

A new species of *Curvemysella* T. Habe, 1959 (Bivalvia: Galeommatoidea) from the Yellow Sea, China

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Abstract. A new species of bivalve, *Curvemysella bajie* sp. nov. [八戒陷腹蛤] (Bivalvia, Galeommatoidea), is described, based on samples collected from Qingdao (Shandong, China). The intertidal zone of the China Yellow and Bohai Sea is home to a large number of *Blepharipoda liberata* (Shen, 1949), which often have clams attached to their bodies. Samples of *B. liberata* were collected from the intertidal zone of Golden Beach in Qingdao and examined for associated molluscs. In addition to description of the shell morphology of *C. bajie* sp. nov., molecular analysis based on four-gene combined dataset (18S + 28S + H3 + COI) also supports its phylogenetic position.

Key words. Qingdao, taxonomy, molecular phylogeny

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INTRODUCTION

Species of the superfamily Galeommatoidea are often found in symbiosis with other invertebrates (Boss 1965; Morton 1972; Ó Foighil 1985; Morton & Scott 1989; Kato 1998; Boyko & Mikkelsen 2002; Goto *et al.* 2007, 2012; Li *et al.* 2012). These galeommatids frequently coexist with crustaceans, and some can transfer hosts when the crustacean molts (Itani *et al.* 2002). The genus *Curvemysella* T. Habe, 1959, in particular, is commonly associated with hermit crabs and obtains protection, increased food availability, and oxygenated water from their hosts (Williams & McDermott 2004).

Habe (1959) established the genus *Curvemysella*, which currently has only one described species, *Curvemysella paula* (A. Adams, 1856). *Curvemysella paula* has a crescent-shaped shell and lives in gastropod shells occupied by hermit crabs. There has been little research on this genus. Goto *et al.* (2007) studied the obligate commensalism between *C. paula* and hermit crabs and concluded that *C. paula* does not affect the breeding and feeding of the crabs, but that the water flow generated by hermit crabs facilitates feeding in *C. paula*. Morton (2017) studied the biology and functional morphology of *C. paula* and found that it lives in small

groups, where the largest and oldest individual is female, the smallest and youngest is a male, and individuals with medium-sized shells are hermaphroditic.

The present study reports a new species of *Curvemysella* from Qingdao, Shandong, China, which is symbiotic with *B. liberata*, a species of mole crab. *Curvemysella bajie* sp. nov. mostly lives inside the gill chamber of this mole crab. Although the shell shape and living environment of the new species differ from those of *C. paula*, we confirmed the new species' position within *Curvemysella* by the irregular, concentric growth lines on the shell surface, the long lateral teeth in the right valve, and the equilateral, triangular foot. A molecular analysis based on a combined 4-gene dataset (18S + 28S + H3 + COI) also support the new species' phylogenetic position.

MATERIALS AND METHODS

Specimens from Golden Beach, Huangdao District, Qingdao, China, in April 2023 (Fig. 1) were collected by Yue Ming He and preserved in 95% ethanol. Photographs were taken with a SOPTOP SZX12 stereomicroscope and an OD500F camera (Sunny Optical Technology, Ningbo, China). The specimens are stored in the Museum of Biol-

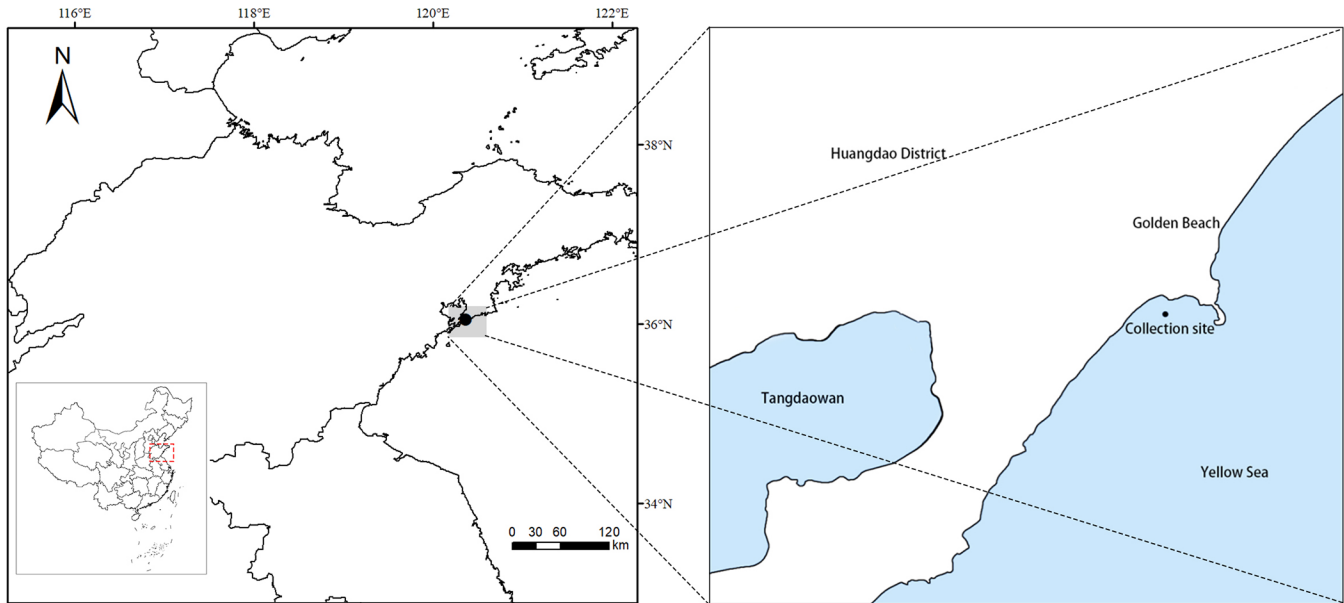


Figure 1. Known distribution and collection site of *Curvemysella bajie* sp. nov. at Qingdao, China.

ogy, Nanchang University (NCUMB), Nanchang 330031, China.

Total genomic DNA was extracted from tissue ethanol-preserved specimens using a Trelief TM Animal Genomic DNA kit (Tsingke Biotech Co. Ltd). Partial sequences of the 18S, 28S, H3 and COI genes were amplified using the following primers: 18Sa2.0, 18Sbi (Giribet *et al.* 1996) for 18S; D1 (Colgan *et al.* 2003) and D3 (Vonnemann *et al.* 2005) for 28S; H3F, H3R (Colgan *et al.* 1998) for H3; and LCO1490, HCO2198 (Folmer *et al.* 1994) for COI.

Each PCR reaction was performed in a total volume of 20 μ L, including 9 μ L of PCR mix, 8 μ L of double distilled water, 1 μ L of each primer and 1 μ L of the DNA template. The PCR conditions were as follows: initial denaturation at 95 $^{\circ}$ C for 3 min; 35 cycles of denaturation at 95 $^{\circ}$ C for 40 s, annealing at 55 $^{\circ}$ C for 30 s and extension at 72 $^{\circ}$ C for 30 s; and final extension at 72 $^{\circ}$ C for 7 min. Both ends of sequences were obtained by automated sequencing using Applied Biosystems 3730 in Sangon Biotech Co. Ltd. (Shanghai, China). To clarify the generic relationship of this new species, sequences of 56 specimens representing 34 genera downloaded from GenBank and 11 sequences generated in this study were used for following molecular phylogenetic analysis (Table 1). Sequences were aligned using MAFFT v. 7.505 based on the L-INS-i method (Katoh & Standley 2013). Gap sites were removed with trimAl v. 1.2rev57 (Capella-Gutiérrez *et al.* 2009) using the “-automated1” command. Genetic distances were calculated using MEGA X (Kumar *et al.* 2018).

The best substitution model was selected using the Bayesian Information Criterion (BIC) in ModelFinder v. 2.2.0 (Kalyaanamoorthy *et al.* 2017). Bayesian-inference and maximum-likelihood analyses were performed using MrBayes v. 3.2.7 (Ronquist *et al.* 2012) and IQ-TREE v. 2.2 (Minh *et al.* 2020), respectively, with reference to the selected model of sequence evolution. We performed the 2 million generations of the Metropolis-coupled Markov chains (one cold chain) for Bayesian-inference phylogenetics, with sampling every 1,000 generations. The first 25% of sampled trees were discarded as burn-in when the standard deviation of split frequencies of the two runs was less than 0.01; the remaining trees were then used to create a 50% majority-rule consensus tree and to estimate Bayesian posterior probabilities (BPP). For maximum likelihood, we generated 10 starting trees using IQ-TREE and then performed branching swapping. Node support for maximum-likelihood phylogenetics was determined using 1000 rapid bootstrap (BS) replicates.

RESULTS

Molecular data

The alignments of 18S, 28S, H3, and COI sequences are 2019, 1181, 329, and 658 bp, respectively. The GTR+F+I+G4 model was selected as the best-fit of nucleotide substitution by the BIC criterion. The 18S, 28S, H3, and COI *p*-distances between the new species and *C. paula* are 0.5%, 3.3%, 2.6%, and 19.8%, respectively.

Table 1. List of species used for molecular phylogenetic analyses, with their GenBank accession numbers. Accession numbers with an asterisk indicate the sequences obtained in this study.

Family	Species	18S rRNA	28S rRNA	H3	COI
Galeommatidae	<i>Anisodevonia ohshimai</i>	AB714754	AB714797	AB714838	AB714878
	<i>Arthritica japonica</i>	AB714755	AB714798	AB714839	AB714879
	<i>Basterotia carinata</i>	AB714780	AB714823	AB714861	AB714902
	<i>Basterotia gouldi</i>	AB714781	AB714824	AB714862	AB714903
	<i>Basterotia</i> sp. 1	AB714782	AB714825	AB714863	AB714904
	<i>Borniopsis</i> aff. <i>ariake</i>	AB714776	AB714819	AB714858	AB714899
	<i>Borniopsis</i> aff. <i>nodosa</i>	AB714777	AB714820	AB714859	AB714900
	<i>Borniopsis macrophthalmensis</i>	AB714775	AB714818	AB714857	AB714898
	<i>Borniopsis ochetostomae</i>	AB714773	AB714816	AB714855	—
	<i>Borniopsis subsinuata</i>	AB714774	AB714817	AB714856	AB714897
	<i>Borniopsis yamakawai</i>	AB714756	AB714799	AB714840	AB714880
	<i>Brachiomya stigmatica</i>	AB714753	AB714796	—	AB714877
	<i>Curvemysella paula</i>	AB714757	AB714800	AB714841	AB714881
	<i>Curvemysella paula</i>	—	KX376110	KX375846	—
	<i>Curvemysella bajie</i> sp. nov.	PQ451482*	PQ452780*	PQ473526*	PQ451479*
	<i>Curvemysella bajie</i> sp. nov.	PQ451483*	PQ452781*	PQ473527*	PQ451480*
	<i>Curvemysella bajie</i> sp. nov.	—	PQ452782*	PQ473528*	PQ451481*
	<i>Devonia semperi</i>	AB714758	AB714801	AB714842	AB714882
	<i>Divariscintilla toyohiwakensis</i>	AB714745	AB714788	AB714831	AB714869
	<i>Entovalva lessonothuriae</i>	AB714759	AB714802	AB714843	AB714883
	<i>Ehippodonta gigas</i>	AB714746	AB714789	AB714832	AB714870
	<i>Galeomma</i> sp. 1	AB714747	AB714790	AB714833	AB714871
	<i>Kellia porculus</i>	AB714760	AB714803	AB714844	AB714884
	<i>Koemya setoensis</i>	AB907562	AB907568	AB907573	AB907574
	<i>Koemya arcuata</i>	AB907557	AB907563	AB907569	AB474955
	<i>Kurtiella</i> aff. <i>bidentata</i>	AB714765	AB714808	—	AB714889
	<i>Kurtiella bidentata</i>	KF741629	KF741655	—	—
	<i>Kurtiella pedroana</i>	—	KX376195	KX375917	—
	<i>Kurtiella tumida</i>	—	KX376206	KX375841	—
	<i>Lasaea undulata</i>	AB714761	AB714804	AB714845	AB714885
	<i>Litigiella pacifica</i>	AB714762	AB714805	AB714846	AB714886
	<i>Melliteryx puncticulata</i>	AB714763	AB714806	AB714847	AB714887
	<i>Montacutona sigalionidcola</i>	LC485247	LC485248	LC485249	LC485250
	<i>Montacutona japonica</i>	—	KX376107	KX375844	—
	<i>Montacutona</i> sp.	AB714764	AB714807	AB714848	AB714888
	<i>Mysella charcoti</i>	KC429372	KC429474	KC429205	—
	<i>Mysella</i> sp.1	—	KX376208	KX375946	—
	<i>Mysella vitrea</i>	AM774519	AM779693	KX375945	—
	<i>Neaeromya rugifera</i>	AB714766	AB714809	AB714849	AB714890
	<i>Nipponomontacuta actinariophila</i>	AB714767	AB714810	AB714850	AB714891
	<i>Nipponomysella oblongata</i>	AB714768	AB714811	AB714851	AB714892
	<i>Nipponomysella subtruncata</i>	AB714769	AB714812	AB714852	AB714893
	<i>Paraborniola matsumoto</i>	AB714770	AB714813	AB714853	AB714894
	<i>Peregrinamor gastrochaenans</i>	AB714771	AB714814	—	AB714895
	<i>Peregrinamor ohshimai</i>	AB714772	AB714815	AB714854	AB714896
	<i>Platomysia rugata</i>	LC126833	LC126832	—	—

Table 1. Continued.

Family	Species	18S rRNA	28S rRNA	H3	COI
Galeommatidae	<i>Pseudogaleomma</i> sp. 1	AB714748	AB714791	AB714834	AB714872
	<i>Pythina deshayesiana</i>	AB714778	AB714821	—	—
	<i>Salpocola philippinensis</i>	AB714779	AB714822	AB714860	AB714901
	<i>Scintilla</i> aff. <i>hydatina</i>	AB714750	AB714793	AB714835	AB714874
	<i>Scintilla rosea</i>	AB714749	AB714792		AB714873
Veneridae	<i>Irus mitis</i>	AB714785	AB714828	AB714866	AB714906
Mactridae	<i>Meropesta nicobarica</i>	AB714786	AB714829	AB714867	—
Solecurtidae	<i>Azorinus minutus</i>	AB714783	AB714826	AB714864	AB714905
Solenidae	<i>Solen strictus</i>	AB714787	AB714830	AB714868	AB714907
Gastrochaenidae	<i>Gastrochaena cuneiformis</i>	AB714784	AB714827	AB714865	—

The phylogenetics indicates that *Curvemysella* is a monophyletic group with full support (BPP = 1.00, BS = 100) and *C. bajie* n. sp. is sister to the type species, *C. paula*. *Curvemysella* is sister to *Montacutona* + *Nipponomysella oblongata* (Yokoyama, 1922) with strong support (BPP = 1.00, BS = 97) (Fig. 2). All genera involved in this study are monophyletic, except for species of the genera

Borniopsis T. Habe, 1959, *Scintilla* Deshayes, 1856, *Montacutona* G. Yamamoto & T. Habe, 1959, *Nipponomysella* G. Yamamoto & T. Habe, 1959, *Kurtiella*, and *Mysella* Angas, 1877.

Systematics

Superfamily Galeommatoidae J.E. Gray, 1840

Family Galeommatidae *sensu* Ponder, 1998

Genus *Curvemysella* T. Habe, 1959

Type species. *Pythina paula* A. Adams, 1856 by original designation.

Curvemysella bajie Chen & He sp. nov.

Figures 2–6

ZooBank registration. urn:lsid:zoobank.org:act:82337D D1-468D-406E-925E-DA14410D9CD3

Type locality. China, Shandong, Qingdao County [青岛市], Huangdao District [黄岛区], Golden Beach [金沙滩], 35.9548°N, 120.2465°E (Fig. 1), collected by Yue Ming He, 2023.x.4.

Type materials. Holotype (Fig. 3): shell length 7.63 mm, shell height 6.32 mm; NCUQD23601.

Paratypes: 4 shells, shell length 6.44–7.63 mm, shell height 5.26–6.32 mm, NCUQD23602–05; locality and habitat as for the holotype.

Diagnosis. Shell subovate to subtrigonal, with ventral mar-

gin slightly convex, slightly inflated, equivalve, with faint commarginal growth lines. In right valve, anterior lateral tooth anteriorly slightly curved, and the teeth gradually disappear as they extend to the top of the shell. Foot short and thick, triangular.

Description. Shell (Figs 3, 4) subovate to subtrigonal, with ventral margin slightly convex, thin, small (shell length 2.95–8.75 mm, shell height 2.16–7.24 mm) and fragile. Outer shell surface dark brown but slightly yellow; prodissoconch lens-shaped, slightly inflated, with faint commarginal growth lines, located slightly posterior to mid-length of shell. Posterior end shorter than anterior end; posteroventral margin rounded but incurved slightly near prodissoconch. Right valve hinge tooth delimiting with dorsal shell margin two grooves to accommodate margin of opposite valve. In right valve, anterior lateral tooth anteriorly slightly curved and the teeth gradually disappear as they extend to the top of the shell; posterior lateral tooth smaller; convex tooth of the left valve not obvious (Fig. 5A, B). Ligamental pit deeply recessed.

Body yellowish white, without tentacles. Anterior and posterior adductor muscles ovate. Labial palps small. Foot short and thick, triangular, and white (Fig. 5C).

Etymology. The specific name “bajie” originates from the name of “Ba-Jie Zhu”, a character in an ancient Chinese mythological novel, who is lazy, loves to eat, and was appointed by Buddha as the manager to clean the altar; the position is dedicated to eating food delivered by Buddhist devotees. The name alludes to the fact that the new species obtains food from its hosts. We suggest the Chinese common name 八戒陷腹蛤.

Habitat and distribution. This species lives in the fine sand of intertidal beaches in symbiosis with a species of mole crab, *B. liberata* (Figs 5D–F, 6A–D). Most of specimens of *C.*

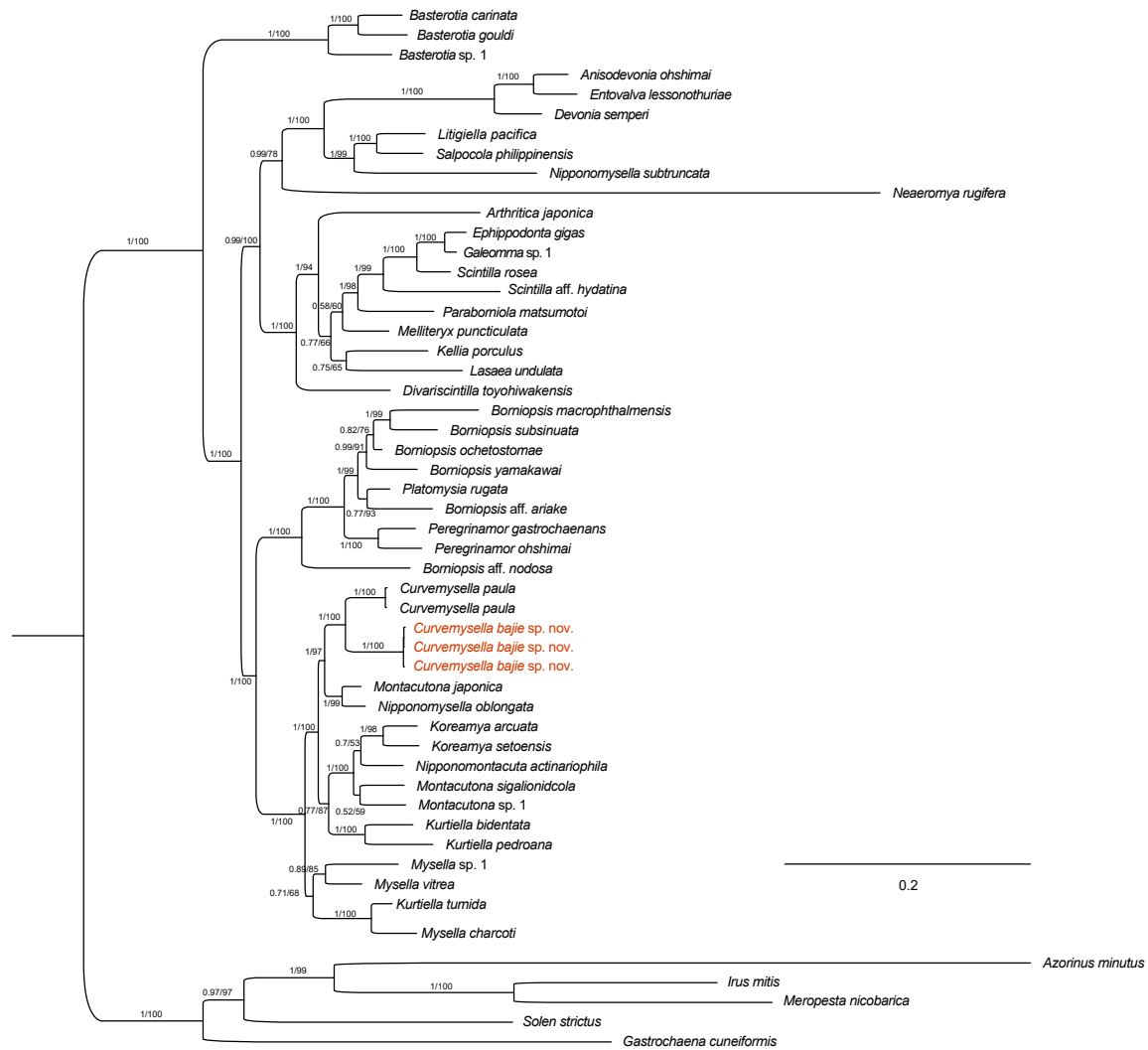


Figure 2. Bayesian phylogenetic tree based on the combined dataset of 18S, 28S, H3 and COI genes. Numbers above branches indicate Bayesian posterior probabilities followed by maximum-likelihood bootstrap support values.

bajie were found in the gill chambers of *B. liberata*, with only a few attached to the ventral surfaces of *B. liberata*. Specimens of *C. bajie* living in the gill chambers were significantly larger than those on the ventral surfaces.

This species is known from the type locality only.

Remarks. *Curvemysella bajie* has a subovate to subtrigonal shell, which easily distinguishes it from the crescent-shaped *C. paula*. The new species also has protruding and cracked lateral teeth, while *C. paula* lacks lateral teeth. The shell of *C. paula* is ventrally concave and inequivalve, whereas the ventral margin is convex and the shell is equivalve in *C. bajie*.

DISCUSSION

The phylogenetic topologies that the family Galeommataceae formed a monophyletic and divided into five large lin-

eages, species of genus *Basterotia* M. Hörnes, 1859 form a monophyletic group and falls to the base of the tree; species of genus *Koemya* Lützen, Hong & Yamashita, 2009, *Nipponomontacuta*, *Montacutona*, *Kurtiella*, *Curvemysella* and *Mysella* were nested in a monophyletic group and sister to the lineages including species of genus *Borniopsis*, *Platomyssia* T. Habe, 1951, and *Peregrinamor* K. Shôji, 1938. Species of genus *Arthritica* H. J. Finlay, 1926, *Ehippodonta* R. Tate, 1889, *Galeomma* W. Turton, 1825, *Scintilla*, *Paraborniola* T. Habe, 1958, *Melliteryx* T. Iredale, 1924, *Kellia* W. Turton, 1822, *Lasaea* T. Brown, 1827, and *Divariscintilla* A.W.B. Powell, 1932 were nested in a monophyletic group and sister to the lineages including species of genus *Anisodevonia* M. Kato, 1999, *Entovalva* A. Voeltzkow, 1890, *Devonia* N.N. Winckworth, 1930, *Litigiella* T.A. di. Monterosato, 1909, *Salpocola* Lützen, Kosuge & Jespersen, 2008 and *Neaeromya*

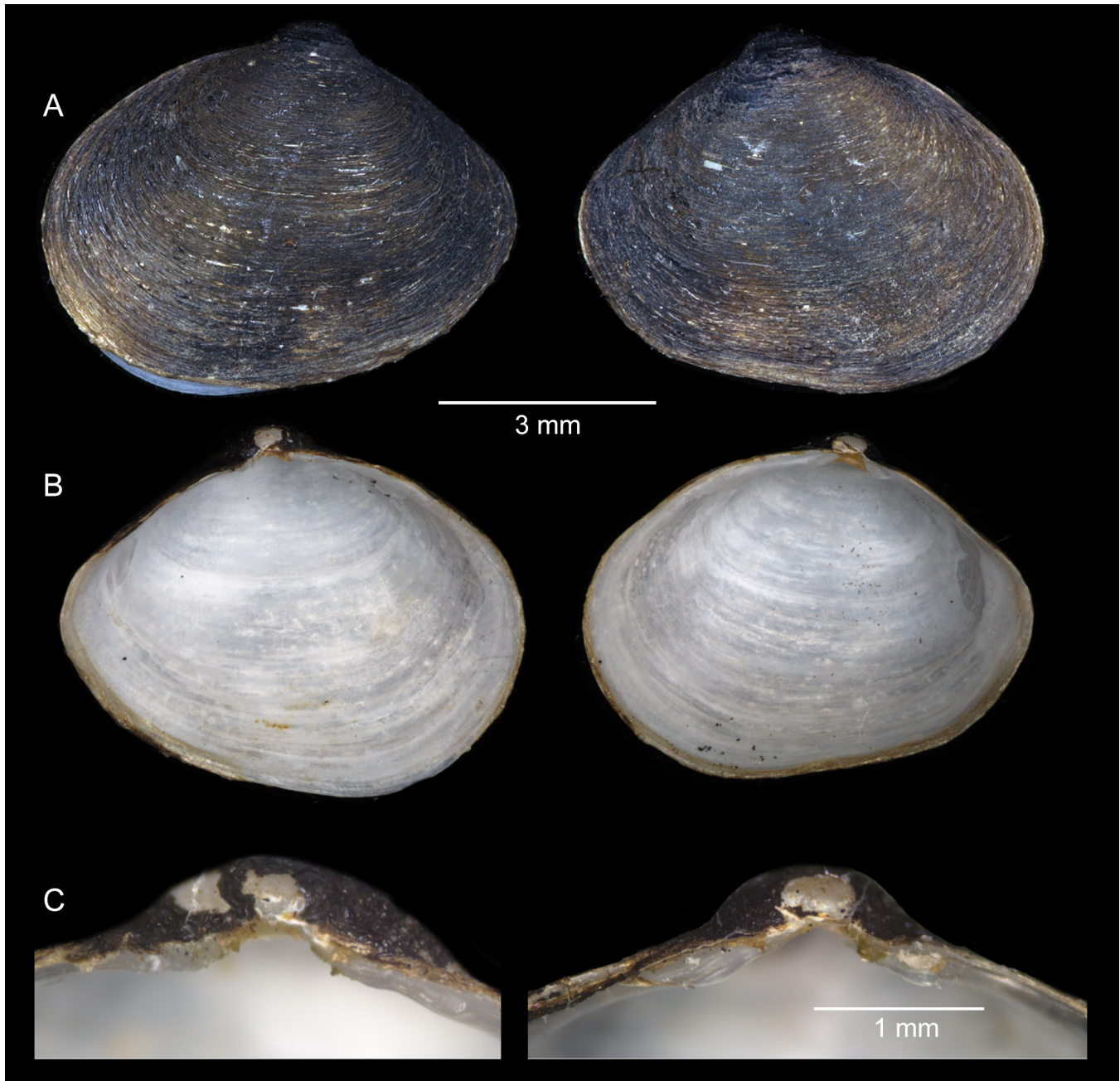


Figure 3. *Curvemysella bajie* sp. nov. Shells: holotype NCUQD23601. **A**, outer surface of left and right valve. **B**, inner surface of left and right valve. **C**, hinge structure of left and right valves. Scale bar A, B = 3 mm, C = 1 mm.

W.M. Gabb, 1873. The phylogenetic topologies here are similar to Goto *et al.* (2019); however, the inner relationships of Galeommatidae differ slightly. Such as *Arthritica japonica* is sister to *Lasaea undulata* in Goto *et al.* (2019), but in our study the phylogenetic relationship between *A. japonica* and *L. undulata* is relatively distant and *L. undulata* is sister to *Kellia porculus*. This may be due to the partition model and choice of software. Gato *et al.* (2019) suggest that genus *Koreamya* Lützen, Hong & Yamashita, 2009 and

Nipponomontacuta Yamamoto & Habe, 1959 are synonyms of *Montacutona* Yamamoto & Habe, 1959, which consistent with the phylogenetic tree of this study. However, *M. japonica* does not form a monophyletic group with *M. sigalionicola* in this study. Other genera appear to be paraphyletic or polyphyletic including *Borniopsis*, *Kurtiella*, *Mysella*, and *Scintilla*. This may be due to the simple classification that used to be based only on the morphology of shells. Therefore, a more comprehensive anatomy and genetic analyses

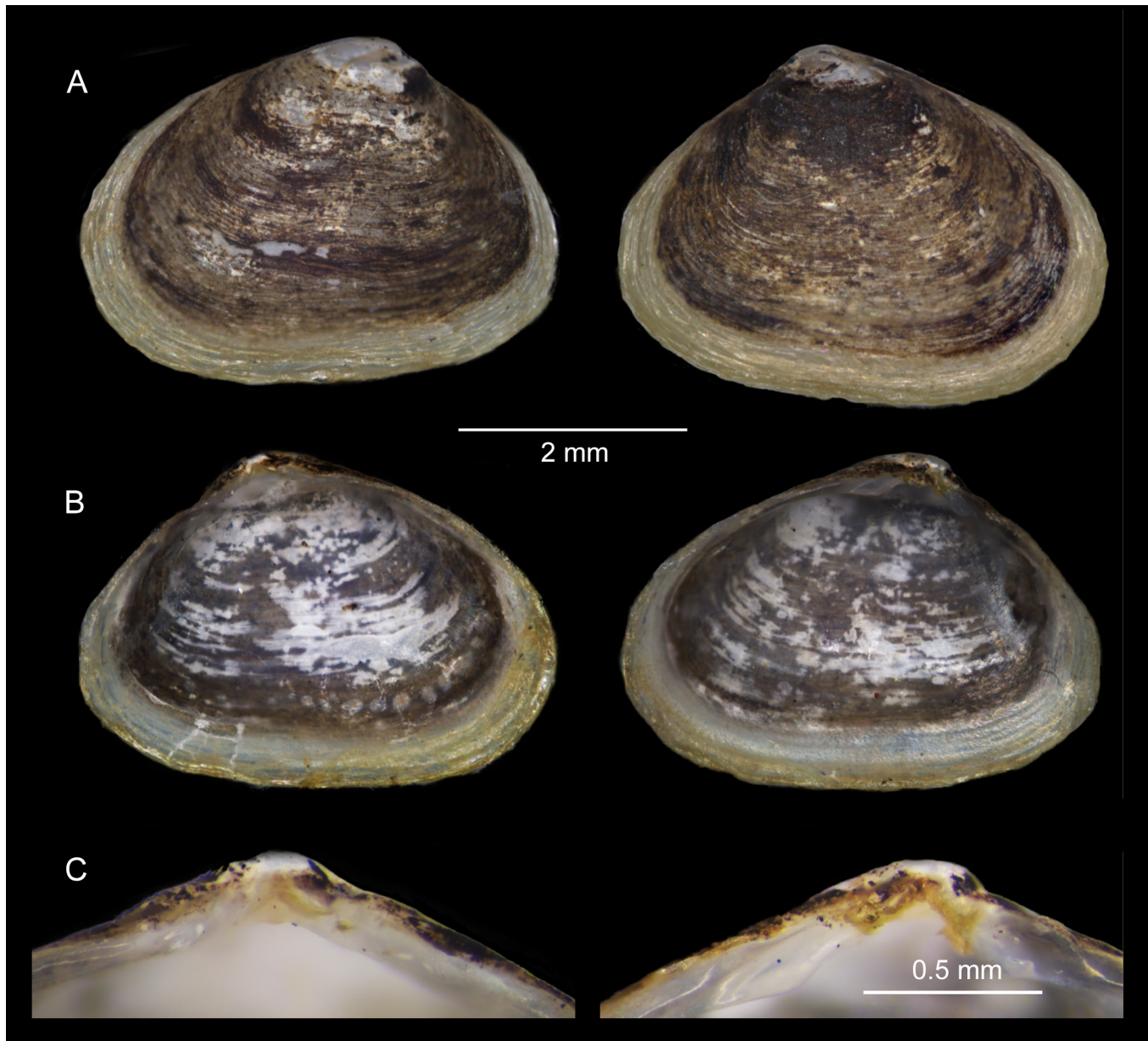


Figure 4. *Curvemysella bajie* sp. nov. Subadult shells. **A**, outer surface of left and right valve. **B**, inner surface of left and right valve. **C**, hinge structure of left and right valves. Scale bar A, B = 2 mm, C = 0.5 mm.

are important to better addressing the relationships between species of these genera.

Both molecular and morphological evidence support the new species taxonomic status. The molecular phylogenies analyses show that *C. bajie* is sister to *C. paula*, forming a monophyletic group with full support (BPP = 1, BS = 100), and sister to *Nipponomysella oblongata* and *Montacutona japonica*. Species of *Curvemysella* possess irregular, concentric growth lines on the outer shell surface and a small, triangular resilifer below the beaks. The right valve has a long

lateral tooth, whereas the left valve is nearly edentulate. The foot resembles an equilateral triangle, and the mantle is smooth. However, due to the different hosts of parasitism, the shell morphology of species in the genus *Curvemysella* may vary. The shape of *C. paula* is specialized to adapt to its hermit crab host (to fit snugly onto the snail axis), so its form may not be well-suited for other species within the genus that do not live in association with hermit crabs, such as the new species *C. bajie* sp. nov. In this case, a crescent-shaped shell may not provide much assistance.

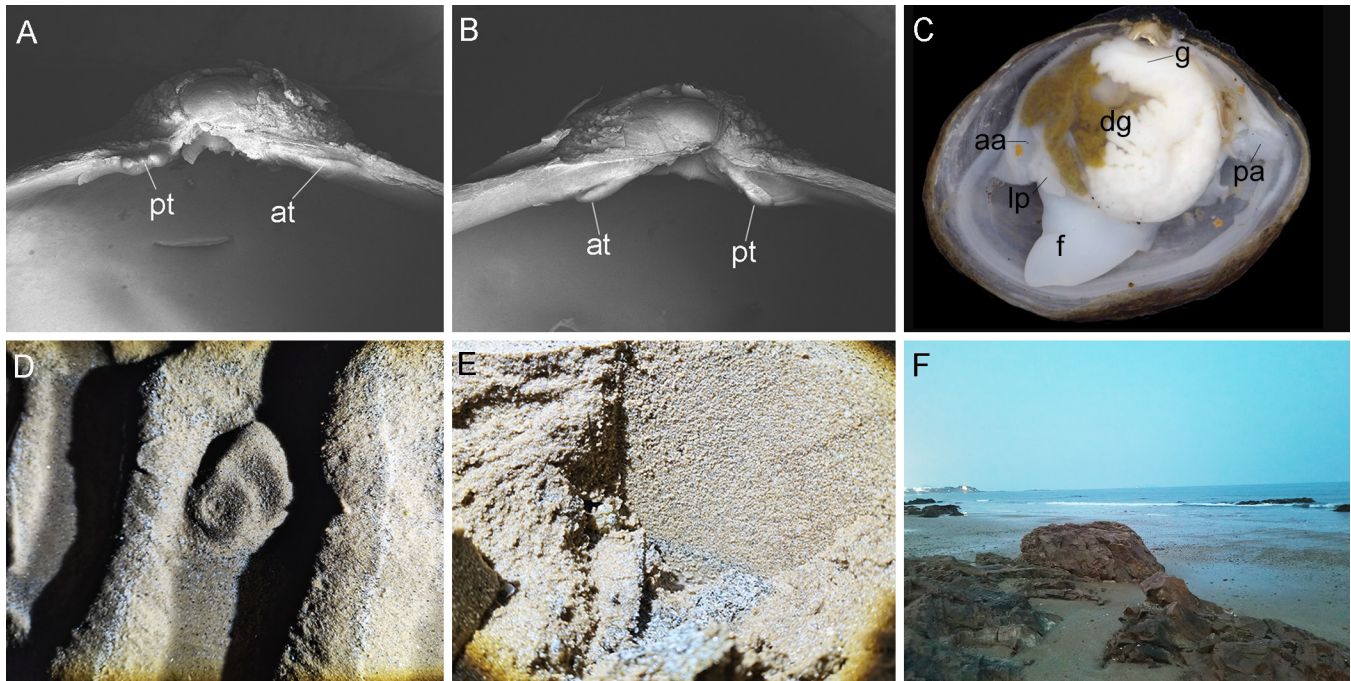


Figure 5. Hinge, body, and habitat of *Curvemysella bajie* sp. nov. **A, B**, hinge structure of left and right valves. **C**, anatomy. **D, E**, *Blepharipoda liberata* burrow. **F**, natural habitat. Abbreviations: aa, anterior adductor muscle; at, anterior lateral tooth; dg, digestive gland; f, foot; g, gonad; lp, labial palp; pa, posterior adductor; pt, posterior lateral tooth.

Observations were made on *B. liberata* reared in the laboratory. When *B. liberata* molt their exoskeleton, individuals located in the gill chamber are less prone to shed, so they

have a more stable growth environment. In clams reared alone, some clams died after a week, while those live in symbiosis with *B. liberata* can survive more than a year. Due to space limitations, many large individuals have certain deformities. Most specimens do not have byssal threads, and more individuals in the gill chamber than lateroventral surfaces. This is similar to the observation results of Bhaduri *et al.* (2017) on *Kurtiella pedroana* (Dall, 1899). This may allow them to receive the water flow efficiently for breathing and filtering (Goto *et al.*, 2019). We also found a small amount of *Kurtiella* sp. on *B. liberata*. We have not found this *Kurtiella* on other crustaceans and have not found them free-living.

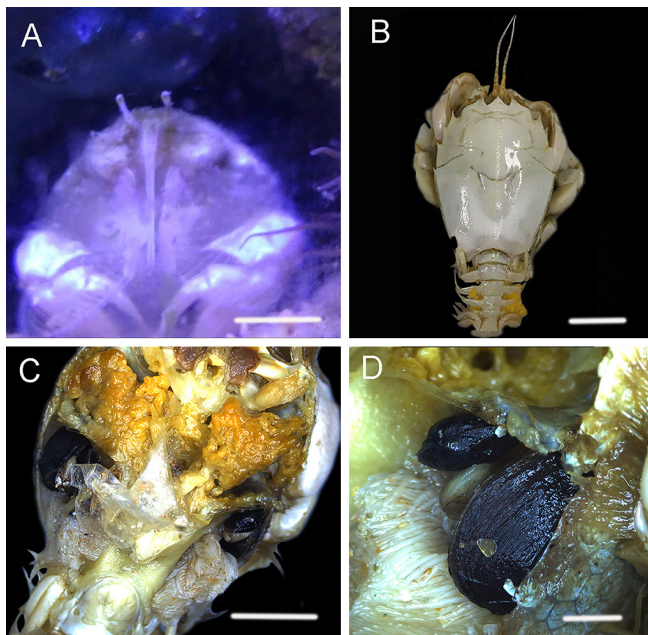


Figure 6. *Curvemysella bajie* sp. nov. and its host, *Blepharipoda liberata*. **A**, living state of *B. liberata*. **B–D**, *B. liberata* with *C. bajie* attached. Scale bars: A = 5 mm, B = 10 mm, C = 5 mm, D = 2 mm.

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