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Description of a new species of the genus *Xyrosaris* Meyrick (Lepidoptera: Yponomeutidae) from the Far East of Russia with notes on congeneric species

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Abstract

A new species, *Xyrosaris insularis* **sp. n.**, was found in the Far East of Russia. Most of the specimens were obtained through the rearing of larvae that fed on *Celastrus orbiculatus* Thunb. (Celastraceae). The genetic distances between the mtCOI sequences in *X. insularis* and congeneric species are in the range 1.2–13.9%. Minimal genetic distance (1.2%) was discovered between new species and *X. lichneuta* Meyrick from Shaanxi (China), which is lower than the standard mtCOI barcoding threshold of 2% for species delineation, but both taxa differ well in the genital morphology. The description of a new species is accompanied by illustrations of variations in the pattern, by the genitalia of both sexes, and by larva on its host plant.

Key words: Ermine moths, new species, host plant, molecular analysis, COI, genetic distances, East Asia

Introduction

The genus *Xyrosaris* Meyrick, 1907 was proposed for the species *dryopa* Meyrick from Australia (Meyrick 1907). It differs from other genera of the family Yponomeutidae by relatively long antennae, palpi with brush-like tuft on the third segment concealing it, forewings with tufts of raised scales; by valva with a long harpa bearing strong spines in males and a more or less developed convex sterigma with long setaceous lobes on the posterior margin in females. Currently the genus *Xyrosaris* Meyrick is considered valid, although it was merged with a related genus *Zelleria* Stainton soon after its establishment (Meyrick 1928). However, later E. Meyrick continued to describe species within *Xyrosaris* without a nomenclatural act of the generic name validation.

The genus *Xyrosaris* up to the present study included 11 species distributed in East Asia, East and South Africa, Madagascar, Rodrigues Is., North-East and South-West India, Sri Lanka, Australia, and Central America (Agassiz 2019; Lewis & Sohn 2019). Two species of them are recorded now in East Asia: *X. lichneuta* Meyrick in the Russian Far East, China, and Japan (Moriuti 1977; Ponomarenko 2016; Ponomarenko & Sinev 2022), and *X. lirinopa* Meyrick in China (Meyrick 1922).

The present work is based on the material collected from the southernmost of the Russian Far East. As a result of this study, a species significantly differing in genital morphology from all known species belonging to the genus *Xyrosaris* was discovered. Collected specimens showed great variability in the ground colour and pattern of the forewings. To confirm the conspecificity of the collected specimens and delineate the new species, a molecular analysis based on the mtCOI fragment was performed. As a result, the conspecificity of the collected specimens and evidence that they belong to a new species was provided.

Material and methods

Material. Specimens belonging to a new species were attracted to the light of mercury Lamp 250 W and 400 W in Furugelm Island in 2012 and reared from larvae, which were collected on *Celastrus orbiculatus* Thunb. (Celastraceae)

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in Russkii Island in 2022. The moths were processed as dry material for morphological study. The abdomens of some adults reared from larvae were preserved in 96 % ethanol for genetic research. The numbers of vouchers of DNA samples are listed in the subparagraph "Type material" of the paragraph Description of a new species. In total, 115 specimens were investigated in the present morphological study, 68 specimens of them were reared from larvae; the abdomens of 9 specimens are sampled for molecular analysis for the mtCOI fragment. In addition to the original data obtained in the present study, the available data from GenBank (NCBI) and from Barcode of Life Data Systems BOLD (Ratnasingham & Hebert 2007) on *Xyrosaris* spp. were included in the molecular study. The GenBank Accession Nos. and BOLD Sequence ID of these sequences are indicated in Table 1.

TABLE 1. List of COI sequences of the species from genera *Xyrosaris* Meyrick and *Zelleria* Stainton taken from GenBank and BOLD bases for molecular study.

Name of species (as identified in GenBank and BOLD)	**Country of sample origin**	**Voucher number**	**GenBank Accession Nos.**	**BOLD Sequence ID**
Xyrosaris lichneuta Meyrick, 1918	South Korea: Cheongju	JCS–08–1006	KF523851.1	LTOLB064–08.COI–5P
Xyrosaris lichneuta Meyrick, 1918	China: Shaanxi	BIOUG14237–G10	–	GMCHD605–14.COI–5P
Xyrosaris lichneuta Meyrick, 1918	China: Shaanxi	BIOUG14502–B02	–	GMCHM714–14.COI–5P
Xyrosaris secreta Meyrick, 1912	Kenya: Nyeri	USNM ENT 00194581	KF643226	AFMIC104–12.COI–5P
Xyrosaris dryopa Meyrick, 1907	Australia: New South Wales	10ANIC–02855	HQ922318.1	ANICF858–10.COI–5P
Xyrosaris acroxutha Turner, 1923	Australia: Queensland	10ANIC–02857	HQ922319.1	ANICF860–10.COI–5P
Xyrosaris acroxutha Turner, 1923	Australia: New South Wales	10ANIC–02859	KF396818.1	ANICF862–10.COI–5P
Xyrosaris sp.	South Africa: Gauteng	BIOUG06231–C03	–	LSAFA453–13.COI–5P
Xyrosaris sp.	Costa Rica: Guanacaste	SJC–08–2227	KF492175.1	LTOL1048–11.COI–5P
Zelleria hepariella Stainton, 1849	Finland	MM08657	HM874029.1	LEFIE303–10.COI–5P
Zelleria hepariella Stainton, 1849	Austria: Vorarlberg	TLMF Lep 07400	KM572196	PHLAG721–12.COI–5P
Zelleria hepariella Stainton, 1849	Germany: Bavaria	BC ZSM Lep 50951	KX040445	ODOPE170–11.COI–5P
*Zelleria oleastrella (*Millière, 1867)	South Africa: Gauteng	BC ZSM Lep 70145	–	GWOTL409–13.COI–5P
*Zelleria oleastrella (*Millière, 1867)	Spain: Comunidad Valenciana	TLMF Lep 03973	JN287234	PHLSA323–11.COI–5P

In the description of a new species, the terminology of the genital structures follows Klots (1970). The holotypes and paratypes of a new species and vouchers of samples processed for molecular study are deposited in the Federal Scientific Center of the East Asia Terrestrial Biodiversity (FSC of Biodiversity), Far Eastern Branch of Russian Academy of Sciences (Vladivostok).

Morphological study. The standard lepidopterological techniques (Falkovitsh & Stekolnikov 1978) of genitalia preparation included maceration of the soft tissue in 10–15 % KOH. The membranous parts of the genitalia were stained using chlorazol black. Structures of the genitalia were studied using a Nikon SMZ–10 stereomicroscope. Following their examination, the genitalia of both sexes were slide-mounted using Euparal following the technique described by Robinson (1976). Images of the genitalia were captured using an Olympus SZX16 stereomicroscope with a DP74 Nikon digital camera.

Molecular study. Genomic DNA from abdominal muscles was extracted following the protocol recommended in the Purification of Genomic DNA from insects appended to Qiagen DNeasy Blood & Tissue Kit (Qiagen GmbH, Hilden, Germany), with the following modifications. Since genitalia in micromoths have diagnostic significance, the abdomen of each sample was not ground for lysis to save copulative apparatus for further slide-mounting with Euparal as a voucher. One individual of each species was sampled for genomic DNA. PCR-sequencing of the COI fragment was made by the Sanger method. In PCR, the primer combination LCO1490: 5'–GGTCAACAAATCATAAAGATATTGG–3' and HCO2198: 5'–TAAACTTCAGGGTGACCAAAAAATCA–3' after Folmer *et al.* (1994) was used. The stages of PCR–sequencing and reaction mixture are described in detail by Ponomarenko *et al.* (2021). PCR fragments were sequenced in Genetic Analyser 3130xl, (Applied Biosystems, USA). Sequence visualization and export for editing and alignment were done with the Program Sequence Scanner v 1.0 (Applied Biosystems 2005). As a result, the COI barcoding fragment, 617–711 bp sequences were obtained from 9 samples collected in the Russian Far East. After editing and alignment, the resulting fragment included in the molecular analysis was 614 bp. The editing, alignment, and analysis of the obtained nucleotide sequences were performed using the software packages FinchTV 1.4.0. (Patterson *et al.* 2004) and MEGA–7 (Kumar *et al.* 2016).

Genetic comparative analysis. Genetic analysis based on the mtCOI fragment was performed using MEGA–7 software packages. The original nucleotide sequences of COI for 9 Far Eastern samples were included in comparative genetic analysis, as well as data on 6 *Xyrosaris* species of the world fauna from the Genbank and Bold databases, 2 of which are not currently identified. In addition, the genus *Zelleria* Stainton was included in the molecular analysis as an outgroup, and its relationships with *Xyrosaris* was confirmed in the recently published phylogenetic study for Yponomeutoid moths (Sohn *et al.* 2013). Since the genus *Zelleria* is characterized by high morphological diversity of the included species, in addition to the type species of the genus *Z. hepariella* Stainton, the species *Z. oleastrella* (Millière), morphologically very different from the latter, was additionally chosen as outgroup species. Samples of the indicated species with high-quality sequences, the numbers of which are listed in Table 1, were included in the analysis. The tree with inferred relationships between *Xyrosaris* species on the base of mtCOI fragment was constructed by Neighbor-Joining statistical method, Kimura 2-parameter model. The genetic divergences (evolutionary distances) between nucleotide sequences of the mtCOI fragment in *Xyrosaris* species were estimated by the Pairwise Distance method, using Kimura 2-parameter model (Kimura 1980).

Descreption of a new species

Xyrosaris insularis Ponomarenko et Beljaev **sp. n.**

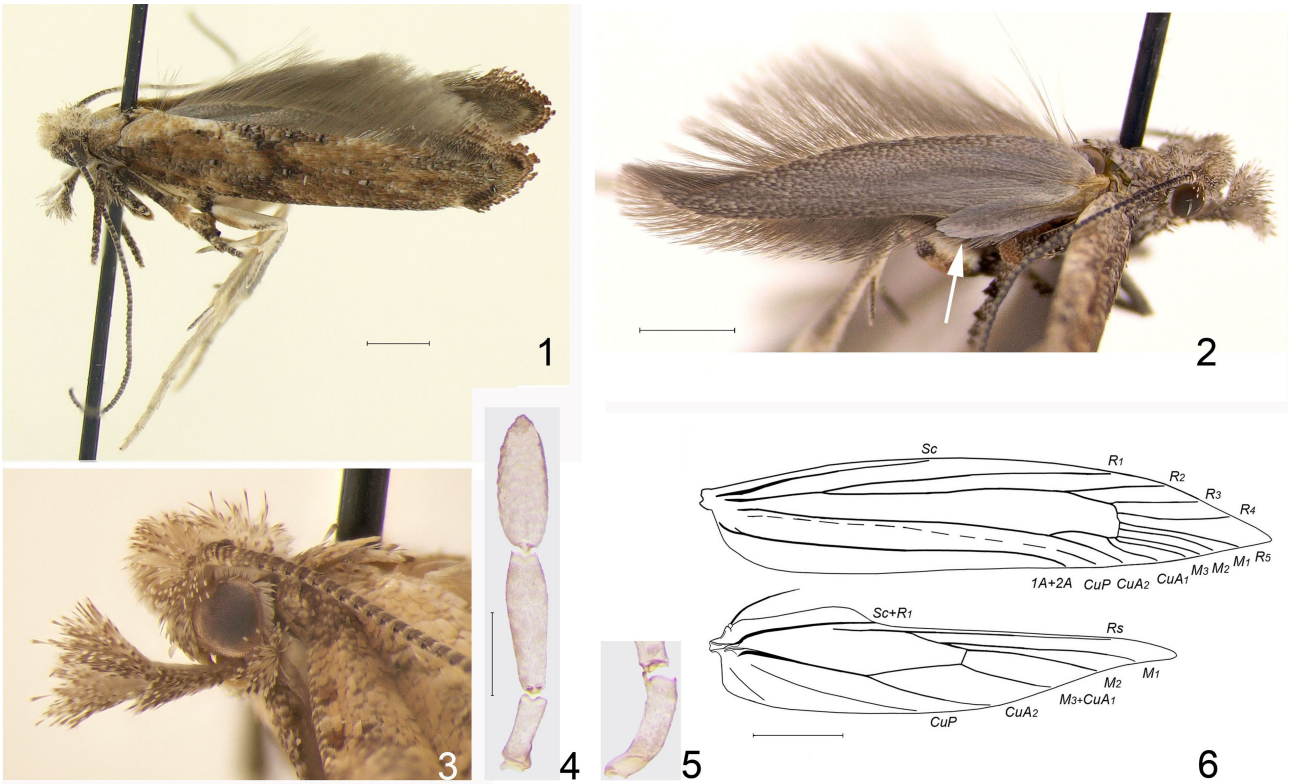
Type material. Holotype: ♂, **Russia**, Primorskii Krai, 1 km SW of Vladivostok, Russkii Isl., Rogozin cape, 42°59'13" N 131°44'47" E, 18.07.2022, reared from *Celastrus orbiculatus*, gen. slide 181 MP (leg. E. Beljaev).

Paratypes: **Russia**: 1 ♀, same locality, date, collector and host plant, gen. slide 182 MP; 33 ♂, 40 ♀, same locality and host plant, 22.08–09.09.2022, gen. slide 190 (♂) MP (leg. M. Ponomarenko and E. Beljaev), voucher Nos / DNA Nos – 777 (♀), 22.08.2022; 778 (♂), 23.08.2022; 781 (♂) 25.08.2022; 782 (♂), 783 (♂), 784 (♂), 785 (♂), 785 (♂), 29.08.2022; 788 (♂), 31.08.2022; 29 ♂, 17 ♀, Khasanskii distr., 59 km SW Slavyanka, Furugelm Isl., 42°27′55″ N 130°55′10″ E, 20–22.09.2012, gen. slide 186 (♂) YuZ, 187, 189, 191 (♂♂), 188, 192, 193 (♀♀) MP (leg. M. Ponomarenko).

Diagnosis. A new species is similar to *X. lichneuta* Meyrick, 1918, *X. dryopa* Meyrick, 1907 and *X. obtorta* Meyrick, 1924 by the labial palpi with third segment bearing a dense brush-like tuft concealing its apex, and by some elements of forewing pattern, specifically by oblique dark stripe on the dorsal half before the middle and light small costal spot at 4/5 of forewing. A new species can be easily distinguished in the male genitalia by a relatively large valval harpa bearing strong thorns on the triangular distal part and in the female genitalia by sterigma covered with strong setae externally and having sclerotized lobes on the anterior margin. In the related species *X. lichneuta* and *X. dryopa* valval harpa is slender, slightly dilated distally and without thorns, and sterigma lacks strong setae on the external surface; furthermore, it is without lobes on the anterior margin.

Adult (Figs 1–10). Forewing length 6.0–7.6 mm. Head covered with raised elongated scales, with light-grey apices (Fig. 3). Palpi also covered with elongated scales, concolorous to those on the head; the first segment is short and arched, the second and third segments are flattened dorso-ventrally, the second segment dilated at distal 2/3,

third segment slightly shorter than second one and hidden in long, loose bundle (Figs 4, 5). Eyes large, diameter 3/4 of head length along the longitudinal body axis. Antenna filiform, with alternating light grey and dark grey rings, 4/5 wing length. Forewing elongated, rather narrow, with raised tufts of scales light at apices. Coloration and pattern of the wing are very variable (Figs 1, 7–10). Ground colour uniformly dark or light reddish-brown, slightly darker in distal third, some specimens with light-grey ground colour along basal half of dorsal margin. The pattern of wing, if distinct, is formed by a dark-brown transverse polyline, as a mirror image of the Greek symbol sigma (Σ), before the middle, brown wide longitudinal band on the basal third of the wing, dark-brown costal margin at basal third, concolorous two spots (costal one on sub-apex and another on tornus) and a light small mark in a small concavity at 4/5 of costal margin; distal third with two greyish or reddish-brown longitudinal bands under the median axis and along the dorsal margin. In many specimens, only some of the described elements are visible. Fringe motley, three stripes of dark brown scales alternating with light ones border the wing apex. Hindwing brownish-grey, with apex curved backward and basal lobe about 1/3 of wing length, surrounded by elongated light scales along the costal margin and $Sc+R_1$, forming shiny plate when opening wings (Fig. 2); fringe grey. Forewing with *Sc* to costa at about 2/5 of wing length; R_1–R_4 to costa, each separate at the base, R_4 and R_5 separate basally; R_5, M_1–M_3, CuA_1 and CuA_2 to dorsal margin, each separate basally; *CuP* present at distal part only, *1A* and *2A* merged. Hindwing with $Sc+R_1$ to costa at about 1/3 of wing length, *Rs* to costa at about 6/7 of wing length, M_1 and M_2 close at base, M_3 and CuA_1 merged (after Moriuti, 1977), M_3+CuA_1 and CuA_2 remote basally, *CuP* to 2/5 of dorsal margin (Fig. 6).

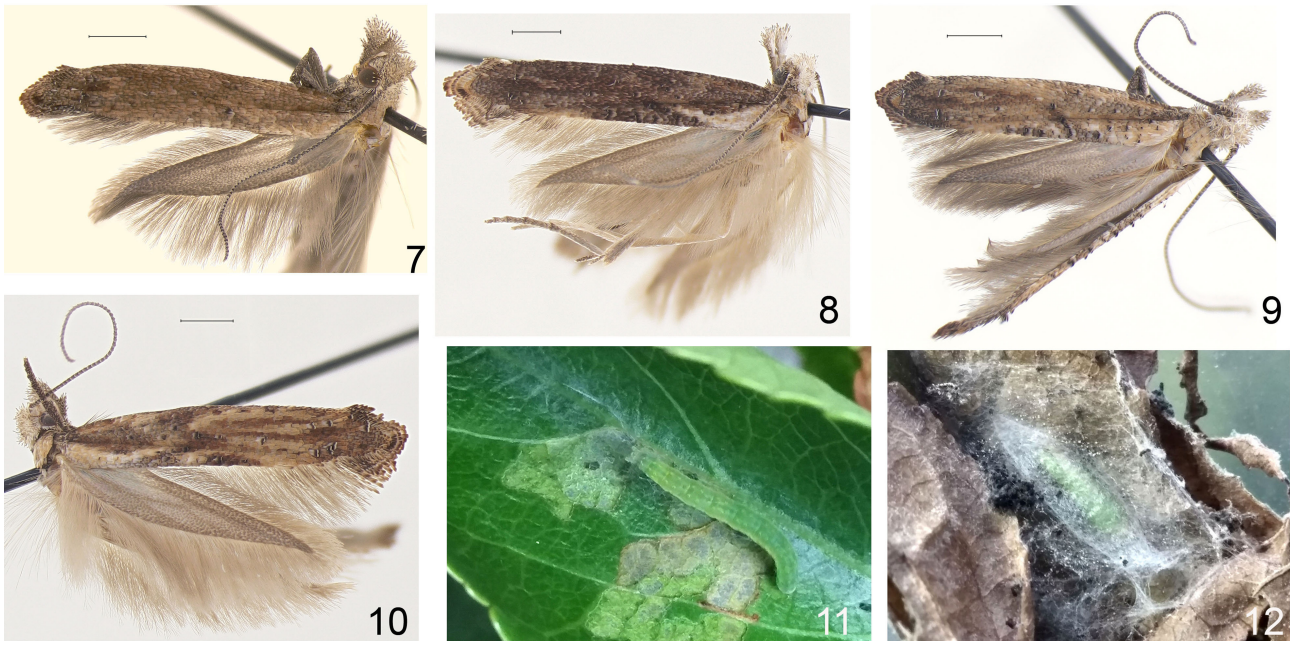


FIGURES 1–6. External morphology of adult of *Xyrosaris insularis* **sp. n.** 1, holotype, male; 2, paratype, male, hindwing with basal lobe on costa (shown with a white arrow); 3, head, lateral view; 4, palpus, dorso-ventral view, distal segment above; 5, basal segment of palpus, lateral view, enlarged; 6, wing venation. Scale bar for figures 1–4, 6—1 mm; for figure 5—0.5 mm.

Second abdominal sternite with a relatively deep rounded incision between long well-developed apodemes, distinct longer venulae, and sclerotized arch between them (Fig. 17).

Male genitalia (Figs 13–16). Uncus more or less triangular; socius arched, narrowed distally, with a thorn at the apex. Tuba analis wide and membranous, with ventral linear sclerotization. Tegumen arcuate, with longitudinal sclerotized comb-like muscular apodeme at anterior 1/4. Gnathos large bucket-shaped, curved at the middle, its basal part consisting of two narrow band-like arms and its distal part finely spiny and with a median gutter-shaped cavity, enclosing the aedeagus; ventral sclerotized ridge roundly convex or sinuous and with lateral projections between basal and distal parts of gnathos (Figs 15, 16). Valva with almost parallel dorsal and ventral edges, slightly notched before dorsal protruding corner; dorso-basal process narrow and long, at about 1/5 of total valval length;

harpa slightly longer than valval length, with inflation at the middle and 4–7 strong thorns along the convex edge of expanded distal part. Vinculum triangular ventrally and narrow laterally, with saccus more or less bulbous distally. Aedeagus slender, longer than valva, tube-like, with sclerotized sides at distal third and ring-like basal scape, cornuti composed of minute spines in distal fourth.



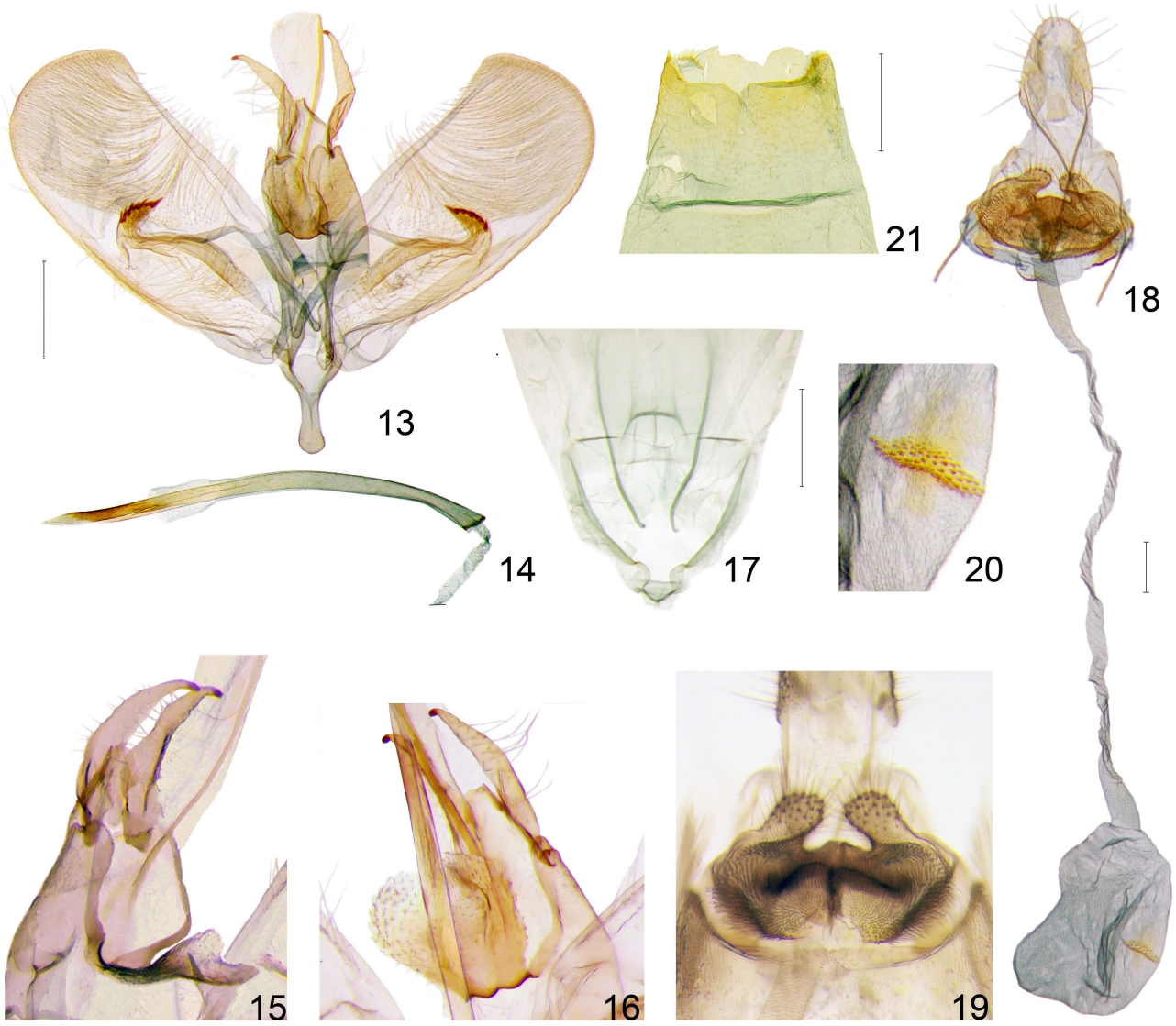
FIGURES 7–12. Adults, paratypes, and preimaginal stages of *Xyrosaris insularis* **sp. n.** 7–10—variations of wing pattern: 7, 9—males, Russkii Is.; 8, 10—males, Furugelm Is.; 11—larva on leaf of *Celastrus orbiculatus* with skeletonized upper surface; 12—cocoon with larva in process of pupation. Scale bar 1 mm.

Female genitalia (Figs 18–20). Ovipositor relatively moderate, intersegmental membrane between 9th and 8th abdominal segments almost 2 times shorter than the length of papillae anales. The latter sclerotized laterally. Sclerotized plate between the base of papillae anales is distinct, triangular, and almost 1/3 of the papilla analis length. 8th tergite is deeply notched on the posterior edge. Apophysis anterioris branched in the posterior part, its dorsal arm merged with the lateral edge of 8th tergite and its ventral branch joined with strongly sclerotized and ventrally convex 8th sternite forming sterigma; the anterior not branched part is three times shorter than apophysis posterioris. Sterigma densely covered with short strong setae on external surface; posterior edge with rounded lobes bearing long setae; anterior edge with a rounded cut at the middle and ear-like lobes laterally. These lobes joined with the posterior margin of the 7th sternite, the latter with a relatively deep cut and sclerotized laterally (Figs 19, 21). Ostium round, placed behind inflated middle part of sterigma. Antrum sclerotized, cylindrical, ductus bursae membranous, long and narrow, three times longer than corpus bursae, slightly dilated towards corpus bursae. Corpus bursae is more or less pear-shaped with signum at about the middle of the lateral side; signum with triangular thorns on a transversal gutter-like part and with one anterior lobe-like and two posterior triangular sclerotizations. Both ductus and corpus bursae with microtrichia on the inner side.

Distribution. Russia (south of the Far East).

Bionomics. Numerous larvae of different ages were collected on *Celastrus orbiculatus* Thunb. (Celastraceae), growing in a narrow strip of the sea coast along rocks and rocky slopes on 12.08.2022. The larvae were predominantly light green in colour with a light grey head and prothoracic shield. The head of larvae is wider than thorax, with distinct epicranial suture dividing it into two slightly inflated halves. They fed on leaves folded in the form of a cradle with silk threads (Fig. 11). In the laboratory, larvae began to pupate from 14.08.2022 onwards. Pupation took place in a loose silken cocoon (Fig. 12). The duration of pupal development in the laboratory was 7–10 days. Imago emerged from 22.08 to 09.09.2022.

Considering the capture of the first 2 specimens of this species in the middle of July and the rearing of specimens in late August–early September, it can be stated that *X. insularis* has 2 generations in the south of Primorskii Krai.



FIGURES 13–21. Abdominal morphostructures of *Xyrosaris insularis* **sp. n.** 13–17, male: 13, male genitalia, ventral view, holotype, GS 181 MP; 14, aedeagus, lateral view, holotype, GS 181 MP; 15, uncus and deflected gnathos, latero-ventral view, paratype; 16, gnathos supporting aedeagus, ventral view, paratype; 17, 2nd abdominal sternite, paratype; 18–21, female: 18, female genitalia, ventral view, paratype, GS 182 MP; 19, 8th abdominal sternite, ventral view, paratype; 20, signum, paratype; 21, 7th abdominal segment, ventral view, paratype. Scale bar 0.5 mm with the exception of enlarged figures 15, 16, 19, 20.

Etymology. The name of the species, *insularis*, is derived from the Latin *insula*, meaning island, and corresponds to the insular habitat of the species.

Remarks. Since the genetic distance between sequences of the new species and specimen from South Korea 0%, they might be conspecific, however other independent character set as detailed genitalia morphology needs to be examined. In case the specimens from Russia, Primorskii Krai, presented in this study, and the specimens captured in South Korea are conspecific, then the distributional range of *X. insularis* includes the territory of this country. To confirm this further investigation is required.

Discussion

Comparative analysis of COI fragment sequences in *Xyrosaris* species

On the built neighbor-joining tree the samples from East Asia (Russian Far East, South Korea and China) were united in one clade consisting of two clusters with bootstrap support 99 % (Fig. 22). The first cluster includes

samples of a new species, *Xyrosaris insularis*, from the Russian Far East together with a sample from South Korea, and the second cluster includes samples from China (Shaanxi). Samples from South Korea and China presented in Genbank and BOLD were identified as *X. lichneuta*. However, specimens from the Russian Far East used for sequence analysis and identified as the new species *Xyrosaris insularis* Ponomarenko et Beljaev differ well from *X. lichneuta* by male and female genitalia (Figs 13, 18). The rooting of the South Korean sample together with the samples from the Russian Far East and the genetic distance between them of 0 % may indicate the probable conspecificity of these samples and, this fact requires re-identification of the South Korean specimen posted in the Genbank and BOLD databases.

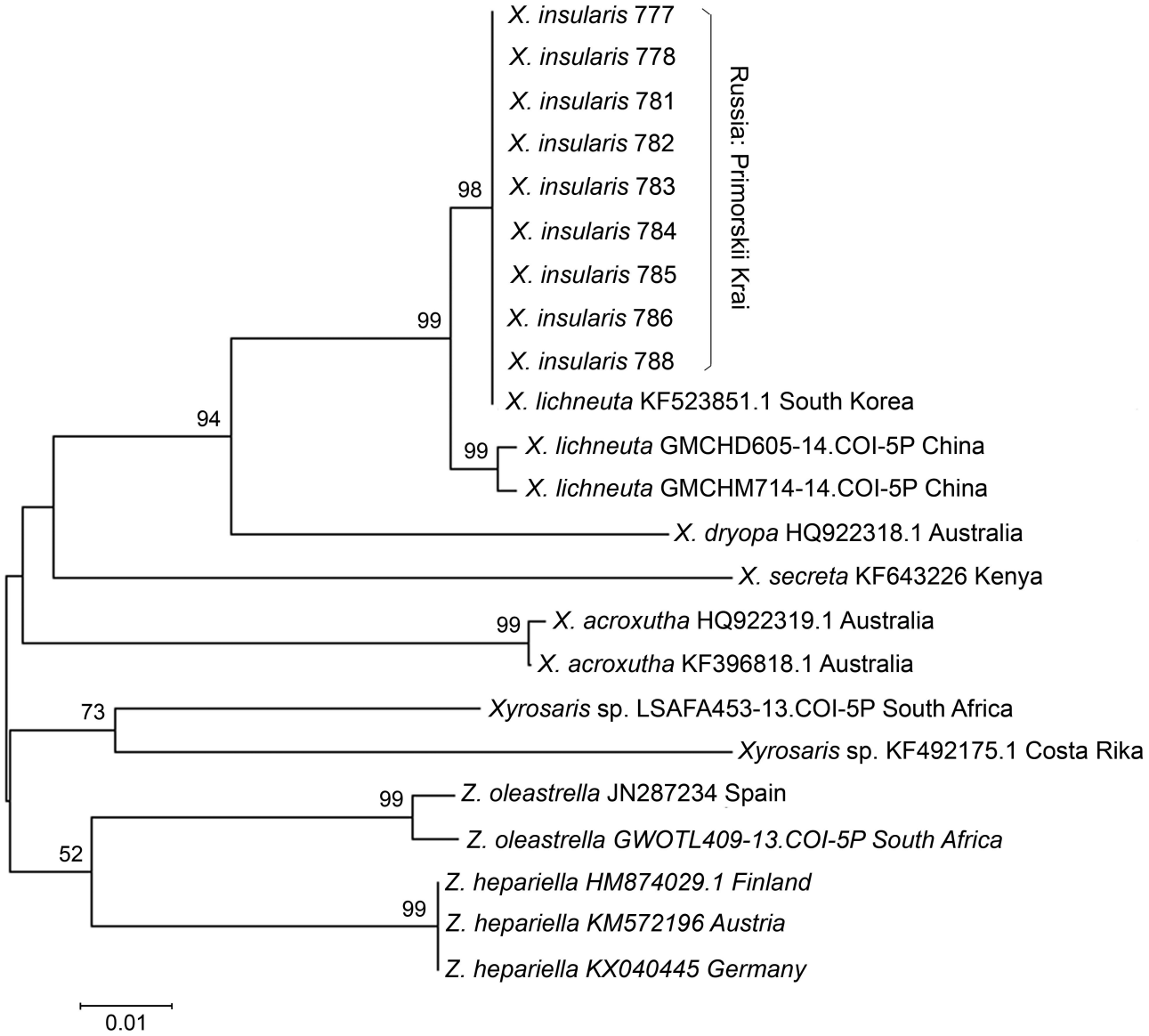


FIGURE 22. Neighbor-Joining tree of *Xyrosaris* species on the base of sequences of COI fragment. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is given for those greater than 50 %.

In general, East Asian species (*Xyrosaris insularis* and *X. lichneuta* from China) are characterized by weak genetic divergence on the barcode fragment, with the interspecific genetic distance between them 1.2 % (Fig. 2). The intraspecific genetic distance of specimens *X. lichneuta* from China (n=2) is 0.4 %. The remaining species of the genus *Xyrosaris* with available molecular data are more divergent on the barcode fragment from East Asian species. The rooting of the Australian species *X. dryopa* along with the East Asian species was most highly supported (bootstrap support 94 %). According to the pairwise distances analysis, *X. dryopa* turned out to be the nearest neighboring species to East Asian species with an interval of genetic distances 7.8–8 %. The similarity between *X. dryopa* and the East Asian species in the morphology of the male genitalia was noted by Moriuti (1977: Figs 336,

337). According to the present study, another Australian species, *X. acroxutha*, has larger genetic distances from East Asian species, 10.9–11.4 %. The maximum divergence was found between East Asian species and *X. secreta* from Kenya—12.3–12.6 %. It should be noted that the East Asian species are less divergent from the Australian species than the East and South African ones. Also, maximum genetic distances were revealed between East African species *X. secreta* and Australian *X. dryopa*—15.3 %.

An unidentified species from South Africa and Costa Rica are united in a separate cluster and rooted along with clusters of *Zelleria* spp. with bootstrap support lower than 50 %, which is generally considered unreliable.

No	Species/ Sequence No /Country		23	22	21	20	19	18	17	16	15	14	13	12	
1	*X. insularis* 777			0,010	0,078	0,078	0,078	0,118	0,093	0,102	0,105	0,140	0,114	0,107	23
2	*X. insularis* 778	0,000			0,080	0,080	0,080	0,118	0,098	0,105	0,107	0,138	0,112	0,109	22
3	*X. insularis* 781	0,000	0,000			0,000	0,000	0,147	0,100	0,114	0,112	0,114	0,111	0,109	21
4	*X. insularis* 782	0,000	0,000	0,000			0,000	0,147	0,100	0,114	0,112	0,114	0,111	0,109	20
5	*X. insularis* 783	0,000	0,000	0,000	0,000			0,147	0,100	0,114	0,112	0,114	0,111	0,109	19
6	*X. insularis* 784	0,000	0,000	0,000	0,000	0,000			0,109	0,132	0,135	0,170	0,137	0,142	18
7	*X. insularis* 785	0,000	0,000	0,000	0,000	0,000	0,000			0,116	0,119	0,135	0,123	0,111	17
8	*X. insularis* 786	0,000	0,000	0,000	0,000	0,000	0,000	0,000			0,002	0,134	0,121	0,112	16
9	*X. insularis* 788	0,000	0,000	0,000	0,000	0,000	0,000	0,000	0,000			0,137	0,123	0,114	15
10	*X. lichneut* a KF523851.1 South Korea	0,000	0,000	0,000	0,000	0,000	0,000	0,000	0,000	0,000			0,153	0,126	14
11	*X. lichneuta* GMCHD605-14.COI-5P China	0,012	0,012	0,012	0,012	0,012	0,012	0,012	0,012	0,012	0,012			0,080	13
12	*X. lichneuta* GMCHM714-14.COI-5P China	0,012	0,012	0,012	0,012	0,012	0,012	0,012	0,012	0,012	0,012	0,004			
13	*X. dryopa* HQ922318.1 Australia	0,078	0,078	0,078	0,078	0,078	0,078	0,078	0,078	0,078	0,078	0,080	0,080		
14	*X. secreta* KF643226 Kenya	0,123	0,123	0,123	0,123	0,123	0,123	0,123	0,123	0,123	0,123	0,126	0,126	0,153	
15	*X. acroxutha* HQ922319.1 Australia	0,112	0,112	0,112	0,112	0,112	0,112	0,112	0,112	0,112	0,112	0,114	0,114	0,123	0,137
16	*X. acroxutha* KF396818.1 Australia	0,109	0,109	0,109	0,109	0,109	0,109	0,109	0,109	0,109	0,109	0,112	0,112	0,121	0,134
17	*Xyrosaris* sp LSAFA453-13.COI-5P South Africa	0,107	0,107	0,107	0,107	0,107	0,107	0,107	0,107	0,107	0,107	0,111	0,111	0,123	0,135
18	*Xyrosaris* sp KF492175.1 Costa Rika	0,135	0,135	0,135	0,135	0,135	0,135	0,135	0,135	0,135	0,135	0,142	0,142	0,137	0,170
19	*Z. hepariella* HM874029.1 Finland	0,102	0,102	0,102	0,102	0,102	0,102	0,102	0,102	0,102	0,102	0,109	0,109	0,111	0,114
20	*Z. hepariella* KM572196 Austria	0,102	0,102	0,102	0,102	0,102	0,102	0,102	0,102	0,102	0,102	0,109	0,109	0,111	0,114
21	*Z. hepariella* KX040445 Germany	0,102	0,102	0,102	0,102	0,102	0,102	0,102	0,102	0,102	0,102	0,109	0,109	0,111	0,114
22	*Z. oleastrella* JN287234 Spain	0,105	0,105	0,105	0,105	0,105	0,105	0,105	0,105	0,105	0,105	0,109	0,109	0,112	0,138
23	*Z. oleastrella* GWOTL409-13.COI-5P South Africa	0,107	0,107	0,107	0,107	0,107	0,107	0,107	0,107	0,107	0,107	0,107	0,107	0,114	0,140
		1	2	3	4	5	6	7	8	9	10	11	12	13	14

FIGURE 23. Interspecific and intraspecific genetic distances in the genus *Xyrosaris*.
Zelleria hepariella and *Z. oleastrella* are included as outgroup representatives.

Conclusion

Species of the genus *Xyrosaris* are characterized by a similar appearance of adults, which makes it impossible to accurately identify specimens without dissection of the genitalia. According to the results of comparative genetic analysis, in this genus the interspecific distances on barcode fragment COI may be lower than the standard threshold for species delimitation; this fact also does not allow to perform species differentiation. Therefore, the identification of specimens used for molecular study by appearance may be erroneous, and, as a consequence, the association of nucleotide sequences with the genus *Xyrosaris* will be incorrect. The dissection of the genitalia for species identification is an obligation. Only an integrated approach using both molecular genetic data and morphological data obtained from the dissection of the genitalia makes the correct identification possible and excludes taxonomic errors. This approach was demonstrated in the present study. The discovery of a series of moths belonging to the East Asian species of the genus *Xyrosaris* with significantly different genitalia and relatively low genetic divergence requires a revision of this genus as a whole.

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