ASED http://e-ASED.org
Animal Systematics, Evolution and Diversity

Anim. Syst. Evol. Divers. *Vol. 40, No. 4: 276-284, October 2024*
https://doi.org/10.5635/ASED.2024.40.4.009

The First Report of the Feather Mite *Alloptes obtusolobus* (Acari: Alloptidae) from the Vega Gull *Larus vegae* (Charadriiformes: Laridae) in Korea

Sung-Yeon Yoo[1], Jong-Kyeong Hwang[1], Sergey V. Mironov[2], In-Ki Kwon[1], Deokki Kim[1], Yeong-Deok Han[1,*]

[1]Research Center for Endangered Species, National Institute of Ecology, Yeongyang 36531, Korea
[2]Zoological Institute, Russian Academy of Sciences, Universitetskaya Embankment 1, Saint-Petersburg 199034, Russia

ABSTRACT

The alloptid feather mite *Alloptes* (*Sternalloptes*) *obtusolobus* Dubinin 1951, isolated from the Vega Gull *Larus vegae* Palmén, 1887 (Charadriiformes: Laridae), is recorded for the first time in Korea. This mite can be clearly distinguished from the closest species, *A.* (*S.*) *oxylobus* Dubinin, 1951, by the following characteristics: in males, the length of the gento-anal field is over 140, the distance between setae *4b* and *g* is less than 2/5 the distance between setae *g* and *h2*, and setae *4a* and *ps3* are usually at the same transverse level; in females, the opisthosomal lobes are slightly shorter than wide at the base, the terminal cleft is equal to or shorter than the supranal concavity, and the ambulacral discs of legs IV extend slightly beyond the lobar apices. This study provides a morphological redescription of *A.* (*S.*) *obtusolobus*, supplemented with photographs and with partial sequences of mitochondrial cytochrome *c* oxidase subunit I (*COI*) as the DNA barcode marker, since its recent record in the Korean fauna.

Keywords: *Alloptes* (*S.*) *obtusolobus*, *COI*, feather mite, Korea, Vega Gull

INTRODUCTION

The feather mite genus *Alloptes* Canestrini, 1879 (Analgoidea: Alloptidae), with 55 described species, is one of the most specious genera of the family (Gaud, 1972; Vasyukova and Mironov, 1991; Kivganov and Mironov, 1992; Mironov and Palma, 2006, Han et al., 2021, 2022). Representatives of this genus are associated with birds of the order Charadriiformes, with the exception of one questionable record from museum specimens of procellariiform hosts. The genus is divided into four subgenera: *Alloptes* Canestrini, 1879, *Apodalloptes* Gaud, 1972, *Conuralloptes* Gaud, 1972, and *Sternalloptes* Mironov, 1992 (Gaud, 1972; Kivganov and Mironov, 1992).

The subgenus *Sternalloptes* is distinguished from other subgenera in the following combination of morphological characters. In both sexes of *Sternalloptes*, genual setae *mG*II are short spine-like with a widely rounded apex; in males, the opisthosoma is triangular with a gradually expanded posterior end, and idiosomal setae *h3* could be present or absent; in females, idiosomal setae *f2* and *ps1* are absent (Kivganov and Mironov, 1992; Han et al., 2021; Hernandes and Brito, 2022). This subgenus comprises 21 valid species known from avian hosts of the families Dromadidae, Laridae, and Stercorariidae (Charadriiformes: Lari) (Gaud, 1976; Vasyukova and Mironov, 1991; Kivganov and Mironov, 1992; Mironov and Kivganov, 1993; Han et al., 2021; Hernandes and Brito, 2022). *Alloptes* (*S.*) *fauri* Gaud, 1957, found on the Black-tailed Gull *Larus crassirostris* Vieillot, 1818, is the only species of this subgenus, which has been reported so far in Korea (Han and Min, 2019).

The Vega Gull, *Larus vegae* Palmén, 1887, is a large gull belonging to the genus *Larus* Linnaeus, 1758 (Charadriiformes: Laridae) and is one of six Arctic endemics (Olsen and Larsson, 2004; Gilg et al., 2023; Gill et al., 2024). Status of some species in the genus *Larus* is disputable, because of interspecific hybridization, including *L. vegae*, which is sometimes considered a subspecies of the American Herring Gull, *L. smithsonianus* Coues, 1862, or the European Herring Gull,

***To whom correspondence should be addressed**
Tel: 82-54-680-7331, Fax: 82-54-680-7279
E-mail: kingpanda8618@nate.co.kr

eISSN 2234-8190

L. argentatus Pontoppidan, 1763 (Crochet et al., 2002; Collinson et al., 2008; Sternkopf et al., 2010; Dickinson and Remsen, 2013; Clements et al., 2023). Although taxonomic controversies remain, *L. vegae* can be clearly distinguished morphologically and geographically from other gull species. It breeds in northeastern Siberia and is known to winter in China, Japan, Korea, and Taiwan (Liebers et al., 2004; Olsen and Larsson, 2004). In a recent study on the flyways and migratory behavior of *L. vegae* using GPS loggers, individuals captured in Korea and Russia showed results consistent with those obtained previously (Gilg et al., 2023).

Larus vegae (= *L. argentatus vegae*) has been reported to be a host for four feather mites: *Alloptes* (*Sternalloptes*) *obtusolobus* Dubinin, 1951 (Alloptidae), *Laronyssus marinus* (Trouessart, 1886), *Laronyssus martini* (Trouessart, 1885), and *Zachvatkinia larica* Mironov, 1989 (Avenzoariidae) (Dubinin, 1951, 1956; Mironov, 1989). In Korea, there were no records of feather mites from *L. vegae*.

We collected the feather mite *A.* (*S.*) *obtusolobus* from the wing feathers of *L. vegae* while conducting the Offshore Wind Power Related Survey and Tracking Investigation for Endangered shorebirds. In the present study, we provide morphological description of the feather mite *A.* (*S.*) *obtusolobus* and present partial sequences of its mitochondrial cytochrome *c* oxidase subunit I (*COI*) as DNA barcodes for comparison with other species of the genus *Alloptes*.

MATERIALS AND METHODS

Material sampling and description

We captured a juvenile of *L. vegae* using a bownet in Nomulport, Gyeongsangbuk-do, South Korea. Before attaching the GPS tracker, mite samples were collected using 3M Scotch Magic Tape (3M, St. Paul, MN, USA) from the wing feathers, and then immediately preserved in 99% ethanol for 24 h. The collected mite samples were separated from the Scotch tape under a dissecting microscope using a dissecting needle, and cleared in 10% lactic acid for 24 h at room temperature. Permanent mite specimens were mounted on microscope slides using PVA mounting medium (BioQuip, Rancho Dominguez, CA, USA). The mite specimens were observed under a light microscope (DM2500; Leica, Wetzlar, Germany). Images were taken with a digital camera (7D; Canon, Tokyo, Japan) attached to a light microscope and assembled and edited using Adobe Illustrator and Photoshop CS5 (Adobe Systems Incorporated, San Jose, CA, USA).

Species redescriptions is provided according to the standard formats used for the corresponding species of the genus *Alloptes* (Mironov and Palma, 2006; Han et al., 2021, 2022; Hernandes and Brito, 2022). Terminology, idiosomal, and leg chaetotaxy follow those of Gaud and Atyeo (1996), with minor corrections for coxal chaetotaxy by Norton (1998). All measurements are in micrometers (μm). All the examined specimens were deposited at the National Institute of Biological Resources (NIBR), Korea. The classification and scientific names of the birds follow the IOC World Bird List (Gill et al., 2024).

DNA sequencing

The genomic DNA extraction was performed from each of the two specimens using the LaboPas Tissue Genomic DNA Isolation Kit Mini (Cosmo Genetech Inc., Seoul, Korea) according to the manufacturer's instructions. The *COI* barcode fragment was amplified using site-specific primers (bcdF05: 5′-TTTTCTACHAAYCATAAAGATATTGC-3′ and bcdR04: 5′-TATAAACYTCDGGATGNCCAAAAAA-3′) under the following cycling conditions (Dabert et al., 2008): 2 min at 94°C; 40 cycles of 98°C for 15 s, 50°C for 30 s, and 68°C for 60 s; and a final extension at 68°C for 5 min. The amplified products were sequenced on an ABI 3100 automated sequencer (Perkin-Elmer, Foster City, CA, USA). Sequence assembly, alignment, and trimming were performed using the Geneious 8.1.9 software (Kearse et al., 2012).

Two partial *COI* sequences of *A. obtusolobus* were aligned with those of ten other *Alloptes* species registered in the National Center for Biotechnology Information (NCBI) database using Geneious v. 8.1.9 (Table 1). Pairwise distances between sequences were computed using the Kimura two-parameter (K2P) substitution model with the Mega X v. 10.1.7 software (Kumar et al., 2018).

SYSTEMATIC ACCOUNTS

Order Sarcoptiformes Reuter, 1909
Family Alloptidae Gaud, 1957
Subfamily Alloptinae Gaud, 1957
Genus *Alloptes* Canestrini, 1879
Subgenus *Sternalloptes* Mironov, 1992

[1]***Alloptes** (***Sternalloptes***) ***obtusolobus*** **Dubinin, 1951 (Figs. 1–3)**

Alloptes obtusolobus Dubinin 1951: 249, fig. 70; Radford, 1958: 132; Atyeo and Peterson, 1967: 98; 1970: 130; Černý, 1967: 13; Jablonska, 1986: 59, table 3; Choe and Kim, 1991: 818, 819, figs. 3, 4; Vasyukova et al., 1996: 617, table 5; Galloway et al., 2014: 167, 181.

Alloptes (*Conuralloptes*) *obtusolobus*: Gaud, 1976: 12, 14, 16, 20, figs. 2, 4; Vasyukova and Mironov, 1991: 88, 95, fig. 68.

Korean name: [1]*짧은꼬리갈매기깐깃털진드기 (신칭)

Table 1. List of *Alloptes* species used in molecular analysis and the respective references

Species	Collection host	Collection locality	GenBank accession No.	Reference
Alloptes (*Alloptes*) *aschizurus*	*Chionis albus*	King George Island, Antarctica	MZ489638	Han et al. (2021)
Alloptes (*Apodalloptes*) *orthogramme*	*Actitis hypoleucos*	Cheongyang-gun, Korea	MK456598	Han and Min (2019)
Alloptes (*Conuralloptes*) *calidridis*	*Calidris alpina*	Michigan, USA	KU203101	Klimov et al. (2017)
Alloptes (*C.*) *chionis*	*Chionis albus*	King George Island, Antarctica	MZ489639	Han et al. (2021)
Alloptes (*C.*) *limosae*	*Limosa limosa*	Asan-si, Korea	MK456600	Han and Min (2019)
Alloptes (*C.*) *neolimosae*	*Limosa limosa*	Asan-si, Korea	OM102971	Han et al. (2022)
Alloptes (*C.*) *procerus*	*Numenius phaeopus*	Taean-gun, Korea	MK456602	Han and Min (2019)
Alloptes (*Sternalloptes*) *antarcticus*	*Stercorarius maccormicki*	King George Island, Antarctica	MZ489641	Han et al. (2021)
Alloptes (*S.*) *fauri*	*Larus crassirostris*	Ulleung-gun, Korea	MK456605	Han and Min (2019)
Alloptes (*S.*) *obtusolobus*	*Larus vegae mongolicus*	Irkutskaya Oblast, Russia	KU203100	Klimov et al. (2017)
Alloptes (*S.*) *obtusolobus*	*Larus vegae vegae*	Yeongdeok-gun, Korea	PP859274-PP859275	This study
Alloptes (*S.*) *stercorarii*	*Stercorarius parasiticus*	Kongsfjorden, Svalbard	KF018833	Dabert et al. (2015)

Alloptes (*Sternalloptes*) *obtusolobus*: Kivganov and Mironov, 1992: 199.
Alloptes lari: Gaud, 1957: 109, 111, 112, figs. 1C, 2D (in part).

Material examined. 3 males and 3 females (NIBR No. NIBRIV0000913692–NIBRIV0000913697) from the Vega Gull, *L. vegae* (Palmén) (Charadriiformes: Laridae), Korea, Gyeongsangbuk-do (36°26′44″N, 129°26′5″E), 28 Nov 2023, coll. Han Y.-D.

Description. Male (range for three specimens, Figs. 1, 2). Idiosoma, length × width, 350–375 × 213–220. Length of hysterosoma 220–250. Prodorsal shield (Fig. 1A): length 75–77, width at posterior margin 98–110, posterolateral corners angular, posterior margin concave. Scapular setae *se* situated on small plates near lateral margins of prodorsal shield, their bases separated by 108–113. Setae *c2* filiform, 31–36 long. Subhumeral setae *c3* narrowly lanceolate, 16–17 × 1.5–2. Distance between prodorsal and hysteronotal shields along midline 15–33. Hysteronotal shield: greatest length 248–265, width at anterior margin 110–120, anterior margin medially concave, lateral margins with small oblique incisions at bases of setae *d2* and fused laterally with bases of epimerites IV. Opisthosoma shaped as equilateral triangle with posterior end strongly expanded; width at level of setae *h2* 55–56. Length of interlobar septum 83–91. Terminal lamella with three pairs of roughly rectangular festoons; incision between inner pair narrow slit-like (Fig. 2C). Setae *h3* present; setae *ps2* short setiform (Fig. 2D). Macrosetae *h2* cylindrical, not expanded in medial part. Distances between dorsal setae: *c2* : *d2* 60–65, *d2* : *ps1* 175–203.

Epimerites I fused into a Y, with stem about half the total length of epimerites. Bases of trochanters I flanked by narrow sclerotized bands connecting bases of corresponding epimerites; sclerotized bands at bases of trochanters II incomplete (Fig. 1B). Pregenital sclerites distant from each other and connect inner ends of epimerites IIIa and anterior margin of paragenital apodeme (Fig. 1B). Coxal fields III open in anteromedian angle, coxal fields IV closed. Length of genito-anal field 158–168. Genital arch: 20–24 × 30–33. Coxal setae *4b* situated posterior to level of setae *3a*. Bases of setae *4a* on soft tegument. Setae *ps3* situated on L-shaped adanal shields. Distances between ventral setae: *3a* : *4b* 7–10, *4b* : *g* 39–45, *4b* : *4a* 60–63, *g* : *ps3* 20–24, *ps3* : *ps1* 108–115, *4a* : *4a* 120–125.

Distal ends of genua I, II with small dorsal spines (Fig. 2A). Setae *mG* of genua I long spine-like with acute apex, setae *mG*II shaped as short thick spine with blunt apex (Fig. 2B). Legs IV, excluding pretarsus, 245–248 long. Distal margin of tibia IV without small spine (Fig. 2E). Tarsus IV 54–58 long, with claw-like apex; setae *d* small spine like situated at level of seta *f*; setae *e* minute spine-like, barely distinct, situated

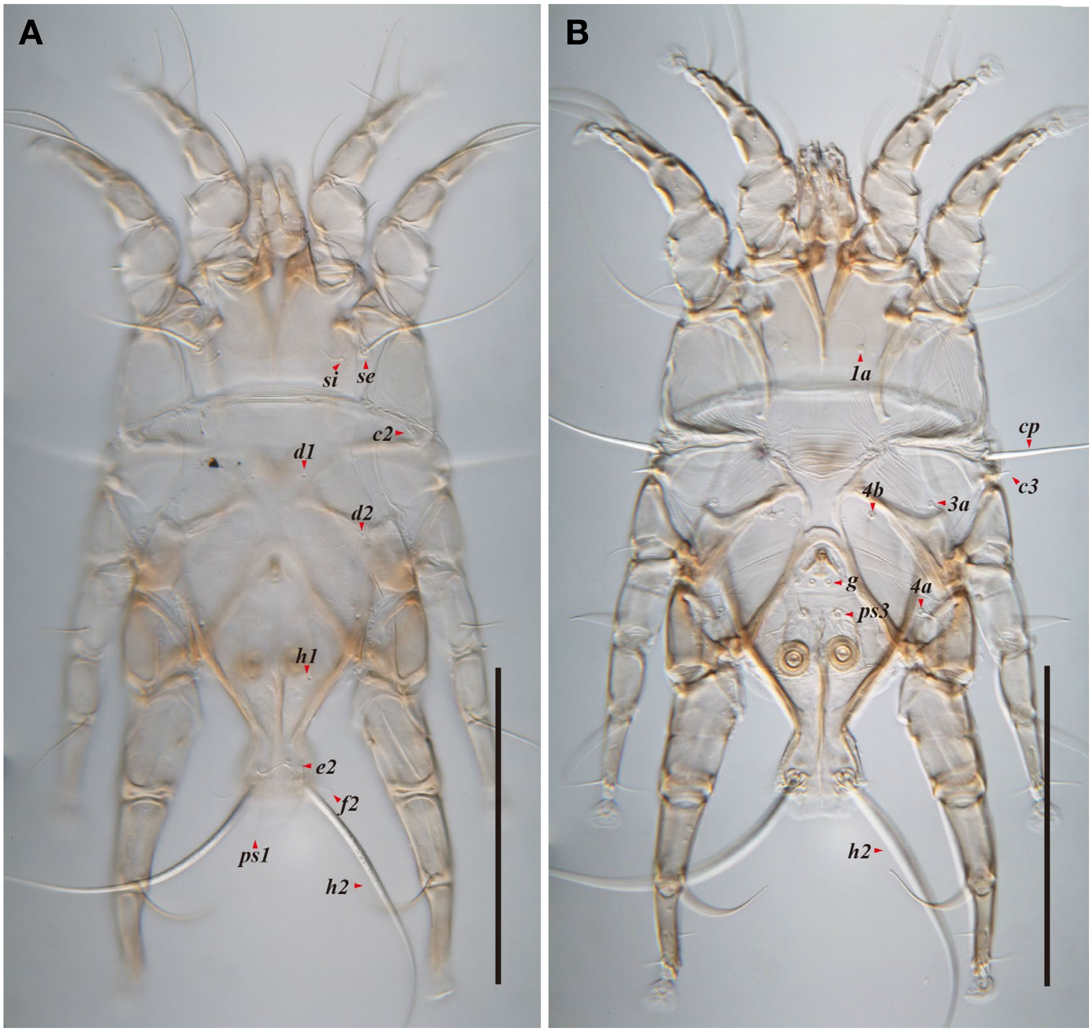

Fig. 1. Male of *Alloptes* (*Sternalloptes*) *obtusolobus* Dubinin, 1951. A, Dorsal view; B, Ventral view. Scale bars: A, B = 200 μm.

near tarsal apex; setae *r* and *w* in basal two-third of the segment (Fig. 2F). Solenidion ϕ of tibia IV 70–80 long, slightly longer that this segment.

Female (range for three specimens, Fig. 3). Idiosoma, length × width, 410–425 × 195–200 (Fig. 3A). Hysterosoma 275–290 long. Prodorsal shield: shaped as in male, 70–83 × 95–99. Setae *se* on small sclerites, separated by 108–110. Setae *c2* filiform, about 29–30 long. Setae *c3* narrowly lanceolate, 15.5–16.5 × 2.5–3. Distance between prodorsal and hysteronotal shields along midline 30–45. Hysteronotal shield: greatest length 270–285, width at anterior margin 77–82, anterior margin straight, surface without ornamentation, posterior part more heavily sclerotized than posterior one. Setae *h1* situated slightly anterior to level of setae *e2*. Setae *f2* and *ps1* absent. Supranal concavity ovate, opened posteriorly, delimited from terminal cleft by a pair of small extensions at level of setae *h2*. Opisthosomal lobes short, slightly wider than long at base; terminal cleft as an inverted U, 21–24 long, 27–29 wide (Fig. 3B). Distances between dorsal setae: *c2* : *d2* 75–80, *d2* : *e2* 135–140, *e2* : *h2* 34–41, *h2* : *h3* 14–16, *h2* : *h2* 57–62, *h3* : *h3* 32–35.

Epimerites I fused into a Y, with stem about one-third the total length of epimerites. Bases of trochanters I flanked by narrow sclerotized bands connecting bases of corresponding epimerites, bands at trochanters II not developed (Fig. 3B). Epimerites IVa barely distinct. Epigynum thick bow-shaped, without lateral extensions, with obliquely cut ends, 24–27 × 61–64. Legs I, II as in the male. Legs IV with ambulacral discs extending slightly beyond level of opisthosomal lobe apices (Fig. 3B). Length of tarsal solenidia: ϕIII 36–39, ϕIV 15–19.

Remarks. *Alloptes* (*Sternalloptes*) *obtusolobus* was first described by Dubinin (1951) based on specimens from the Caspian Gull, *Larus cachinnans* Pallas, 1811, collected from

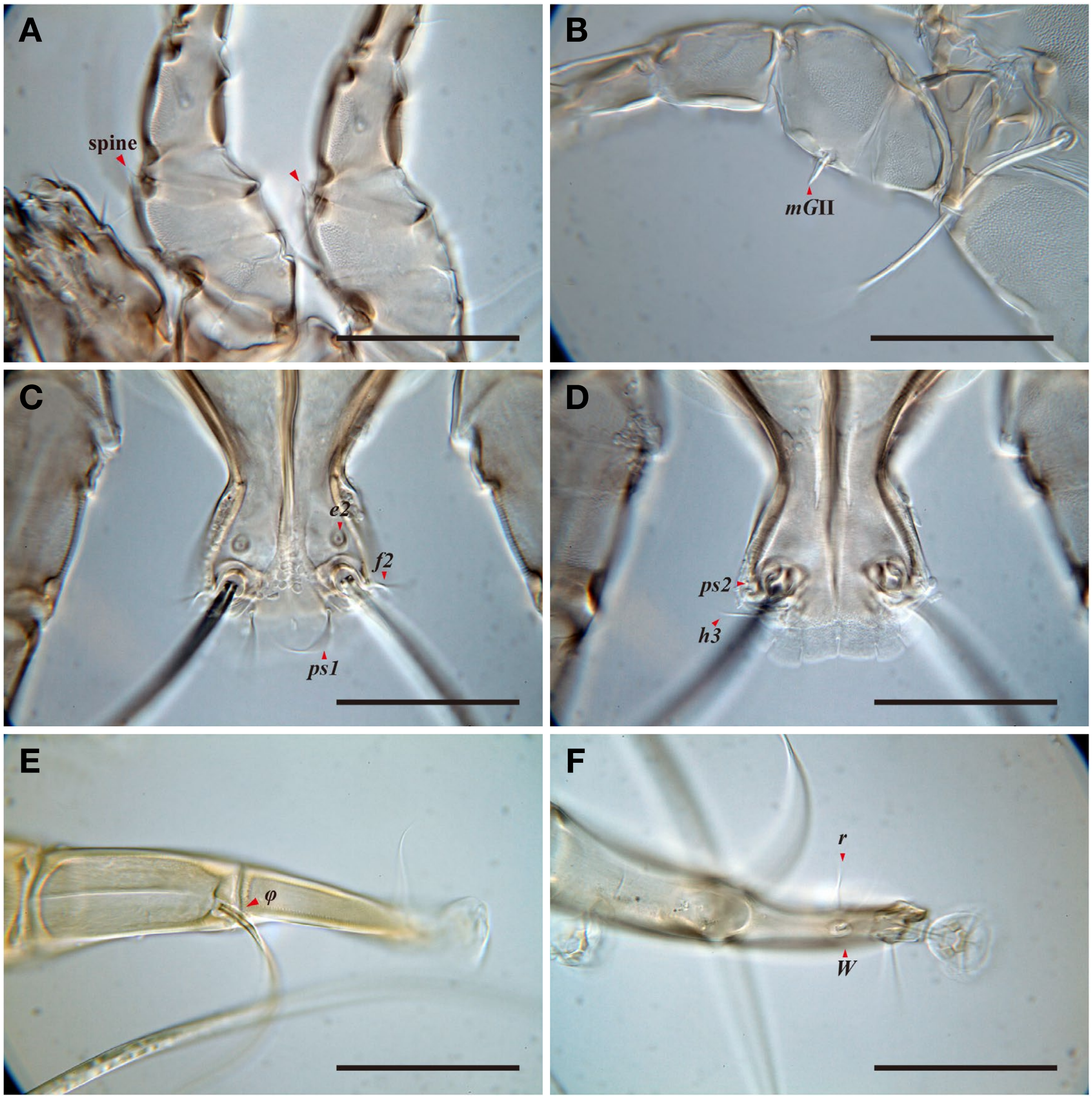

Fig. 2. Male of *Alloptes* (*Sternalloptes*) *obtusolobus* Dubinin, 1951, details. A, Legs I and II; B, Seta *mG* of leg II; C, Dorsal view of opisthosoma; D, Ventral view of opisthosoma; E, Dorsal view of tarsus and tibia IV; F, Ventral view of tarsus IV. Scale bars: A–F = 50 μm.

Lake Chany in Western Siberia, Russia. Additionally, this mite has been recorded on 18 species of gull (Charadriiformes: Laridae): *Chroicocephalus genei* (Brème, 1839) (=*L. genei*), *Chr. saundersi* Swinhoe, 1871 (=*L. saundersi*), *Ichthyaetus ichthyaetus* (Pallas, 1773) (=*L. ichthyaetus*), *I. melanocephalus* (Temminck, 1820) (=*L. melanocephalus*), *Larus argentatus* Pontoppidan, 1763, *L. canus* Linnaeus, 1758, *L. crassirostris* Vieillot, 1818, *L. dominicanus* Lichtenstein, 1823, *L. fuscus* Linnaeus, 1758 (=*L. taimyrensis*), *L. glaucoides* Meyer, 1822 (=*L. leucopterus* Vieillot), *L. marinus* Linnaeus, 1758, *L. vegae* Palmén, 1887, *Leucophaeus pipixcan* (Wagler, 1831), *Pagophila eburnean* (Phipps, 1774), *Rhodostethia rosea* (MacGillivray, 1824), *Rissa brevirostris* (Bruch, 1855), *R. tridactyla* (Linnaeus, 1758), and *Xema sabini* (Sabine, 1819) (see Dubinin, 1951; Černý, 1967; Atyeo and Peterson, 1970; Gaud, 1976; Jablonska, 1986; Choe and Kim, 1991; Vasyukova and Mironov, 1991; Vasyukova et al., 1996; Galloway et al., 2014).

Alloptes (*S.*) *obtusolobus* and *A.* (*S.*) *oxylobus* Dubinin, 1951, two closely related species, are readily distinct from other species of the subgenus *Sternalloptes* in having the following combination of features in males: the opisthosoma is roughly equilateral in shape with strongly enlarged posterior end, setae *h3* are present, and the pregenital apodemes are strongly sclerotized and widely separated from each other. *Alloptes* (*S.*) *obtusolobus* differs from *A.* (*S.*) *oxylobus* in the

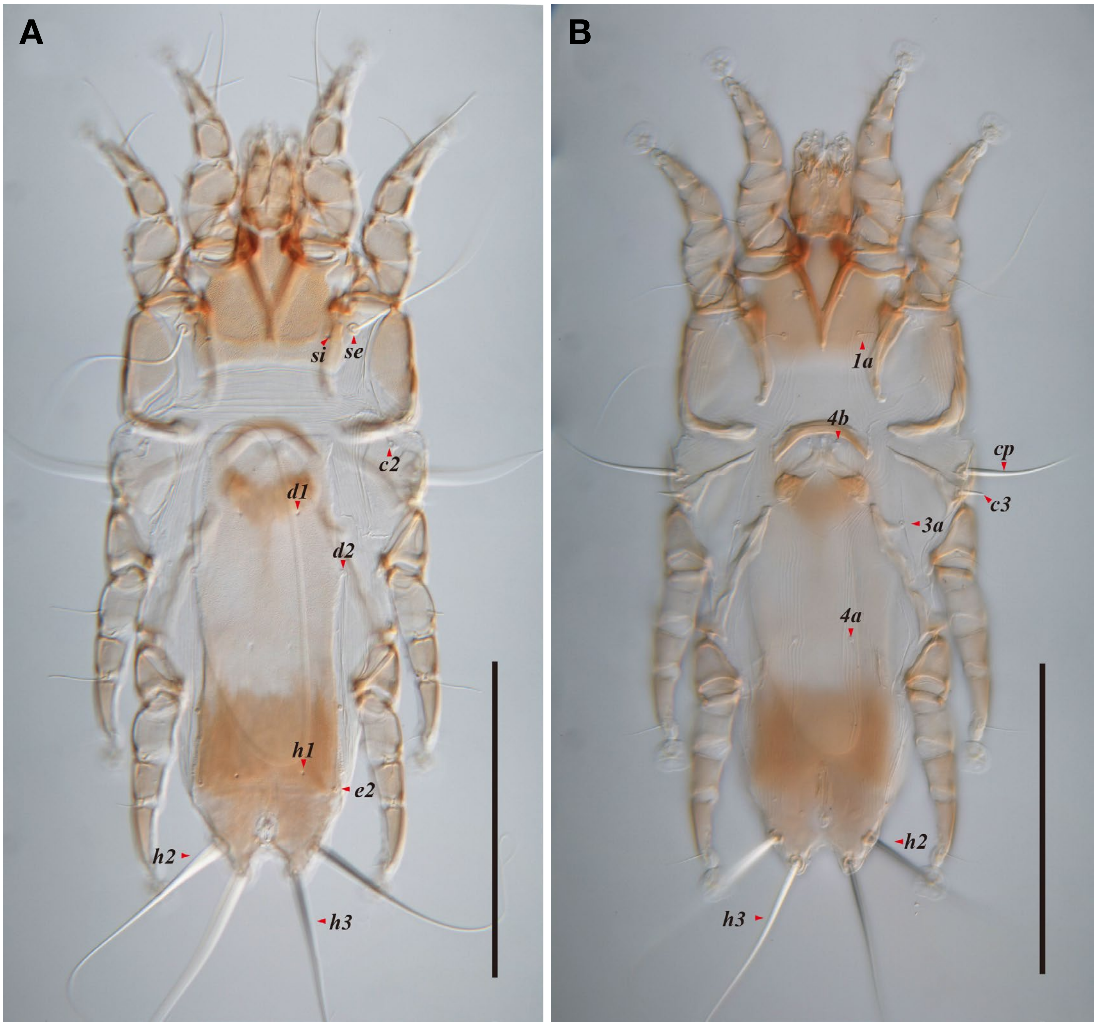

Fig. 3. Female of *Alloptes* (*Sternalloptes*) *obtusolobus* Dubinin, 1951. A, Dorsal view; B, Ventral view. Scale bars: A, B=200 μm.

following characteristics: in males of *A. obtusolobus*, the length of the gento-anal field is over 140, the distance between setae *4b* and *g* is less than 2/5 the distance between setae *g* and *h2*, and setae *4a* and *ps3* are approximately at the same transverse level; in females, the opisthosomal lobes are slightly shorter than wide at the base, the terminal cleft is equal to or shorter than the supranal concavity, and the ambulacral discs of legs IV extend slightly beyond the lobar apices. In males of *A. oxylobus*, the length of the gento-anal field is shorter than 140, the distance between setae *4b* and *g* is longer than 2/5 the distance between setae *g* and *h2*, and setae *ps3* are slightly anterior to the level of setae *4a*; in females, the opisthosomal lobes are distinctly longer than wide at base (1.2–1.4 times), the terminal cleft is distinctly longer than the supranal concavity, and the ambulacral discs of legs IV do not extend the level of lobar apices (Dubinin, 1951; Gaud, 1976; Vasyukova and Mironov, 1991). The morphology of the Korean specimens agrees well with the descriptions and illustrations given by the previous researchers.

The DNA barcode sequence of the mitochondrial *COI* gene was obtained from two Korean specimens and deposited in GenBank under the accession numbers PP859274–PP859275. Intraspecific genetic distances based on 531 bp sequences from *A.* (*S.*) *obtusolobus* ranged from 0.2–18.6%, of which the genetic difference between specimens from *L. vegae vegae* (Korea) and *L. vegae mongolicus* (Russia) was 18.6%. Interspecific genetic distances within the genus *Alloptes* ranged between 14.7–24.5% (Table 2). In taxonomic studies of feather mites using molecular data, the *COI* barcodes showed lower intraspecific and higher interspecific genetic distances with a threshold, in most cases, about 5–6%, suggesting usefulness of this criterion for species delimitation and identification (Dabert et al., 2008, 2011; Jinbo et al., 2011; Glowska et al., 2014; Klimov et al., 2019, 2022). However, hosts of

Table 2. Pairwise genetic distances (*p*-distance) among 11 *Alloptes* species based on mitochondrial cytochrome *c* oxidase subunit I (*COI*) sequences

Species (GenBank accession No.)	*COI* distances (%)											
	1	2	3	4	5	6	7	8	9	10	11	12
1. *Alloptes* (*Alloptes*) *aschizurus* (MZ489638)												
2. *Alloptes* (*Apodalloptes*) *orthogramme* (MK456598)	22.0											
3. *Alloptes* (*Conuralloptes*) *calidridis* (KU203101)	17.3	17.5										
4. *Alloptes* (*C.*) *chionis* (MZ489639)	21.8	17.3	18.1									
5. *Alloptes* (*C.*) *limosae* (MK456600)	20.9	18.1	17.5	18.3								
6. *Alloptes* (*C.*) *neolimosae* (OM102971)	20.3	18.1	19.2	19.2	18.6							
7. *Alloptes* (*C.*) *procerus* (MK456602)	19.8	17.1	16.4	16.8	14.7	18.1						
8. *Alloptes* (*Sternalloptes*) *antarcticus* (MZ489641)	21.1	19.4	18.8	22.2	20.9	20.5	20.7					
9. *Alloptes* (*S.*) *fauri* (MK456605)	23.4	21.7	23.2	23.2	21.1	21.8	20.7	20.7				
10. *Alloptes* (*S.*) *obtusolobus* (KU203100)	24.1	21.5	22.0	21.1	24.5	24.1	23.2	22.4	22.2			
11. *Alloptes* (*S.*) *obtusolobus* (this study)	23.2	21.1	22.2	22.6	23.5	24.1	21.8	22.8	22.8	18.6		
12. *Alloptes* (*S.*) *obtusolobus* (this study)	23.4	21.3	22.4	22.8	23.5	24.3	22.0	23.0	23.0	18.6	0.2	
13. *Alloptes* (*S.*) *stercorarii* (KF018833)	20.3	19.0	18.5	19.6	19.6	20.9	21.3	15.6	19.6	20.9	20.2	20.3

multihost feather mites, such as *Proctophyllodes musicus* Vitzthum, 1922 (Analgoidea: Proctophyllodidae) and *Analges passerinus* (Linnaeus, 1758) (Analgoidea: Analgidae), showed intraspecific variation of *COI* barcodes over 7% (Doña et al., 2015a, 2015b; Klimov et al., 2017; Dabert et al., 2022).

In conclusion, the Korean specimens of *A.* (*S.*) *obtusolobus* showed no differences from the previously described morphological descriptions, but the *COI* barcode sequences showed the difference from the Russian specimen similar to the rate of interspecies variation. *Alloptes* (*S.*) *obtusolobus* is recorded as a multihost species inhabiting the plumage of many gull species worldwide (Dubinin, 1951; Černý, 1967; Atyeo and Peterson, 1970; Gaud, 1976; Choe and Kim, 1991; Vasyukova and Mironov, 1991; Galloway et al., 2014). Although this mite species can be easily identified according to its current taxonomic concept, morphological variability of this mite from different hosts and parts of the world is not well studied. The original description of *A.* (*S.*) *obtusolobus* is rather brief and based on specimens collected from a number of various gull species from Eurasia and even belonging to different genera (Dubinin, 1951); a careful taxonomic redescription was made only by Gaud (1976) based on specimens from several gull species from Europe and northern Africa; and a few works provided some illustrations (Gaud, 1957; Vasyukova and Mironov, 1991). Therefore, although specimens of *A.* (*S.*) *obtusolobus* collected from different hosts have not been precisely compared in a morphological aspect, and DNA barcode information has been obtained for specimens from only two gull species, our results indicate a high probability that this mite species is a complex of several cryptic species.

ORCID

Sung-Yeon Yoo: https://orcid.org/0000-0002-5741-1690
Jong-Kyeong Hwang: https://orcid.org/0000-0001-6409-6732
Sergey V. Mironov: https://orcid.org/0000-0003-0417-5687
In-Ki Kwon: https://orcid.org/0000-0003-4000-3380
Deokki Kim: https://orcid.org/0000-0002-1302-4330
Yeong-Deok Han: https://orcid.org/0000-0002-6625-8966

CONFLICTS OF INTEREST

Yeong-Deok Han, a contributing editor of the Animal Systematics, Evolution and Diversity, was not involved in the editorial evaluation or decision to publish this article. The remaining authors declare no conflicts of interest.

ACKNOWLEDGMENTS

The authors wish to thank Dr. Min-Seung Yang and Dr.

Seung-Gu Kang (Research Center for Endangered Species, National Institute of Ecology, Korea) for bird trapping and collection of feather mites. This study was supported by the National Institute of Ecology's the "study on interactions between habitat characterisrics and life history traits of endangered insects and invertebrates" (NIE-B-2024-48) and Korea Environment Institute's project the "Offshore Wind Power Related Survey and Tracking Investigation for Endangered shorebirds (II)" (NIE-2023-89). The permit for bird catching was officially approved by the Korean local government through the National Institute of Ecology.

REFERENCES

Atyeo WT, Peterson PC, 1967. Astigmata (Sarcoptiformes): Proctophyllodidae, Avenzoariidae (feather mites). Antarctic Research Series, 10:97-103. https://doi.org/10.1029/AR010p0097

Atyeo WT, Peterson PC, 1970. Acarina: Astigmata: Analgoidea: feather mites of South Georgia and Heard Islands. Pacific Insects Monographs, 23:121-151.

Černý V, 1967. Catalogo de la fauna Cubana. XX. Lista de los acaros parasitos de aves reportadas de Cuba. Trabajos de Divulgacion, Museo Felipe Poey de la Academia de Ciencias de Cuba, 45:1-23.

Choe JC, Kim KC, 1991. Microhabitat selection and adaptation of feather mites (Acari: Analgoidea) on murres and kittiwakes. Canadian Journal of Zoology, 69:817-821. https://doi.org/10.1139/z91-122

Clements JF, Rasmussen PC, Schulenberg TS, Iliff MJ, Fredericks TA, Gerbracht JA, Lepage D, Spencer A, Billerman SM, Sullivan BL, Wood CL, 2023. The eBird/Clements checklist of Birds of the World: v2023 [Internet]. Cornell Lab of Ornithology, Ithaca, Accessed 24 Apr 2024, <https://www.birds.cornell.edu/clementschecklist/download/>.

Collinson JM, Parkin DT, Knox AG, Sangster G, Svensson L, 2008. Species boundaries in the herring gull and lesser black-backed gull complex. British Birds, 101:340-363.

Crochet PA, Lebreton JD, Bonhomme F, 2002. Systematics of large white-headed gulls: patterns of mitochondrial DNA variation in western European taxa. The Auk, 119:603-620. https://doi.org/10.1093/auk/119.3.603

Dabert J, Ehrnsberger R, Dabert M, 2008. *Glaucalges tytonis* sp. n. (Analgoidea, Xolalgidae) from the barn owl *Tyto alba* (Strigiformes, Tytonidae): compiling morphology with DNA barcode data for taxon descriptions in mites (Acari). Zootaxa, 1719:41-52. https://doi.org/10.11646/zootaxa.1719.1.2

Dabert J, Mironov SV, Dabert M, 2022. The explosive radiation, intense host-shifts, and long-term failure to speciate in the evolutionary history of the feather mite genus *Analges* (Acariformes: Analgidae) from the European passerines. Zoological Journal of the Linnean Society, 195:673-694. https://doi.org/10.1093/zoolinnean/zlab057

Dabert M, Bigoś A, Witaliński W, 2011. DNA barcoding reveals andropolymorphism in *Aclerogamasus* species (Acari: Parasitidae). Zootaxa, 3015:13-20. https://doi.org/10.11646/zootaxa.3015.1.2

Dabert M, Coulson SJ, Gwiazdowicz DJ, Moe B, Hanssen SA, Biersma EM, Pilskog HE, Dabert J, 2015. Differences in speciation progress in feather mites (Analgoidea) inhabiting the same host: the case of *Zachvatkinia* and *Alloptes* living on arctic and long-tailed skuas. Experimental and Applied Acarology, 65:163-179. https://doi.org/10.1007/s10493-014-9856-1

Dickinson EC, Remsen JV, 2013. The Howard & Moore complete checklist of the birds of the world. 4th ed. Vol. 1. Non-passerines. Aves Press, Eastbourne, pp. 1-401.

Doña J, Diaz-Real J, Mironov S, Bazaga P, Serrano D, Jovani R, 2015a. DNA barcoding and minibarcoding as a powerful tool for feather mite studies. Molecular Ecology Resources, 15:1216-1225. https://doi.org/10.1111/1755-0998.12384

Doña J, Moreno-García M, Criscione CD, Serrano D, Jovani R, 2015b. Species mtDNA genetic diversity explained by infrapopulation size in a host-symbiont system. Ecology and Evolution, 5:5801-5809. https://doi.org/10.1002/ece3.1842

Dubinin VB, 1951. Feather mites of birds of the Baraba Steppe. Report I. Feather mites of waterfowl and wading birds of the orders of rails, grebes, palmipedes, anserines, herons, gulls and limicoles. Parazitologicheskii Sbornik, 13:120-256 (in Russian).

Dubinin VB, 1956. Feather mites (Analgesoidea). Part III. Family Pterolichidae. Fauna SSSR, Paukoobraznye, Vol. 6, Fasc. 7. AN SSSR, Moscow-Leningrad, pp. 1-813 (in Russian).

Galloway TD, Proctor HC, Mironov SV, 2014. Chewing lice (Insecta: Phthiraptera: Amblycera, Ischnocera) and feather mites (Acari: Astigmatina: Analgoidea, Pterolichoidea): ectosymbionts of grassland birds in Canada. In: Arthropods of Canadian grasslands, Vol. 3. Biodiversity and systematics, part 1 (Eds., Cárcamo HA, Giberson DJ). Biological Survey of Canada, Ottawa, pp. 139-188.

Gaud J, 1957. Acariens plumicoles (Analgesoidea) parasites des oiseaux du Maroc. I. Proctophyllodidae. Bulletin de la Société des Sciences Naturelles et Physiques du Maroc, 37: 105-136.

Gaud J, 1972. Acariens sarcoptiformes plumicoles (Analgoidea): parasites sur les oiseaux Charadriiformes d'Afrique. Annales du Musée Royale de l'Afrique Centrale, Série 8, Sciences Zoologiques, 193:1-116.

Gaud J, 1976. Acariens sarcoptiformes plumicoles parasites sur les oiseaux Lariformes et Columbiformes d'Afrique. Annales du Musée Royale de l'Afrique Centrale, Série 8, Science Zoologique, 214:1-101.

Gaud J, Atyeo WT, 1996. Feather mites of the World (Acarina, Astigmata): the supraspecific taxa. Annales du Musée Royal de l'Afrique Centrale, Sciences Zoologiques, 277, Part 1: 1-193 (text), Part 2:1-436 (illustrations).

Gilg O, van Bemmelen RSA, Lee H, Park JY, Kim HJ, Kim DW, Lee WY, Sokolovskis K, Solovyeva DV, 2023. Flyways and migratory behaviour of the Vega gull (*Larus vegae*), a little-known Arctic endemic. PLoS ONE, 18:e0281827. https://doi.org/10.1371/journal.pone.0281827

Gill F, Donsker D, Rasmussen P, 2024. IOC World Bird List (v14.1). Doi 10.14344/IOC.ML.14.1 [Internet]. Accessed 24 Apr 2024, <http://www.worldbirdnames.org/>.

Glowska E, Dragun-Damian A, Broda L, Dabert J, Dabert M, 2014. DNA barcodes reveal female dimorphism in syringophilid mites (Actinotrichida: Prostigmata: Cheyletoidea): *Stibarokris phoeniconaias* and *Ciconichenophilus phoeniconaias* are conspecific. Folia Parasitologica, 61:272-276. https://doi.org/10.14411/fp.2014.030

Han YD, Min GS, 2019. Four unrecorded species of genus *Alloptes* (Acari: Sarcoptiformes: Alloptidae) from charadriiform birds in South Korea. Animal Systematics, Evolution and Diversity, 35:63-72. https://doi.org/10.5635/ASED.2019.35.2.005

Han YD, Mironov SV, Kim JH, Min GS, 2021. Feather mites (Acariformes, Astigmata) from marine birds of the Barton Peninsula (King George Island, Antarctica), with descriptions of two new species. ZooKeys, 1061:109-130. https://doi.org/10.3897/zookeys.1061.71212

Han YD, Mironov SV, Min GS, 2022. Two new species of feather mites (Acariformes, Astigmata) from the black-tailed godwit, *Limosa limosa* (Charadriiformes, Scolopacidae), in Korea. ZooKeys, 1088:81-97. https://doi.org/10.3897/zookeys.1088.80307

Hernandes FA, Brito G, 2022. Feather mites (Acariformes: Astigmata) of the brown noddy, *Anous stolidus* (L.) (Charadriiformes: Laridae), with description of two new species from Brazil. Acarologia, 62:317-331. https://doi.org/10.24349/rblu-98ly

Jablonska J, 1986. Specificity of some mite species of the superfamily Analgesoidea to bird hosts in the Warsaw Zoo. Acta Parsitologia Polonica, 15:55-62.

Jinbo U, Kato T, Ito M, 2011. Current progress in DNA barcoding and future implications for entomology. Entomological Science, 14:107-124. https://doi.org/10.1111/j.1479-8298.2011.00449.x

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, Thierer T, Ashton B, Meintjes P, Drummond A, 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics, 28:1647-1649. https://doi.org/10.1093/bioinformatics/bts199

Kivganov DA, Mironov SV, 1992. A new subgenus and three new species of the feather mite genus *Alloptes* (Analgoidea: Alloptidae) from terns of the Black Sea. Parazitologiya, 26: 198-208 (in Russian).

Klimov PB, Mironov SV, OConnor BM, 2017. Detecting ancient codispersals and host shifts by double dating of host and parasite phylogenies: application in proctophyllodid feather mites associated with passerine birds. Evolution, 71:2381-2397. https://doi.org/10.1111/evo.13309

Klimov PB, Skoracki M, Bochkov AV, 2019. *Cox1* barcoding versus multilocus species delimitation: validation of two mite species with contrasting effective population sizes. Parasites and Vectors, 12:8. https://doi.org/10.1186/s13071-018-3242-5

Klimov PB, Stolbov VA, Kazakov DV, Filimoova MO, Sheykin SD, 2022. A DNA barcoding and photo-documentation resource of water mites (Acariformes, Hydrachnidia) of Siberia: accurate species identification for global climate change monitoring programs. Systematic and Applied Acarology, 27: 2493-2567. https://doi.org/10.11158/saa.27.12.8

Kumar S, Stecher G, Li M, Knyaz C, Tamura K, 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Molecular Biology and Evolution, 35:1547-1549. https://doi.org/10.1093/molbev/msy096

Liebers D, de Knijff P, Helbig AJ, 2004. The herring gull complex is not a ring species. Proceedings of the Royal Society of London Series B: Biological Sciences, 271:893-901. https://doi.org/10.1098/rspb.2004.2679

Mironov SV, 1989. A brief review of the feather mites of the genus *Zachvatkinia* in the USSR (Analgoidea, Avenzoariidae). Parazitologicheskii Sbornik, 36:91-115 (in Russian with English summary).

Mironov SV, Kivganov DA, 1993. New species of feather mites of the superfamily Analgoidea from charadriiformes of Black Sea. Parazitologiya, 27:161-167 (in Russian).

Mironov SV, Palma RL, 2006. Two new feather mite species (Acari: Analgoidea) from the Tuamotu sandpiper *Aechmorhynchus parvirostris* (Charadriiformes: Scolopacidae). Tuhinga - Records of the Museum of New Zealand Te Papa Tongarewa, 17:49-59.

Norton RA, 1998. Morphological evidence for the evolutionary origin of Astigmata (Acari: Acariformes). Experimental and Applied Acarology, 22:559-594. https://doi.org/10.1023/A:1006135509248

Olsen KM, Larsson H, 2004. Gulls of Europe, Asia and North America. Christopher Helm, London, pp. 1-608.

Radford CD, 1958. The host-parasite relationships of the feather mites (Acarina: Analgesoidea). Revista Brasileira de Entomologia, 8:107-170.

Sternkopf V, Liebers-Helbig D, Ritz MS, Zhang J, Helbig AJ, de Knijff P, 2010. Introgressive hybridization and the evolutionary history of the herring gull complex revealed by mitochondrial and nuclear DNA. BMC Evolutionary Biology, 10:348. https://doi.org/10.1186/1471-2148-10-348

Vasyukova TT, Borisov ZZ, Isaev AP, Yakovlev FG, 1996. Ecological and faunistic features of bird ectoparasites (biting lice and feather mites) in Verkhoyansk region. Uspekhi Sovremennoi Biologii, 116:607-620.

Vasyukova TT, Mironov SV, 1991. Feather mites of Anseriformes and Charadriiformes of Yakutia. Systematics. Nauka, Siberian Dept, Novosibirsk, pp. 1-200 (in Russian).

Received June 17, 2024
Revised July 24, 2024
Accepted August 26, 2024