fragment, **E** Maximum likelihood tree based on *28s* rRNA gene fragment, **F** Bayesian Inference tree based on *28s* rRNA gene fragment

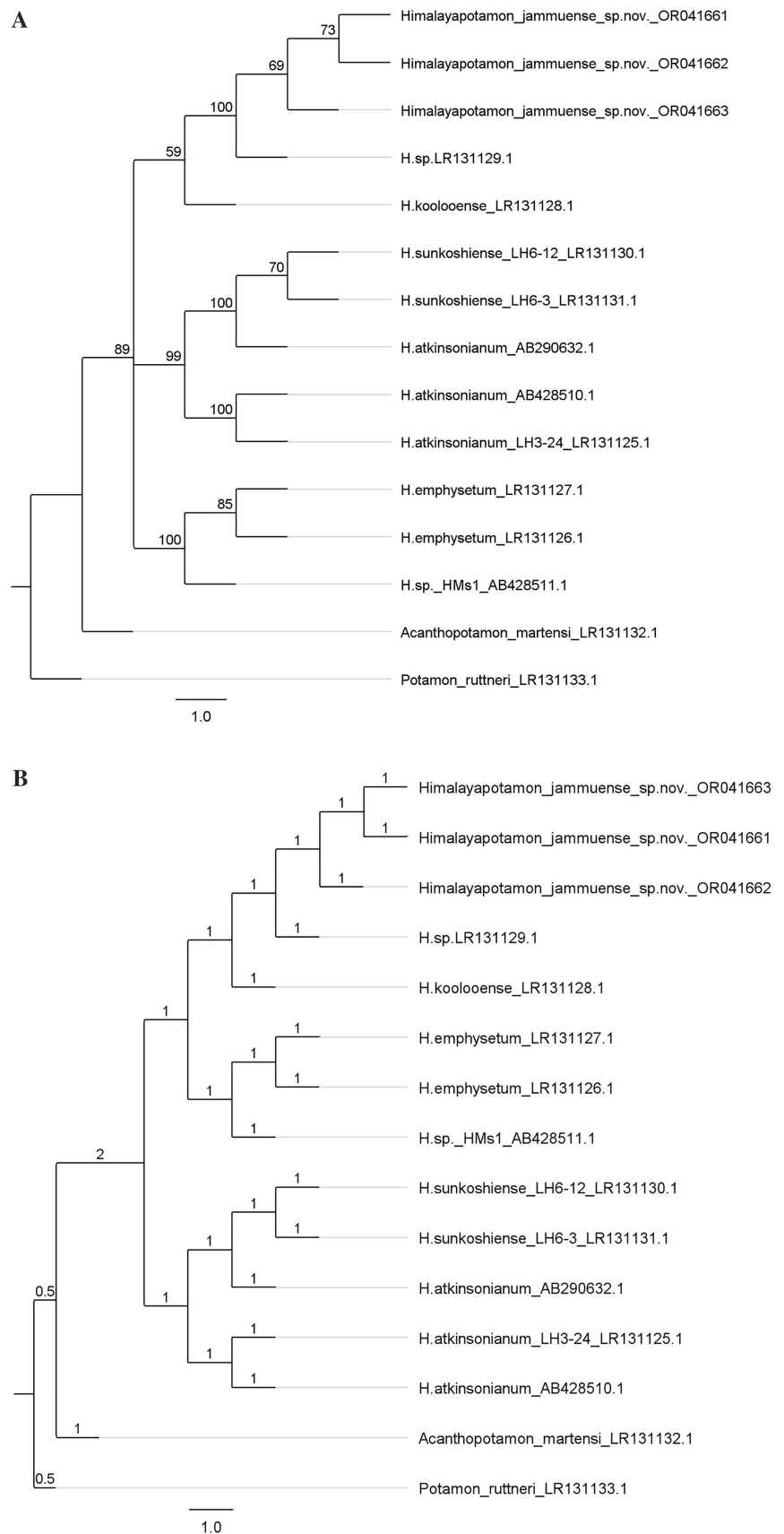


Fig. 7 (continued)

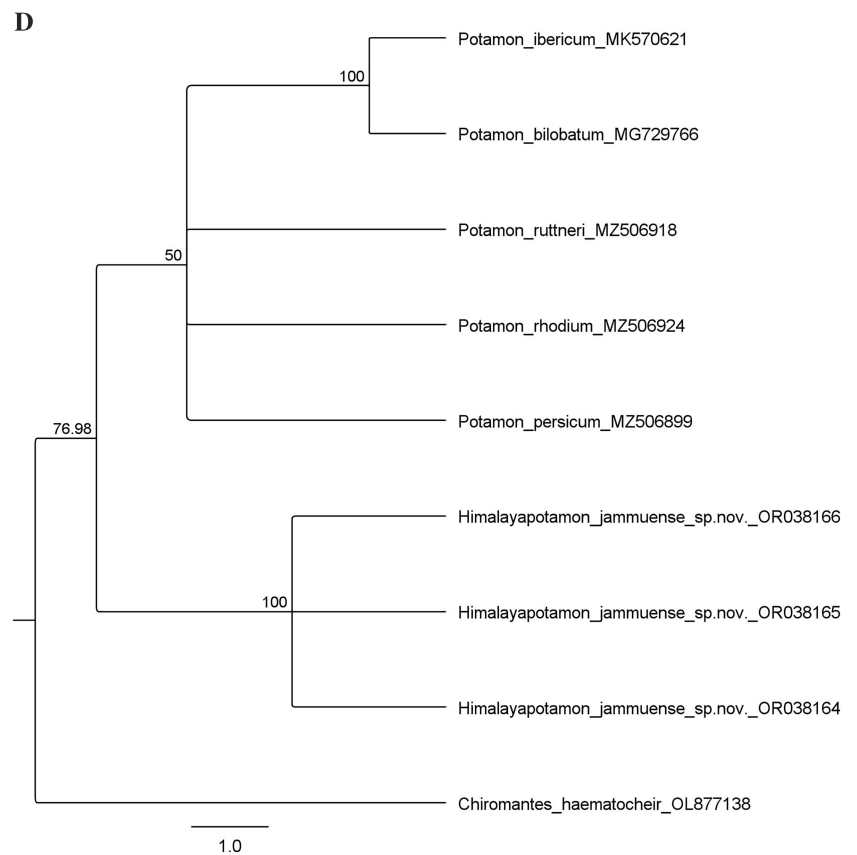
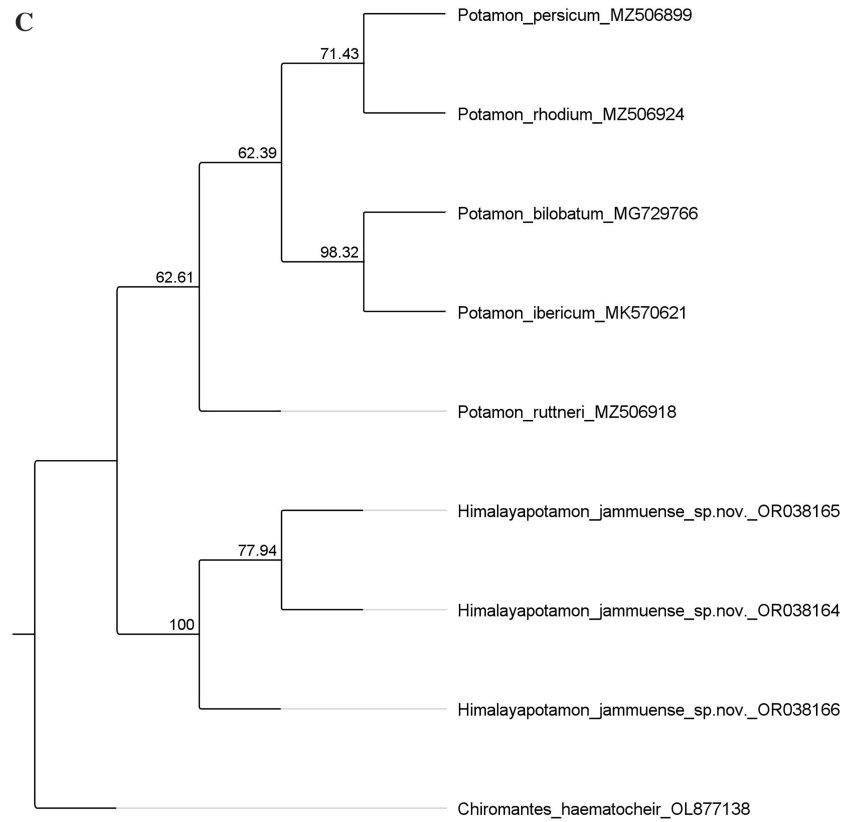
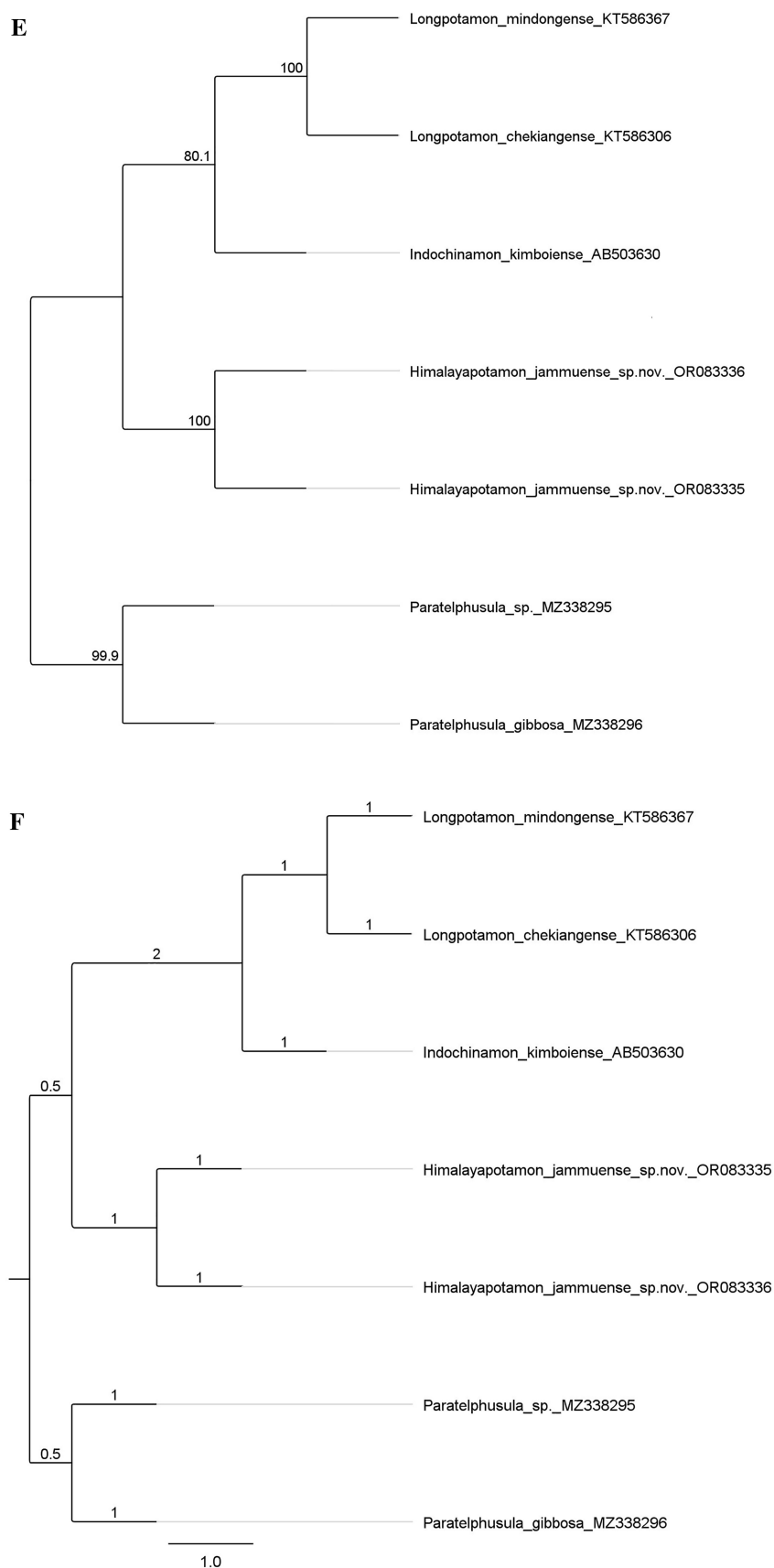


Fig. 7 (continued)



ML tree of 16s rRNA gene the new species can be seen forming a clade with *H. robertsonianum* and *H. koolooense* which are also biogeographically the nearest species of *Himalayapotamon*, *H. robertsonianum* towards western part of Jammu and Kashmir *i.e.*, from Muree Hills of Pakistan and *H. koolooense* towards the southern part of Jammu and Kashmir *i.e.*, Punjab, the next adjoining state. Important zoogeographical data regarding distribution of *Himalayapotamon* species within the Indus drainage has already been provided by Klaus and Brandis (2018). Thus, the present study strongly supports the theory put forth by the authors and fills the gap as suggested by them regarding presence of *Himalayapotamon* species within the range between *H. chambaensis*, *H. koolooense* and *H. robertsonianum*. The results interpreted correspond to the information generated only by 16s rRNA gene, but on the other hand other genes as *cox1* and 28s rRNA gene cannot be neglected as they can provide a better insight into the species level identification of various taxa. Thus, a wide range of molecular markers can be used so as to authenticate not only the species delimitation concept but also in better understanding of zoogeography and paleogeography of the organism.

Key to species of Genus *Himalayapotamon* Pretzmann 1966 (modified from Mitra and Valarmathi 2017).

1. Gonopod 1 terminal segment strongly bent outwards, relatively long and slender—— 2
- Gonopod 1 terminal segment straight or slightly bent outwards, relatively short and stout——3
2. Gonopod 1 terminal segment long, elongated, strongly bent outwards, up to 70–80° in mature male, Gonopod 2 distal segment strongly coiled, tip turned and very long——*H. emphysetum* (Mitra & Valarmathi 2017)
- Gonopod 1 terminal segment long, broadly triangular, Gonopod 2 distal segment hook-like, bent strongly——*H. marinelli* (Pretzmann 1963)
3. Gonopod 1 terminal segment bent outwards, conical, short, tapering at tip, Gonopod 2 terminal segment hook-like——*H. garhwalense* (Pati & Singh 2017)
- Gonopod 1 terminal segment somewhat bent outwards or straight, Gonopod 2 nearly straight——4
4. Short additional crest present between post-orbital cristae and epi-branchial corner, Gonopod 1 terminal segment blunt, triangular, convex inter distal part of subterminal segment, V-shaped flexible zone——*H. emphysetum* (Alcock 1909)
- Short additional crest present between post-orbital cristae and epi-branchial corner, Gonopod 1 terminal segment conical, stout, flexible zone U-shaped, subterminal segment broad——*H. jammuense*

Conclusion

In this study, we describe a new species of freshwater crabs from Poonch district of Jammu and Kashmir, Northern India. The species has been seen to be well within the definition of the genus *Himalayapotamon*, supported both by morphological and molecular characters.

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Author contributions Conceptualization: HK, SL, SM & NS. Data collection: HK. Diagnosis: HK. Original draft preparation: HK & NS. Finalization of manuscript: SL, SM, KRD & KN.

Data availability All the data generated in the current study has been presented either in the main text or in figures.

Declarations

Conflict of interest The authors declare that there is no conflict of interest.

Ethical approval No approval by an ethical committee was required to achieve the goals of the present study.

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