Zootaxa 5706 (1): 079–092
https://www.mapress.com/zt/

Article

ISSN 1175-5326 (print edition)
ZOOTAXA
ISSN 1175-5334 (online edition)

https://doi.org/10.11646/zootaxa.5706.1.5
http://zoobank.org/urn:lsid:zoobank.org:pub:34D2DB65-44F8-4F51-968E-82AA37F2AECF

Taxonomic study of the flower chafer genus *Gametis* Burmeister, 1842 (Coleoptera: Scarabaeidae: Cetoniinae) in Japan, with a description of a new species from Tarama-jima Island and Minna-jima Island, the Miyako Islands, southwestern Japan

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Abstract

A new species of the flower chafer genus *Gametis* Burmeister, 1842, *Gametis polita* Seshima & Yoshida, **sp. nov.**, is described from Tarama-jima Island and Minna-jima Island in the Miyako Islands, southwestern Japan, which was formerly misidentified as *Gametis forticula* (Janson, 1881). This is the first new species of the subfamily Cetoniinae *sensu stricto* described from Japan in approximately half a century. Using molecular and morphological evidence, we conclude that the genus *Gametis* comprises three species in Japan: *G. forticula* (Janson, 1881), *G. polita* **sp. nov.**, and *G. ishigakiana* (Nomura, 1959), which was formerly treated as a subspecies of *G. forticula*. In addition, *G. forticula miyakoana* (Nomura, 1959) and *G. forticula yonakuniana* (Nomura, 1959) are transferred to subspecific status under *G. ishigakiana*.

Key words: Cetoniini, cryptic species, molecular phylogeny, taxonomy, the Ryukyus

Introduction

The genus *Gametis* Burmeister, 1842 (Coleoptera: Scarabaeidae: Cetoniinae) comprises eight species and several subspecies distributed across East Asia and Southeast Asia (Nomura 1959; Sakai & Nagai 1998; Bezděk 2016). In this genus, taxa exhibit significant individual variation, and the morphological differences between taxa are often subtle, both of which make classification challenging (Sakai 2012). Additionally, species- and subspecies-level delimitation within this genus has never been assessed using molecular analysis.

In Japan, two *Gametis* species, *G. jucunda* (Faldermann, 1835) and *G. forticula* (Janson, 1881), are distributed (Sakai 2012; Bezděk 2016). *Gametis forticula* has been classified into seven subspecies based on morphological characteristics (Sakai & Nagai 1998). Additionally, Wada (1985) reported that a morphologically distinct population of *G. forticula* from Tarama-jima Island exhibited distinct morphological characteristics and suggested that this population may represent a distinct subspecies. However, given the minor interspecific differences within this genus, taxonomic studies integrating molecular data alongside morphological analyses are required.

In this study, the taxonomic status of the *G. forticula* population from Tarama-jima Island, as well as that of the Japanese subspecies, is examined using both morphological characteristics and DNA analyses.

Accepted by A. Bezděk: 3 Sept. 2025; published: 9 Oct. 2025

Materials and methods

Morphological observations and measurements

All morphological observations and measurements were conducted using dried specimens. Observations were made under a stereomicroscope (SMZ1270, Nikon), while photographing and measurements were performed using a digital microscope (VHX-7000, Keyence) and Click Measure v.2.4.0.15 (Onochi-lab). In addition, specimen photographs were also taken by a digital camera (Canon EOS 5D Mark IV) with a Canon MP-E 65 mm macro lens, combined using Helicon Focus® v.8.2.18. (Helicon Soft Ltd.), and live habitus photographs were taken by a digital camera (Nikon D500) with a Sigma 17–70 mm macro lens. These photographs were retouched using Adobe Photoshop 2024 (Adobe Inc.). The male genitalia were removed from the specimens and macerated overnight in a 10% potassium hydroxide (KOH) solution. After rinsing thoroughly with distilled water, the male genitalia were completely dried and observed.

Terminology for morphological structures follows Krikken (1984) and Sakai & Fujioka (2007). Specimens examined including type material are deposited in the following institutions and private collections: Ehime University Museum, Matsuyama, Japan (EUMJ), the private collection of Kaoru Wada (PCKW), the private collection of Yûhi Seshima (PCYS), and the private collection of Kaoru Sakai (PCKS).

DNA extraction, PCR amplification, and sequencing

Two protocols, the "Chelex" method and the "QIAGEN" method, were employed for DNA extraction. In both methods, a single mesotarsus was removed from each specimen and used for DNA extraction. The remaining body of each specimen was air-dried and preserved as a voucher specimen for subsequent morphological study.

In the Chelex-TE and Proteinase K-based method, i.e., "Chelex" method, total genomic DNA was extracted from specimens preserved in 99.5% ethanol. The detached mesotarsus was placed into a microtube containing 105 μL of extraction buffer, consisting of 100 μL of 10% Chelex-TE and 5 μL of QIAGEN Proteinase K. The sample was incubated at 56 °C for 24 hours to extract DNA, followed by heating at 99 °C for 10 minutes to inactivate Proteinase K.

In the "QIAGEN" method, total genomic DNA was extracted using the DNeasy® Blood & Tissue Kit (QIAGEN), following the manufacturer's standard protocol with a single modification: the volume of Buffer AE was adjusted to 60 μL instead of the default amount. The DNA extraction method used for each specimen is summarized in Table 1.

TABLE 1. Specimen used in molecular phylogenetic analysis, with DNA extraction methods and accession numbers. Em. = emergence.

Taxa	Extraction method	Sample number	Collecting date	Locality	Accession no.
					COI
Gametis polita **sp. nov.**	Chelex	GFT-01	21–24. VI. 2024	Tarama Is.	LC867624
	Chelex	GFT-02	21–24. VI. 2024	Tarama Is.	LC867625
Gametis forticula forticula	Chelex	GFF-09	26. III. 2025	Zamami Is.	LC867636
	Chelex	GFF-10	10. III. 2025	Okinawa Is.	LC867637
	Chelex	GFF-12	10. III. 2025	Okinawa Is.	LC867638
	Chelex	GFF-14	10. III. 2025	Okinawa Is.	LC867639
Gametis forticula miyakoana	QIAGEN	GFM-04	11. III. 2022	Irabu Is.	LC867633
Gametis forticula ishigakiana	QIAGEN	GFI-05	15. III. 2022	Ishigaki Is.	LC867635
	QIAGEN	GFI-06	15. III. 2022	Ishigaki Is.	LC867632
Gametis forticula yonakuniana	QIAGEN	GFY-02	25. III. 2021	Yonaguni Is.	LC867626
	QIAGEN	GFY-03	25. III. 2021	Yonaguni Is.	LC867627

.....continued on the next page

TABLE 1. (Continued)

Taxa	Extraction method	Sample number	Collecting date	Locality	Accession no.
					COI
	QIAGEN	GFY-04	25. III. 2021	Yonaguni Is.	LC867628
	QIAGEN	GFY-05	25. III. 2021	Yonaguni Is.	LC867634
Gametis jucunda	QIAGEN	GJG-01	19. VIII. 2022	Gunma	LC867629
	QIAGEN	GJG-02	19. VIII. 2022	Gunma	LC867630
	QIAGEN	GJT-03	11. V. 2022	Tsushima Is.	LC867631
Cetonia pilifera	Chelex	CPP-01	28. IV. 2024	Kanagawa	LC881770
Cetonia roelofsi roelofsi	Chelex	CR-02	9. X. 2021 Em. 4. IV. 2022	Yakushima Is.	LC881771
Cetonia roelofsi gotoana	Chelex	GRG-03	14–17. VII. 2024	Fukue Is.	LC881772

Partial mitochondrial COI gene regions were amplified and sequenced using the primers, CI-J-2183 (Jerry) and TL2-N-3014 (Pat) (Simon *et al*. 1994). Each PCR mastermix consisted of 1 μL of template DNA, 5 μL of KOD One polymerase, 3.9 μL of distilled water (DW), and 0.3 μL each of forward and reverse primers, for a final volume of 10.5 μL. PCR amplification was carried out using a MiniAmp Thermal Cycler (Thermo Fisher Scientific, U.S.) under the following cycling conditions: 40 cycles of 98 °C for 10 seconds, 53 °C for 5 seconds, and 68 °C for 1 second, followed by a final extension at 68 °C for 7 minutes.

Successful amplification was confirmed by electrophoresis on a 2% TAE agarose gel. PCR products were purified using ExoSAP-IT (Applied Biosystems), and the purified products were sequenced bidirectionally by Azenta Japan Corporation.

Phylogenetic analysis

To infer phylogenetic relationships and calculate genetic distances among the examined taxa, a set of 19 newly obtained COI sequences (797 bp) from all Japanese species of the genera *Gametis* and *Cetonia* was analyzed. In addition, four COI sequences of *Oxythyrea funesta* (Poda, 1761) (GenBank accession nos. OP279088, OP279113, OP279119, and OP279121) were also used as outgroups. Multiple sequence alignment was performed using MUSCLE (Edgar 2004) integrated within MEGA 11 (Kumar *et al*. 2018).

Phylogenetic analysis was conducted using the Maximum Likelihood (ML) method (Felsenstein 1981) in IQ-TREE 3 v3.0.1 for Windows (Wong *et al*. 2025). Codon positions were treated as separate partitions, and the most suitable substitution model for each was selected based on the Bayesian Information Criterion (BIC) using ModelFinder (Kalyaanamoorthy *et al*. 2017). The selected models were as follows: 1st codon: TN+F; 2nd codon: F81+F; 3rd codon: TN+F+G4.

To evaluate the reliability of the inferred nodes, 1,000 replicates of both the Ultrafast Bootstrap (UFBoot; Hoang *et al*. 2018) and Shimodaira-Hasegawa-like approximate likelihood ratio test (SH-aLRT; Shimodaira & Hasegawa 1999) were conducted. The resulting tree was visualized using FigTree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/).

Pairwise genetic distances among COI sequences were calculated in MEGA 11 using the Kimura 2-parameter (K2P) model (Kimura 1980). Standard errors were estimated through 1,000 bootstrap replicates (Felsenstein 1985). To infer the interspecific threshold for genetic distance in the COI region of the primer sets used in this study, the divergence between two Japanese species of the closely related genus *Cetonia*, *C. pilifera* (Motschulsky, 1860) and *C. roelofsi* Harold, 1880 was also calculated in the same way.

Results

Phylogenetic position and genetic distances

In the phylogenetic tree, *Gametis forticula* is divided into five distinct monophyletic clades represented by *G. jucund*, *G. f. forticula*, *G. f. yonakuniana*, *G. f. ishigakiana* + *G. f. miyakoana*, and the unique population of *G. forticula* from Tarama-jima Island, respectively (Fig. 37). The monophyly of the Tarama-jima population was strongly supported by both UFBoot and SH-aLRT values, and they are separated from *G. jucunda* and all Japanese subspecies of *G. forticula*, previously treated as conspecific, by a genetic distance (K2P) of over 5 % (Table 2). Moreover, *G. f. forticula* and three southern Ryukyus subspecies are separated from other Japanese species of *Gametis* by a genetic distance (K2P) of approximately 5 % (Table 2). In contrast, *G. f. yonakuniana* is from *G. f. ishigakiana* + *G. f. miyakoana* by a genetic distance (K2P) of approximately 3 % (Table 2).

The genetic distance between *Cetonia* species, *C. pilifera* and *C. roelofsi*, is calculated as 4.96 % (SE = 0.85 %).

TABLE 2. Pairwise genetic distances (K2P) among *Gametis* species from Japan based on partial COI sequences. Mean genetic distances are shown below the diagonal, and standard error estimates are shown above the diagonal.

Taxa	Accession no.	1	2	3	4	5	6
1. G. polita **sp. nov.**	LC867624–LC867625		0.00816	0.00851	0.00840	0.00799	0.00969
2. G. forticula forticula	LC867636–LC867639	0.05063		0.00805	0.00797	0.00849	0.00958
3. G. forticula miyakoana	LC867633	0.05303	0.04992		0.00226	0.00595	0.00905
4. G. forticula ishigakiana	LC867632, LC867635	0.05301	0.05127	0.00568		0.00576	0.00905
5. G. forticula yonakuniana	LC867626–LC867628, LC867634	0.05501	0.06019	0.02827	0.02892		0.00975
6. G. jucunda	LC867629–LC867631	0.06867	0.07432	0.06113	0.06227	0.07256	

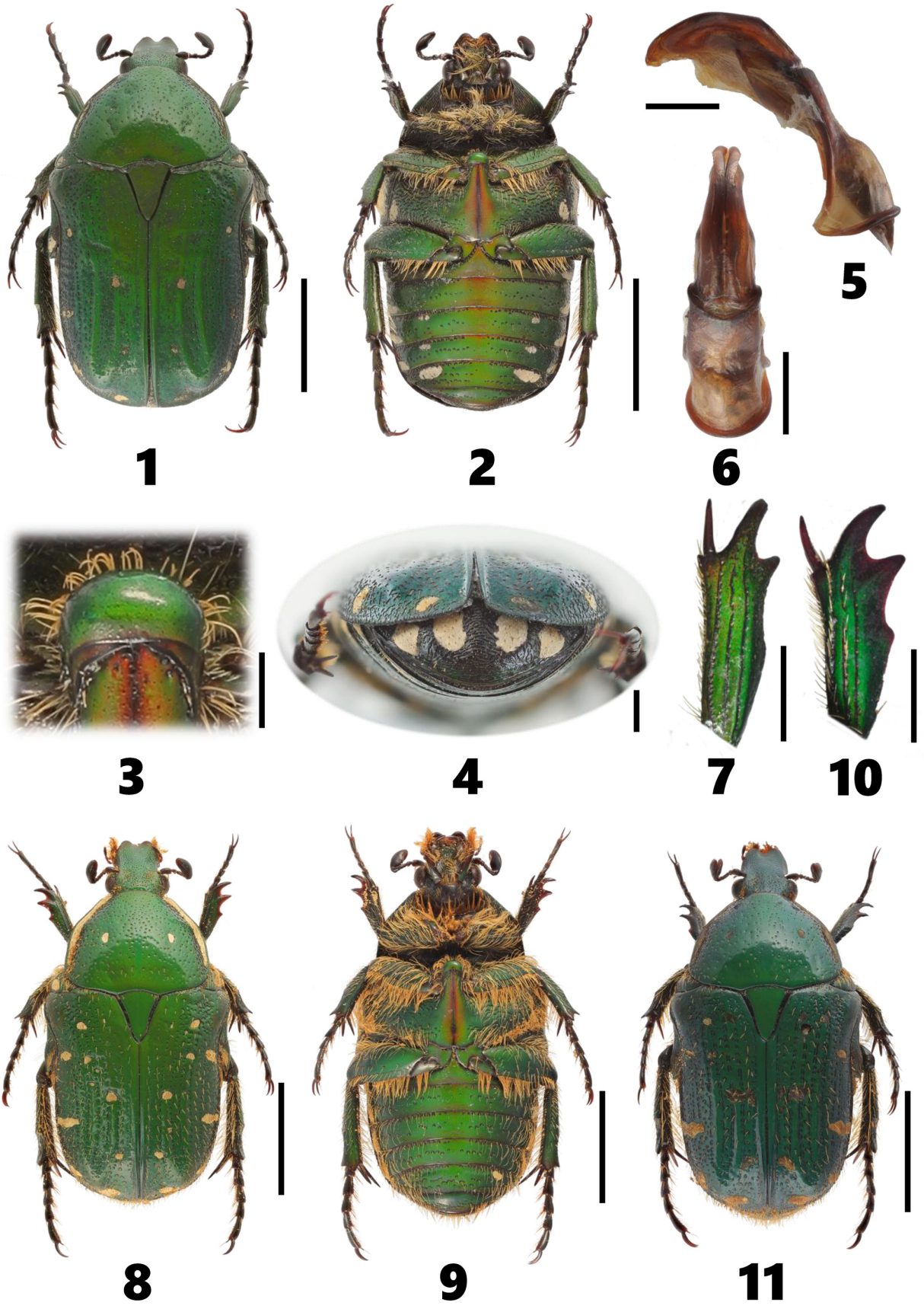
Taxonomy

***Gametis polita* Seshima & Yoshida, sp. nov.**
[Japanese name: Hisui-koao-hanamuguri]
(Figs. 1–11, 28–29)

Type locality. Mitsuse park, Tarama-jima Is., the Miyako Isls., Okinawa-ken, Japan.

Type material. *Holotype*, ♂ (Figs. 1–7). [JAPAN] Mitsuse park, Tarama-jima Is., the Miyako Isls., Okinawa-ken, 21–24. VI. 2024, Fubito Aizawa leg. (EUMJ). *Paratypes*: (3 ♂♂, 82 ♀♀). [JAPAN] 64 ♀♀ (EUMJ, PCKW, PCYS, PCKS), Tarama-jima Is., Tarama-son, the Miyako Islands, Okinawa pref., 1. IV. 1983, Kaoru Wada leg.; 3 ♂♂, 13 ♀♀ (EUMJ, PCYS), same data as holotype; 1 ♀ (PCYS), Shiokawa, Tarama-jima Is., 14. VI. 2025, Yûhi Seshima leg.; 4 ♀♀ (PCYS), near Miyako Minna Island Lighthouse, Minna-jima Is., 20. VI. 2024, Fubito Aizawa leg.

Description. Holotype, male (Figs. 1–7)**.** Body oval, without tomentum; body length measured from anterior margin of clypeus to elytral apex 13.98 mm; maximum width measured around humeri 7.57 mm. Color glossy green, enamel-like, with several white round maculae; head mostly green, with anterior margins tinged slightly pale red; antennae reddish brown to black; pronotum, scutellum, and elytra glossy, green to pale red; pronotum with longitudinal white macula present along each lateral declivity, with an additional pair of small inner white spots medially; elytra with four white maculae arranged along each outer margin, with two additional ones on each middle area; pygidium glossy black and slightly greenish, with four conspicuously large white maculae; venter mostly glossy, green, with a faint reddish tint; prosternum glossy black; mesosternum with large white maculae along each lateral margin; abdominal ventrites 1, 2, and 5 with single pair of white maculae, 3 and 4 with two pairs of white maculae; protibiae shiny green anteriorly and dark shiny green posteriorly; meso- and metatibiae dark green; tarsi dark reddish brown to black with a greenish tint and glossy.



FIGURES 1–11. *Gametis polita* **sp. nov.**: 1–7, male (holotype); 1–2, habitus, dorsal (1), and ventral views (2); 3, mesosternal process, ventral view; 4, pygidium, dorsal view; 5, parameres, lateral view; 6, parameres, dorsal view; 7, right protibia, anterior view. 8–11, female (paratype); 8–9, habitus, dorsal (8) and ventral views (9); 10, right protibia, anterior view; 11, color variation, dorsal view. Scale bars = 5 mm (1–2, 8–9, 11); 1 mm (4–7, 10); 0.5 mm (3).

Head (Figs. 1–2). Symmetrical and elongate; dorsal surface moderately shiny and sparsely punctated; interocular width equals 5.3 transverse eye diameters; median side depression. Clypeus with anterior margin deeply depressed at middle, with sparser punctures evenly distributed; apex slightly reflexed dorsally. Frons laterally with punctures coarser and slightly denser than those on clypeus, medially with sparser punctures but similar in size to those on clypeus. Eyes large, laterally protruding, partially covered by an elongate eye-canthus extending laterad. Antennal club approximately as long as the footstalk.

Pronotum (Fig. 1). Trapezoidal, approximately as long as wide, moderately convex dorsally, with gently curved lateral margins with posterior margin weakly and roundly emarginate at middle; surface entirely glabrous. Punctation composed of a mixture of coarse and fine punctures, becoming sparser and finer on posteromedial area. A distinct longitudinal white macula is present along each lateral declivity, with an additional pair of small inner white spots medially.

Scutellum (Fig. 1). Triangular with length 1.2 times as long as width, elongate, nearly flat; surface moderately shiny, smooth, without punctures, entirely glabrous.

Elytra (Fig. 1). Somewhat elongate, with a broad base, largely glabrous but distally with some short setae on declivity. Two distinct costae on each elytron extending from middle to the distal declivity, meeting each other at distal end. Punctures on outer areas large and moderately dense, occasionally contiguous and forming C- or U-shaped impressions; punctures on inner areas somewhat large and sparser, notably sparse around scutellum.

Pygidium (Fig. 4). Broad, pentagonal; surface flat, coarsely and densely, rugose in part.

Venter (Figs. 2–3). Prosternum broad, densely rugose. Mesosternum broad densely with punctures sometimes contiguous and forming wavy or C-shaped impressions; mesosternal process developed and broadly rounded. Abdomen with 2–3 transverse rows of C-shaped punctures on each ventrite; ventrite 6 noticeably short and compressed, protruded ventrally.

Legs (Figs. 1–2, 7). Femora densely covered with long setae. Protibiae apically with two distinct outer teeth, with one rudimentary outer tooth at middle; posterior surface with three longitudinal grooves, apically with one well-developed spur. Meso- and metatibiae each equipped with two well-developed apical spurs. Length ratios of tarsomeres I–V approximately 1.0 : 1.7 : 1.6 : 1.6 : 2.0; tarsomere I short, tarsomeres II–V elongate; claws slender and simple.

Aedeagus (Figs. 5–6). Parameres elongate and symmetrical; sub-apices without any distinct swelling; apices curved outward. Each paramere with outer margins shallowly depressed at just after middle.

Sexual dimorphism (Figs. 8–11)**.** Females differ from males as follows: third outer tooth of protibia well-developed; abdominal ventrite 6 not protruded ventrally.

Variability (Figs. 1–11)**.** Body length measured from anterior margin of clypeus to elytral apex 11.96–15.53 mm, maximum width measured around humeri 6.07–8.10 mm (n = 20, including both sexes). The body color ranges from green to deep green, pale reddish green and shiny. Maculae ranges from white to light yellowish brown, occasionally with a small macula on scutellum; One or two small maculae sometimes present at base of elytron, sometimes absent in some individuals; one or two pairs of maculae sometimes occurring on abdominal ventrites 1 to 5, but sometimes absent in some specimens. Dorsal surface of elytra either glabrous or bears sparse setae in some individuals.

Etymology. The specific epithet "polita" refers to the glossy green appearance of this new species, a distinguishing morphological characteristic.

Distribution. Japan: Ryukyu Islands: Miyako Islands (Tarama-jima Island, and Minna-jima Island) (Fig. 38)

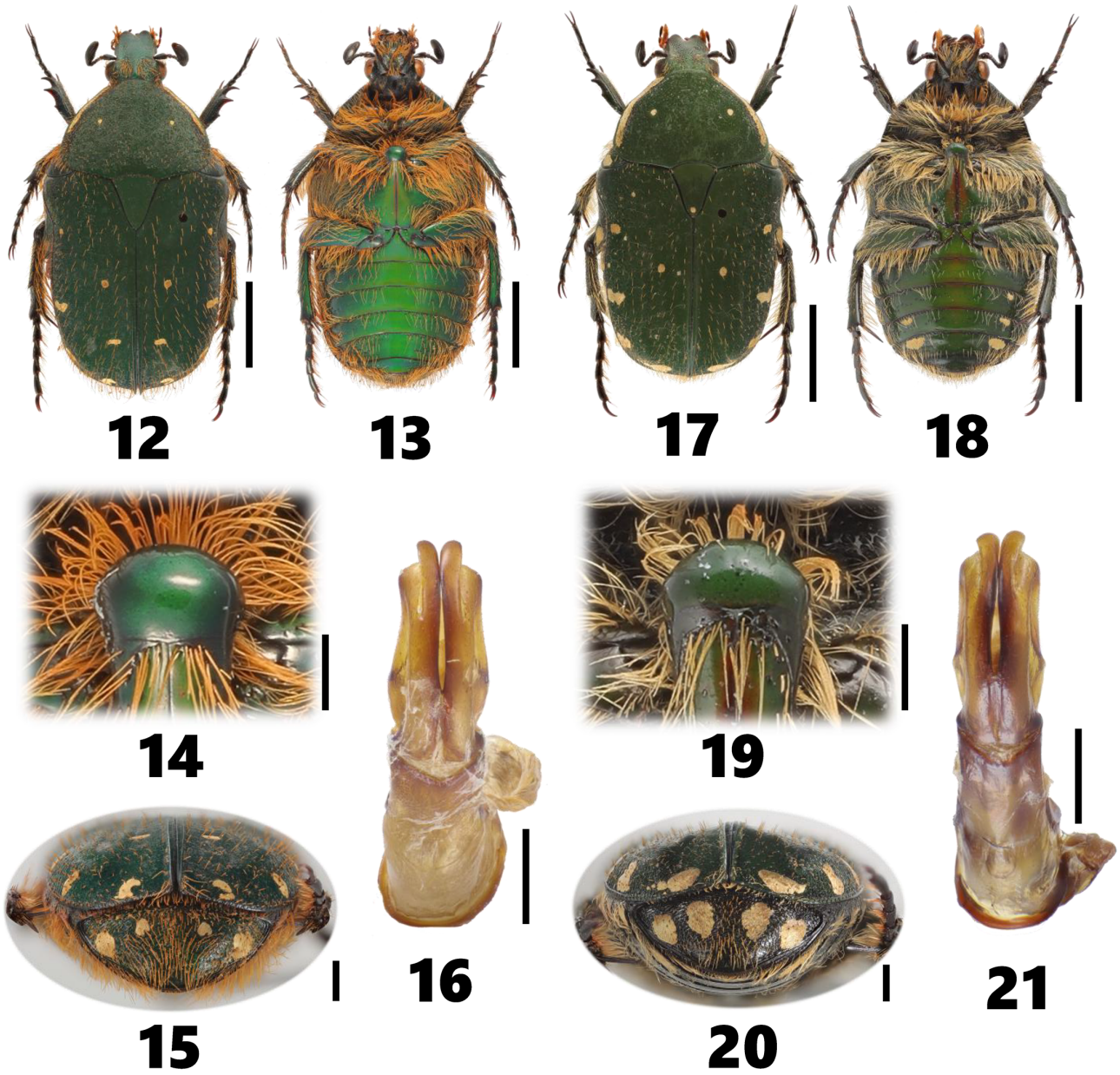
Differential diagnosis. This new species is morphologically similar to *G. forticula* (Figs. 12–16, 30–31) and *G. ishigakiana* (Figs. 17–27, 32–35) but is identified by the following combination of characteristics (Figs. 1–11, 28–29): absence of tomentum on the dorsum; body enamel-like glossy; punctures on elytra large (Figs. 28–29); denser punctation around the scutellum compared to *G. ishigakiana yonakuniana* (Figs. 29, 35); subapical part of parameres lacking any distinct swelling laterally (Fig. 6).

Remarks. In Tarama-jima Island, *G. ishigakiana* is distributed sympatrically with this new species. The two species were distinguished based on their external morphology.

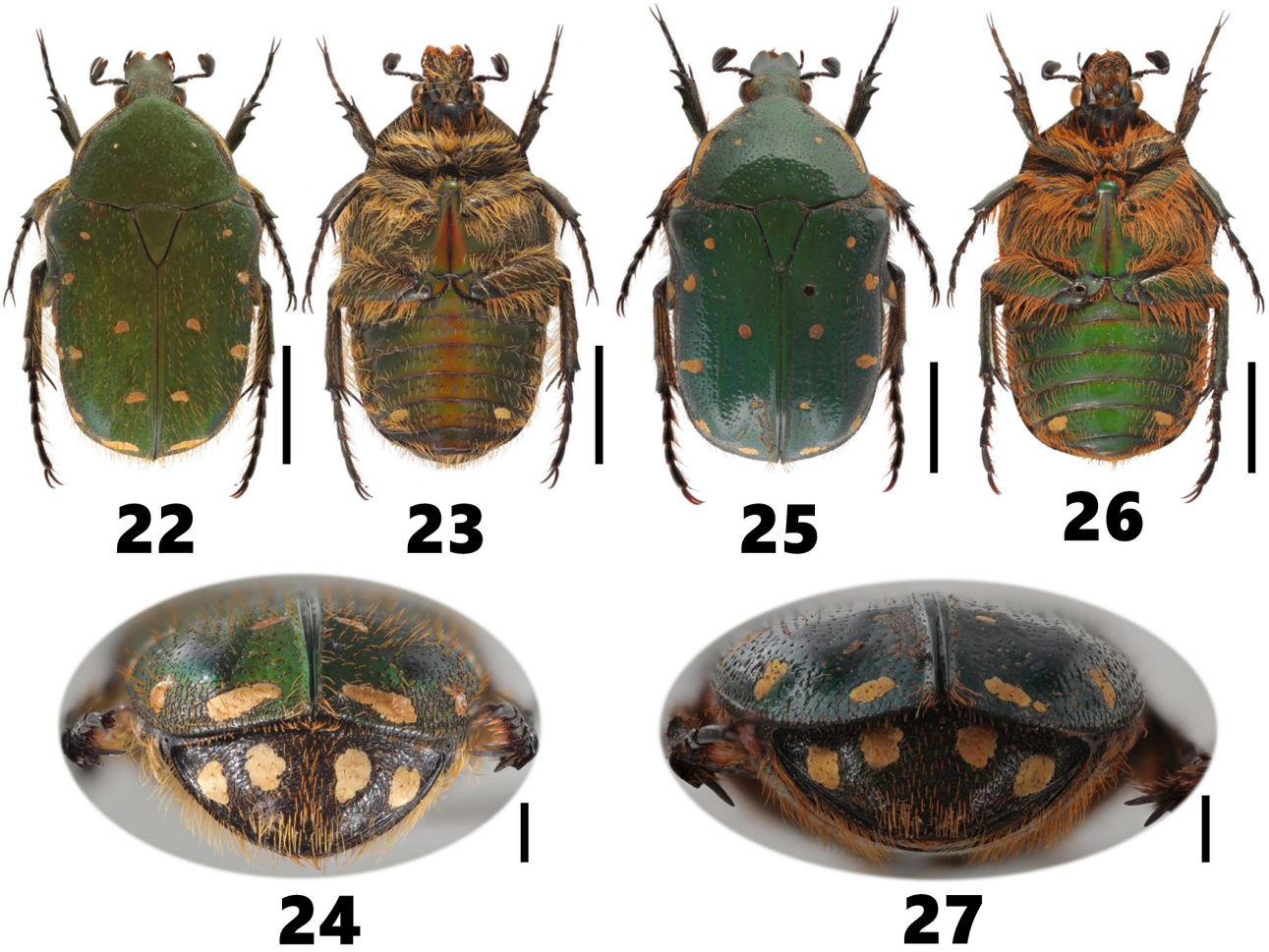
This new species was collected from the flowers of *Premna serratifolia* L. (Fig. 36).

***Gametis ishigakiana* (Nomura, 1959)**
[Japanese name: Ishigaki-koao-hanamuguri]
(Figs. 17–27, 32–35)

Oxycetonia jucunda ishigakiana Nomura, 1959: 53.
Oxycetonia jucunda miyakoana Nomura, 1959: 53.
Oxycetonia jucunda yonakuniana Nomura, 1959: 53.
Gametis forticula ishigakiana: Mikšič 1982: 182.
Gametis forticula miyakoana: Mikšič 1982: 182.
Gametis forticula yonakuniana: Mikšič 1982: 182.



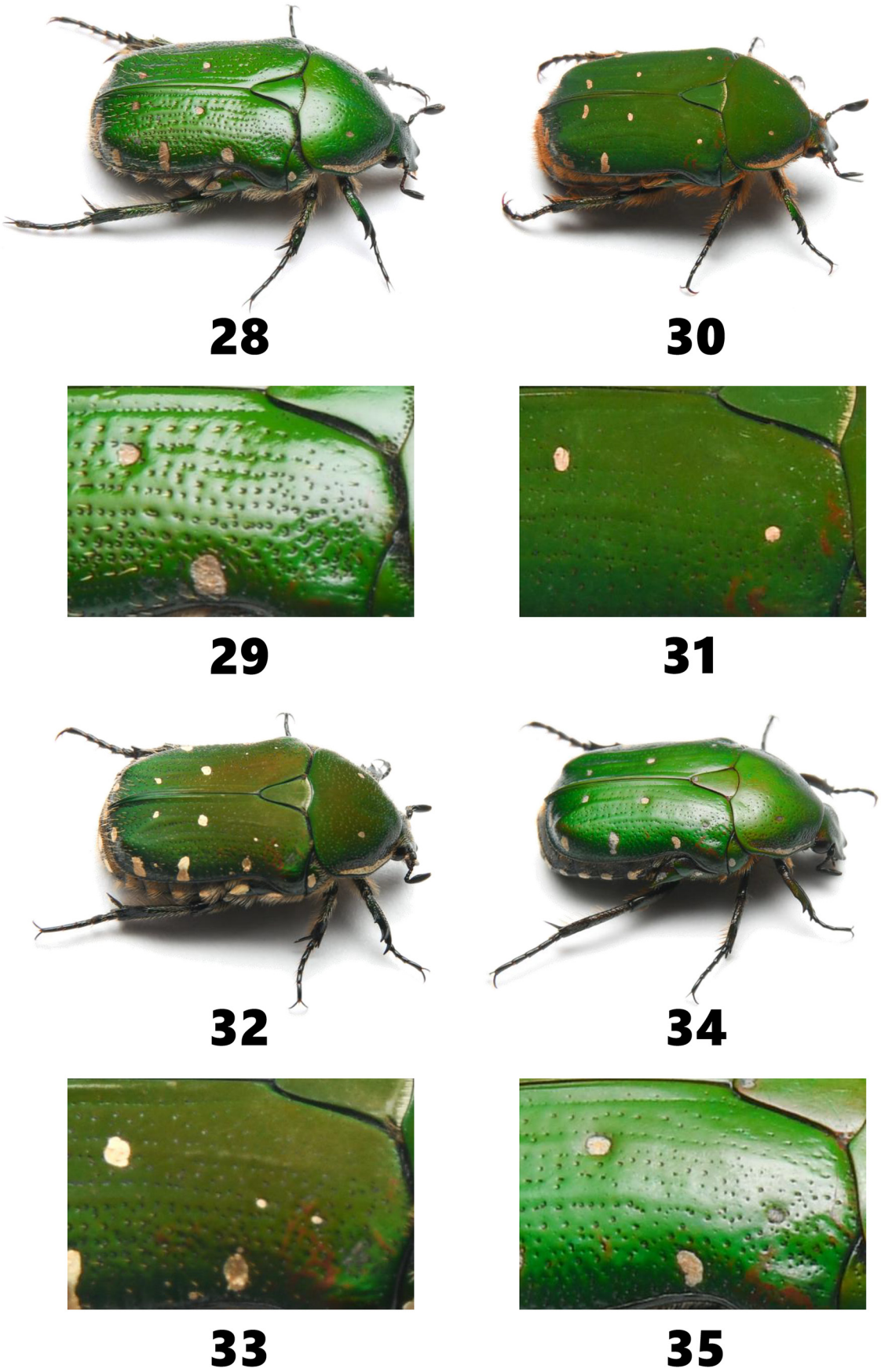
FIGURES 12–21. *Gametis forticula*: 12–16, male; 12–13, habitus, dorsal (12) and ventral views (13); 14, mesosternal process, ventral view; 15, pygidium, dorsal view; 16, parameres, dorsal view. *Gametis ishigakiana ishigakiana*, male; 17–21; 17–18, habitus, dorsal (17) and ventral views (18); 19, mesosternal process, ventral view; 20, pygidium, dorsal view; 21, parameres, dorsal view. Scale bars = 5 mm (12–13, 17–1); 1 mm (15–16, 20–21); 0.5 mm (14, 19).



FIGURES 22–27. *Gametis ishigakiana miyakoana*: 22–24, male; 22–23, habitus, dorsal (22) and ventral views (23); 24, pygidium, dorsal view. *Gametis ishigakiana yonakuniana*: 25–27, male; 25–26, habitus, dorsal (25) and ventral views (26); 27, pygidium, dorsal view. Scale bars = 5 mm (22–23, 25–26); 1 mm (24, 27).

Specimens examined. *Gametis ishigakiana miyakoana*. (10 ♂♂, 31 ♀♀). [JAPAN: Miyako Islands] 5 ♂♂, 20 ♀♀ (EUMJ, PCWK), Nobarrugoshi, Miyako-jima Island, 30. III. 1984, Kaoru Wada leg.; 1 ♀ (PCYS), Tako park, Shimojikurima, Kurima-jima Island, 13. III. 2022, Yûhi Seshima leg.; 1 ♂, 3 ♀♀ (PCYS), Irabumaesatozoe, Irabu-jima Island, 13. V. 2021, Tomoya Saeki leg.; 1 ♀ (PCYS), Mt. Maki, Irabuikemazoe, Irabu-jima Island, 11. III. 2022, Yûhi Seshima leg.; 4 ♂♂, 6 ♀♀ (PCYS), same locality, 12. III. 2022, Yûhi Seshima leg.; *Gametis ishigakiana ishigakiana*. (4 ♂♂, 54 ♀♀). [JAPAN: Yaeyama Islnads] 49 ♀♀ (EUMJ, PCKW), Mt. Banna, Ishigaki-jima Island, 4. IV. 1983, Kaoru Wada leg.; 4 ♂♂, 1 ♀ (PCYS), Mt. Buzama, Kabira, Ishigaki-jima Island, 15. III. 2021, Yûhi Seshima leg.; 1 ♀ (PCYS), Haemi, Iriomote-jima Island, 26. III. 2019, Tomoya Saeki leg.; 3 ♀♀ (PCKW), Taketomi-jima Island, 5. IV. 1983, Kaoru Wada leg.; *Gametis ishigakiana yonakuniana*. (2 ♂♂, 11 ♀♀). [JAPAN: Yaeyama Islands] 1 ♂ (PCKW), Hikawa, Yonaguni-jima Island, 30. III. 1980, H. Uraoka leg.; 5 ♀♀ (PCKW), Higashi-zaki, Yonaguni-jima Island, 30. VII. 1985, H. Tanaka leg.; 1 ♀ (PCKW), Kubura-bari, Yonaguni-jima Island, 30. VII. 1985, H. Tanaka leg.; 1 ♀ (PCKW), Kubura, Yonaguni-jima Island, 31. VII. 1985, H. Tanaka leg.; 1 ♂, 4 ♀♀ (EUMJ, PCYS), Mt. Inbi-dake, Yonaguni-jima Island, 24. III. 2023, Takumi Aiso leg.

Distribution. *Gametis ishigakiana ishigakiana*. Japan: Ryukyu Islands: Miyako Islands (Tarama-jima Is.) and Yaeyama Islands (Ishigaki-jima Is., Iriomote-jima Is., Hatoma-jima Is., Kohama-jima Is., Taketomi-jima Is., Kuroshima Is., and Aragusuku-jima Is. (= Kamiji-jima Is.)). *Gametis ishigakiana miyakoana*. Japan: Ryukyu Islands: Miyako Islands (Miyako-jima Is., Ogami-jima Is., Irabu-jima Is., Kurima-jima Is., and Minna-jima Is.). *Gametis ishigakiana yonakuniana*. Japan: Ryukyu Islands: Yonaguni-jima Is. (Fujioka 2001; Sasaki *et al*. 2002; Yamazaki *et al*. 2015; Kusui 2012, 2017, 2019; this study).



FIGURES 28–35. Live specimens of *Gametis*, dorso-lateral view. 28–29, *Gametis polita* **sp. nov.**, 28, habitus, 29, punctures on elytra; 30–31, *Gametis forticula*, 30, habitus, 31, punctures on elytra; 32–33, *Gametis ishigakiana ishigakiana*, 32, habitus, 33, punctures on elytra; 34–35, *Gametis ishigakiana yonakuniana*, 34, habitus, 35, punctures on elytra.

Remarks. The subspecies, *Gametis ishigakiana miyakoana* (Nomura, 1959) (Figs. 22–24) and *G. ishigakiana yonakuniana* (Nomura, 1959) (Figs. 25–27, 34–35), are herein transferred from *G. forticula* to *G. ishigakiana* based on both morphological characteristics and mitochondrial COI gene sequence data.

The three subspecies were described on the same paper by Nomura (1959). Among them, *G. f. ishigakiana* is the most widely distributed and common. Following recommendation 24A of the International Code of Zoological Nomenclature (ICZN 1999), *G. f. ishigakiana* is selected here as the nominotypical subspecies under the First Reviser Rule.

Key to species of the genus *Gametis* in Japan

1 Head and venter black; lateral margins of pronotum broadly bordered with black area; lateral margins of parameres straight in dorsal view . . . . . *G. jucunda* (Faldermann, 1835)

\- Head and venter green to red; lateral margins of pronotum either unbordered with black area or bordered with a very narrow black line; lateral margins of parameres not straight in dorsal view 2

2 Dorsum without tomentum, glossy, enamel-like appearance; punctures on elytra large (Figs. 28–29); subapical part of parameres (Fig. 6) not laterally expanded . . . . . *G. polita* **sp. nov.**

\- Dorsum covered with tomentum or, if lacking tomentum glossy; punctures on elytra small (Figs. 30–35); subapical part of parameres (Figs. 16, 21) laterally expanded. 3

3 Mesosternal process narrow (Fig. 14); abdominal ventrites lacking maculae (Fig. 13); pygidium with small maculae (Fig. 15); apex of parameres (Fig. 16) somewhat elongated . . . . . *G. forticula* (Janson, 1881)

\- Mesosternal process moderately broad (Fig. 19); abdominal ventrites with several maculae (Figs. 18, 23, 26); pygidium with large maculae (Figs. 20, 24, 27); apex of parameres (Fig. 21) somewhat shortened. . . . . *G. ishigakiana* (Nomura, 1959)

FIGURE 36. Habitat of *Gametis polita* **sp. nov.**, Tarama-jima Island (type locality). Photo by Fubito Aizawa.

Discussion

The taxonomic status of species of the Japanese *Gametis*, *G. forticula* and *G. jucunda*, has been a subject of long-standing debate. In earlier studies, there were two contrary opinions: they are different species (Mikšič 1982; Kurosawa 1985) or conspecific (Arrow 1913; Sawada 1950; Nomura 1959). Currently, the prevailing view considers them distinct species, based on morphological characteristics and their sympatric occurrence (Sakai 2003, 2012). In this study, we present the first DNA-based analysis of interspecific relationships within the Japanese *Gametis*. The genetic distances between *G. jucunda* and any formerly recognized subspecies of Japanese *G. forticula* exceed 6 % (Table 3) as well as the distance between two distinct species of the genus *Cetonia* (4.96 %). Therefore, the two Japanese species of the genus *Gametis* are supported as being distinct species.

Furthermore, the population of *Gametis* from Tarama-jima Island, previously suggested to be a distinct subspecies of *G. forticula* due to its unique morphological features (Wada 1985; Sakai 2012), was found to be genetically distinct from *G. jucunda* as well as any formerly recognized subspecies of Japanese *G. forticula*, with genetic distances of more than 5 % (Table 3). The Tarama-jima population can also be distinguished from other congeners by the following morphological characteristics: tomentum on dorsum absent; body enamel-like glossy; punctures on elytra large; subapical part of parameres not laterally expanded. This result clearly supports the recognition of the Tarama-jima population as a distinct species. In addition, a population exhibiting the same morphological characteristics as the Tarama-jima population is confirmed from Minna-jima Island. Therefore, both the Tarama-jima and Minna-jima populations are described as a new species, *G. polita* **sp. nov.**

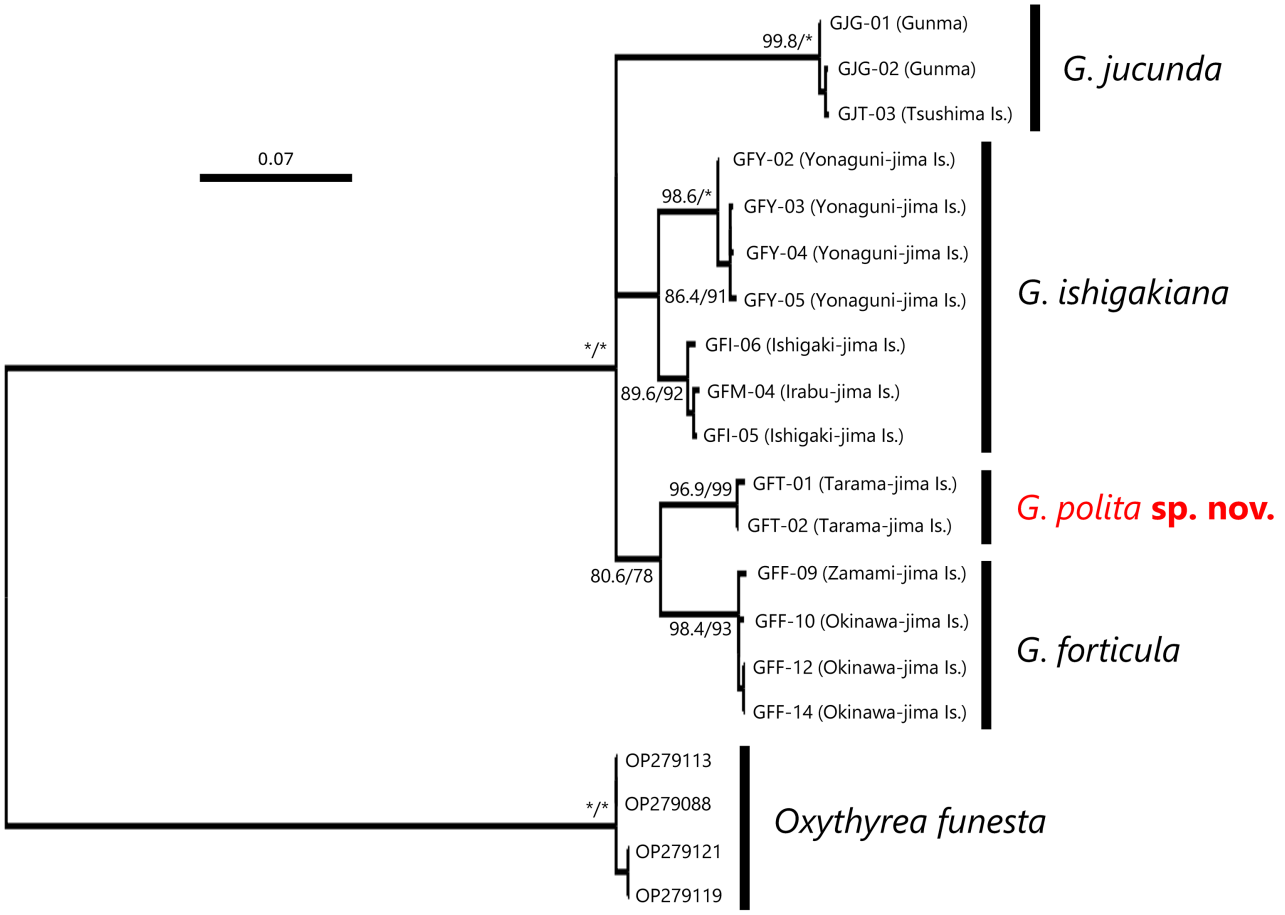


FIGURE 37. Phylogenetic tree of *Gametis* based on mitochondrial COI region, using the ML methods. Values at nodes represent Shimodaira-Hasegawa approximate likelihood ratio test values (SH-aLRT) / Ultrafast bootstrap values (UFBoot). Asterisk (*) indicates 100 %.

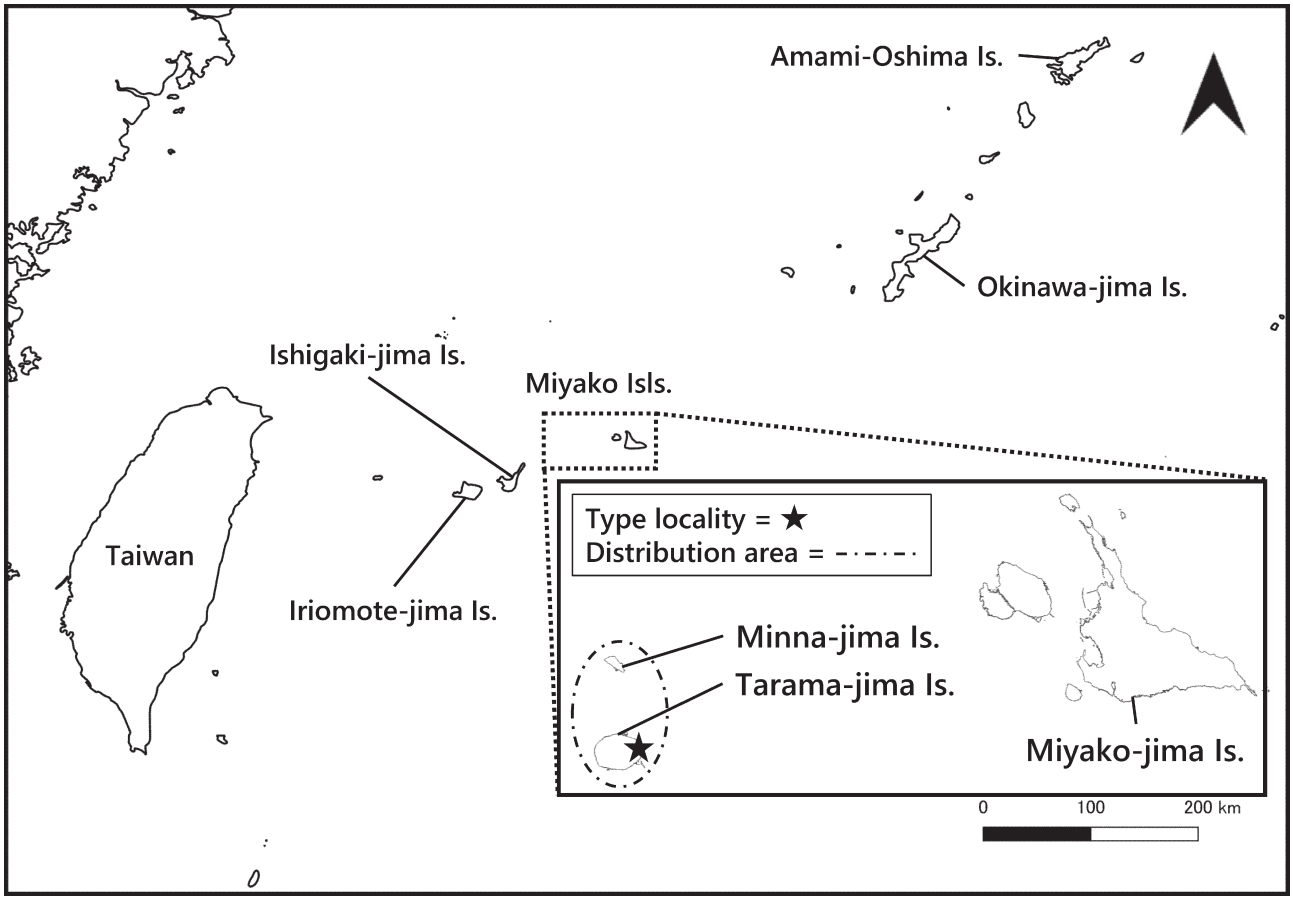


FIGURE 38. Map showing the distribution of *Gametis polita* **sp. nov.**

This study also revealed that the subspecies formerly placed under *G. forticula* in southern Ryukyus (as *G. f. ishigakiana*, *G. f. miyakoana*, and *G. f. yonakuniana*) (Fig. 37) are genetically differentiated from the nominotypical subspecies (*G. f. forticula*) with genetic distances slightly higher than one of two *Cetonia* species (approximately 5 %; Table 3), which suggests potential species-level differentiation. Among the formerly recognized subspecies, *G. f. miyakoana* is nested within *G. f. ishigakiana*, with minimal genetic divergence (<1 %) between these subspecies, supporting previous studies that questioned their subspecific validity due to the lack of distinct diagnostic characters (Mikšič 1982; Sakai 2003). In contrast, *G. f. yonakuniana* forms a monophyletic group with strong support values, with slightly higher divergence from the two subspecies (~3%), and is morphologically distinguishable by its conspicuously glossy dorsal surface (Sakai 2003). Based on these findings, we propose elevating *G. f. ishigakiana* to species rank as *Gametis ishigakiana*, and transferring *G. f. yonakuniana* to subspecific status under this species as *G. ishigakiana yonakuniana*, *Gametis f. miyakoana* is also provisionally transferred to *G. ishigakiana* as *G. ishigakiana miyakoana*, although future morphological and molecular studies may support its synonymization with *G. ishigakiana ishigakiana*.

In this paper, the taxa formerly regarded as *Gametis forticula* in Japan are taxonomically revised with molecular and morphological evidence. However, the taxonomic status of the three subspecies distributed in Taiwan, *G. forticula formosana* (Nomura, 1959), *G. forticula kotoensis* (Nomura, 1959), and *G. forticula lutaoensis* (Kobayashi, 1989), has not been reassessed. Further reassessment of their taxonomic treatment, incorporating not only morphological but also DNA-based analyses, will be required in future studies.

Acknowledgements

We sincerely thank Assos. Prof. Katsuyuki Eguchi (TMU) for insightful comments on this study and for providing reagents and equipment for molecular experiments. We are deeply grateful to Prof. Kaoru Wada (Meisei University)

for providing important literature and specimens essential to this study. We are also grateful to Mr. Takumi Aiso (Miyagi), Mr. Kyosuke Iwasaki, Mr. Takehito Yanagihara (TUA), Mr. Tomoya Saeki (Kanagawa), and Mr. Kaoru Sakai (Tokyo) for kindly providing important specimens and materials. We thank Mr. Fubito Aizawa (Tokyo) for kindly providing important specimens and ecological photography. We would like to express our appreciation to Mr. Koki Hayashi, Mr. Toshimichi Nagai, Mr. Joe Kutsukake (TMU), and Mr. Yuto Shirao (Tokyo) for their assistance with molecular experiments. We are grateful to Meisei University and Mr. Ryosuke Ishida (Meisei University) for support with morphological measurements. We sincerely thank Laboratory of Entomology (TUA) for providing photography equipment, and Mr. Shu Arai (TUA) for the assistance. We further thank Mr. Tadafumi Nakata, Mr. Taichi Morino (Okinawa), and Mr. Takanao Hashimoto (Kyushu University) for their help in field investigations. This study was supported by the Sasakawa Scientific Research Grant from the Japan Science Society and JST SPRING, Japan Grant Number JPMJSP2156.

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