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# DESCRIPTION OF KIMUNPSOCUS TAKUMAI N. GEN. & N. SP. FROM HOKKAIDO, JAPAN (PSOCODEA: 'PSOCOPTERA': PSOCIDAE: PTYCTINI)

*By* KAZUNORI YOSHIZAWA

*Abstract*

YOSHIZAWA, K., Description of *Kimunpsocus takumai* n. gen. & n. sp. from Hokkaido, Japan (Psocodea: 'Psocoptera': Psocidae: Ptyctini). *Ins. matsum. n. s*. 65: 149–155, 4 figs.

A new genus and species of the tribe Ptyctini, *Kimunpsocus takumai*, was described based on the specimens collected in Hokkaido, Japan. Morphologically, *Kimunpsocus* is apparently a member of the tribe Ptyctini and is similar to *Loensia* in the forewing markings and venation. However, independence of this new genus was supported morphologically and molecularly.

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## Introduction

Recently, I had an opportunity to examine a unique undescribed psocid species collected in Hokkaido, Japan. Based on the morphological examination, the undescribed species is clearly assigned to the tribe Ptyctini of the family Psocidae, but its exact systematic placement could not be decided. Superficially, the species is similar to the genus *Loensia* Enderlein, 1924, in the forewing venation and markings. However, some important differences in genitalic morphology were observed between *Loensia* and the undescribed species. Therefore, I also extracted DNA from the species and appended the data to the matrix presented in Yoshizawa & Johnson (2008). The resultant tree supported that the species composes a monophyletic group with the genera *Arabopsocus* Lienhard, 2008, *Camelopsocus* Mockford, 1965, *Loensia*, and *Oreopsocus* Roesler, 1939, but is not assignable to any of these genera. Based on this morphological and molecular evidence, I here erect a new genus, *Kimunpsocus*, for the undescribed species, described here as *K. takumai* n. sp..

I thank Akira Ueda for collecting and supplying the specimens examined in this study, Takuma Yoshida for sorting them out from the samples collected by A. Ueda, and E. L. Mockford for review of the manuscript.

## Systematics

### Genus *Kimunpsocus* new

Diagnosis. Distal margin of labrum with nine median sensilla, three of them placoids. Setae on antenna much longer in males than in females. Forewing (Fig. 1) heavily pigmented; Rs and M fused for short distance; posterior margin of pterostigma angled, without spur vein; areola postica nearly triangular in shape. Male (Fig. 2): Anterior margin of clunium deeply hollowed dorsally. Epiproct (Fig. 2AB) chair shaped; epiproct lobe trilobed. Hypandrium (Fig. 2D) with single median strap. Phallosome (Fig. 2E) closed anteriorly, with long process posteriorly and with pair of asymmetrical expansions posterolaterally. Female (Fig. 3): Ventral valve of gonapophyses long, external valve with well developed posterior lobe (Fig. 3B). Internal plate without

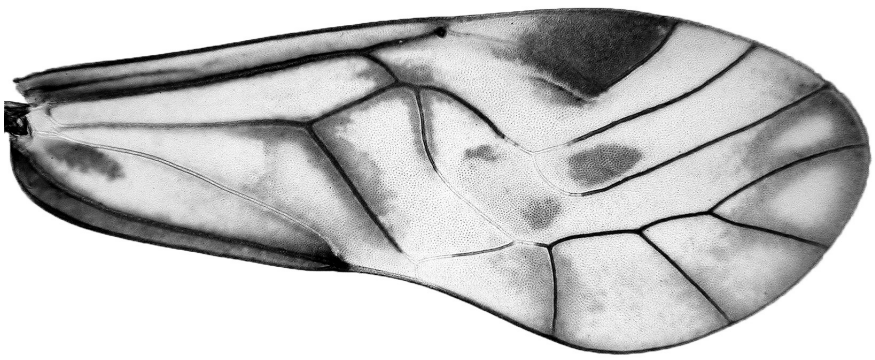

Fig. 1. Forewing of *Kimunpsocus takumai*, male.

sclerotization nor pigmentation.

Etymology. 'Kimun' means mountain in the language of the native Hokkaido people, Ainu. This genus is known only from the mountainous regions of Hokkaido to date.

Type species. *Kimunpsocus takumai* n. sp.

*Kimunpsocus takumai* n. sp.
(Figs 1–3)

Description. Male. Head. White in ground color; vertical and orbital markings broad and blackish brown; coronal suture black; frontal suture dorsally bordered with broad blackish brown band; frons with pair of pale brown bands medially; gena without marking; eye black, small, IO/D = 1.7; ocelli white, ocellar field black; antennal socket bordered with blackish brown band; postclypeus brown; anteclypeus blackish brown. Anenna brown, pedicel and scape darker. Mouth parts mostly brown.

Thorax. Prothorax blackish brown. Meso- and metathorax mostly blackish brown except membranous regions white; mesonotum with white region medially and posterolateral margin of lateral lobe of scutum, and with narrow white longitudinal line on anterior lobe of scutum medially; anterior lobe of metascutum white.

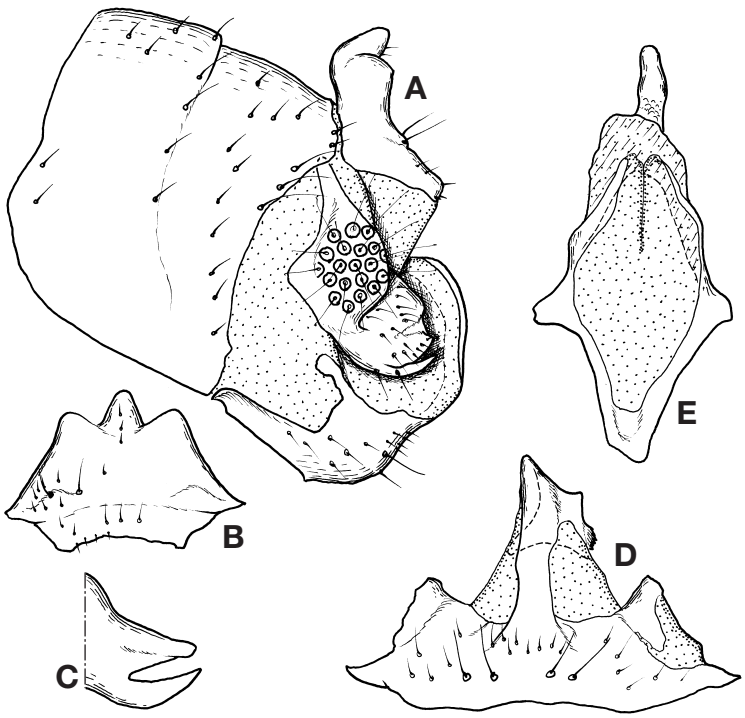


Fig. 2. Male (holotype) terminal structures of *Kimunpsocus takumai*. A, terminalia, lateral view; B, epiproct, posterior view; C, distal part of paraproct, ventrolateral view; D, hypandrium, ventral view; E, phallosome, ventral view.

Legs. Almost uniformly blackish brown; basal half of all tibiae paler.

Forewing (Fig. 1) hyaline with brownish tinge, extensively with blackish brown markings; nodal band (sensu Günther, 1974) not continuous, only recognized along veins and distal end of cell cup; distal 2/3 of pterostigma pigmented; cell r3 with oval spot basally; cell r5 with pair of spots in basal half; distal margin widely pigmented from posterior margin of cell r3 to distal margin of areola postica but faint in cell m3, marginal pigmentation with light spot in middle of each cell; cell cup with long spot basally; cell a uniformly blackish brown; Rs and M fused for short distance; posterior margin of pterostigma angled, without spur vein; areola postica triangular in shape.

Hindwing hyaline with brownish tinge; cell cup brown; veins blackish brown.

Abdomen white dorsally, laterally with blackish brown longitudinal band, brown ventrally.

Terminalia (Fig. 2). Anterodorsal margin of clunium deeply concave in V-shape. Epiproct (Fig. 2AB) chair shaped; epiproct lobe expanded antero-dorsally, narrowing dorsally in posterior view, its dorsal margin three-lobed, lobes directed posterodorsally. Paraproct (Fig. 2AC) with distal lobe well projected posteriorly, rather thin and pointed in ventrolateral view; distal process long. Hypandrium (Fig. 2D) asymmetrical; posterolateral corner strongly bent anteriorly; posteromedially with median strap, its apical part strongly skewed rightward and bent anteriorly. Phallosome (Fig. 2E) closed, pointed anteriorly, with weakly sclerotized parameres, posterolaterally with asymmetrical expansions, left expansion stronger than right one; posteromedially with long process rounded apically.

Length. Forewing 4.0–4.2 mm; hindwing 3.0–3.1 mm; body 1.9–2.1 mm.

Female. Generally as in male except for following. IO/D = 2.0; dorsal band of frontal suture narrow.

Genitalia (Fig. 3). Subgenital plate (Fig. 3A): egg guide strongly constricted to narrow and rounded posterior margin; anterior arm short and wide, anterior margin

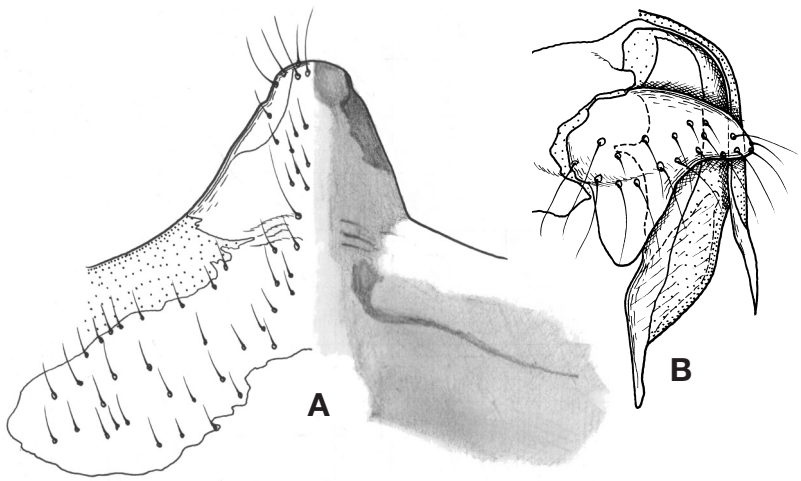


Fig. 3. Female genitalia of *Kimunpsocus takumai*. A, subgenital plate, ventral view, showing structure (left) and pigmentation (right); B, gonapophyses, ventral view.

deeply concave in semicircular shape. Gonapophyses (Fig. 3B): ventral valve long; dorsal valve with broad sclerotized portion dorsally; external valve with broad and long posterior lobe. Internal plate without obvious sclerotization nor pigmentation.

Length. Forewing 4.4–4.6 mm; hindwing 3.1–3.3 mm; body 2.6–2.8 mm.

Holotype male, N43º40' E143º06', alt. 993m, Sekihoku-toge, Kamikawa-cho, Hokkaido, 27. vi–18. vii. 2008, Malaise Trap, A. Ueda leg. (DNA extraction ID: KY416; GenBank accession ID: GQ231535–GQ231538). Paratypes: 3 males 4 females, N43º40' E143º01', alt. 947m, Ginsendai, Kamikawa-cho, Hokkaido, 27. vi–18. vii. 2008, Malaise Trap, A. Ueda leg.; 1 male, same locality and collector as for holotype, 6–27. vi. 2008; 3 males 4 females, same data as for holotype; 1 male, N43º38' E144º29', alt. 217m, Teshikaga-cho, Hokkaido, 26. vi–17. vii. 2008, Malaise Trap, A. Ueda leg.; 1 female, same locality and collector, 17. vii–7. viii. 2008. All specimens are stored in the Hokkaido University Insect Collection.

Etymology. The specific epithet is dedicated to Takuma Yoshida of the laboratory of Systematic Entomology, Hokkaido University, who discovered and sorted out this unique psocid from the enormous insect samples collected by Malaise Trap.

Distribution. Japan (Hokkaido).

## Discussion

The chair-shaped epiproct of the present new species clearly shows that the species is a member of the tribe Ptyctini. In contrast, systematic placement of this species within the tribe is morphologically difficult to decide. By molecular-based phylogenetic analyses, the species is placed within a lineage composed of the genera *Arabopsocus*, *Camelopsocus*, *Loensia*, and *Oreopsocus* (referred to as ACLO lineage in the following lines: Fig. 4), and statistical supports for the ACLO lineage are high (99% posterior probability and 82% bootstrap support). In this tree, *Loensia* is split into two different lineages, and *L. conspersa* composes a monophyletic group with *Oreopsocus* and *Arabopsocus*: supports for this monophyletic group are fairly high (91% PP and 73.8% BS). Morphlogically, *L. conspersa* is quite different from the type species of *Loensia* in male genitalic structures (Mockford, 1993; K. Yoshizawa, personal examination) and thus probably represents a different genus in its own. The tree also shows that assignment of the present new species to any known genus of the ACLO lineage is not supported molecularly.

Within the ACLO lineage, the present species shows the closest morphological similarities with the genus *Loensia* as follow: forewing heavily pigmented; areola postica triangular in shape; hypandrium with asymmetrical median strap bent upward and forward at apex; phallosome with pair of posterolateral expansions. In contrast, all species of *Loensia* except for the heterogeneous species, *L. conspersa*, have a process to the left of hypandrial median strap (autapomorphy of the genus), and the present species lacks this important apomorphy of *Loensia*. Heavily pigmented forewing is widely observed throughout Psocidae, and it even might represent a plesiomorphic condition in the ACLO lineage. In addition, the other character states listed above can also be observed in other genera as follow: triangular areola postica in Oreopsocus; similar hypandrial structure in *Camelopsocus*; posterolateral expansions of phallosome in *Oreopsocus* and *Camelopsocus*. Therefore, the above-mentioned similarities between the present species and *Loensia* do not provide morphological evidence for their closest phylogenetic relationship.


Fig. 4. The maximum likelihood tree estimated by PAUP* (Swofford, 2002) showing the systematic position of *Kimunpsocus takumai*. Data and methods are from Yoshizawa & Johnson (2008), but non-Ptyctini exemplars are eliminated from the analyses. Therefore, the tree is unrooted. Substitution model was selected based on the Akaike Information Criterion as implemented in Modeltest (GTR+I+G: Posada & Crandall, 1998). The data include nuclear 18S rDNA, Histone 3 and wingless and mitochondrial 12S rDNA, 16S rDNA and COI genes but, for *K. takumai*, partitions of Histone 3 and wingless are missing. Numbers associated to branches are Bayesian posterior probability (>90%) calculated with MrBayes (four chains for 200,000 MCMC generations, sampled every 1000 generations, first 100 trees were excluded as burnin: Ronquist & Huelsenbeck, 2003) and likelihood bootstrap support value (>50%) calculated with PHYML (1000 replicates, NNI branch swapping with ML tree as a starting tree: Guindon & Gascuel, 2003). Aligned data matrix is available from http://kazu.psocodea.org/data.

As discussed above, neither molecular nor morphological data provide evidence for the systematic assignment of the present new species to any known genus so that independent generic status of *Kimunpsocus takumai* can be justified from two independent data sets. The genus is now represented only by a single species, and it is difficult to point out the apomorphic character states which are important to characterize the genus. However, the trilobed epiproct lobe and presence of the long posterior process and asymmetrical posterolateral expansions of the phallosome are autapomorphic to *K. takumai* and probably useful to characterize the genus.

All the members of the ACLO linage are distributed in either western Eurasia (Europe and UAE) or North America, and *Kimunpsocus* is the first representative of the lineage in eastern Asia. Therefore, discovery of this genus is also interesting biogeographically, but further faunal and phylogenetic investigations are needed to clarify the origin and biogeographical history of this lineage.

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