

Chewing lice from high-altitude and migrating birds in Yunnan, China, with descriptions of two new species of *Guimaraesiella*

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Abstract. In total, 366 birds representing 55 species in 24 families and eight orders, were examined for chewing lice (Phthiraptera: Amblycera, Ischnocera) in two high-altitude localities in Yunnan Province, China. In Ailaoshan, almost all of the birds examined were resident passeriforms, of which 36% were parasitized by chewing lice. In Jinshanyakou, most birds were on migration, and included both passerine and non-passerine birds. Of the passerine birds caught in Jinshanyakou, only one bird (0.7%) was parasitized by chewing lice. The prevalence of *Myrsidea* and *Brueelia*-complex lice on birds caught in Ailaoshan was higher than in previous reports. Of the chewing lice identifiable to species level, three represent new records for China: *Actornithophilus hoplopteri* (Mjöberg, 1910), *Maculinirmus ljosalfar* Gustafsson & Bush, 2017 and *Quadriceps sinensis* Timmermann, 1954. In total, 17 new host records are included, of which we describe two as new species in the *Brueelia*-complex: *Guimaraesiella (Cicchinella) ailaoshanensis* sp. nov. ex *Schoeniparus dubius dubius* (Hume, 1874) and *G. (C.) montisodalis* sp. nov. ex *Fulvetta manipurensis tonkinensis* Delacour & Jabouille, 1930.

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Key words. *Guimaraesiella*, *Myrsidea*, new host records, new species, Phthiraptera, Yunnan.

Introduction

Most published records of chewing lice (Phthiraptera) from Southeast Asia have been from non-passeriform birds and the chewing lice of passeriform birds in the region are poorly known. The only large-scale survey is that reported by McClure *et al.* (1973). However, most of the specimens recorded in that study were never identified to species level; for example, specimens from over 80 host species spanning 22 families and

four orders were listed as *Brueelia* sp. Moreover, most of the unidentified species recorded by McClure *et al.* (1973) have never subsequently been described.

In recent years, this has begun to change. A large number of new host records and species have been described from across South and Southeast Asia (Hellenthal & Price, 2003; Mey, 2004, 2017; Price *et al.*, 2006; Sychra *et al.*, 2009; Eduardo & Villa, 2011; Najer *et al.*, 2012a, 2012b, 2014; Mey & Barker, 2014; Gustafsson & Bush, 2017; Gustafsson *et al.*, 2018a, 2018b,

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2018c, 2019). However, despite this recently increased interest in the chewing louse fauna of the region, no chewing lice are yet known from the majority of passeriform species in Southeast Asia.

To partially address this data deficiency, we report the results of a chewing louse collection trip to Yunnan Province, China, August to September 2018. In addition, we describe two new species of chewing lice in the *Brueelia*-complex genus *Guimaraesiella* Eichler, 1949. Both of these new species parasitize babblers, comprising one of the most speciose groups of birds in South China.

Materials and methods

Bird capture

Two different sites were visited in the same mountain range that runs through South-Central Yunnan Province: Ailaoshan in Jingdong County and Jinshanyakou in Zhenyuan County. Bird collection was carried out between 28 August and 9 September 2018 at Ailaoshan and between 10 September 2018 and 15 September 2018 at Jinshanyakou.

At the first site, birds were caught by dawn-to-dusk mist-netting at an elevation of around 2420 m. Nets were put up at or near the forest edge, or at the edge of tea plantations. Nearby forest included both primary and secondary growth, often with dense undergrowth of bamboo. Some nets were also put in more open areas, with soggy, *Sphagnum*-dominated ground, as well as scattered bushes (e.g. *Rhododendron*, *Salix*) and bamboo. A maximum of 10 nets (each 12 m long) was used; however, not all nets were used at all times, and nets were moved to new localities after 3–5 days as the number of birds caught in that place declined. Nets were checked for birds approximately every hour. Birds were examined at the nets, and some birds (e.g. recent fledglings) were released without further examination because they were deemed too fragile to undergo fumigation safely. Birds were kept in separate bags, which were shaken out after use.

At the second site, migrating birds were caught at night using a mist-net suspended in front of coloured lights at Jinshanyakou, Yunnan, China, at an elevation of about 2360 m. This station is part of a regular experiment that is examining the effects of light pollution on migrating birds (Zhao *et al.*, 2014). Lights were turned on between 20.00 hours and 06.00 hours, rotating hourly between red, yellow, green and blue light. The net was put up in the outskirts of a primary forest, with alpine meadow-like sections. This area is in a pass through the Ailao Mountain Range, and a natural choke point for bird migration in the area. The net was monitored continuously and birds were collected as soon as they hit the net. Bags were only used when many birds hit the net at the same time. All birds were checked for parasites before ringing; Vas & Fuisz (2010) showed that banding may reduce the louse loads of birds, and checking for parasites before ringing is therefore preferable.

Birds were identified to species using Arlott (2017); however, the bird taxonomy used in the present study follows Clements *et al.* (2018), which differs in the generic placement of some species. The focus of the collection was songbirds; however, all

birds caught were examined for parasites. Parasites from hosts other than songbirds are not considered further, beyond their inclusion in Table 1.

Fumigation and louse collection

Two different methods of fumigation were used during this collection trip. At the first site, birds were fumigated with ethyl acetate for 5–10 min in a zip-lock bag, with the birds' heads outside the bag. One paper clamp was placed on each side of the bird's head to keep the zip-lock bag closed during fumigation. At the second site, glass jars were used instead of zip-lock bags, with cloth collars fitted around the bird's neck using a drawstring, again with the birds' heads outside the jars.

As a result of the size limitations of jars, and the impracticability of putting larger birds in jars, some large cuckoos and lapwings were placed in larger bags even at the second site. This also proved impractical for some bird species, which, instead, were examined only manually. Specific areas of the birds were examined visually for lice in the order: wings (underside), flanks, stomach, lower rump, lower neck, wings (upper side), back, upper rump, upper neck, head. We examined heads last because lice may naturally move towards the head of dead or stressed birds (the so-called Drost effect) (Eichler, 1970). Examining other body parts first is therefore more likely to yield accurate microhabitat data for lice collected from live birds.

Fumigation was carried out either outdoors or in well-ventilated areas, aiming to minimize the irritation of ethyl acetate on the birds. During fumigation (both in bags and in jars), the head of the bird was examined for lice visually, using a forceps. All sides of the head were examined, with particular attention being paid to the chin and the neck. Lice, eggs or mites were removed from the head and put in 95% ethanol. After fumigation, birds were ruffled gently over a white paper, and any lice falling off were collected. The primaries and secondaries were examined visually for mites, and a small number of these were collected from each bird using a forceps. After examination, birds were released. Mites collected will be treated in a separate publication, and are not discussed further.

Selected lice were slide-mounted in accordance with the procedure outlined by Palma (1978), except that a small cut was made through the pterothorax on one side, between coxae II and III after immersion in KOH for approximately 24 h. The gut content was emptied through this hole either by lightly pressing the abdomen with a needle or, if this was not sufficient, by entering a hooked needle into the cut, and pulling the stomach out. Specimens were mounted in Hoyer's medium instead of Canada balsam. All louse specimens collected are deposited at the Guangdong Institute of Applied Biological Resources, Guangzhou, China (GIABR); apart from the specimens described below, these were maintained in absolute ethanol in a freezer at -80°C for DNA studies.

Lice in the *Brueelia*-complex were identified to genus and, where possible, species, using the keys provided in Gustafsson & Bush (2017), Gustafsson *et al.* (2018a, 2018c, 2019). Lice in the genus *Myrsidea* will form the core of a partial revision of this genus by the second investigator of the present study (L. Lei) and were not identified to species level here. *Quadraceps sinensis*

Table 1. Summary of the birds examined at Ailaoshan and Jinshan, Yunnan Province, China, and the lice that were collected.

Host species	Louse species	E	I	P (%)	♂	♀	N	Location
<u>Pelecaniformes</u>								
<u>Ardeidae</u>								
<i>Ardeola bacchus</i>	—	3	0					JS
<i>Ixobrychus eurhythmus</i>		1	0					JS
<i>Nycticorax nycticorax</i>		6	0					JS
<u>Gruiformes</u>								
<u>Rallidae</u>								
<i>Zapornis bicolor</i>	—	1	0					JS
<i>Zapornis fusca erythrothorax</i>	—	2	0					JS
<u>Charadriiformes</u>								
<u>Charadriidae</u>								
<i>Vanellus cinereus</i>	<i>Actornithophilus hoplopteri</i> (Mjöberg, 1910) ‡	7	4	57	9	10	8	JS
	<i>Quadriceps sinensis</i> Timmermann, 1954 †		1	14	6	3	0	JS
<u>Cuculiformes</u>								
<u>Cuculidae</u>								
<i>Chrysococcyx xanthorhynchus xanthorhynchus</i>	—	1	0					JS
<i>Clamator jacobinus</i>	—	1	0					JS
<i>Cuculus canorus bakeri</i>	—	3	0					JS
<i>Cuculus optatus</i>	—	8	0					JS
<i>Cuculus poliocephalus</i>	<i>Cuculoecus</i> sp. *	20	6	30	8	9	2	JS
	<i>Cuculicola</i> sp. *		1	5	2	1	0	JS
<i>Cuculus saturatus</i>	—	1	0					JS
<i>Cuculus</i> sp. indet.	—	1	0					JS
<u>Columbiformes</u>								
<u>Columbidae</u>								
<i>Streptopelia tranquebarica humilis</i>	—	1	0					JS
<i>Treron sphenurus sphenurus</i>	—	1	0					JS
<u>Coraciiformes</u>								
<u>Alcedinidae</u>								
<i>Halcyon pileata</i>	—	1	0					JS
<u>Piciformes</u>								
<u>Picidae</u>								
<i>Picumnus innominatus malayorum</i>	—	1	0					ALS
<u>Passeriformes</u>								
<u>Acrocephalidae</u>								
<i>Arundinax aedon aedon</i>	—	7	0					JS
<u>Hirundinidae</u>								
<i>Delichon dasypus</i>	—	1	0					JS
<u>Laniidae</u>								
<i>Lanius cristatus</i>	—	120	0					JS
<i>Lanius tephronotus tephronotus</i>	—	4	0					ALS (n = 1), JS (n = 3)
<u>Leiothrichidae</u>								
<i>Actinodura strigula yunnanensis</i>	<i>Myrsidea</i> sp.	4	2	50	3	1	0	ALS
<i>Alcippe fratercula yunnanensis</i>	<i>Myrsidea</i> sp. *	4	1	25	0	1	0	ALS
	<i>Resartor</i> sp. *		4	100	1	8	4	ALS
<i>Heterophasia desgodinsi desgodinsi</i>	<i>Resartor albofulvus</i> Gustafsson <i>et al.</i> 2018	1	1	100	1	4	0	ALS
<i>Minla ignotincta mariae</i>	<i>Myrsidea</i> sp. *	1	1	100	0	0	3	ALS
<u>Locustellidae</u>								
<i>Locustella certhiola</i> ssp.	—	3	0					JS
<i>Locustella tacsanowskia</i>	—	5	0					JS
<u>Muscicapidae</u>								
<i>Enicurus leschenaulti sinensis</i>	<i>Penenirmus</i> sp. *	1	1	100	0	1	0	ALS
<i>Ficedula hyperythra hyperythra</i>	<i>Philoaterus</i> sp. *	24	1	4	0	1	0	ALS (n = 23), JS (n = 1)
	<i>Ricinus mugimaki</i> (Uchida, 1915)		2	8	0	2	0	ALS

Table 1. Continued

Host species	Louse species	E	I	P (%)	♂	♀	N	Location
<i>Ficedula sapphira sapphira</i>	—	1	0					ALS
<i>Ficedula strophciata stropciata</i>	—	2	0					JS
<i>Ficedula tricolor diversa</i>	—	1	0					ALS
<i>Larvivora cyane</i>	—	2	0					JS
<i>Monticola solitarius pandoo</i>	—	1	0					JS
Muscicapidae sp. indet.	—	1	0					ALS
<i>Niltava sundara denotata</i>	<i>Myrsidea</i> sp.	11	5	45	8	13	8	ALS
Nectarinidae								
<i>Aethopyga nipalensis koelzi</i>	—	2	0					ALS
Oriolidae								
<i>Oriolus chinensis diffusus</i>	<i>Maculinirmus ljosalfar</i> Gustafsson & Bush, 2017†	1	1	100	8	5	4	JS
Paradoxornithidae								
<i>Fulvetta manipurensis tonkinensis</i>	<i>Guimaraesiella montisodalis</i> n. sp. *	24	6	25	9	4	2	ALS
	<i>Myrsidea</i> sp. *		8	33	7	6	5	ALS
<i>Lioparus chrysotis amoenus</i>	<i>Myrsidea</i> sp. *	11	8	73	4	9	28	ALS
	<i>Resartor extraneus</i> Gustafsson <i>et al.</i> 2018		3	27	5	2	0	ALS
<i>Suthora nipalensis poliotis</i>	<i>Myrsidea</i> sp. *	10	3	30	1	2	5	ALS
Paridae								
<i>Parus monticolus yunnanensis</i>	—	2	0					ALS
<i>Sylviparus modestus modestus</i>	—	16	0					ALS
Pellorneidae								
<i>Schoeniparus castaneiceps exul</i>	<i>Myrsidea</i> sp. *	2	1	50	1	1	11	ALS
<i>Schoeniparus dubius dubius</i>	<i>Guimaraesiella ailaoshanensis</i> n. sp. *	15	7	47	5	6	2	ALS
	<i>Myrsidea</i> sp. *		14	93	27	34	64	ALS
Phylloscopidae								
<i>Phylloscopus claudiae</i>	<i>Penenirmus</i> sp. *	7	1	14	1	1	0	ALS
<i>Phylloscopus maculipennis maculipennis</i>	—	6	0					ALS
<i>Seicercus affinis affinis</i>	—	1	0					ALS
<i>Seicercus valentini valentini</i>	—	1	0					ALS
Scotocercidae								
<i>Cettia castaneocoronata ripleyi</i>	—	3	0					ALS
Sittidae								
<i>Sitta himalayensis</i>	—	1	0					ALS
Stenostiridae								
<i>Culicicapa ceylonensis calochrysea</i>	—	1	0					ALS
Timaliidae								
<i>Cyanoderma ruficeps davidi</i>	<i>Myrsidea</i> sp.	3	3	100	5	0	9	ALS
<i>Pomatorhinus ruficollis reconditus</i>	—	1	0					ALS
Zosteropidae								
<i>Yuhina diademata</i>	—	1	0					ALS
<i>Yuhina gularis</i>	<i>Myrsidea</i> sp. *	4	2	50	0	0	3	ALS
<i>Yuhina occipitalis</i>	—	1	0					ALS
Total		366						

Only two bird species were caught at both collection localities (*Lanius tephronotus* and *Ficedula hyperythra*); the number for each locality is given in parentheses after the locality name. The lice from *F. hyperythra* were all collected at Ailaoshan; no lice were found on *L. tephronotus* in either locality.

*Denotes new host records.

†Denotes new records for China.

ALS, Ailaoshan; E, examined birds; I, infested birds; JS, Jinshan; N, nymphs; P, prevalence. Note that both McClure *et al.* (1973) and Najer *et al.* (2012a) reported *Myrsidea* sp. from *Alcippe morrisoniana*, which was previously considered conspecific with *A. fratercula*. No records of *Myrsidea* are known to us from hosts explicitly identified as *A. fratercula* and we therefore consider this to be a new host record.

Timmermann, 1954, was identified based on comparisons with the original description. *Actornithophilus hoplopteri* (Mjöberg, 1910) was identified using the key of Clay (1962). *Ricinus mugimaki* (Uchida, 1915) was identified based on Rheinwald (1968). No identification keys to species of *Cuculicola*, *Cuculoecus*, *Philopterus* or *Penenirmus* on passerines have been published, and most species descriptions are inadequate; therefore, we were unable to accurately identify species in these genera.

Specimens were examined in a Eclipse Ni (Nikon Corp.) Illustrations were drawn by hand using a drawing tube. Line drawings were scanned, collated and edited in GIMP (www.gimp.org). Measurements were made from live images in NIS-Elements (Nikon Corp.). All measurements are given as ranges in millimeters (mm): total length (along midline); head length (along midline); head width (at temples); prothoracic width; pterothoracic width; and abdominal width (at segment V, unless otherwise noted).

Terminology for morphological and setal characters (and consequent abbreviations) is used in accordance with Gustafsson & Bush (2017) and Gustafsson *et al.* (2019): anterior dorsal seta (*ads*); anterior mesosomal seta (*ames*); accessory post-spiracular seta (*aps*); dorsal submarginal seta (*dsms*); gonoporal posterior mesosomal seta (*gpms*); lateral posterior mesosomal seta (*lpms*); preocular seta (*pos*); parameral setae 1–2 (*pst1–2*); vulval marginal seta (*vms*); vulval oblique seta (*vos*); vulval submarginal seta (*vss*).

Results

In total, 366 birds were examined for lice, of which 70 (19.1%) were infested with lice (Table 1). One hundred and sixty-two birds of 32 species were examined in Ailaoshan, and 204 birds of 27 species were examined in Jinshanyakou. Fifty-nine birds (36.4%) were parasitized by some species of louse in Ailaoshan, whereas, in Jinshanyakou, only 11 birds (5.4%) were parasitized. If non-passerines are excluded, the percentages are 36% and 0.7%, respectively. Only one non-passerine bird was examined in Ailaoshan, and this was not parasitized by chewing lice. By contrast, 58 non-passerine birds were examined in Jinshanyakou, of which 10 (17%) were parasitized by chewing lice.

Seventeen new host records were found (Table 1), of which most were only identified to genus level. Of the six louse species identified to species level, three constitute new records for China: *Actornithophilus hoplopteri* (Mjöberg, 1910), *Maculinirmus ljosaljar* Gustafsson & Bush, 2017 and *Quadriceps sinensis* Timmermann, 1954. Moreover, two new species were identified: *Guimaraesiella ailaoshensis* **sp. nov.** and *Guimaraesiella montisodalis* **sp. nov.** No species of *Myrsidea* were identified to species level because partial revisions of this genus are in preparation to clarify useful morphological characters and species limits. We expect several of the *Myrsidea* species listed in Table 1 to represent new species, which will be described in future studies.

In addition to chewing lice, 2878 feather mites were collected from 71 hosts (prevalence = 19.4%): 66 hosts in Ailaoshan (prevalence = 40.7%) and five hosts in Jinshanyakou (prevalence = 2.4%). Moreover, two hippoboscid flies were collected

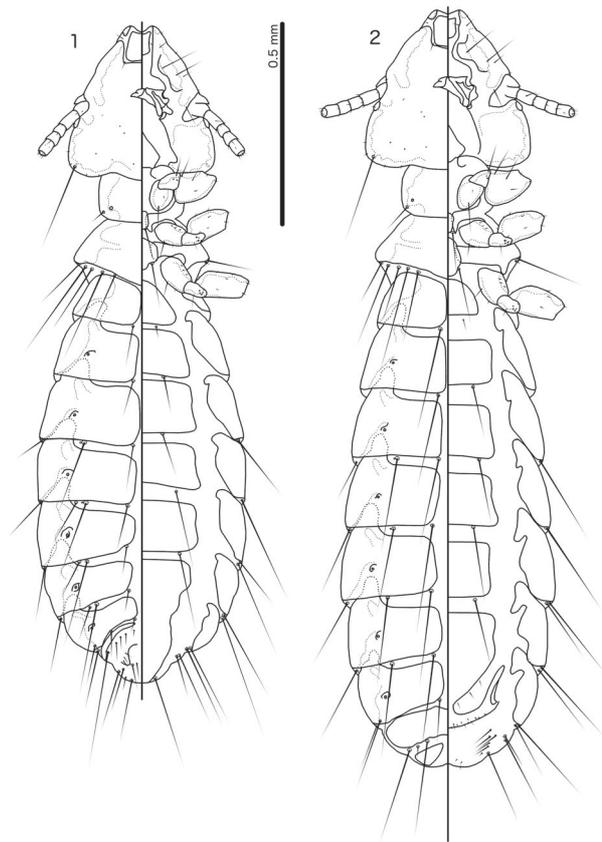


Fig. 1–2. *Guimaraesiella (Cicchinella) montisodalis* **sp. nov.** ex *Fulvetta manipurensis tonkinensis*. **1**, male habitus, dorsal and ventral views. **2**, female habitus, dorsal and ventral views.

from two different *Lanius cristatus* in Jinshanyakou. These records are not discussed further here.

New species

Guimaraesiella (Cicchinella) montisodalis *new species*

Figs 1–7.

<http://zoobank.org/urn:lsid:zoobank.org:act:F046A381-49CF-47AB-8D57-B8EF02B1D669>.

Type host. *Fulvetta manipurensis tonkinensis* Delacour & Jabouille, 1930 – *Manipur fulvetta* (Paradoxornithidae).

Type locality. Ailaoshan, Yunnan Province, China.

Diagnosis. *Guimaraesiella montisodalis* **sp. nov.** keys to *G. tenella* Gustafsson *et al.*, 2019, in the key of Gustafsson *et al.* (2019), with which it shares the characters: dorsal preantennal suture completely surrounds dorsal preantennal plate (Fig. 3) but

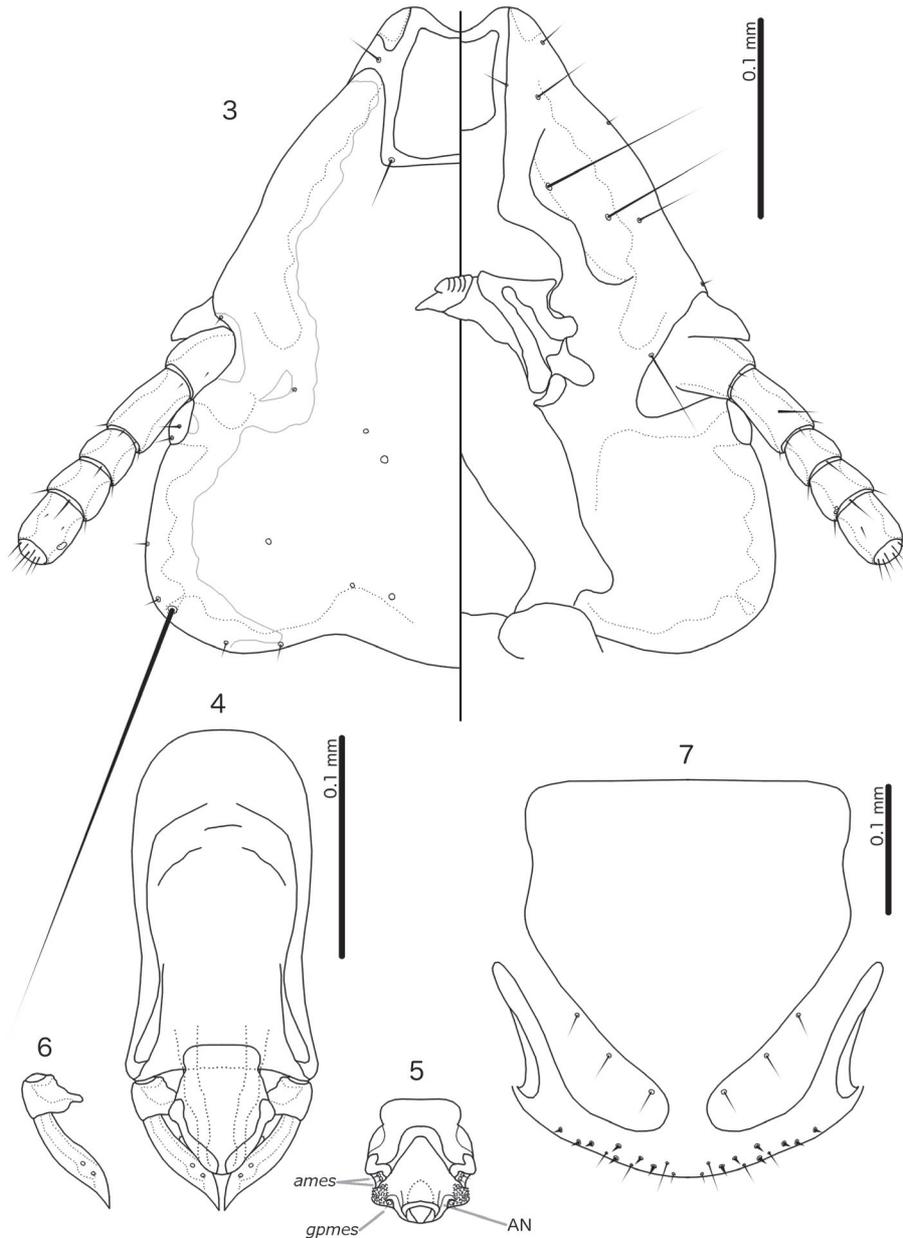


Fig. 3–7. *Guimaraesiella (Cicchinella) montisodalis* sp. nov. ex *Fulvetta manipurensis tonkinensis*. **3**, male head, dorsal and ventral views. **4**, male genitalia, dorsal view. **5**, male mesosome, ventral view. **6**, male paramere, ventral view. **7**, female subgenital plate and vulval margin, ventral view. *ames*, anterior mesosomal setae; AN, arched nodus; *gpmes*, gonoporal posterior mesosomal setae.

suture not clear in all examined specimens of *G. montisodalis*); *aps* typically absent on male tergopleurite IV (Fig. 1) but present on one side in three of eight examined males; see below); distal mesosome with rugose nodi laterally and arched nodi median to these (AN in Fig. 5); only three setae on each side of mesosome. These two species can be separated by the characters: head shape of *G. montisodalis* unique within *Guimaraesiella (Cicchinella)*, and very distinct compared with that of *G. tenella*, with lateral margins of preantennal area convex proximally and concave distally in *G. montisodalis* (Fig. 3) but largely concave in *G. tenella*; pleural incassations wider in *G. montisodalis* (Figs 1,

2) than in *G. tenella*; female subgenital plate of different shape in the two species (Fig. 7); ventral mesosomal sclerite extends anterior to proximal margin of mesosome in *G. tenella* but not in *G. montisodalis* (Fig. 5); gonopore subterminal in *G. montisodalis* (Fig. 5) but ventral in *G. tenella*; rugose nodi extensive in *G. montisodalis* (Fig. 5) but limited to fringed lateral margin of mesosome in *G. tenella*; lateral margin of mesosomal lobes with arched nodi anterior to rugose nodi in *G. montisodalis* (Fig. 5) but without such nodi in *G. tenella*.

Remarkably, *G. montisodalis* is also somewhat similar to species in the *G. diaprepes* species group, only known from

Hawai'i and the Andes (Gustafsson & Bush, 2017). Species in this group also have prominent posterolateral rugose nodi, extensive lateral nodi proximal to the rugose nodi, and males lack *aps* on tergopleurite IV. Moreover, at least in *G. diaprepes*, the dorsal preantennal suture completely surrounds the dorsal anterior plate. However, there are significant differences between *G. montisodalis* and the species in the *G. diaprepes* group, suggesting that these similarities may be convergent. Females of species in the *G. diaprepes* group lack complete cross-pieces (present in *G. montisodalis*), gonopore is ventral (subterminal in *G. montisodalis*), the *gpmes* are ventral (marginal in *G. montisodalis*) and, in at least *G. diaprepes*, there are dorsal *pms* on the distal mesosome (no such setae in *G. montisodalis*). Because only four species are known in the *G. diaprepes* group [Gustafsson & Bush, 2017; Mey, 2017 (as *Mohoaticus*)], little is presently known about the variation in this group. We presently do not consider these two groups to be closely related.

Description. Both sexes. Head rounded triangular (Fig. 1), frons concave, lateral margins of preantennal area convex, except distal section with concave lateral margins. Marginal carina broad, with undulating inner margin. Dorsal preantennal suture reaches lateral margin of head, and completely surrounds dorsal anterior plate. Head chaetotaxy and pigmentation patterns as in Fig. 3; *pos* located on eye. Preantennal nodi large, bulging. Preocular nodi much larger than postocular nodi. Marginal temporal carina of moderate width, with undulating inner margin. Gular plate spade-shaped.

Male. Thoracic and abdominal segments and chaetotaxy as in Fig. 1. *aps* absent on tergopleurite IV in holotype and four of seven paratypes but present on one side of remaining three paratypes. Basal apodeme with rounded anterior end and concave lateral margins (Fig. 4). Proximal mesosome broadly rectangular (Fig. 5); ventral sclerite does not extend anterior to proximal margin. Mesosomal lobes with two arched nodi on each side, one at approximately mid-length and one near distal end; lateral margins of mesosome concave between nodi but with prominent rugose nodi near distal arched nodi. Gonopore shallowly crescent-shaped, subterminal. Chaetotaxy: 2 *ames* sublaterally on each side anterior to proximal arched nodi; 1 *gpmes* on each side lateral to distal arched nodi; *lpms* not visible. Parameral heads with median finger-like extension (Fig. 6); distal parameres partially everted in all examined males but appear to be elongated distal to the *pst1-2*; distal section here illustrated tentatively.

Measurements as in Table 2.

Female. Thoracic and abdominal segments and chaetotaxy as in Fig. 2. Subgenital plate without reticulation, lateral margins concave, connection to cross-piece narrow (Fig. 7). Vulval margin gently rounded, with two or three short, slender *vms* and six to eight short, thorn-like *vss* on each side; four or five short, slender *vos* on each side of subgenital plate; distal *vos* median to *vss*. Measurements as in Table 2.

Etymology. The species epithet is derived from 'mons', Latin for 'mountain', and 'sodalis', Latin for 'companion', referring to

Table 2. Measurements of the two species of *Guimaraesiella* described in the present study.

Dimension	<i>Guimaraesiella montisodalis</i>		<i>Guimaraesiella ailaoshanensis</i>	
	♂ (n = 8 *)	♀ (n = 5)	♂ (n = 4)	♀ (n = 2)
TL	1.40–1.62	1.72–1.92	1.17–1.25	1.56–1.58
HL	0.33–0.36	0.36–0.39	0.32–0.34	0.36
HW	0.33–0.39	0.38–0.41	0.32–0.33	0.35–0.36
PRW	0.20–0.22	0.22–0.24	0.17–0.20	0.20–0.21
PTW	0.33	—	0.27–0.28	0.29–0.32
AW	0.37–0.49	0.45–0.51	0.36–0.43	0.44

*For AW, n = 7; for TL, n = 6.

AW, abdominal width (at segment V); HL, head length (along midline); HW, head width (at temples); PRW, prothoracic width; PTW, pterothoracic width; TL, total length (along midline). All measurements are in millimeters. As a result of the slide-mounting technique (see Materials and methods), pterothoracic width could be measured in only a small number of specimens (n = 2♂ and 0♀ for *G. montisodalis*, and n = 2♂ and 2♀ of *G. ailaoshanensis*).

the altitudinal distribution of the host (and, as far as is presently known, the louse).

Type material. Ex *Fulvetta manipurensis tonkinensis*: **Holotype** ♂, Ailaoshan, Yunnan Province, China, D. R. Gustafsson, K. Luo, L. Lei, 5 September 2018, J3757 (GIABR). **Paratypes:** 1♂, 1♀, same data as holotype, D. R. Gustafsson, K. Luo, L. Lei, 5 September 2018, J3757 (GIABR). 4♂, same locality as holotype, D. R. Gustafsson, K. Luo, L. Lei, 2 September 2018, J3738 (GIABR). 2♂, same locality as holotype, D. R. Gustafsson, K. Luo, L. Lei, 28 August 2018, J3708 (GIABR). 1♀, same locality as holotype, D. R. Gustafsson, K. Luo, L. Lei, 2 September 2018, J3729 (GIABR).

Non-type material: one nymph, same data as holotype (GIABR). 1 nymph, same locality as holotype, J3708 (GIABR).

Non-type material (in ethanol): 1♂, same data as holotype, D. R. Gustafsson, K. Luo, L. Lei, 5 September 2018, J3757 (GIABR). 1 nymph, same locality as holotype, D. R. Gustafsson, K. Luo, L. Lei, 28 August 2018, J3708 (GIABR). 1♀, same locality as holotype, D. R. Gustafsson, K. Luo, L. Lei, 28 August 2018, J3687 (GIABR). 1♀, same locality as holotype, D. R. Gustafsson, K. Luo, L. Lei, 29 August 2018, J3699 (GIABR).

Remarks. The morphological similarities between *G. montisodalis* and *G. tenella* outlined above suggest a close relationship between these two species; however, there are also substantial differences that suggest that the similarities could be a result of convergence or parallelism. Because only one species of *Guimaraesiella* is known in the *G. tenella* group and *G. montisodalis* is the first species in this genus to be described from a host in the family Paradoxornithidae, we presently do not consider *G. montisodalis* to be a member of the *G. tenella* species group. Instead, we tentatively erect the informal *G. montisodalis* species group, characterized by the characters (*sensu* Gustafsson *et al.*, 2019): (a) dorsal preantennal suture completely surrounds

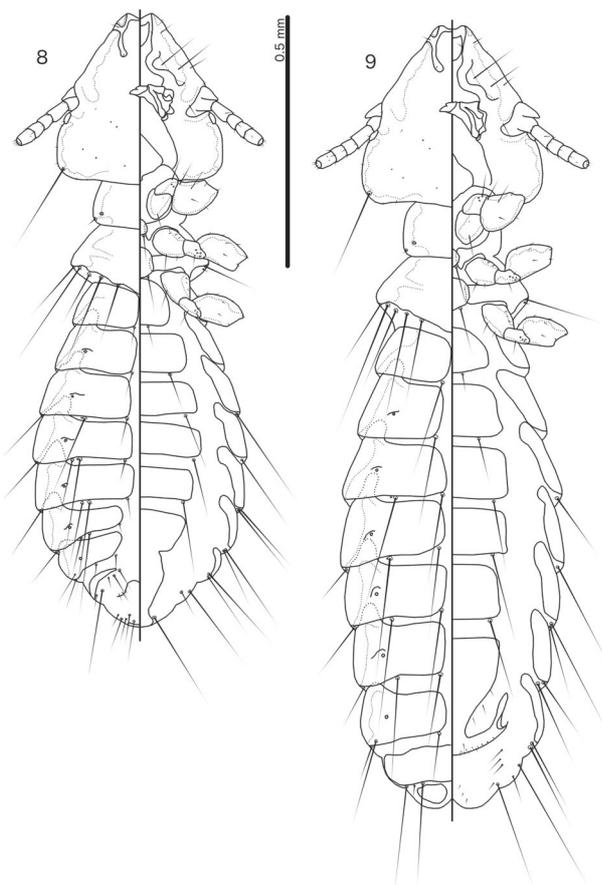


Fig. 8–9. *Guimaraesiella (Cicchinella) ailaoshanensis* sp. nov. ex *Schoeniparus dubius dubius*. **8**, male habitus, dorsal and ventral views. **9**, female habitus, dorsal and ventral views.

dorsal preantennal plate; (b) *aps* generally absent from male tergopleurite IV (but may be present on one side); (c) mesosome with anterior and posterior arched nodi on each side; (d) mesosomal ventral sclerite present as arched thickening on mesosome, not protruding anterior to the proximal margin of the mesosome; (e) rugose nodi present lateral to distal arched nodi of mesosome; (f) female subgenital plate roughly pentagonal. As more species in these species groups become known, the relationship between these groups will need to be reassessed.

Notably, two female *Guimaraesiella* collected from the same host species belong to a different species of *Guimaraesiella* (sample J3727, GIABR). No other small babbler were caught at the same time, and these lice thus likely represent a case of natural straggling.

Guimaraesiella (Cicchinella) ailaoshanensis new species

Figs 8–14.

<http://zoobank.org/urn:lsid:zoobank.org:act:071D86E4-2A77-4B31-B613-24C59FB57752>.

Type host. *Schoeniparus dubius dubius* (Hume, 1874) – rusty-capped fulvetta (Pellorneidae).

Type locality. Ailaoshan, Yunnan Province, China.

Diagnosis. In the key to *Guimaraesiella (Cicchinella)* of Gustafsson *et al.* (2019), *Guimaraesiella ailaoshanensis* sp. nov. keys to couplet 10, and is thus similar to *G. retusa* Gustafsson *et al.*, 2019 and *G. sehri* (Ansari, 1955). Of these two species, *G. ailaoshanensis* is more similar to *G. retusa*, with which it shares characters not found in *G. sehri*: distal nodi of mesosome trapezoidal (Fig. 12), not triangular; dorsal preantennal suture reaches lateral margin of head (Fig. 10); mesosomal ventral sclerite without rugose anterior nodi (Fig. 12). These two species can be separated by the characters: *aps* absent on male tergopleurite IV in *G. ailaoshanensis* (Fig. 8) but present in *G. retusa*; preantennal head longer in *G. ailaoshanensis* (Fig. 10) than in *G. retusa*; female subgenital plate with conspicuous central reticulation in *G. retusa* but with no or at most faint reticulation in *G. ailaoshanensis* (Fig. 14); gonopore with roughly S-shaped lateral sclerites not connected medianly in *G. retusa* but with crossing sclerite in *G. ailaoshanensis* (Fig. 12); distal mesosomal nodi larger and extended farther laterally in *G. ailaoshanensis* (Fig. 12) than in *G. retusa*.

Description. Both sexes. Head nearly triangular (Fig. 10), frons concave, lateral margins of preantennal area more or less straight. Marginal carina broad, with undulating median margin. Dorsal preantennal suture reaches *ads*, *dsms* and lateral margin of head but does not completely separate dorsal anterior plate. Head chaetotaxy and pigmentation pattern as in Fig. 10; *pos* located just behind eye. Preantennal nodi prominent, bulging. Preocular nodi larger than post-ocular nodi. Marginal temporal carina broad, with undulating median margin. Gular plate spade-shaped.

Male. Thoracic and abdominal segments and chaetotaxy as in Fig. 8. Proximal end of basal apodeme diffuse in all examined specimens, and not illustrated; distal section as in Fig. 11. Proximal mesosome irregularly shaped, with an exact shape that differs slightly between specimens; Figs 11 and 12 show the shape of the mesosome in the holotype but paratype specimens have less undulating lateral margins. Ventral sclerite broad, almost reaching anterior end of mesosome. Mesosomal lobes with undulating lateral margins; distal nodi prominent, roughly trapezoidal. Gonopore with anterolateral extensions; ventrally, gonopore is associated with small crossing sclerite, the lateral ends of which are slightly rugose. Chaetotaxy: 2 *ames* microsetae on each side lateral margins of ventral sclerite; 2 *lpmes* microsetae on each side just anterior to triangular nodi; *gpms* not visible. Parameral heads of irregular shape (Fig. 13). Parameral blades proximally with prominent V-shaped thickenings on dorsal side; distal parameral blades somewhat elongated and distal section soft, often bent slightly outward; *pst1*–2 as in Fig. 13. Measurements as in Table 2.

Female. Thoracic and abdominal segments and chaetotaxy as in Fig. 9. Subgenital plate in one female with faint traces of reticulation in central part (not illustrated). Proximal subgenital plate differs in shape between the two examined females; the female collected from the same host as the holotype has a plate shaped

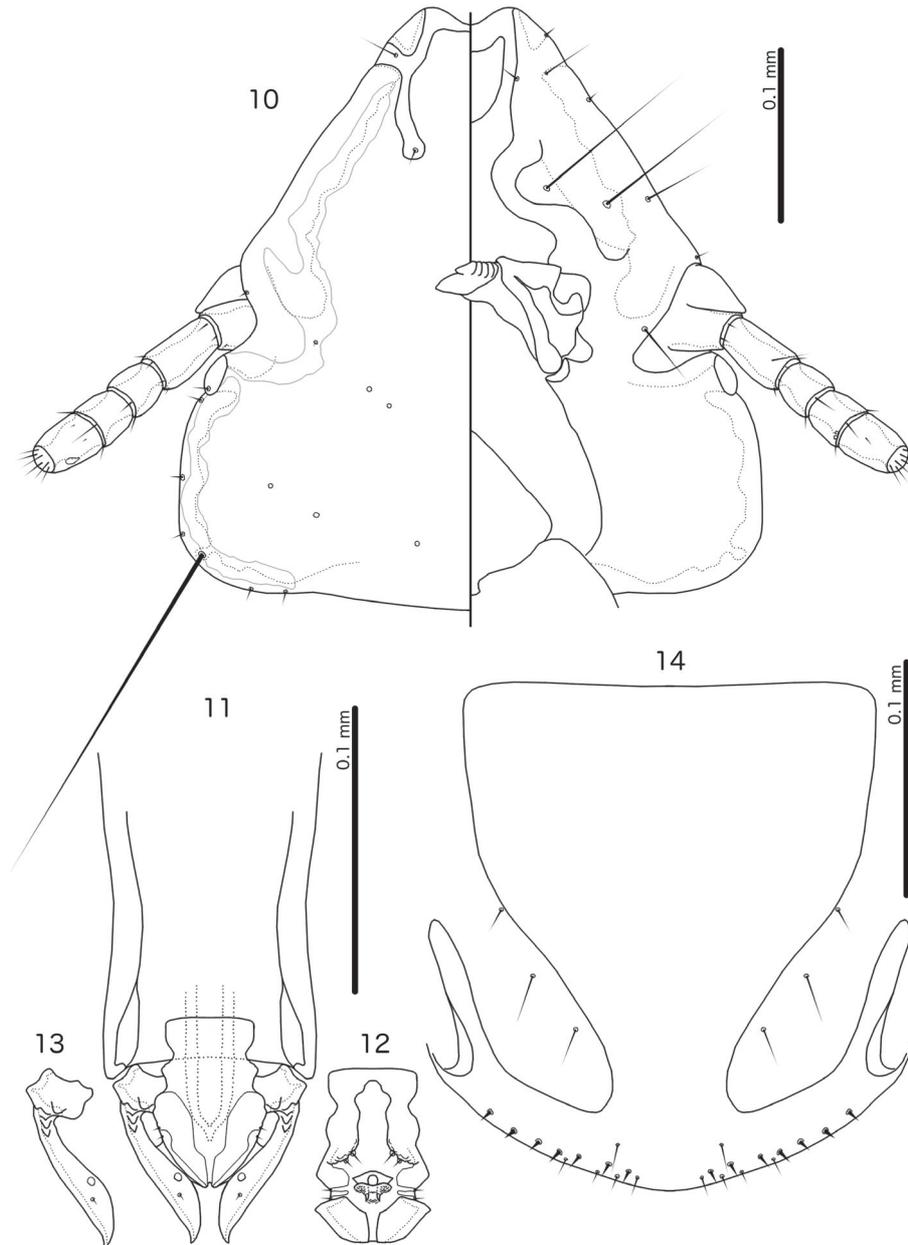


Fig. 10–14. *Guimaraesiella (Cicchinella) ailaoshanensis* sp. nov. ex *Schoeniparus dubius dubius*. **10**, male head, dorsal and ventral views. **11**, male genitalia, dorsal view. **12**, male mesosome, ventral view. **13**, male paramere, ventral view. **14**, female subgenital plate and vulval margin, ventral view.

as in Fig. 14, whereas the other female has a narrower proximal section with more rounded corners. Connection between subgenital plate and complete cross-piece broad. Vulval margin gently rounded, with up to four short, slender *vms* and six to eight short, thorn-like *vss* on each side; up to four short, slender *vos* on each side of subgenital plate but not clearly visible in one female; distal *vos* proximal to *vss*. Measurements as in Table 2.

Etymology. The species epithet is derived from the type locality, Ailaoshan.

Type material. Ex *Schoeniparus dubius dubius*: **Holotype** ♂, Ailaoshan, Yunnan Province, China, D. R. Gustafsson, K. Luo, L. Lei, 2 September 2018, J3748 (GIABR). **Paratypes:** 1♂, 1♀, same data as holotype, D. R. Gustafsson, K. Luo, L. Lei, 2 September 2018, J3748 (GIABR). 2♂, same locality as holotype, D. R. Gustafsson, K. Luo, L. Lei, 5 September 2018, J3759 (GIABR). 1♀, same locality as holotype, D. R. Gustafsson, K. Luo, L. Lei, 30 August 2018, J3722 (GIABR).

Non-type material (in ethanol): 1♂, same data as holotype, D. R. Gustafsson, K. Luo, L. Lei, 2 September 2018, J3748 (GIABR). Two nymphs, same locality as holotype, D. R.

Gustafsson, K. Luo, L. Lei, 30 August 2018, J3714 (GIABR). 2♂, same locality as holotype, D. R. Gustafsson, K. Luo, L. Lei, 30 August 2018, J3721 (GIABR). 2♂, same locality as holotype, D. R. Gustafsson, K. Luo, L. Lei, 4 September 2018, J3749 (GIABR). 2♂, same locality as holotype, D. R. Gustafsson, K. Luo, L. Lei, 5 September 2018, J3758 (GIABR)

Remarks. *Guimaraesiella* (*Cicchinella*) *ailaoshanensis* is the second species of *Guimaraesiella* described from hosts in the Pellorneidae; the first was *Guimaraesiella* (*Cicchinella*) *gombakensis* Gustafsson *et al.*, 2019. Curiously, these two hosts are parasitized by members of different species groups within *G.* (*Cicchinella*): *G.* (*C.*) *gombakensis* belongs to the *gombakensis* species group, whereas *G.* (*C.*) *ailaoshanensis* belongs to the *sehri* species group. *Turdinus* and *Schoeniparus* are not closely related within the Pellorneidae (Gelang *et al.*, 2008; Moyle *et al.*, 2012). More collections from hosts in the Pellorneidae are needed to establish the distribution patterns of the lice in these two species groups.

Discussion

The chewing lice of most Southeast Asian passeriforms remain poorly known. Chu *et al.* (2019) published the first general survey of chewing lice in China, and recorded 28 new species for the Chinese louse fauna and 10 new host records worldwide. In the present study, we add another 17 new host records, three new records for China and two new species derived from a single collection trip to two places in central Yunnan. Many of the unidentified louse species recorded in the present study are also predicted to represent new species. This indicates that the unknown diversity of chewing lice in China and Southeast Asia is likely very high. More extensive surveys are needed to explore the biogeography, host relationships and diversity of chewing lice in this region.

Infestation rates

With the exception of two species of lice each from the Grey-headed Lapwing and the Lesser Cuckoo, all lice were collected from passerine hosts. Lice from non-passerine hosts are not discussed further. The majority of the parasitized passeriform hosts belong either in the Muscicapidae or in one of the 'babbler' families (Leiothrichidae, Paradoxornithidae, Pellorneidae, Timaliidae) (Table 1).

The louse fauna on the birds examined in Ailaoshan was dominated by the genus *Myrsidea*; of the 394 louse specimens collected, 259 (65.7%) were *Myrsidea* spp. Specimens of *Myrsidea* were obtained from 11 host species, with prevalences ranging from 25% to 100%. The prevalence of *Myrsidea* spp. on host species for which we examined 10 individuals or more ranges from 30% to 73%. This is higher than most other published prevalences of *Myrsidea* on Southeast Asian birds, which generally range between 11% and 40% (Gupta *et al.*, 2007; Saxena *et al.*, 2007; Beg *et al.*, 2008; Ahmad *et al.*, 2011). However,

Sychra *et al.* (2014) reported a 100% prevalence of *Myrsidea claytoni* on *Cymbirhynchus macrorhynchus*.

Comparisons with published prevalences of *Brueelia*-complex species are difficult because all of these were published prior to the recent revision of this complex (Gustafsson & Bush, 2017) and the correct genus of many of the published louse records is thus unknown. For example, at least six genera of *Brueelia*-complex lice occur on 'babblers' (Gustafsson & Bush, 2017), although all of the published prevalences for *Brueelia*-complex lice on these hosts are given as '*Brueelia* sp.' Moreover, because more than one species of *Brueelia*-complex lice may occur on the same host species, it is possible that older reports refer to more than one louse species from the same host as '*Brueelia* sp.' Ignoring host species for which only a single specimen was examined, the prevalence of *Brueelia*-complex lice in our study ranges from 25% to 100% (Table 1), which is generally higher than published prevalences for *Brueelia*-complex lice (Sychra *et al.*, 2009; Najer *et al.*, 2012a, 2012b, 2014).

The higher prevalence in the present study compared with other studies of Southeast Asian birds is difficult to explain. The prevalence of lice is known to differ over the year and often shows a peak in August to September (Foster, 1969; Kettle, 1983; Chandra *et al.*, 1990; Galloway & Lamb, 2015; Lamb & Galloway, 2016; Dhoundiyal & Kumar, 2018; but see also Ash, 1960). However, some of the studies in Vietnam were conducted at times of the year similar to that of the present study (Sychra *et al.*, 2009; Najer *et al.*, 2014). The breeding and moulting cycles of the hosts are thus unlikely to have influenced the differences in prevalence of lice between our collections and those in Vietnam.

Our collection sites were at a much higher altitude than any of the collection sites in Vietnam (Sychra *et al.*, 2009; Najer *et al.*, 2012a, 2012b, 2014). The effect of altitude on the ecology of chewing lice is almost entirely unknown, although differences in altitude could conceivably be connected to differences in ambient humidity, which is known to affect chewing louse communities. In particular, *Myrsidea* sp. are entirely absent in less humid parts of its host's range in North American scrub-jays (*Aphelocoma*; Bush *et al.*, 2009) and not found at all in the desert-adapted trumpeter-finch (*Bucanetes*; Carillo *et al.*, 2007). In both these hosts, *Brueelia* s.l. are present in very dry areas. Lice caught at higher altitude in Slovakia also had higher prevalences of lice caught at lower altitudes in the same area (Sychra *et al.*, 2011; Bush *et al.*, 2018); however, many other factors differed between these two studies and the abiotic factors influencing louse prevalence are likely more complicated. Finally, if forest habitats form larger cohesive units at higher altitudes than at lower altitudes (e.g. as a result of farming and villages in the valleys), habitat fragmentation effects may impact on lice differently at different altitudes (Bush *et al.*, 2013).

Notably, our samples in Ailaoshan contain a higher proportion of babblers than any of the studies in Vietnam. Many of these babbler species occur in large flocks post-breeding, which may increase the opportunities for lateral transmission between individuals. Most of the smaller babbler species examined (*Alcippe fratercula*, *Fulvetta manipurensis*, *Lioparus chrysotis*, *Schoeniparus* spp., *Suthora nipalensis*) were almost always caught in groups, often with more than one species caught in the

same net at the same time (data not shown). By contrast, many of the species examined in Vietnam are more solitary.

Some *Brueelia*-complex lice are known to spread between host individuals by phoretic attachment on hippoboscids; this is not known in *Myrsidea*, although recent records have shown that at least some amblyceran lice are capable of phoresy (Bartlow *et al.*, 2016) and phoresy may be more common in amblyceran lice than is currently appreciated. This could potentially influence the prevalence data because our sampling was carried out within the peak period of abundance reported for hippoboscids (Sychra *et al.*, 2008). However, no hippoboscids were observed or collected in Ailaoshan, and only two were collected in Jinshanyakou, each from a different host individual, neither of which was carrying any chewing lice. Because hippoboscids escape readily from hosts, these may have been overlooked in our sampling; however, the undetected presence of hippoboscids does not explain the differences in prevalence between the data obtained in the present study and that from Vietnam because the sampling periods overlap.

By contrast with the higher prevalences of lice in our samples compared with those previously reported from Vietnam, the mean intensity of lice in our sample is much lower (1.96 in Ailaoshan, 0.37 in Jinshanyakou; 1.08 overall) than that reported from Vietnam (3.61–19.2; Sychra *et al.*, 2009; Najer *et al.*, 2012a, 2012b, 2014). The mean intensity is known to be reduced in the post-breeding season compared with the pre-breeding season (Sychra *et al.*, 2011); however, at least some of the Vietnamese data are from the same time of the year as those obtained in the present study (Najer *et al.*, 2012a, 2012b, 2014) and thus cannot explain this difference between the Chinese and Vietnamese data entirely.

The presence of two unidentified *Guimaraesiella* on one *F. manipurensis* (see above) may be the result of natural straggling between birds in mixed-species flocks. The specimens are not conspecific with any known species of *Guimaraesiella* but are not described here because no males were obtained. Both specimens belong to the subgenus *Cicchinella* Gustafsson *et al.* (2019) and many hosts presumably parasitized by lice in this subgenus were observed in Ailaoshan but not caught (data not shown). Unless two species of *Guimaraesiella* naturally occur on the same host, any of these hosts may be the natural host of this undescribed species. No comprehensive study of the effect of participation in the mixed-species flock on the prevalence or host associations of chewing lice has been published. However, mixed-species flocks have been suggested as an explanation for the wide range of host associations seen in some *Brueelia*-complex lice (Gustafsson *et al.*, 2018a). Moreover, participation in mixed-species flocks may explain why closely-related species of lice may occur on distantly-related hosts in several bird families (Gustafsson *et al.*, 2018b). More detailed studies are needed to address the impact of a mixed-species flock on chewing louse biology and evolution.

Impact of migration

Notably, almost no lice were collected from migrating passerines at Jinshanyakou (one bird; 0.7% infested), whereas 59

of 162 (36%) of the resident passerine birds caught at Ailaoshan were infested with chewing lice (Table 1). This is in contrast with the results reported by Chu *et al.* (2019), who found that there were no significant differences in prevalence between resident and migrant birds in China. Several factors may explain this discrepancy. For example, Chu *et al.* (2019) included both passerine and non-passerine birds in their analysis, whereas we considered only passerines. In general, passerines are parasitized by chewing lice less often compared with non-passerines (Sychra *et al.*, 2011; D. R. Gustafsson, unpublished data).

Moreover, Chu *et al.* (2019) did not differentiate between birds that breed in South China and migrate to, for example, South-east Asia (South China Migrants, SCM), and birds that breed in, for example, North China and migrate to South China (North China Migrants, NCM). Migration for the SCM birds would be within the tropical/subtropical region and, even during migration, these birds would not experience any significant differences in external environment; the environment would in this sense not be very different from that of resident birds in South China. By contrast, migration for the NCM birds would be between a temperate or boreal region and a tropical/subtropical region (i.e. between regions with different external environments). This hypothesis may explain the differences between the results of the present and those reported by Chu *et al.* (2019) and would be in line with much lower infestation rates in migratory birds caught in Sweden and Japan (D. R. Gustafsson, unpublished data). However, our present data set from Yunnan is not sufficient to test this hypothesis; future collections in China will focus on the difference between SCM and NCM birds, specifically.

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