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Molecular comments on *Phlyctaenomorpha sinuosalis* from SE Turkey (Lepidoptera, Pyraloidea)

Sibel Kızıldağ¹ Muhabbet Kemal

Abstract: Molecular comments on *Phlyctaenomorpha sinuosalis* from SE Turkey (Lepidoptera, Pyraloidea). *Misc. Pap.* 181: 1-2, 2 figs.
MtCOI barcoding of *Phlyctaenomorpha sinuosalis* is prepared and evaluated here for the first time. For this purpose, a typical and slightly different individuals from SE Turkey are used. In their genetic distance, no difference was seen.
Keywords: *Phlyctaenomorpha sinuosalis*, *Pyraloidea*, *Lepidoptera*, mtCOI barcoding, Turkey.

Within the private Cesa project on the Lepidoptera of Old World, barcoding of the species in the Cesa collection has been started by the authors since 2018. The methods on the molecular analyses, applied by the first author was summarized in some earlier papers (Kemal, *et al.*, 2018; Kemal, Kızıldağ & Koçak, 2018). Within this project, all the barcodes are stored in the Cesa Barcoding Bank for further studies².

In the present paper, mtCOI barcoding of *Phlyctaenomorpha sinuosalis* was performed for the first time. Molecular evaluations of *P. sinuosalis* were made based on the two specimens from Şırnak and Van Province (SE Turkey). In the P2K (Kimura2-Parameter) analysis, the genetic distance between two specimens from different populations was 0.002%. According to this result, these populations are considered as conspecific.

Phlyctaenomorpha Amsel, 1970

Phlyctaenomorpha sinuosalis (Le Cerf, 1913) (Figs. 1, 2)

Phlyctaenodes sinuosalis Le Cerf, [1910], *Bull. Mus. natn. Hist. nat. Paris* 1909 (8): 536. Type: Iran.

Phlyctaenodes sinuosalis: Koçak, 1975, *Atalanta* 6: 29 "Hakkari Province, Zap valley 1400m, 30.vi-2.vii.1972; [Şırnak Prov.]: "Uludere 1100m, 15.vii.1974, A. Koçak leg.

Phlyctaenomorpha sinuosalis: Amsel, 1970, *Beitr. Naturk. Forsch. SüdwDtl* 29: 55.

Range of the species: Turkey (Antalya, İçel, Siirt, Bitlis, Van, Hakkari, Şırnak), North Iraq, South Iran (Fars) (Koçak & Kemal, 2018).

Phlyctaenomorpha sinuosalis is a common and nocturnal species in the southern regions of Turkey. Its taxonomical and faunistical references and distributional information are mentioned above. The species seems rather homogenous morphologically. However some individuals may

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² <http://entcesa.tripod.com/Cesacollection.pdf> [under construction]

perform some differences externally (Figs.1,2). Therefore, further investigation of other populations is also planned from the molecular standpoint.



Figs. 1, 2 – *Phlyctaenomorpha sinuosalis*. Paler form from SE Turkey, Şırnak Prov., Beytüşşebap, Dule valley 1250m, 15.viii.2013, M. Kemal & A.Koçak leg. (left). Typical form from SE Turkey, Van Prov., Gevaş, Balaban 1800m, 21.vi.2006, H.Ö. & L.K. leg. (right).

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Molecular comment on a population of *Anchinia* in SE Turkey, with a taxonomic evaluation (Lepidoptera, Oecophoridae)

Sibel Kızıldağ³ Muhabbet Kemal

Abstract: Molecular comment on a population of *Anchinia* in SE Turkey, with a taxonomic evaluation (Lepidoptera, Oecophoridae). *Misc. Pap.* 181: 3-4, 1 fig.

Anchinia species from Europe and Turkey are evaluated from the molecular standpoint. *Anchinia mukusensis* is proposed as a distinct species from Turkey.

Key words: *Anchinia mukusensis*, mtCOI, Turkey, Van, Hakkari, Turkey.

Kemal & Koçak (2017) described *mukusensis* from Bahçesaray (Van Province) at the subspecific level for the species *Anchinia cristalis*, by using the morphological characters. Later, this taxon was also recorded by the authors from various localities in Hakkari Province (Dağlıca and Zap Valley) (Kemal, Koçak & Uçak, 2018). Geographically, *mukusensis* is confined to the mountainous region of SE Turkey.

In the present paper, the aim was to determine the mtCOI of *mukusensis* and to understand its phylogenetic relationship with other *Anchinia* species of Europe. For this purpose, mtCOI of *mukusensis* and those of *Anchinia* species of Europe, accessible in the BOLD System (Ratnasingham & Hebert 2007) (Fig.1), are compared. As a result of this, the *mukusensis* population has genetic distance between the range 4.47-4.81% with *Anchinia cristalis* and *Anchinia laureolella* populations. This means that the level of the genetic distance of *mukusensis* high enough. Consequently, we propose here the taxon under discussion as a distinct species: *Anchinia mukusensis* (**stat. nov.**).

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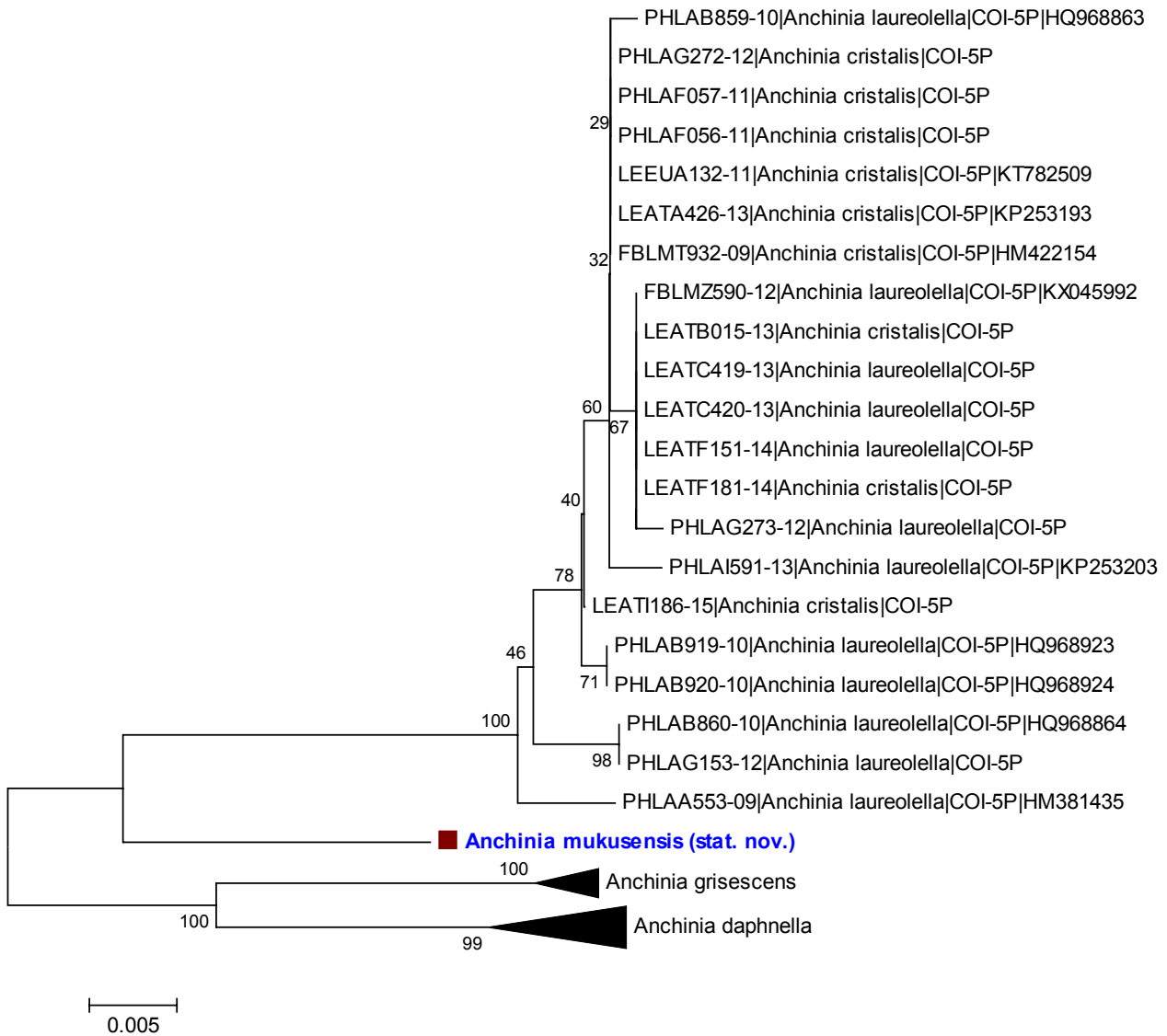


Fig. 1 - Neighbor-Joining Tree for the five species of the *Anchinia*. Bootstrap values (in %, 1000 replicates) are given on each branch.

<http://zoobank.org/References/F2B76392-6A57-45E5-AA6F-C9B6E462056F>

Molecular comments on *Jordanita graeca-chloros* in Ukraine compared with a population in Turkey (Lepidoptera, Zygaenidae)

Sibel Kızıldağ⁴ Muhabbet Kemal

Abstract: Molecular comments on *Jordanita graeca-chloros* in Ukraine compared with a population in Turkey (Lepidoptera, Zygaenidae). *Misc. Pap.* 181: 5-6, 1 fig.
A molecular comparison between *Jordanita graeca-chloros* populations of Ukraine and *Jordanita* from NE Turkey. The problems encountered in this regard are discussed.

Key words: *Jordanita, graeca, chloros, Zygaenidae, Lepidoptera, Ukraine, Turkey, mtCOI*

The aim was to understand the identity of the specimen, collected from Iğdır Province (NE Turkey), by using the molecular data of the species *Jordanita graeca/chloros* from Ukraine, freely accessible from the BOLD System (Kemal & Koçak, 2019: 9). However, it has been encountered with an unexpected problem. The identities of *Jordanita chloros* and *graeca*, listed in the BOLD System looks problematic. Therefore, it cannot be said that benefited from the BOLD System at the level expected (Ratnasingham & Hebert 2007).

In present study, Mitochondrial DNA has been used at species-level to make phylogeny estimate due to the ease of polymerase chain reaction (PCR) amplification and due to maternal inheritance, lack of recombination, and a relatively high mutation rate. The region of the mitochondrial gene Cytochrome oxidase subunit 1(COI) is a powerful barcode for phylogenetics at a low taxonomic level.

In the study, the specimen from Iğdır population was successfully barcoded full length (658bp). The average base composition of cytochrome oxidase subunit I sequences was 40% 256T, 16% 107C, 29% 194A, and 15% 101 G, showing a strong AT bias (68.3%).

Pairwise gene distances based on COI nucleotide sequences were calculated by the Kimura-2 parameter model and phylogenetic analysis were constructed with the neighbor-joining (NJ) in MEGA 6. The nucleotide distance of our population (0.46-0.92%) revealed that *J. graeca* and *J. chloros* in Group I of Ukraine were closely similar (Fig. 1). However, Ukraine populations of *J. graeca* and *J. chloros* in Group II were not close genetically to Iğdır specimen (5.51-5.69%) (Fig.1).

Before the barcoding, it should be questioned whether these two species, which are similar to each other morphologically, have been correctly diagnosed in BOLD. It is suggested that these two groups be re-evaluated and arranged as two different species.

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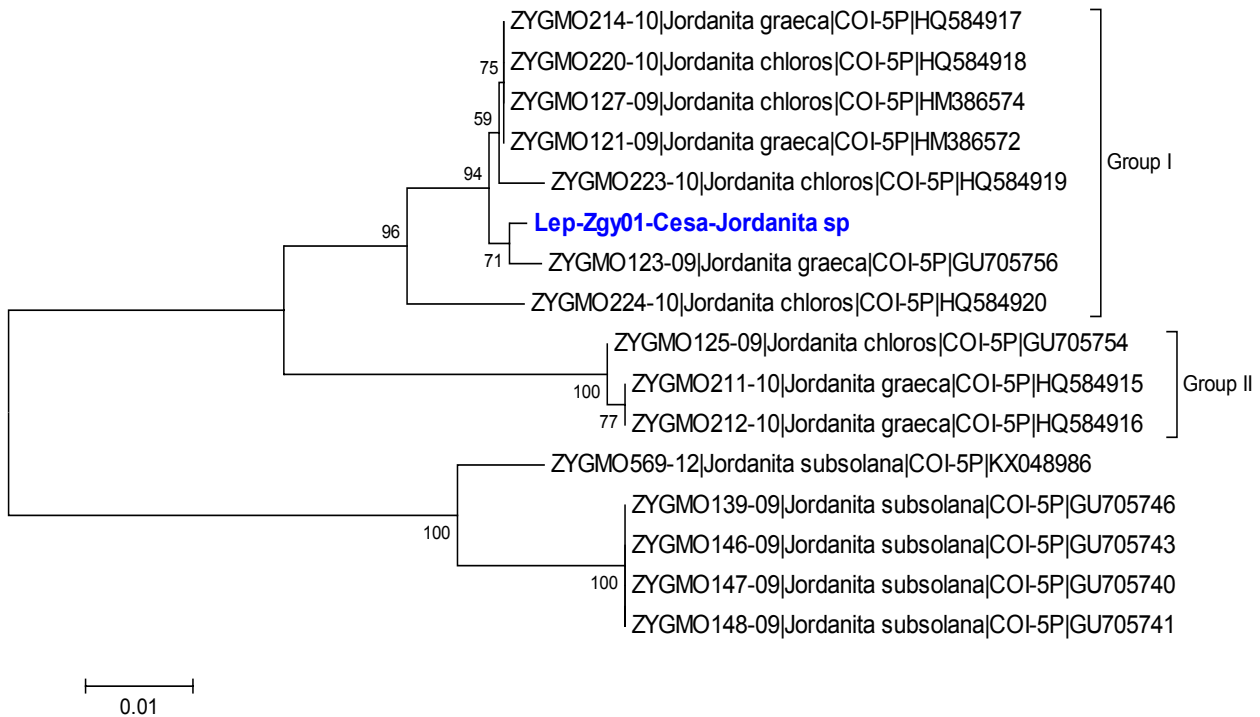


Fig 1. Neighbor-joining tree of the some *Jordanita* species in this study based on sequences of mtDNA COI gene. The bootstrap values are shown at the branching points. *Jordanita subsolana* was used as the outgroup.

<http://zoobank.org/References/D311CEAF-1D86-4A5C-A5E8-9AEBDAF07A02>

Description of a new *Recurvaria* species from East Turkey (Lepidoptera, Gelechiidae)

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Abstract: Description of a new *Recurvaria* species from East Turkey (Lepidoptera, Gelechiidae). *Misc. Pap.* 181: 7-9, 4 figs.

From the molecular standpoint, European and Turkish *Recurvaria* populations are compared. Consequently, a new species of *Recurvaria* from East Turkey is supported. New species, *Recurvaria vanella* (sp. n.) is described and illustrated. Its affinities to other *Recurvaria* species is also discussed.

Key words: *Recurvaria*, *nanella*, *leucatella*, *vanella*, Gelechiidae, Lepidoptera, Turkey, Van, new species, mtCOI.

Recently, Kemal & Koçak (2018) reported a distinct *Recurvaria* species from Van Province, and compared its male genitalia with the related species *Recurvaria nanella*. This was the first species of the genus recorded in East Anatolia. The authors attracted attention to the necessity of the molecular investigation for the final decision on the specific identity.

The mtCOI of this specimen was prepared properly, and compared with the available data of other *Recurvaria* species in different geographic regions of Europe, freely accessible in the BOLD System (Ratnasingham & Hebert 2007). *Recurvaria* specimen from Van was remarkable by significant divergence of the mtDNA barcode (COI fragment of 658 bp).

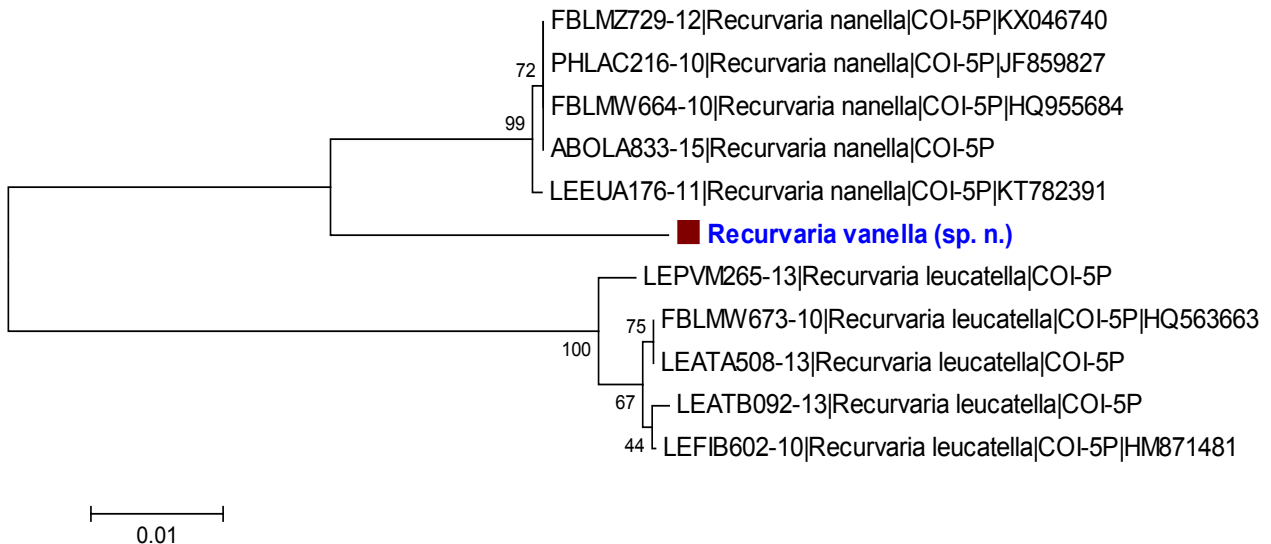


Fig. 1 - Neighbour-joining tree of some *Recurvaria nanella-leucatella* and *R. vanella* (sp. n.) in this study based on the sequences of mtDNA COI gene (only 658 bp). The bootstrap values are shown at the branching points.

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A neighbour-joining tree of DNA barcode data of Van specimen and some European *Recurvaria* species was constructed using Mega 6 under the K2P model for nucleotide substitutions. Van population is genetically closer to those of *Recurvaria nanella* (4.14-4.30%) compared to *Recurvaria leucateella* populations (9.72-9.91%). The population from Van and *Recurvaria nanella* populations are also compatible with this result by clustering in same clade at our phylogenetic tree (Fig.1). It is clear that the specimen under discussion has differ genetically, and belongs to a new species in the genus *Recurvaria*.

The description of this new species is given below.

***Recurvaria vanella* (sp. n.) (Figs. 2-4)**

<http://zoobank.org/NomenclaturalActs/4FB25AA2-F06C-4380-89BE-19D905BFA28D>

Holotype ♂. Rather small-sized gelechiid. Wingspan: 9 mm.

Diagnosis:

External features: Frontal and dorsal side of head smoothly covered by silky, creamy-white, elongated scales. Outer parts of some scales dark brown. Palpus labialis in divergent position, slender, and curved. Covered by creamy scales, more or less ringed by dark brown scales. Third segment creamy and dark brown, its tip creamy. Compound eyes blackish. Antennae ringed by dark brown and creamy scales. Its base covered by creamy scales with a few dark brown dots. Upperside of forewing: Markings and colouration similar to *nanella* to some degree, however creamy scales more densely. Hindwing light brownish.

Male genitalia (GP3023♂), and complete abdominal skin were previously illustrated by the authors (Kemal & Koçak, 2018, *Misc. Pap.* 176: 23, figs. 25-27). Shape of uncus and gnathos somewhat similar to *nanella*. Valva very long, developed as whip, terminal filament sinuous. Medial process of vinculum horseshoe shaped. Sternite VIII and tergite broad and round, not emarginated. Aedeagus small, oblong with conical tip.

Female genitalia: Unknown.

Similar species: *Recurvaria nanella* Hw. This new species differs from *nanella* Hw. especially in the male genitalia (shape of valva, medial process of vinculum, not emarginated viii sternite and tergite).

Genetic data: The genetic distance of the new species to *Recurvaria nanella* (4.14-4.30%), and to *Recurvaria leucateella* (9.72-9.91%).

Type material: 1♂(Holotype). Turkey, Van Province, Gevaş, Altınsaç SE 1680m, reared from larva on *Cerasus* sp. on 30.iv.2016, adult emerged on 01.vi.2016, M. Kemal (in coll. Cesa).

Etymology: The scientific name *vanella* is derived from the collecting locality in Van Province (Turkey).

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Figs. 2-4 – Holotype of *Recurvaria vanella* sp.n. Dorsal view (above). Frontal (bottom left), and lateral view (bottom right) of head, base of antennae, and labial palpi. M. Kemal (Cesa)

<http://zoobank.org/References/507D4E28-C4FD-445C-9412-AD9EA876CB9F>

Comments on the molecular evaluations of some Heterocera species from Uighur Ili (Lepidoptera)

Sibel Kızıldağ⁶ Muhabbet Kemal

Abstract: Comments on the molecular evaluations of some Heterocera species from Uighur Ili (Lepidoptera). *Misc. Pap.* 181: 10-14, 5 figs.

Some species from Uighur Ili are discussed here from the molecular standpoint. Consequently, three species, *Cataclysmes* sp., *Pareulype* sp. and *Hoplodrina* sp. are supported as new taxa. All the species under discussion were first sequenced for the 658-bp DNA barcoding from Uighur Ili.

Key words: *Cataclysmes*, *Pareulype*, *Hoplodrina*, *Scopula*, *Idaea*, *Gnophopsodos*, *Eugnorisma*, *Cryphia*, *Hoplodrina*, *Xestia*, Geometridae, Noctuidae, Lepidoptera, Uighur Ili, mtCOI

Kemal & Koçak (2018) published faunistical information on some Heterocera of Uighur Ili with some taxonomical remarks. Attention was also drawn to the necessity of some molecular investigations on some species. Recently, Kızıldağ, Kemal & Koçak (2019) confirmed the identities of two arctiid subspecies from Uighur Ili from the molecular standpoint. All the species under discussion were first sequenced for the 658-bp DNA barcoding from Uighur Ili. Among them, three species (*Cataclysmes* sp., *Pareulype* sp. and *Hoplodrina* sp.) appear as new taxa, after their molecular evaluations. Comments are given below:

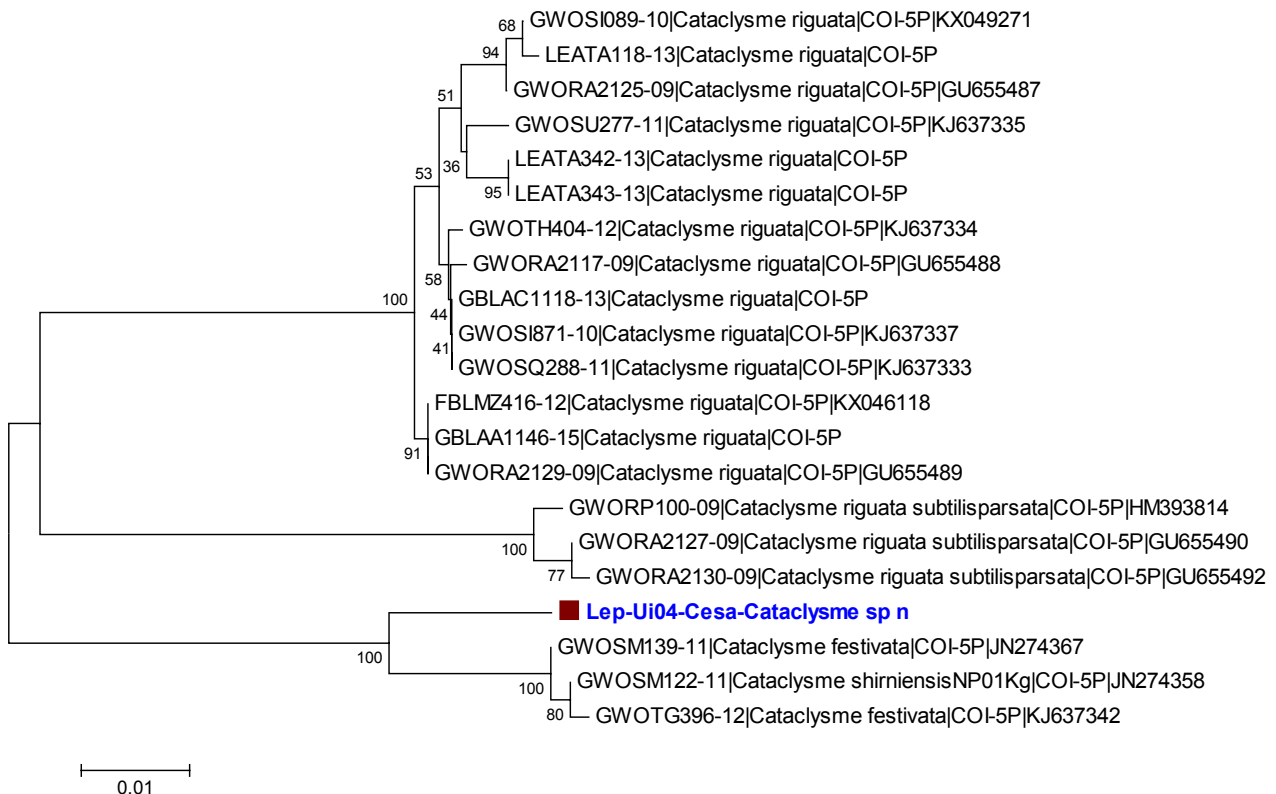


Fig. 1 - Neighbour-joining trees constructed with Kimura 2-parameter distances within and among species of *Cataclysmes*.

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1. Comment on the status of *Cataclysmes* sp. from Uighur Ili versus *Cataclysmes festivata* and *Cataclysmes riguata subtilisarsata*. The interspecific nucleotide divergence among the twenty-one populations, used in the tree and the genetic distance, ranged from 2.99% to 10.34%, with an average of 8.10% (Fig.1). Our population, *Cataclysmes riguata subtilisarsata* with the highest genetic distance to 10.34%, *Cataclysmes festivata* with 2.99% of the shortest genetic distance was obtained. Based on the DNA barcode divergence of similar species as morphological, we describe later the new species *Cataclysmes* sp. n.

2. The Uighur population has an evolutionary distance of 7.21-8.48% from *Pareulype berberata* species and also 9.5-10.5% from *Pareulype lasithiotica*. The genetic distance of the population of *Pareulype consanguinea* reported from China, which is the only registry in BOLD (Ratnasingham & Hebert 2007), from our *Pareulype* population is 13.63%. A new species should be described, because it was deduced rather high genetic distance using mtCOI DNA barcode between the species (Fig.2).

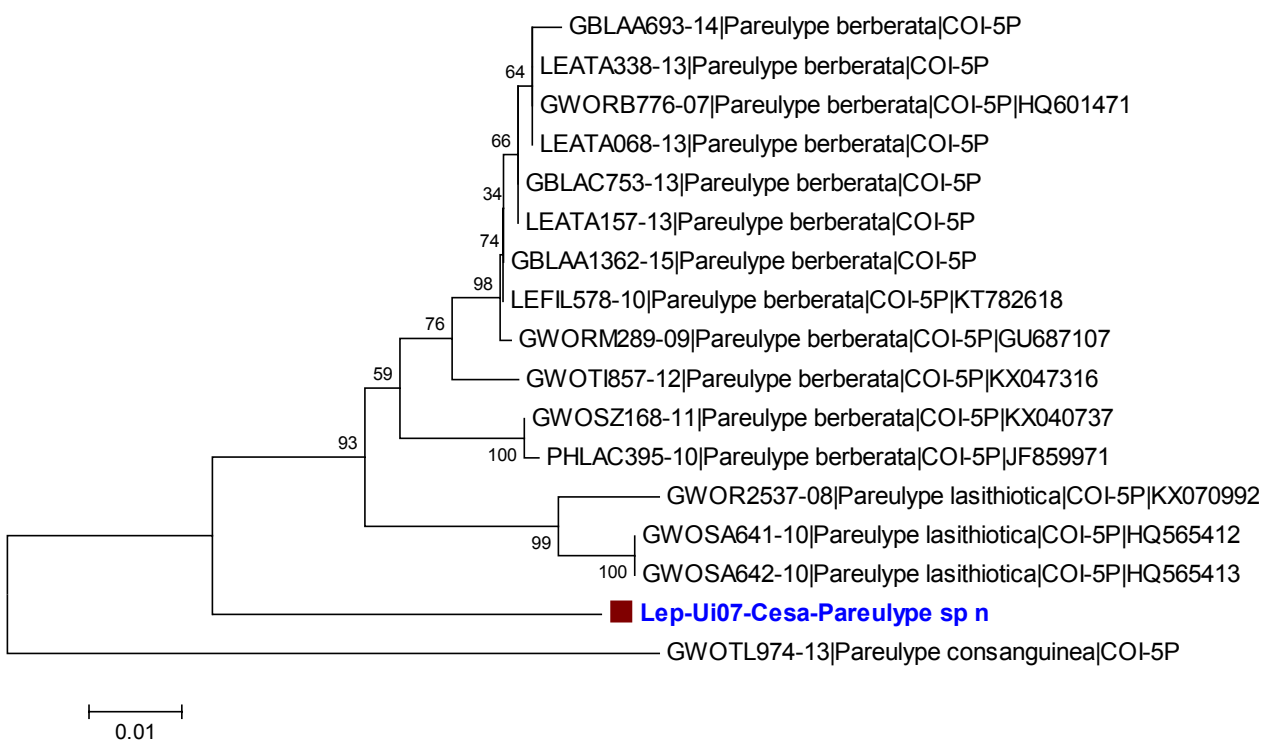


Fig. 2 - Neighbor-joining tree of some *Pareulype* species in this study based on the sequences of mtDNA COI gene (only 658 bp). The bootstrap values are shown at the branching points.

3. Here we evaluated the population of Uighur Ili with 4 populations registered in the BOLD System (Iran, Germany) (Ratnasingham & Hebert 2007). The genetic distance between the specimen from Uighur Ili and the populations of Iran (GWORE1207-08) and Germany (GBLAA2058-15) seems to be appropriate for the subspecies of this group (0.77% and 0.92% respectively). The other Iran population (GWORE1206-08) can be considered as another subspecies (1.87%) (Fig.3). However, the German population (GBLAB832-13) seems to be quite remote from the specimen from Uighur Ili. The taxonomic level of this population should be reassessed.

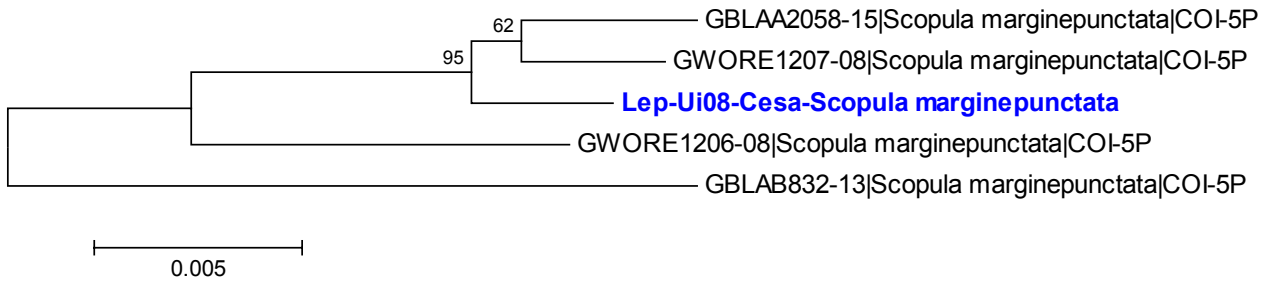


Fig. 3 - Neighbor-joining tree of *Scopula marginepunctata* populations (Germany, Iran and Uighur) in this study based on the sequences of mtDNA COI gene (only 658 bp). The bootstrap values are shown at the branching points.

4. In present study, Uighur Ili specimen was compared with three populations from Austria and a single specimen from China; consequently, its phylogenetic value was estimated. Uighur Ili specimen appears very close to the Austrian populations (0.00% -0.15%) and clustered in Clade A. *Scopula ornata subornata* reported from China (Hebei) is also located to far branch of phylogenetic tree (Fig.4). Uighur Ili population is 2.5% distance as evolutionally from the Chinese population. In result, Uighur Ili specimen is genetically same with the Austrian populations.

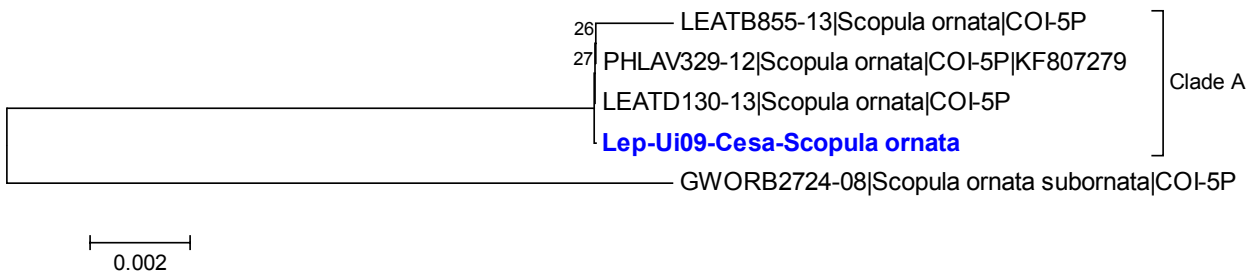


Fig. 4 - Neighbor-joining tree of some *Scopula ornata* populations (Uighur, Austria and Hebei (China)) in this study based on the sequences of mtDNA COI gene (only 658 bp)

5. In this study, Uighur Ili specimen, which was identified as *Hoplodrina* sp. morphologically (Kemal & Koçak, 2018), are investigated their phylogenetic relation with some European populations of five species (658 bp sequences of *Hoplodrina octogenaria*, *Hoplodrina blanda*, *Hoplodrina ambigua*, *Hoplodrina respersa* and *Hoplodrina superstes* in BOLD) (Ratnasingham & Hebert 2007). In constructed phylogenetic tree, Uighur Ili specimen located in Clade *blanda* is genetically the closest to *Hoplodrina blanda* species (2.36%-2.51%). Therefore, it can be said that this specimen belongs to a new species by looking at both the genetic distance and the bootstrap values in the COI gene tree (Fig.5).

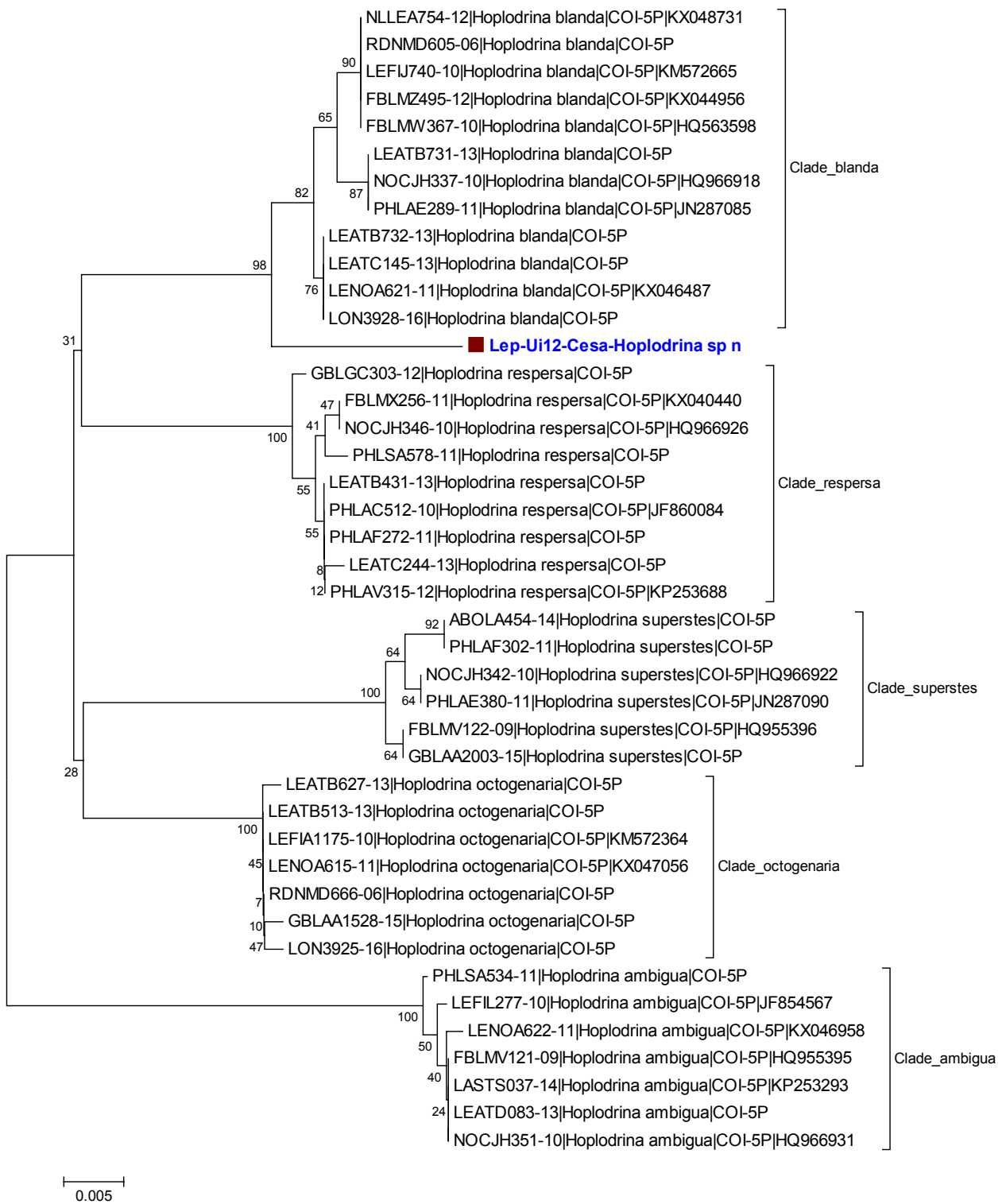


Fig. 5 - Neighbor-joining tree of some *Hoplodrina* species in this study based on the sequences of mtDNA COI gene (only 658 bp). The bootstrap values are shown at the branching points.

New molecular information on some taxa

Geometridae

Gnophopsodos stemmataria specimen from Uighur Ili was first time sequenced for the 658-bp DNA barcoding and saved in Cesa Barcoding Bank (Lep-Ui10-Cesa-Ui05- *Gnophopsodos stemmataria*).

Morphologically identified *Idaea straminata* specimen was first time barcoded from this region and the genetic distance between GBLAB823-13 - *Idaea straminata* obtained from the BOLD System was 0.00%.

Noctuidae

Cryphia rueckbeili specimen from Uighur Ili was first time sequenced for the 658-bp DNA barcoding and saved in Cesa Barcoding Bank (Lep-Ui10-Cesa- *Cryphia rueckbeili*).

Eugnorisma trigonica specimen from Uighur Ili was first time sequenced for the 658-bp DNA barcoding and saved in Cesa Barcoding Bank (Lep-Ui11-Cesa- *Eugnorisma trigonica*).

The specimen from Uighur Ili was compared with European populations of *Xestia baja* registered in BOLD. It should be discussed subspecies status between the populations of this species, because not meaningful p-distance between their COI barcodes (0.00–0.15%). However, *Xestia baja* specimen from Uighur Ili was first time sequenced for the 658-bp DNA barcoding and saved in Cesa Barcoding Bank (Lep-Ui13-Cesa- *Xestia baja*).

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On the nomenclature of two Lymantriidae species in Africa (Lepidoptera)

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Abstract: On the nomenclature of two Lymantriidae species in Africa (Lepidoptera). *Misc.Pap.* 181: 15-16.

This paper deals with the nomenclature of two preoccupied species of the family Lymantriidae from Africa.

Key words: *Lepidoptera*, *Lymantriidae*, Africa, nomenclature, new name.

The following preoccupied names were found by the authors in 2013, and reported in 2015 (Koçak & Kemal, 2015). However, these nomenclatural issues have been neglected and not yet been published. For that reason, two replacement names are proposed below:

Lymantriidae

Dasychira Hübner, [1819]

Dasychira madagascarensis (nom. nov.)

<http://zoobank.org/NomenclaturalActs/FF32B0A9-1253-44F7-8827-BF5B25351481>

Dasychira maculata Griveaud, 1974, *Bull. Mus. Nat. Hist. Paris* 125 (186): 1466-1467, figs. Holotype ♂. Madagascar (MNHN Paris) [secondary homonym of *Laelia bacchans maculata* Wichgraf, 1921, *Int. Ent. Z.* 15 (3): 20. "Sierra Leone"]

Remarks: The names, *Dasychira maculata* Griveaud, 1974 and *Laelia maculata* Wichgraf, 1921 are currently used in the genus *Dasychira* Hbn. Therefore, they are considered as homonyms under the Rules of the ICZN. This homonymy case has been seen by the authors. Koçak & Kemal (2015) mentioned them on page 2693, nr. 53861. The name *Dasychira maculata* Griveaud, 1974 cannot be used validly, as it is junior secondary homonym of *Laelia maculata* Wichgraf, 1921, which is currently synonym of *Dasychira bacchans* (Karsch, 1898). Therefore, we propose here a replacement name for *Dasychira maculata* Griveaud, 1974 (nec *maculata* Wichgraf, 1921), *Dasychira madagascarensis* **nom. nov.**

Euproctis Hübner, [1819]

Euproctis africola (nom. nov.)

<http://zoobank.org/NomenclaturalActs/353C220A-FA61-4650-9CD9-DB52BDB68042>

Laelia aethiopica Bethune-Baker, 1908, *Ann. Mag. Nat. Hist.* (8) 2 (9): 261. "Fort Jameson, N.E. Rhodesia; Uganda and Nigeria". [secondary homonym of *Euproctis aethiopica* Snellen, 1872, *Tijdschr. Ent.* (2) 7 15: 37-38, figs. "Neder-Guinea"].

Remarks: These two names, mentioned above, are currently placed as valid specific names in the genus *Euproctis* Hbn. However, *aethiopica* Bethune-Baker, 1908 is junior secondary homonym of *aethiopica* Snellen, 1872. This homonymy case has been seen by the authors. Koçak & Kemal (2015)

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listed the name on page 2702, nr.54095. The name *Euproctis aethiopica* (Bethune-Baker,1908) cannot be used validly, as it is junior secondary homonym of *Euproctis aethiopica* Snellen,1872. Therefore, we propose here a replacement name for *Laelia aethiopica* Bethune-Baker,1908 (nec Snellen,1872), *Euproctis africola* **nom. nov.**

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