

# A New Species of the Intertidal Limpet *Eoacmaea* (Patellogastropoda: Eoacmaeidae) from Yonaguni Island, Japan and Taiwan

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A new species of intertidal limpet was identified from Yonaguni Island, Japan and southern Taiwan in the present study and described as *Eoacmaea nivea* n. sp. It was previously reported by different authors as *Cellana mauritiana*, or as Acmaeid sp. in Taiwan, and as *Patelloida* sp. in Yonaguni Island, Japan. Based on detailed morphological observations and molecular analyses (COI), *E. nivea* n. sp. is distinguished from other *Eoacmaea* species. *Eoacmaea nivea* n. sp. is presently known from southern Taiwan, and a population on Yonaguni Island, Japan that is very limited. The present study reports a total 11 species of patellogastropod limpet species in Taiwan. The seven species—*Cellana grata*, *Cellana toreuma*, *Nipponacmea nigrans*, *Nipponacmea fuscoviridis*, *Lottia dorsuosa*, *Lottia luchuana* and *Lottia tenuisculpta*—were found in the intertidal on rocky shores along the north to northeastern shores of Taiwan. The five species—*Cellana radiata*, *Lottia luchuana*, *Scutellastra flexuosa*, *Patelloida saccharina* and *E. nivea* n. sp.—can be found mostly within depressions in limestone substrate in southeastern Taiwan. Of these, only *Lottia luchuana* is found throughout Taiwan, and overall has a tropical, not warm-temperate, distribution.

**Key words:** Mollusca, Gastropoda, Limestone, Biogeography, Patellogastropoda.

## BACKGROUND

The limpets belonging to the order Patellogastropoda are common inhabitants of intertidal rocky shores throughout the world oceans, typically as important grazers in intertidal systems (Branch 1985a b). The genus *Eoacmaea* was earlier referred to as the *Patelloida profunda* group (Christiaens 1975; Lindberg and Vermeij 1985). Nakano and Ozawa (2007) revealed that this group is different from other species of the genus *Patelloida* both morphologically and genetically and designated it as a new genus *Eoacmaea* (Nakano and Ozawa 2007). Furthermore, *Eoacmaea* was found to be a basal branch among the recent Patellogastropoda. The

new family Eoacmaeidae was established for this genus (Nakano and Ozawa 2007). However, there are long branch attraction problems due to the long insertions and deletions in Lottioidea of Patellogastropoda to construct the phylogenetic tree (Uribe et al. 2019; Ponder et al. 2020). Although the distinct mt genome organization of *Eoacmaea* is reported (Uribe et al. 2019), the placement of this family is still debated (Uribe et al. 2019; Ponder et al. 2020).

Eoacmaeid limpets formerly assigned as *Patelloida profunda* group are limited to limestone in high to supratidal zone and widely distributed in South Africa, Indo-Pacific and Caribbean. The highest diversity of eoacmaeid limpets can be found in the Indo-West Pacific

(Christiaens 1975; Ponder and Creese 1980; Lindberg and Vermeij 1985; Kirkendale and Meyer 2004). A molecular phylogenetic analysis of the genus *Eoacmaea* based on the two mitochondrial genes, 16S and *COI* has been conducted and results revealed that *Eoacmaea* is genetically highly differentiated in each island and likely harbors undescribed species especially in Indo-West Pacific (Kirkendale and Meyer 2004). Among this undescribed diversity, so far only *Eoacmaea javanica* has been described from Java, Indonesia (Nakano et al. 2005).

The present study describes a new species of *Eoacmaea* from Yonaguni Island, Japan and Taiwan (Kosuge and Sasaki 2002) based on molecular data and detailed morphological and anatomical characters. This species was previously reported as *Cellana mauritiana*,

or as *Acmaeid* sp. in Taiwan (Oyama and Takemura 1959; Takenouchi 1993), and as *Patelloida* sp. in Yonaguni Island, Japan (Kosuge and Sasaki 2002).

## MATERIALS AND METHODS

### Sample collections

Limpets were collected at intertidal shores from Yonaguni Island, Japan. In Taiwan, limpets were collected from Yeliu in northern coastline to Kenting in southern coastline (Fig. 1). The new *Eoacmaea* species described here was collected from the high intertidal to supratidal zones at two localities, the outlying Pacific Island, Green Island and at Jialershui, southern Taiwan.

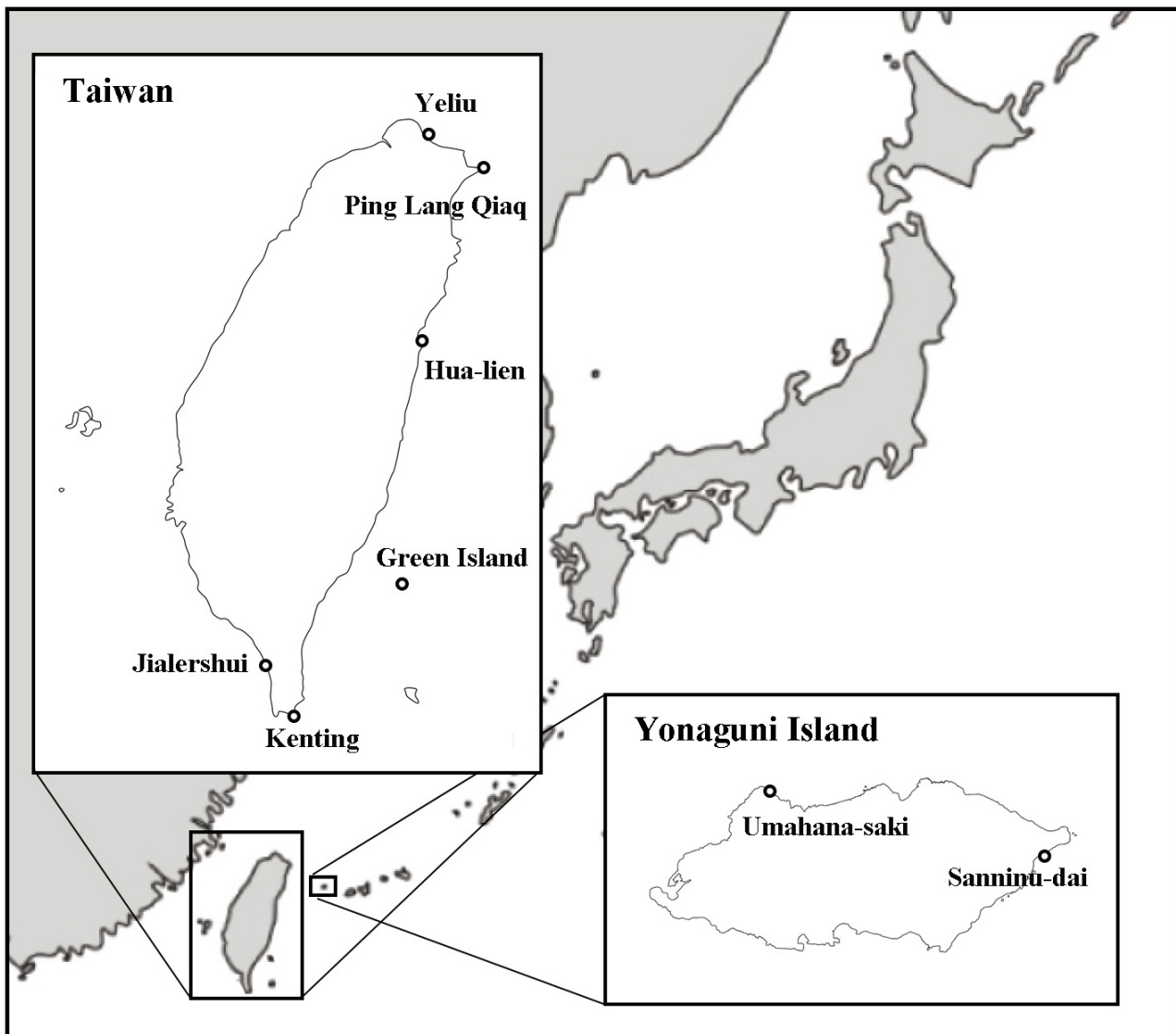


Fig. 1. Collection localities of *Eoacmaea nivea* n. sp. in southeastern Asia.

Living specimens were preserved in 95% ethanol. Details of the specimens are listed in table 1.

### DNA extraction, PCR amplification and DNA sequencing

The protocol of DNA extraction, PCR amplification for *COI* and DNA sequencing followed Nakano and Ozawa (2007).

### Phylogenetic analyses

Sequences were assembled and edited using ATGC. Sequences of *COI*, which lacked any indels across the data set, were aligned manually using MacClade 4.03 (Maddison and Maddison 2002), referring to translated amino acid sequences.

Phylogenetic trees were constructed with neighbour-joining (NJ) (Saitou and Nei 1987), maximum parsimony (MP) (Felsenstein 1988) and Bayesian methods (Ronquist and Huelsenbeck 2003). Bayesian analysis was performed by MrBayes v. 3.1.2 (Ronquist and Huelsenbeck 2003). The choice of substitution model used in Bayesian phylogenetic analyses, GTR + I + G, was selected using MrModelTest v.2.1 (Nylander 2004).

The NJ bootstrap analysis consisted of 10,000 replicates. The MP bootstrap analysis comprised 1,000 replicates of a heuristic search with 10 random

addition sequence replicates and TBR branch-swapping. MrBayes was run with the following settings (nst = 6, rate = invgamma, mcmc ngen = 10,000,000). Trees were sampled every 100 generations. The first 10% of trees were discarded as burn-in.

### Anatomy and radular morphology

The radula from [paratype specimen RM28705] was dissected and placed in 10% KOH at approximately 60°C for 5 min and rinsed in distilled water. The radula was examined by scanning electron microscope (SEM). Terminology used in the morphological description is adopted from Lindberg and Vermeij (1985) and Nakano et al. (2005).

## RESULTS

### Molecular data

In total, seven specimens were newly sequenced in this study. The aligned dataset of 658 bp characters including the outgroup species, *Patella caerulea*, *P. ferruginea* and *P. vulgata*, had 297 variable and 247 parsimony-informative characters. There were no indels across the data sets. All sequences obtained in this study have been deposited in GenBank under Accession numbers (LC598472–LC598478) (Table 1).

**Table 1.** Species identification, localities, voucher numbers and GenBank accession numbers for specimens genetically analyzed in this study

Species	Locality	Specimen voucher	Accession number	DNA-ID
<i>Eoacmaea nivea</i> n. sp.	Umahana-saki, Yonaguni Island, Okinawa, Japan	UMUT-RM28704	LC598472	L708
	Sanninu-dai, Yonaguni Island, Okinawa, Japan	UMUT-RM28705	LC598473	L709
	Umahana-saki, Yonaguni Island, Okinawa, Japan	UMUT-RM28706	LC598474	L710
	Green Island, Taiwan	SMBL-V0595	LC598475	L826
	Green Island, Taiwan	SMBL-V0596	LC598476	L827
	Green Island, Taiwan	SMBL-V0597	LC598477	L828
	Jialershui, Taiwan	ASIZM0001712	LC598478	L1104
<i>Eoacmaea javanica</i> (Nakano, Aswan & Ozawa, 2005)	Sedekan Beach, Java, Indonesia	NUGB-L558	AB238506	L526
<i>Eoacmaea conoidalis</i> (Pease, 1868)	Cook Islands	UF296033	AB238505	L603
<i>Eoacmaea</i> ESU 1	Zanzibar	UF296016	AB238511	L601
<i>Eoacmaea mauritiana</i> (Pilsbry, 1891)	Mauritius	UF296014	AB238510	L626
<i>Eoacmaea albonotata</i> (Smith, 1901)	South Africa	UF295658	AB238508	L605
<i>Eoacmaea profunda</i> (Deshayes, 1863)	Reunion	UF295652	AB238507	L607
<i>Eoacmaea omanensis</i> (Christiaens, 1975)	Gulf of Oman	UF295654	AB238509	L609
<i>Patella caerulea</i> Linnaeus, 1758	Ceuta, Spain	NUGB-L653	AB238577	L653
<i>Patella ferruginea</i> Gmelin, 1791	Ceuta, Spain	NUGB-L655	AB238578	L655
<i>Patella vulgata</i> Linnaeus, 1758	Millport, UK	NUGB-L340	AB238580	L340

Abbreviations: UMUT; The University Museum, The University of Tokyo. SMBL; Seto Marine Biological Laboratory, Kyoto University. ASIZ; Biodiversity Research Museum, Academia Sinica.

**Molecular phylogeny**

All phylogenetic trees—whether constructed using NJ, MP or Bayesian analyses—confirmed the monophyly of *E. nivea* n. sp. Two clades were confirmed; one consists of *Eoacmaea javanica*, *E. nivea* n. sp. and *E. conoidalis*, and the other comprises *E. sp.* from Zanzibar, *E. mauritiana*, *E. albonotata* and *E. omanensis* (Fig. 2). *Eoacmaea profunda* is in the basal branch among *Eoacmaea* species.

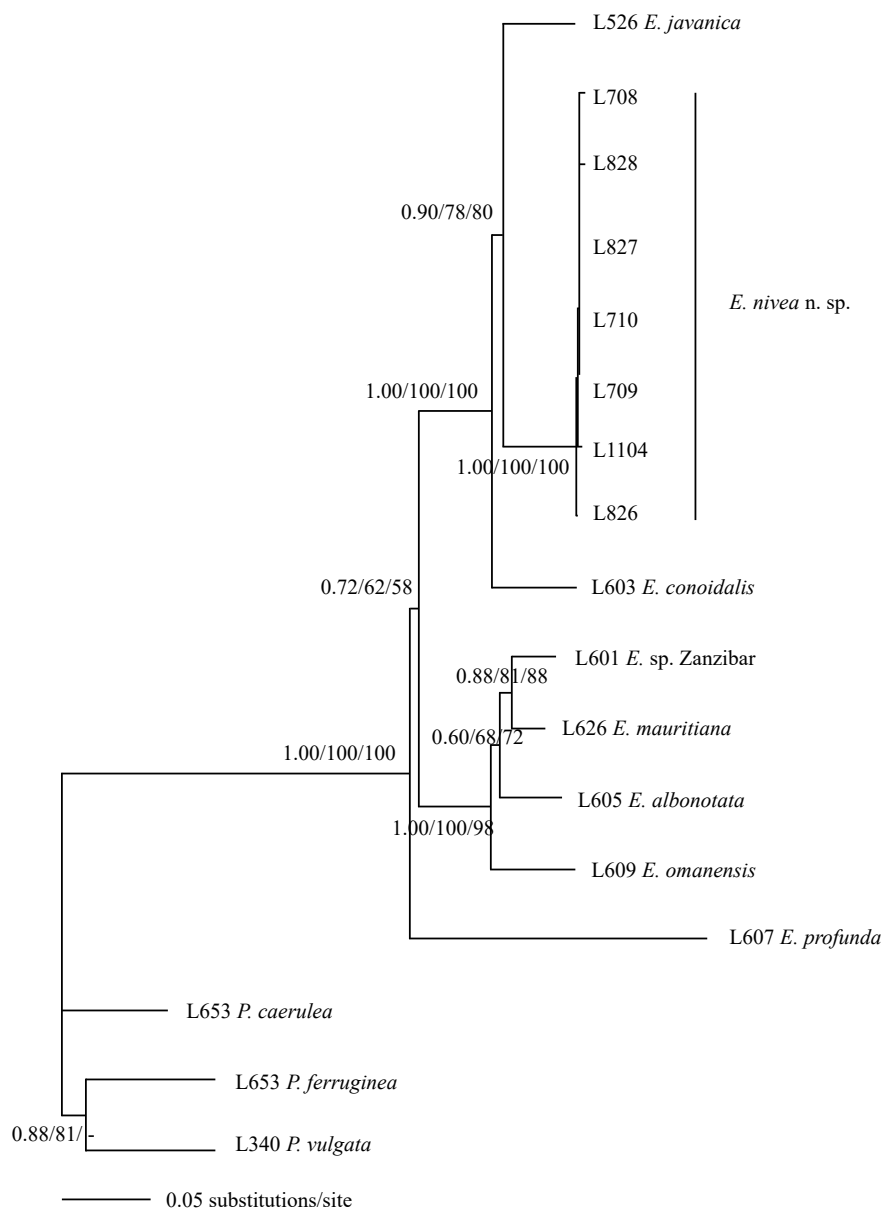
Pairwise genetic distances of *COI* between the species ranged from 6.4–22.2 % in the genus *Eoacmaea* (Table 2). *Eoacmaea nivea* had 0.3–0.6% intraspecific

variation.

**TAXONOMY**

**Family Eoacmaeide Nakano and Ozawa, 2007**  
**Genus *Eoacmaea* Nakano and Ozawa, 2007**  
**Type species *Patella profunda* Deshayes, 1863**

*Diagnosis:* Light-colored shell medium and high in profile. Lateral teeth of radula typically equal size and shape. Habitats limited to limestone in high intertidal to splash zone.



**Fig. 2.** Phylogenetic tree of Bayesian analysis based on the mitochondrial *COI* gene (658 bp). The numbers above each branch are Bayesian posterior probabilities/ NJ bootstrap/ MP bootstrap.



***Eoacmaea nivea* n. sp.**

(Figs. 3–5)

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*Cellana mauritiana* in part, not Pilsbry, 1892: Oyama and Takemura, 1959, Fig. *Cellana* (2). 1, 2.

Acmaeidae sp.: Takenouchi, 1993, Fig. 2C.

*Patelloida* sp.: Kosuge and Sasaki, 2002, Figs. 3A–I.*Eoacmaea* sp.: Nakano, 2017, Fig. 9, Pl. 16

**Material examined:** Holotype, UMUT-RM28074 (Length 20.4 mm, width 16.5 mm, height 8.2 mm), Umahana-saki, Yonaguni Island, Japan. Paratype 1, UMUT-RM28705, Sanninu-dai, Yonaguni Island, Japan. Paratype 2, UMUT-RM28706, Umahana-saki, Yonaguni Island, Japan. Paratype 3, ASIZM0001712, Jialershui, Taiwan. Paratype 4, SMBL-V0595, Green Island, Taiwan. Paratype 5, SMBL-V0596, Green Island, Taiwan. Paratype 6, SMBL-V0597, Green Island, Taiwan.

**Shell morphology**

Shell (Fig. 3) conical, thickened and oval in outline (width/length = 0.78–0.81). Apex located at the anterior 47–53% of shell length, and dorsally pointed as the highest point of shell. Exterior is sculptured by thin radial ribs, which are variable in thickness from evenly to differentially ribbed conditions. Ribs granulate at intersections with growth lines and fine commarginal sculpture. Shell exterior color is almost white except corroded apex in part of examined specimens (UMUT-RM28074). Margin of shell is roughened with minutely projected ends of radial ribs.

From lateral view, anterior and posterior slopes almost straight. Ventral margin apparently concaved, not planar.

From ventral view, shell interior smooth and

lustrous. Shell muscle scar deeply impressed. Interior color white in the marginal area, and yellow to orange in inner area; depth and size of colored area variable among specimens; brown markings may be formed in apical area.

**Anatomy**

Mantle margin (mm: Fig. 4A–C) thick, circumpallial tentacles completely invisible in fixed specimens (may be retracted or tiny length). Foot muscular, well developed and stiffened. Pallial cavity (pc: Fig. 4A–C) possesses a large ctenidium (ctn: Fig. 4D) extending from posterior left to anterior right. A pair of small elongate osphradia attached on floor of pallial cavity. Attachment area of shell muscle (sm) U-shaped, and divided into bundles, more finely in posterior than in anterior.

Mouth (m: Fig. 5A) surrounded by thick outer lip (oli) and laterally extended oral lappets (ola). Eyes (e: Fig. 5B) exist at bases of cephalic tentacles (ct).

Head contains muscular buccal mass (bm). Radular sac (rds: Fig. 5B) forms two loops; first loop (L1) on left posterior, second loop (L2) on right anterior. End of radular sac (ers) enlarged and bulbous behind the buccal mass.

Part of stomach (st: Fig. 4A, C) and intestine (i) visible as pale lines on darker background color of digestive glands (dg) which on dorsal surface of the animal.

Pericardium (pd: Fig. 4A, C) located on the left anterior side of limpet and with a single auricle (au: Fig. 4D) and ventricle (vn). Right kidney (rk) discernible on the right side of the animal.

**Radular morphology**

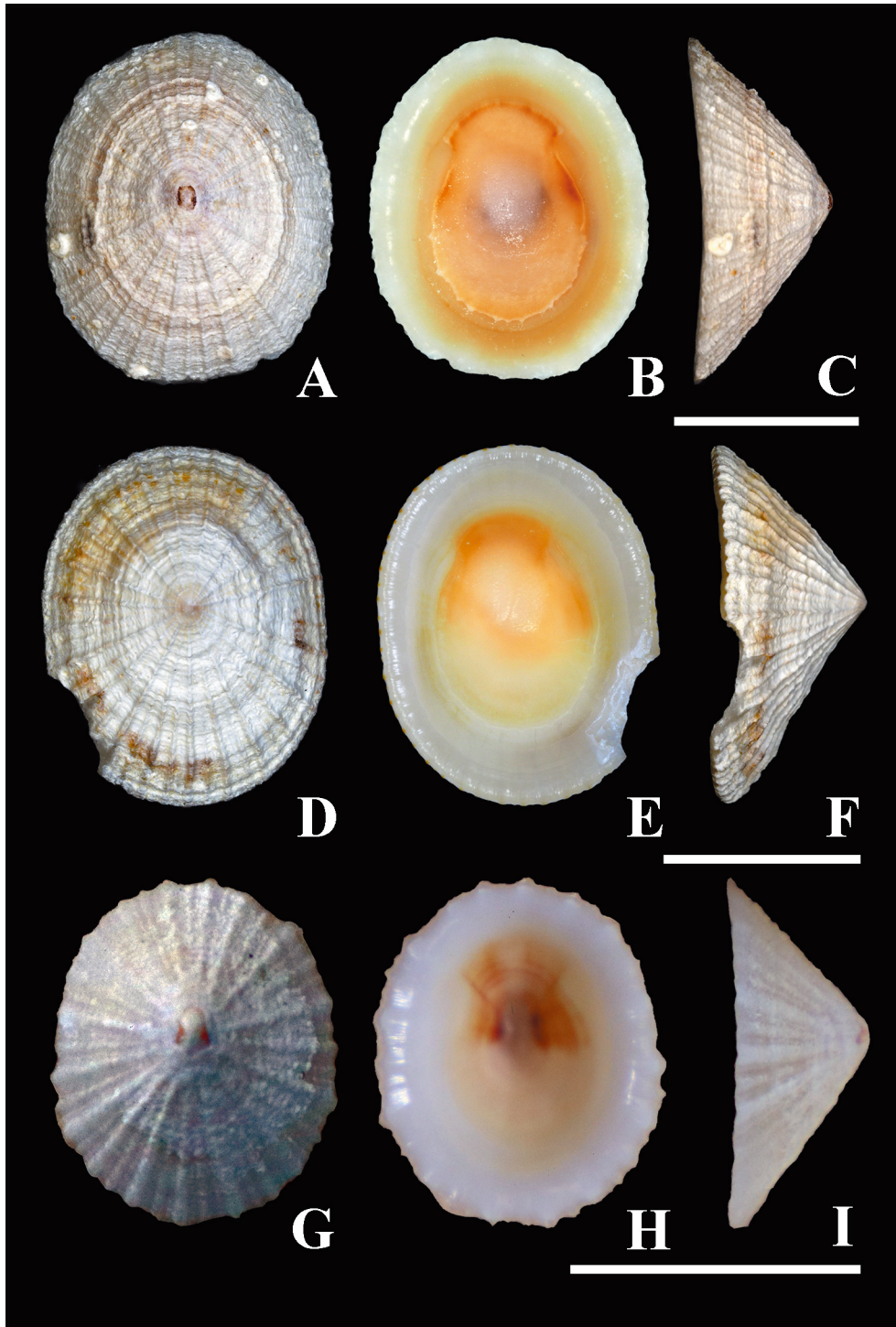
The radular sac contains 75 rows of radular

**Table 2.** Uncorrected *p*-distances within and among species

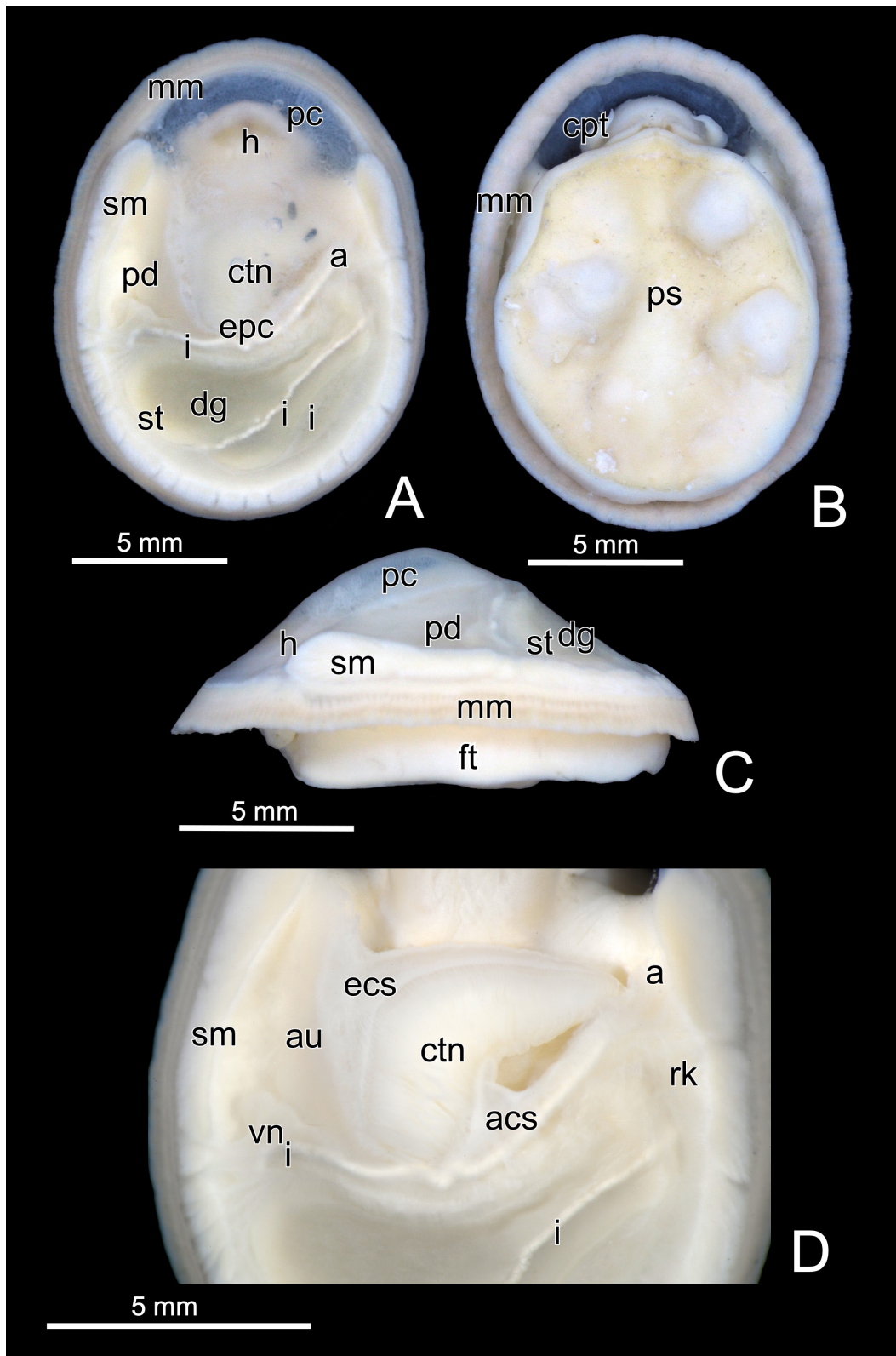
	1	2	3	4	5	6	7	8	9	10	11
1. <i>E. javanica</i>	0.00										
2. <i>E. sp. Zanzibar</i>	13.4	0.00									
3. <i>E. conoidalis</i>	8.5	14.1	0.00								
4. <i>E. albonota</i>	15.2	6.4	15.7	0.00							
5. <i>E. profunda</i>	21.6	20.5	22.1	20.7	0.00						
6. <i>E. omanensis</i>	16.0	8.5	15	7.8	21.1	0.00					
7. <i>E. mauritiana</i>	14.3	13.8	13.8	5.4	19.8	6.8	0.00				
8. <i>E. nivea</i> n. sp.	7.6–8.1	14.6–15.0	8.8–9.1	14.7–15.2	21.9–22.2	15.5–16.0	14.3–14.7	0.3–0.6			
9. <i>P. caerulea</i>	27.5	28.4	26.9	27.5	32.5	27.5	27.4	27.6–28.1	0.00		
10. <i>P. ferruginea</i>	29.1	30.1	29.0	30.2	32.6	29.6	28.6	29.3–29.6	12.3	0.00	
11. <i>P. vulgata</i>	29.6	29.9	29.9	29.0	32.8	29.0	29.4	29.1–29.6	13.8	12.8	0.00

segments in paratype UMUT-RM28075 (Fig. 6A–C). Rows 1–66 have thickly mineralized orange-brown teeth, rows 67–70 are weakly mineralized, and rows 71–75 are organic and translucent. Each radula row

consists of three pairs of lateral teeth and two pairs of marginal teeth. The first teeth are thickest among three pairs; cusps (L1c: Fig. 6D) are almost in contact between the right and left teeth; posterior margins of



**Fig. 3.** Shell morphology of *Eoacmaea nivea* n. sp. A–C, Holotype, UMUT-RM28704, Umahana-saki, Yonaguni Island, Japan; 20.4 × 16.5 × 8.2 mm. D–F, Paratype 1, UMUT-RM28705, Sanninu-dai, Yonaguni Island, Japan; 17.9 × 13.9 × 7.6 mm. G–I, Paratype 3, Jialershui, Taiwan; 11.8 mm × 10.1 mm × 4.9 mm.

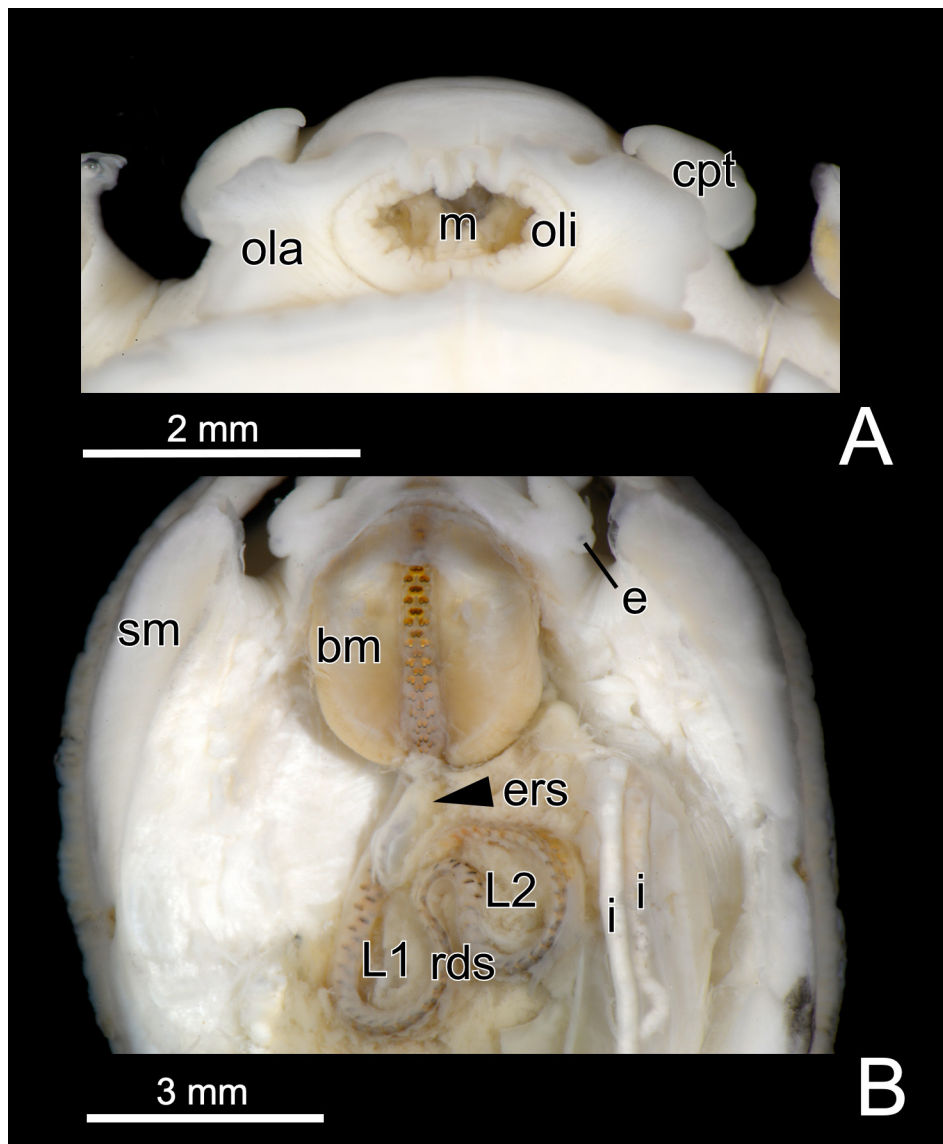


**Fig. 4.** External view of animal. UMUT-RM28074. A, Dorsal view. B, Ventral view. C, Left lateral view. D, Enlarged view of ctenidium and adjacent organs, with mantle removed. Abbreviations: a, anus; acs, afferent ctenidial sinus; au, auricle; cpt, cephalic tentacle; ctn, ctenidium; dg, digestive gland; ecs, efferent ctenidial sinus; epc, end of pallial cavity; ft, foot; h, head; i, intestine; mm, mantle margin; pc, pallial cavity; pd, pericardium; ps, pedal sole; rk, right kidney; sm, shell muscle; st, stomach; vn, ventricle. Animal size: length = 15 mm, width = 12 mm.

their cusps blunt and roundly curved; shafts (L1s: Fig. 6D) stout and short; bases concaved on inner side and broadly fused with second and third teeth on outer posterior side. Second lateral teeth (L2: Fig. 6D, E) almost 50% of first teeth in width and about 55% in length; inner margins of bases are curved towards the midline of the radula. Third lateral teeth (L3) slightly wider than second teeth; bases are mostly hidden in the dorsal view, anterior sides are thinly extended along the first teeth. Posterior margins of cusps of second and third teeth blunt, rounded, and more strongly curved than those of first teeth; boundaries of cusps of second

and third teeth discernible as distinct lines. Marginal teeth (M1, M2: Fig. 6F) tightly overlapped; cusps curved backwards; shafts elongate; bases concealed by anterolateral corners of basal plates of the next row of the radula; inner marginal teeth slightly wider than outer teeth. Basal plates (bp: Fig. 6D) tightly fused between right and left, considerably thickened, and wider than long (height/width = ca. 0.67); anterior margins weakly convex; anterolateral corners obliquely truncated and broadly extended laterally; posterolateral corners straight; posterior margins overlaid by next basal plates.

*Distribution:* The species is restricted to calcareous



**Fig. 5.** Ventral and internal view of animal. UMUT-RM28075. A, Ventral view of mouth region. B, Dorsal view of buccal mass and radular sac, with pallial and visceral organs removed. Abbreviations: bm, buccal mass; cpt, cephalic tentacle; e, eye; ers, end of radular sac; I, intestine; L1, first loop; L2, second loop; m, mouth; ola, oral lappet; oli, outer lip of mouth; rds, radular sac; sm, shell muscle. Size of buccal mass: length = 3.6 mm, width = 2.9 mm.



substrates in Yonaguni Island, Japan and eastern and southern Taiwan (note rock substrate in northern Taiwan is not calcareous).

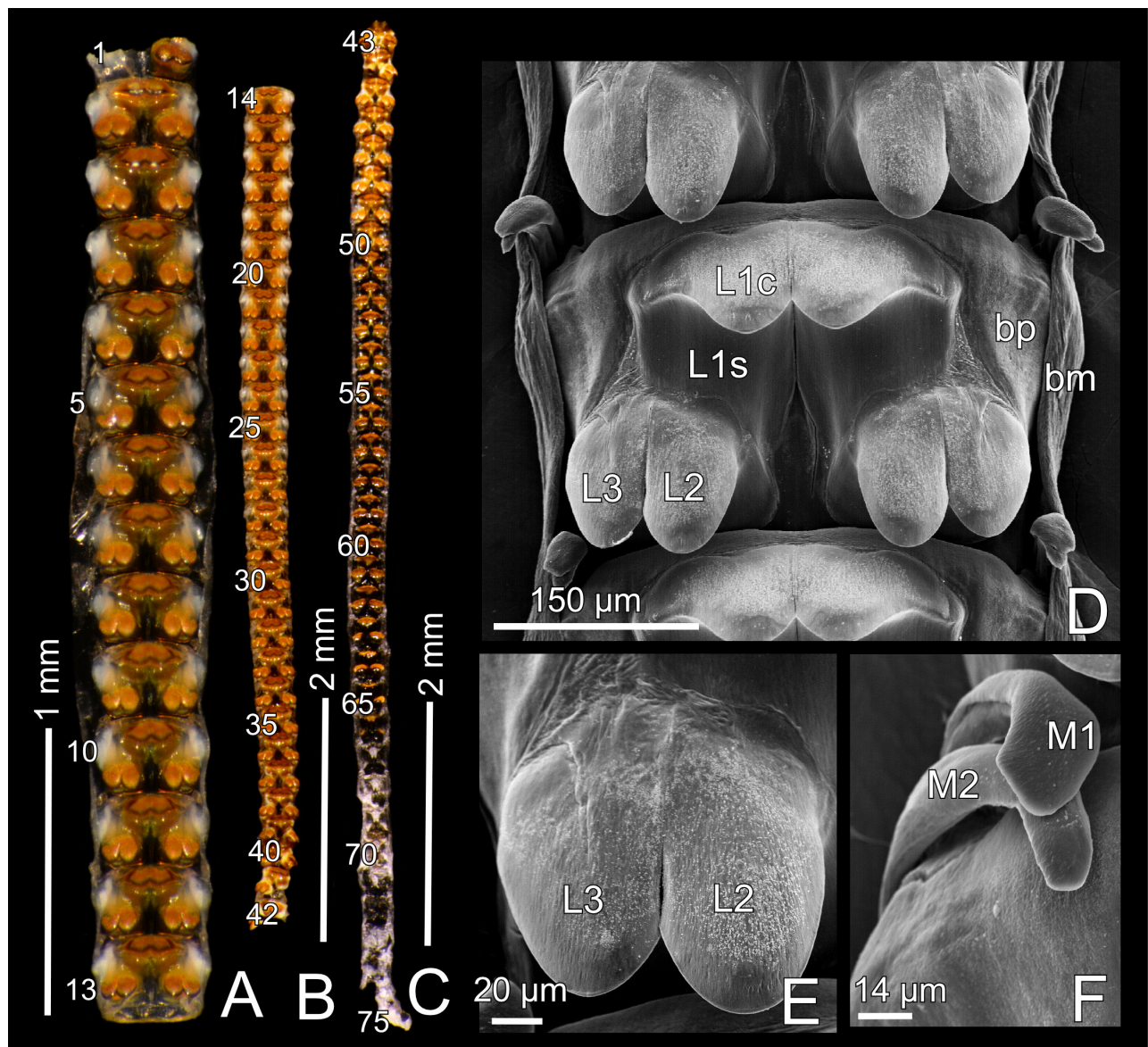
*Habitat:* The species lives in crevices and hollows on vertical limestone faces on exposed shores in the high intertidal to supratidal zone. Although it does not occur in dense communities in Yonaguni Island, Japan and Jialershui, Taiwan, the species is abundant on Green Island and Orchid Island, southeastern Taiwan.

*Etymology:* The species name *nivea* is given for the white color of the shell.

**DISCUSSION**

**Previous identification of *Eoacmaea nivea* n. sp.**

Oyama and Takemura (1959) firstly reported *Eoacmaea nivea* n. sp. from Taiwan as *Cellana mauritiana* in the family Nacellidae. However, judging from the shell morphology and anatomical characters, the identification of *C. mauritiana* in Oyama and Takemura (1959) is not correct. The genus *Cellana* has secondary gills, whereas *E. nivea* n. sp. has a true



**Fig. 6.** Radula. A–C, Radular sac cut into three portions. The numbers 1 to 75 represent the first to 75th rows from the anterior. D–F, Scanning electron micrographs of radular teeth. D, Enlarged view of single radular segment. E, Second and third cusps of lateral teeth. F, Marginal teeth. Abbreviations: bm, basal membrane; bp, basal plate; L1c, cusp of first lateral tooth; L1s, shaft of first lateral tooth; L2, second lateral tooth; L3, third lateral tooth; M1, first marginal tooth; M2, second marginal tooth.

gill. Takenouchi (1993) recorded the *E. nivea* n. sp. from Orchid Island, Taiwan and listed it as Acmaeid sp. Although species in Acmaeidae are similar to lottiid species (e.g., Pilsbry 1891), this scheme was revised based on the shell structure (Lindberg 1986). The genus *Acmaea* was restricted to the type species *Acmaea mitra*. The rest of the former acmaeid species were transferred to the Lottiidae with type species *Lottia gigantea* G. B. Sowerby I, 1834. Later, the definition of Acmaeidae was revised based on molecular data (Nakano and Ozawa 2007; Nakano and Sasaki 2011). The family Acmaeidae is currently composed of three genera: *Acmaea*, *Niveotectura* and *Erginus*. All the species of Acmaeidae are restricted to cold-water in the North Pacific.

Kosuge and Sasaki (2002) reported *Patelloida* sp. (= *Eoacmaea nivea* n. sp.) from Yonaguni Island (chain of Okinawa islands), Japan. According to Lindberg and Vermeij (1985), the genus *Patelloida* consists of two groups. The first group consists of species characterized by low to medium profiles, strong ribs or many fine riblets, reduced third lateral radular teeth, and inhabiting various substrata in exposed rocky shores and sheltered inlets. The second group is referred as the *Patelloida profunda* group by Christiaens (1975). Lindberg and Vermeij (1985) expanded this to include species characterized by moderate to high shell profiles, equal-sized lateral radular teeth, and limited to occupying the limestone in the high intertidal and supratidal zones. Nakano and Ozawa (2007) proposed a new genus, *Eoacmaea*, for the *Patelloida profunda* group based on molecular data and morphological characters. The new species identified in the present study belongs to *Eoacmaea* since it has high shell profile, equal-sized lateral radular teeth, and inhabits limestone substrates in high intertidal zone.

Most of the species of the genus *Eoacmaea* have a similar external shell morphology. However, *E. nivea* n. sp. can be distinguished from congeners by the shell morphology or coloration. Both *E. nivea* n. sp. and *E. javanica* have a similar shell morphology, but the color of the inner shell is different between these two species. The intermediate area between the muscle scar and shell margin of *E. nivea* n. sp. is glossy white, whereas *E. javanica* has glossy orange-yellow to orange. Although *E. conoidalis* also has glossy white in the intermediate area on inner shell, *E. conoidalis* is bigger than *E. nivea* n. sp. The species *Eoacmaea chamorrorum* is different from *E. nivea* n. sp., *E. javanica* and *E. conoidalis* by having dark rays and red markings of the shell.

The genetic distances of *COI* between *E. nivea* n. sp. and the two most closely allied species *E. javanica*, and *E. conoidalis* were 7.6–8.1% and 8.8–9.1%, respectively, whereas *E. nivea* had 0.3–0.6% intraspecific variation.

Molecular analyses further confirmed that *E. nivea* n. sp. is genetically distinguished from other *Eoacmaea* species. Therefore, the species identity of *E. nivea* n. sp. is supported by both molecular data and morphological characters.

## Biogeography

Almost all Patellogastropoda species display pelagic larval development and all display lecithotrophic development (Lindberg 1998). The duration of the larval period depends on temperature and ranges from a few days in the tropics to up to 10 days in cooler waters (e.g., Amio 1963; Nakano et al. 2020). Recent molecular work has attempted to estimate planktonic dispersal distances during the larval period (Bird et al. 2007; Goldstien et al. 2006; Sá-Pinto et al. 2008; Nakano et al. 2010). These works suggested that patellogastropod limpets can disperse up to 100–200 km from their parent populations during the larval period. However, patterns of oceanographic currents, fragmentation of calcareous rocky shores and region with inhospitable ranges of sandy shores can affect the larval dispersal and settlement locations. The distribution of Japanese Patellogastropoda species are strongly affected by the Kuroshio Current (Nakano et al. 2009 2010) along the Pacific Japanese coastlines. The Kuroshio Current flows from the Philippines via Taiwan and Yonaguni Island to the west side of the Ryukyu Islands and reaches the Pacific coast of Honshu Island, Japan. *Eoacmaea nivea* n. sp. is abundant on limestone substrates in southeastern Taiwan, including Green Island and Orchid Island, and less abundant on Yonaguni Island, even though Taiwan and Yonaguni Island are only 100 km apart. The strong Kuroshio Current probably transports the larvae of *E. nivea* n. sp. along from southeastern Taiwan northward to Yonaguni Island. The small-sized population of the species on Yonaguni Island may be a result of limited episodic larval dispersal from southern Taiwan.

## Diversity of Patellogastropoda in Taiwan

During the field survey in Taiwan, we found a total 11 species of patellogastropod limpets in Taiwan. *Cellana grata* (Gould, 1859), *Cellana toreuma* (Reeve, 1855), *Nipponacmea nigrans* (Kira, 1961), *Nipponacmea fuscoviridis* (Teramachi, 1949), *Lottia dorsuosa* (Gould, 1859), *Lottia luchuana* (Pilsbry, 1901), *Lottia tenuisculpta* Sasaki and Okutani, 1994 were found in the intertidal rocky shores along the northern and northeastern coasts of Taiwan, whereas *Cellana radiata* (Born, 1778), *Lottia luchuana*, *Scutellastra flexuosa* (Quoy and Gaimard, 1834),

*Patelloida saccharina* (Linnaeus, 1758) and *E. nivea* n. sp. were only found on limestone in southeastern Taiwan waters, including Green Island and Orchid Island. The other patellogastropod limpets are warm-temperate species and (except *L. luchuana*) also distributed in mainland of Japan, whereas the *Eoacmaea* group are all tropical species that are widely distributed in the Indo-West Pacific (and in other tropical regions worldwide). Therefore, the fauna of Patellogastropoda in Taiwan is characterized by both warm-temperate and tropical species.

*Nipponacmea fuscoviridis* is known to be widely distributed in Japan, Korea, China, Hong Kong and Taiwan (Sasaki and Nakano 2007; Yu et al. 2014; Sharina et al. 2017; Sasaki 2017). However, previous molecular analysis has suggested that the Taiwan population is significantly different (Yu et al. 2014). The Taiwan population may be an endemic species, for which *Nipponacmea formosa* (Christiaens, 1980) is available. Further morphological and anatomical observations are needed to elucidate the validity of *N. formosa*.

According to Powell (1973), *Cellana radiata* is classified into four subspecies: *Cellana radiata radiata* (Born, 1778), *Cellana radiata orientalis* (Pilsbry, 1891), *Cellana radiata enneagona* (Reeve, 1854) and *Cellana radiata capensis* (Gmelin, 1791). Molecular analysis has revealed that six genetically distinct clades corresponding to these four species and two additional phylogenetic clusters provisionally interpreted as separate species that remain to be formally separated (Nakano and Ozawa 2007; Nakano et al. 2009; herein). *Patelloida saccharina* and *Scutellastra flexuosa* are also thought to be species complexes (Paulay and Mayer 2002; Kirkendale and Meyer 2005). These three species complexes are all widely distributed in the Indo-West Pacific, and all are in need of further sampling and detailed analyses to elucidate the species boundaries.

## CONCLUSIONS

We conducted a molecular phylogenetic analysis based on a partial *COI* sequence (658 bp) and detailed morphological and anatomical comparison for eoacmaeid limpets collected from Yonaguni Island, Japan and Jialershui and Green Island, Taiwan. As a result, the present species is genetically and morphologically different from the other *Eoacmaea* species. We described it as *Eoacmaea nivea* n. sp. in this paper. *Eoacmaea nivea* n. sp. is abundant in the limestone in southeastern Taiwan (*i.e.*, Green Island and Orchid Island), but the population of the species in Yonaguni Island was very limited, which may be a

result of only occasional larval dispersal from southern Taiwan via the larval or adult rafting dispersal provided by the strong Kuroshio Current.

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**Competing interests:** The authors declare that they have no conflict of interest.

**Availability of data and materials:** All specimens used in this study are deposited in museum collections as stated in table 1. All genetic data newly sequenced in this study are deposited in GenBank under the accession numbers.

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