



Tribal assignment of the genus *Eumera* Staudinger, 1892, using multi-gene analysis, with description of a new species from Iran (Lepidoptera: Geometridae: Ennominae)

DOMINIC WANKE^{1,2*}, ASGHAR SHIRVANI³, AXEL HAUSMANN⁴, LEIDYS MURILLO-RAMOS⁵ & PASI SIHVONEN⁶

¹State Museum of Natural History Stuttgart, Entomology, Rosenstein 1, D-70191 Stuttgart, Germany

✉ dominic.wanke@smns-bw.de; <https://orcid.org/0000-0001-5390-8993>

²University of Hohenheim, Systematic Entomology (190n), Garbenstr. 30, D-70599 Stuttgart, Germany

³Department of Plant Protection, Faculty of Agriculture, Shahid Bahonar University of Kerman, Kerman, Iran

✉ shirvani@uk.ac.ir; <https://orcid.org/0000-0002-4647-1030>

⁴SNSB-ZSM, Bavarian State Collection of Zoology, Münchhausenstr. 21, D-81247 Munich, Germany

✉ hausmann.a@snsb.de; <https://orcid.org/0000-0002-0358-9928>

⁵Grupo Biología Evolutiva, Department of Biology, Universidad de Sucre, Sincelejo, Sucre, Colombia

✉ leidys.murillo@biol.lu.se; <https://orcid.org/0000-0002-8256-105X>

⁶Finnish Museum of Natural History, Zoology Unit, University of Helsinki, P.O. Box 17, FI-00014

✉ pasi.sihvonen@helsinki.fi; <https://orcid.org/0000-0003-2237-9325>

*Corresponding author. ✉ dominic.wanke@smns-bw.de

Abstract

The geometrid moth genus *Eumera* Staudinger, 1892 consists of five yellow-orange-pinkish species distributed in the western Palearctic, with uncertain tribal classification within the geometrid subfamily Ennominae. In this study, we explored the phylogenetic position of the genus *Eumera*. Therefore, a concatenated dataset was analyzed, which includes one mitochondrial and up to ten protein-coding genetic markers per taxa. Moreover, we compared some external and internal morphological traits to other closely related genera. Our phylogenetic inference and comparative morphology suggested that *Eumera* should be included in the tribe Prosoplophini. In addition, a new species, *Eumera rajaeii* sp. nov. Wanke & Shirvani is described from southern Iran, and diagnosed by molecular data and morphological features. The distribution of the Iranian species is shown on a map. We illustrate external characters and male genitalia of three closely related *Eumera* species.

Key words: *Colotois*, DNA barcoding, *Himeromima*, phylogeny, Prosoplophini, systematics, taxonomy, *Wilemania*

Introduction

In recent years, our knowledge of the classification of geometrid moths has been enhanced particularly by molecular phylogenetic studies (e.g., Sihvonen *et al.* 2011; Önap *et al.* 2016; Jiang *et al.* 2017; Ban *et al.* 2018; Brehm *et al.* 2019; Murillo-Ramos *et al.* 2019). Despite this, we are just beginning to understand the relationships at the tribal- and genus levels, and this is a vast task in the family Geometridae, with about 24.000 known species (Müller *et al.* 2019; Rajaei *et al.* 2022). This is also true for the European Geometridae; for example, Müller *et al.* (2019) listed two genera for the subfamilies Larentiinae and 12 genera for Ennominae of uncertain tribal association. Ennominae include also the genus *Eumera* Staudinger, 1892, which is given special attention here in this study.

The genus *Eumera* was described in 1892 by Staudinger based on the type species *Eumera regina* Staudinger, 1892 from northern Turkey (Amasia, Zara). Later, a second species was added to this genus, when Prout (1929) described *E. mulier* based on a female holotype from Nicosia in the northern part of Cyprus. In 1932, Wehrli described the subspecies *E. regina turcosyrica* from Turkey (Marasch [Kahramanmaraş]; Akschehir) and Syria (Akhis [Maydan İkbis]), which he later regarded as valid species (Wehrli 1934), followed by the description of *E.*

hoeferi Wehrli, 1934 from Turkey (Kurdistan, Malatia [Malatya]). Finally, Wehrli (1940), described the subspecies *E. hoeferi transcaucasica* from Nakhichevan, (Dzhuga (Arax River)). 68 years later, a further species was added to the genus *Eumera*, *E. lewandowskii*, from southwestern Jordan by Fischer (2008). Thus, today a total of five species are assigned to the genus *Eumera*, all distributed in the western Palearctic region but only one species has its distribution range in Iran (Skou & Sihvonen 2015; Müller *et al.* 2019; Hausmann *et al.* 2020; Rajaei *et al.* 2022; Rajaei *et al.* 2023).

Eumera species are large moths (wingspan 35–40 mm), with only limited information on their biology (Fischer 2008; Skou & Sihvonen 2015). Species of this genus are early autumnal, flying from August to early November (Skou & Sihvonen 2015). Caterpillars of *E. regina* have been found on *Acer monspessulanum* and were reared on *Prunus triloba* (Skou & Sihvonen 2015). Moths of this genus are characterized by their yellow to orange wing colouration, rarely with light pink elements of the wing pattern (Skou & Sihvonen 2015). The outer wing margins are slightly wavy with well-pronounced medial and postmedial lines. In the male genitalia, uncus and gnathos are absent, and the ventral margin of the valva bears a distinct hook. In the female genitalia large and broad ovipositor, short apophyses anteriores, lamella antevaginalis with a weakly sclerotized ridge, and weakly sclerotized signum are diagnostic. The genus *Eumera* is classified in the geometrid subfamily Ennominae but its tribal association is still uncertain (Skou & Sihvonen 2015; Müller *et al.* 2019). Earlier, *Eumera* was considered to be a member of the tribe Colotoini by Viidalepp (1996), whereas Hausmann *et al.* (2011) placed it in Ennomini. This study aims to clarify the systematic position of this genus using a multi-gene molecular phylogenetic analysis, including one mitochondrial and up to ten protein-coding nuclear gene regions, along with the examination of morphological characters. In addition, a new *Eumera* species is described from the southern Iranian province Kerman.

Material and methods

Examined type material and specimens are deposited in the following collections: CN-SHBUK—Collection of Noctuidae, Shahid Bahonar University of Kerman, Kerman, Iran; NHMUK—Natural History Museum London, United Kingdom; SMNK—Staatliches Museum für Naturkunde Karlsruhe, Germany; SMNS—Staatliches Museum für Naturkunde Stuttgart, Germany; SNSB/ZSM—Zoologische Staatssammlung München, Germany; ZFMK—Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany; ZMH—Finnish Museum of Natural History, University of Helsinki, Finland.

Examined material

Eumera regina: 1 ♂, Macedonia, Petrina, Planina, Ochrid, 1600 m, 20.viii.1955, leg. Dr. F. Kasy, g.prep. 1327/2022 D. Wanke; 1 ♂, Griechenland, Fokida Nom, Chrisso bei Delphi, 17.ix.2002, leg. M. Salmen, g.prep. 1328/2022 D. Wanke; 1 ♂, [Croatia], Sukosan, e.l., 1.ix.[19]65, leg. Czipka, g.prep. 1329/2022 D. Wanke; 1 ♂, 1 ♀, [Croatia], Dalmatien, ex coll. W. Pfitzenmeier Stuttgart, g.preps (♂) 1330 (♀) 1331/2022 D. Wanke; **all in SMNS.**

Eumera turcosyrlica: Syntypes [both labeled with ‘Typ’] 1 ♂, 1 ♀, Syr. sept. [Turkey], Taurus c. Marasch, 6–900 m, x.[19]30, leg. Einh. Slr., g.preps (♂) 5576 (♀) 1318/2022 D. Wanke; non-type specimens: 1 ♂, Syr. sept. [Turkey], Taurus c. Marasch, 6–900 m, x.[19]30, leg. Einh. Slr., g.prep. 1319/2022 D. Wanke; 1 ♂, Asia min. [Turkey], Akschehir, 10.–20.ix.[19]31, coll Wagner, Wien, g.prep. 1320/2022 D. Wanke; **all in ZFMK.**

1 ♂, Asia min. [Turkey], Aksehir, 25.viii.1966, leg. Czipka, g.prep. 1324/2022 D. Wanke; **in SMNS.**

Eumera hoeferi: Holotype ♂, Asia min. [Turkey], Malatya-Tecde, 20.ix., g.prep. 5570; Paratype [labelled as Allotype] 1 ♀, Asia min. [Turkey], Malatya-Tecde, 20.ix., g.prep. 1317/2022 D. Wanke; **all in ZFMK.**

Paratype 1 ♂, Asia min. [Turkey], Malatya-Tecde, 20.ix., NHMUK 014173742, g.prep. NHMUK 010317504; non-type specimens: 1 ♂, Iran, Fars, Straße Chiraz-Kazeroun, Fort Sine-Sefid, ca. 2200 m, 10.ix.1937, coll. Brandt, NHMUK 014173743, g.prep. NHMUK 010317503; 1 ♀, Iraq, Kurdistan, Rowanduz, 8.x.1936, E.P. Wiltshire, NHMUK 014173744, g.prep. NHMUK 010317505; 1 ♂, Iraq, Kurdistan, Rayat, 14.x.[19]36, E.P. Wiltshire, NHMUK 014173745, g.prep. NHMUK 010317506; **all in NHMUK.**

1 ♂, 1 ♀, Türkei, Kleinasien, Prov. Siirt, 3 km NE Baykan, 750 m, 14.x.1985, g.preps (♂) 1322 (♀) 1323/2022 D. Wanke; **all in SMNS.**

Morphological examination

Wing pattern and male genitalia were examined and original descriptions used for a critical review, as well as additional specimens from different localities were investigated. Documentation of external characters was carried out using an Olympus E3 digital camera. For the genitalia preparation, standard techniques were used (Robinson 1976) and if the vesica was everted, it was done following the protocol described in Sihvonen (2001). Genitalia was embedded in Euparal as permanent slides. A Keyence VHX-5000 microscope was used for their photography.

Distribution map preparation

Geographical coordinates were traced using ‘Google Earth Pro’ (vers. 7.3.6.9326 for Mac) and the distribution pattern was plotted and prepared in QGIS (vers. 3.22.8 for Mac). For the preparation of the elevation profile in QGIS, Global Multi-resolution Terrain Elevation Data 2010 (GMTED2010) downloaded from <https://earthexplorer.usgs.gov>, was used.

DNA extraction and amplification

Extraction of DNA of *Eumera rajaeii* **sp. nov.** Wanke & Shirvani was carried out at the molecular laboratory of the State Museum of Natural History Stuttgart. Therefore, prior to genitalia dissection, the whole abdomen of the holotype was used for lysis (details available in Hundsdoerfer & Kitching 2010), following the manufacturer’s protocol of the DNeasy Blood and Tissue kits (Qiagen, Hilden, Germany).

Amplification of the “barcode” fragment (658 base-pairs of the 5’ terminus) of the mitochondrial Cytochrome-C Oxidase I of *Eumera rajaeii* **sp. nov.** Wanke & Shirvani, was performed using standard protocols (Ivanova *et al.* 2006) and amplification of nuclear genes of *Eumera rajaeii* **sp. nov.** Wanke & Shirvani was conducted following the protocols of Wahlberg and Wheat (2008) and Wahlberg *et al.* (2016) at the molecular laboratory of the State Museum of Natural History Stuttgart. All PCR amplification products were sent to MacroGen for sequencing.

Extraction and amplification of the “barcode” fragment of all other *Eumera* and *Apocolotois* species used in barcoding analysis were performed at the Canadian Centre of DNA barcoding (CCDB, Guelph), in the framework of the Lepidoptera campaign of the International Barcode of Life program (iBOL; www.lepbarcoding.org).

Phylogenetic analysis

In addition to the data generated in this study, we retrieved up to ten sequences per species of 655 Ennominae taxa, as well as two Oenochrominae and three Geometrinae as outgroups from the dataset of Murillo-Ramos *et al.* (2019) (see Supplementary Table). The concatenated length of the alignment was 7,662 bp.

To reveal the phylogenetic position of *Eumera* within Geometridae, we conducted the phylogenetic analysis under a Maximum-likelihood (ML) approach in IQ-TREE2 V2.0.7 (Minh *et al.* 2020). The dataset was partitioned by genes. We evaluated support for nodes with 1000 ultrafast bootstrap (UFBoot2) approximations (Hoang *et al.* 2018), and SH-like approximate likelihood ratio test (Guindon *et al.* 2010). We selected the best substitution model with ModelFinder (Kalyaanamoorthy *et al.* 2017). To reduce the risk of overestimating branch supports in UFBoot2 test, we implemented the *-bnni* option. We visualized and edited the trees in FigTree v1.4.3.

TABLE 1. Interspecific genetic distances between six species of the genus *Eumera* and one species of the genus *Apocolotois* (in %), calculated with MEGA X. Note: The small genetic differences (< 2 %) of the species *E. lewandowskii*, *E. turcosyrlica* relative to *E. regina* question their status on species level. However, this is beyond the scope of this study and needs further investigation.

	<i>E. turcosyrlica</i>	<i>E. lewandowskii</i>	<i>E. regina</i>	<i>E. hoeferi</i>	<i>E. mulier</i>	<i>E. rajaeii</i> sp. nov. Wanke & Shirvani
<i>E. lewandowskii</i>	1.72					
<i>E. regina</i>	1.90	1.76				
<i>E. hoeferi</i>	5.17	5.17	4.52			
<i>E. mulier</i>	6.52	6.28	5.80	7.18		
<i>E. rajaeii</i> sp. nov. Wanke & Shirvani	6.44	6.39	6.20	6.12	6.67	
<i>A. almatensis</i>	9.78	9.78	9.09	10.92	11.35	9.81

Barcoding analysis

For the maximum likelihood analysis for *Eumera* species (with 1000 bootstrap replications), and calculation of genetic distances, MEGA X was used (Kumar *et al.* 2018, Stecher *et al.* 2020) (K2P model: Kimura 1980).

All specimens used for COI analysis are given in table 2 along with their sampling site, sample ID, and process ID numbers. Their sequences, photographs, and metadata are accessible in BOLD (Barcode of Life Datasystems) in the public dataset DS-EUMERA (doi: dx.doi.org/10.5883/DS-EUMERA).

TABLE 2. *Eumera* and *Apocolotois* specimens used in the COI maximum likelihood analysis, with identification, sampling site, sample ID and process ID in the Barcode of Life Data Systems (BOLD).

Taxon Identification	sampling site	Sample ID	Process ID
<i>A. almatensis</i>	China, Hebei, Chongli, Baiqi, 1350 m, 09.ix.2007, leg. C. Wang	BC ZSM Lep 12975	GWORD885-08
<i>A. almatensis</i>	China, Hebei, Chongli, Baiqi, 1350 m, 23.ix.2006, leg. C. Wang	BC ZSM Lep 13014	GWORD924-08
<i>A. almatensis</i>	China, Hebei, Chongli, Shizigou, 1650 m, 13.ix.2007, leg. C. Wang	BC ZSM Lep 13350	GWORB2670-08
<i>A. almatensis</i>	Kazakhstan, Almaty, Tien Shan, Turgen, 27.ix.2010, leg. G. Nazymbetova	BC ZSM Lep 80107	GWOR5397-13
<i>E. hoeferi</i>	Turkey, Malatya, Malatya, 2 km S Erkenek, Resadiye pass, 1550 m, 15.ix.2009, leg. R. Fiebig & S. Rothe	BMB Lep 00771	GWOTD1021-12
<i>E. hoeferi</i>	Turkey, Tunceli, 9.5 km NE Ovacik, 1400 m, 24.viii.2009, leg. R. & S. Fiebig	BMB Lep 00772	GWOTD1022-12
<i>E. lewandowskii</i>	Jordan, Ma'an, Al-Aqabah, Wadi Musa nr Petra, 1030 m, 12.x.2007, leg. S: Lewandowski & K. Tober	BC ZSM Lep 11461	GWORA593-08
<i>E. mulier</i>	Cyprus, Limassol, nr. Agios Joannis, 920 m, 03.x.2000, leg. H. Fischer	BC ZSM Lep+ 0020	GWOR3008-08
<i>E. mulier</i>	Cyprus, Larnaca, nr. Lefkara, 790 m, 01.x.2004, leg. S. Lewandowski	BC ZSM Lep 11478	GWORA610-08
<i>E. mulier</i>	Cyprus, Larnaca, nr. Lefkara, 790 m, 01.x.2004, leg. S. Lewandowski	BC ZSM Lep 11479	GWORA611-08
<i>E. mulier</i>	Cyprus, Larnaca, nr. Lefkara, 790 m, 01.x.2004, leg. S. Lewandowski	BC ZSM Lep 11480	GWORA612-08
<i>E. regina</i>	Turkey, Cankiri, Ic Anadolu, Ilgaz, 900 m, 09.ix.1997, leg. T. Drechsel & H. Loebel	BC ZSM Lep 09080	GWORA494-08
<i>E. regina</i>	Turkey, Cankiri, Ic Anadolu, Ilgaz, 900 m, 09.ix.1997, leg. T. Drechsel & H. Loebel	BC ZSM Lep 09081	GWORA495-08
<i>E. regina</i>	Turkey, Cankiri, Ic Anadolu, Ilgaz, 900 m, 09.ix.1997, leg. T. Drechsel & H. Loebel	BC ZSM Lep 09082	GWORA496-08
<i>E. regina</i>	Croatia, Splitsko-dalmatinska, Dalmatia, NP Mt. Biokovo, Rastovac, 221 m, 13.ix.2007, leg. I. Mihoci, M. Vajdic	RCIM 0017	GWOSI017-10
<i>E. turcosyrica</i>	Israel, Northern, Mt. Hermon, 2000 m, 30.xi.2003, leg. Mueller, Kravchenko	BC ZSM Lep 00250	GWOR250-07
<i>E. turcosyrica</i>	Jordan, Al Asimah, Jabal Ma'uda, 100 m, 31.x.2002, leg. Li, Mueller	BC ZSM Lep 00334	GWOR334-07
<i>E. turcosyrica</i>	Lebanon, Mount Lebanon, Arab ei Laqlouq, 1600 m, 29.ix.2008, leg. Floriani, Saldaitis	BC ZSM Lep 19578	GWORP792-09
<i>E. turcosyrica</i>	Syria, Idlib, Al Barah, 659 m, 15.x.2010, leg. S. Lewandowski & K. Tober	BC ZSM Lep 52709	GWOSN598-11
<i>E. rajaeii</i> sp. nov. Wanke & Shirvani	Iran, prov. Kerman, Dalfard, waterfall, 2204 m, 16.ix.2021, leg. Asghar Shirvani	SMNS Lep 002347	GMECA086-23

Results

In total, eight genes (COI, ArgK, Ca-ATPase, EF-1 α , GAPDH, IDH, MDH, RpS5) of the holotype of *Eumera rajaeii* sp. nov. Wanke & Shirvani were successfully amplified and sequenced. In molecular phylogenetic analysis, *Eumera rajaeii* sp. nov. Wanke & Shirvani clustered as sister to *Himeromima* near *aulis* (Druce, 1892) within the tribe Prosoplophini (fig. 1). Moreover, the results of our morphological examination support the assignment of *Eumera* to the tribe Prosoplophini (see figs 2–5 and Systematics part of Discussion).

Our results from the barcoding analysis revealed a genetic p-distance of *Eumera rajaeii* sp. nov. Wanke & Shirvani of 6.12 % difference from the nearest species *E. hoeferi*. Description of the new *Eumera* species is given in the taxonomy part of the Discussion.

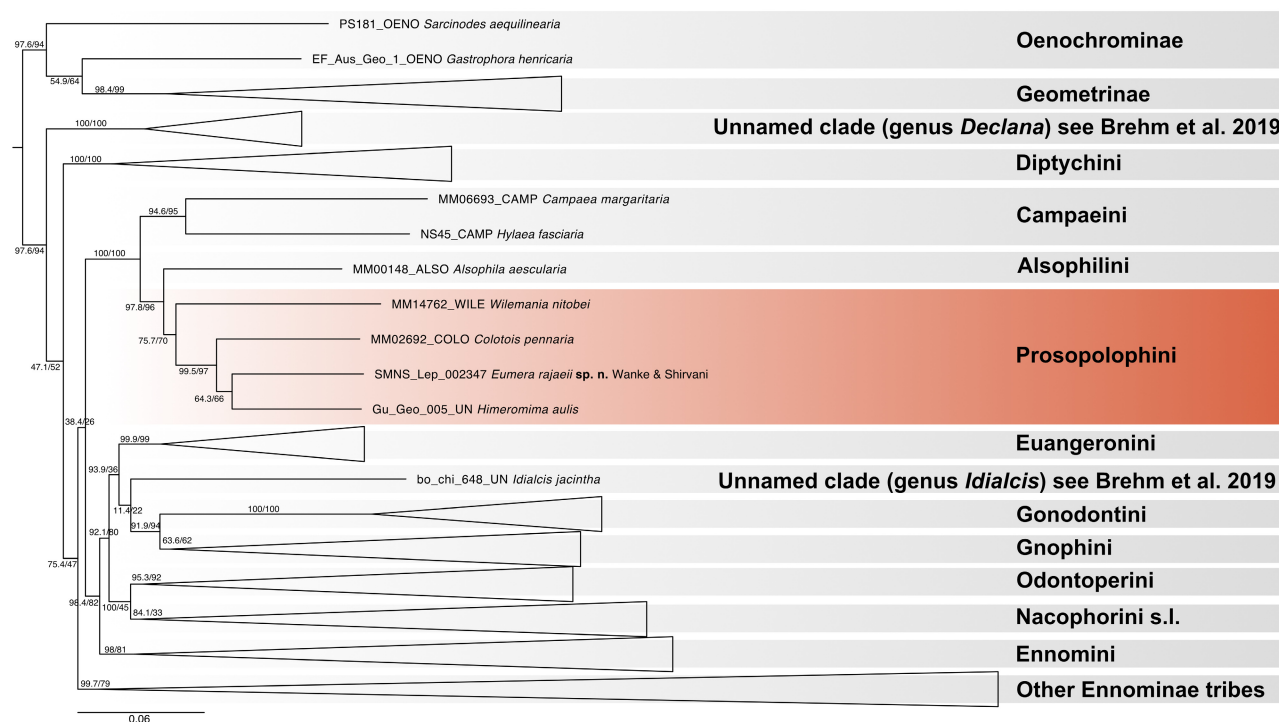


FIGURE 1. Phylogenetic position of *Eumera rajaeii* sp. nov. Wanke & Shirvani within Ennominae, supporting the classification of the genus *Eumera* in Prosoplophini. The maximum likelihood tree is based on up to ten genes, and the numbers above the branches are SH-aLRT support (%) / ultrafast bootstrap support (%). The dataset is based on Murillo-Ramos *et al.* (2019), supplemented with *Eumera rajaeii* sp. nov. Wanke & Shirvani (see Supplementary Table).

Discussion

Systematics

Eumera rajaeii sp. nov. Wanke & Shirvani, *Himeromima* near *aulis* (Druce, 1892), *Colotois pennaria* (Linnaeus, 1761), and *Wilemania nitobei* (Nitobe, 1907) grouped together in the multi-gene phylogeny (fig. 1) and those are morphologically similar (figs 2–5). In addition, *Dorsispina furcicornaria* Nupponen & Sihvonen, 2013, *Chondrosoma fiduciarum* Anker, 1854, *Apochima flabellaria* (Heeger, 1838), and *Dasycorsa modesta* (Staudinger, 1879), which have thus far not been included in molecular phylogeny, but the structures are well-known (Nupponen & Sihvonen 2013; Skou & Sihvonen 2015; Müller *et al.* 2019) are morphologically similar. Males share bipectinate antennae, often wings have pale spots in the terminal area, and the genitalia have diagnostic bilobed uncus (single in *D. modesta*; homology of dorsal structures in some Prosoplophini taxa is unclear, that of *E. regina* identified as scaphium in Skou & Sihvonen (2015)), which is either symmetrical or asymmetrical, valva is simple and relatively wide, sacculus sclerotized marginally and with a spine-shaped saccular process, the short and small aedeagus bears a simple vesica. Female genitalia are not known for all these species, but the examined taxa share large papillae anales, corpus bursae are simple and membranous, and signum is absent (small, weakly stellate signum is present in *W. nitobei*).

Many of the above-mentioned taxa have earlier been assigned to the tribes Colotoini (e.g., Viidalepp 1996), or Gonodontini Forbes, 1948 (Pohl *et al.* 2016), while Beljaev (2016) considered Colotoini Wehrli, 1940, Wilemanini Wehrli, 1941 and Compsopterini Herbulot, 1963 junior synonyms of Prosoplophini Warren, 1894. The type genus of Prosoplophini is *Compsoptera* Blanchard, 1845, which has thus far not been included in molecular phylogeny. The morphology of *Compsoptera* is illustrated in Skou and Sihvonen (2015). *Alsophila aescularia* (Denis &

Schiffermüller, 1775), currently classified in Alsophilini Herbulot, 1962, is sister to Prosopolophini in the molecular phylogeny (fig. 1). It is morphologically different from Prosopolophini lineage (see e.g., Hausmann 2001), therefore, we consider Alsophilini valid on tribe level.

The disjunct biogeography of Prosopolophini is striking. In the phylogenetic tree, *Eumera* and *Himeromima* are sister taxa, the former occurring from southern Europe across the Near East to Iran in the Palearctic (Skou & Sihvonen 2015), the latter from Mexico to the northern parts of South America (Pitkin 2002). All other Prosopolophini species are found in the Palearctic, except *C. pennaria*, which shows a Holarctic distribution. It is not excluded that this disjunct zoogeographical pattern will become supplemented and modified when additional genera will be included in the molecular phylogenetic analysis, which may turn out to be closer relatives to *Eumera*.

Taxonomy

Eumera rajaeii sp. nov. Wanke & Shirvani

(figs 4, 16, 21)

Material examined. Holotype ♂, Iran, prov. Kerman, Dalfard, waterfall, 28°59'58"N, 57°35'15"E, 2204 m, 16.ix.2021, leg. Asghar Shirvani, g.prep. 1321/2022 D. Wanke; **in SMNS**.

Paratypes 2 ♂, Iran, prov. Kerman, Baft, Khabr, 2360 m, 28°51'0"N, 56°22'22"E, 7–8.x.2021, leg. Asghar Shirvani; **all in SMNS**.

2 ♂, Iran, prov. Kerman, Sarbizhan, Shingera, 2850 m, 29°5'8"N 57°32'50"E, 25.viii.2022, leg. Asghar Shirvani, g.prep. AS880m A. Shirvani; 1 ♂, Iran, prov. Kerman, Baft, Dehsard, 15.viii.2022, leg. Mehrabi, g.prep. AS882m A. Shirvani; 1 ♂, Iran, prov. Kerman, Baft, Khabr, 2522 m., 28°45'34"N 56°29'5"E, 2.ix.2022, leg. Kamyab & Shirvani, g.prep. AS881m A. Shirvani; **all in CN-SHBUK**.

1 ♂, Iran, prov. Kerman, Baft, Khabr, 2360 m, 28°51'0"N, 56°22'22"E, 7–8.x.2021, leg. Asghar Shirvani; **in SMNK**.

2 ♂, Iran, prov. Kerman, Baft, Khabr, 2360 m, 28°51'0"N, 56°22'22"E, 7–8.x.2021, leg. Asghar Shirvani; **all in SNSB/ZSM**.

1 ♂, Iran, prov. Kerman, Baft, Khabr, 2522 m., 28°45'34"N 56°29'5"E, 2.ix.2022, leg. Kamyab & Shirvani; 1 ♂, Iran, prov. Kerman, Sarbizhan, Shingera, 2850 m, 29°5'8"N 57°32'50"E, 25.viii.2022, leg. Asghar Shirvani; **all in ZMH**.

Description. *Wings and body* (figs 4, 16). Wingspan ♂ 30–37 mm (forewing length ♂ 17–20 mm). Antennae bipectinate. Frons protruding, prominently yellow scaled. Chaetosemata present as two small patches, located between eyes' margin and antennal bases. Labial palpi strongly reduced, about one-fifth eye diameter. Proboscis reduced. Head, thorax and abdomen concolorous with wings. Forewing basal area, terminal area, and costa brownish-yellow pink with some olive green, terminal area olive green. Terminal line and fringes pink with some brown spots. Medial and postmedial lines brown, pink highlighted. Medial line weakly pronounced. Postmedial line neatly curved. Hindwing brownish-pink, basal and medial area pink, terminal area olive-green. Medial line absent. Postmedial line narrow, brown.

Male genitalia (figs 4, 21). Uncus (homology tentative) triangular. Gnathos absent. Valva long and thin. Costa of valva and ventral margin of sacculus strongly sclerotized. Sacculus with spine-shaped process. Juxta large, posteriorly narrowing. Saccus large and elongated. Aedeagus strongly s-shaped. Vesica without cornuti.

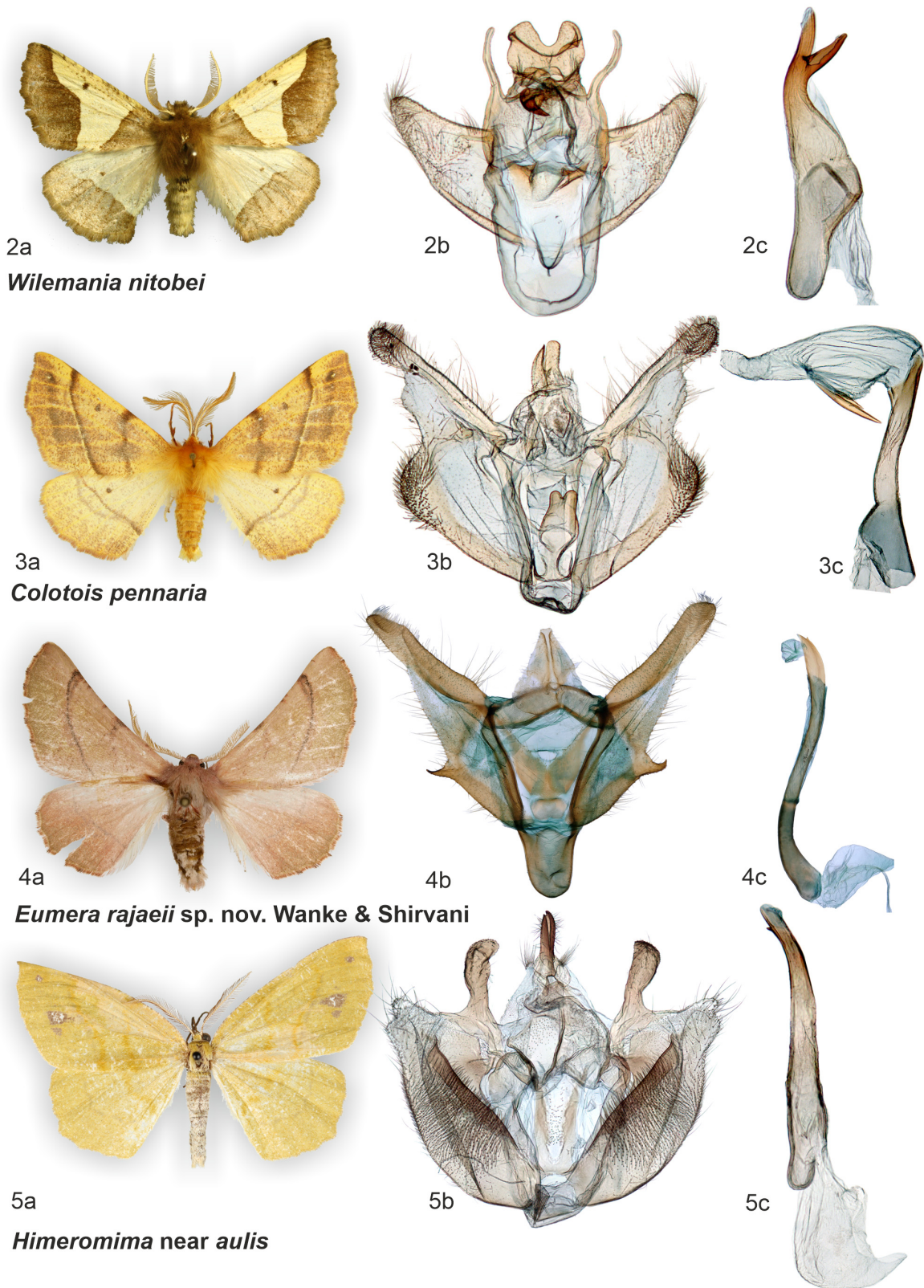
Female genitalia. Unknown.

Diagnosis. In Iran, only *E. hoeferi* is reported from the southern province Fars (Brandt 1939, Viidalepp 1996), which we can confirm here as a specimen was available from this province in the collection of the NHMUK (see examined material). Nevertheless, the new species is - in addition to *E. hoeferi* - also compared with *E. regina* and *E. turcosyrlica*. In the forewing postmedial line neatly curved (rather straight in *E. regina*, *E. turcosyrlica* and *E. hoeferi*) (figs 6–16). Two white spots in the terminal area of the forewing absent (similar in *E. hoeferi*; two white spots present in *E. regina* and *E. turcosyrlica*). In the male genitalia differences are minute and quantitative: saccus more elongated and aedeagus strongly s-shaped compared to *E. regina*, *E. turcosyrlica* and *E. hoeferi* (figs 17–21). See also DNA barcoding.

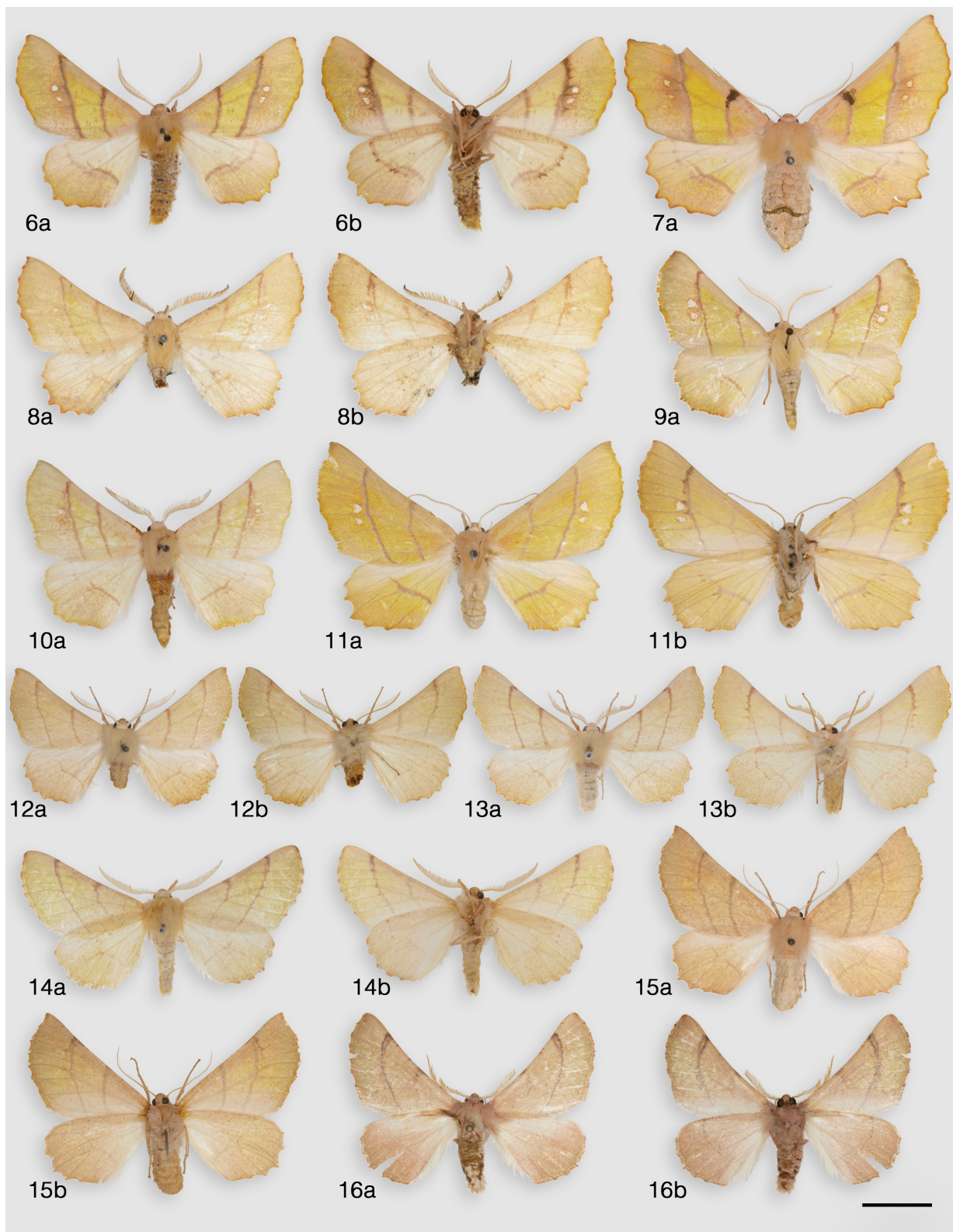
Phenology. Type specimens collected from August to October.

Biology. Unknown.

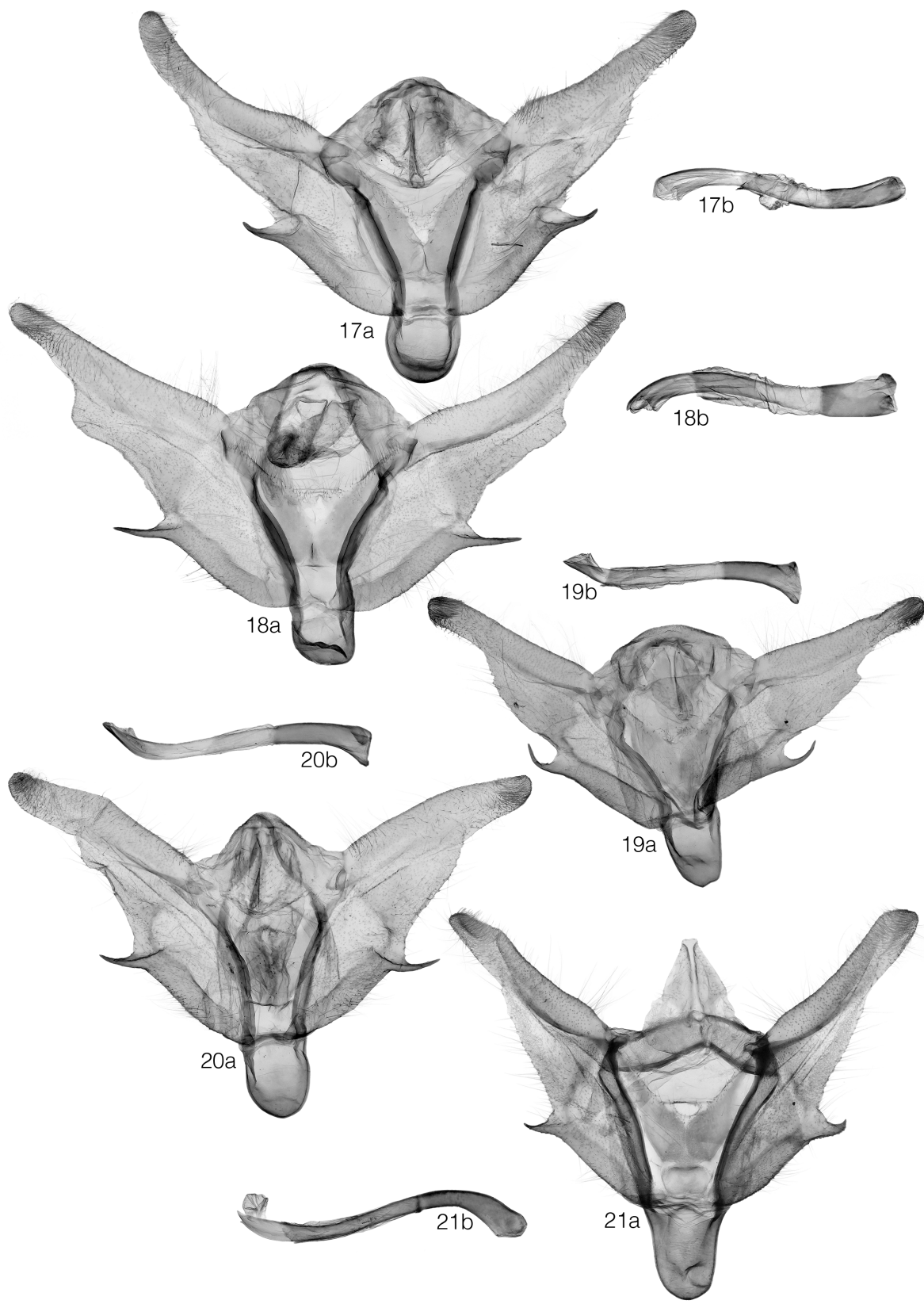
Habitat. Type specimens were collected from rocky mountainous regions covered with shrubs and trees at altitudes from 2204 m up to 2850 m.



FIGURES 2–5. Adults, male genitalia and aedeagus of *Eumera rajaeii* sp. nov. Wanke & Shirvani and related genera based on the molecular phylogeny shown in Figure 1. We classify these genera and several other (see text for details), in tribe Prosopopolophini. 2: *Wilemania nitobei* (Japan, Bushi, Iruma, Saitama-kea, 24.xi.1973, coll. NHMUK, g.prep. Sihvonen 1867); 3: *Colotois pennaria* (a: Sweden, Södermanland, Ågeta, 21.ix.1973, coll. Skou; b–c. Finland: Vantaa, Königstedt, 2–9.ix.1995, coll. Sihvonen, g.prep. Sihvonen 1862); 4: *Eumera rajaeii* sp. nov. Wanke & Shirvani (Iran, Kerman, Dalfard, 16.ix.2021, coll. SMNS, g.prep. 1321/2022 D. Wanke); 5: *Himeromima near aulis* (Mexico, Orizaba, May 1896, coll. NHMUK, g.prep. Sihvonen 2873). Figures are not to scale.



FIGURES 6–16. Wing colouration and pattern of *Eumera* species. 6–7: *E. regina* (6: Macedonia, Petrina, g.prep. 1327/2022 D. Wanke; 7: [Croatia], Dalmatien, g.prep. 1331/2022 D. Wanke); 8–11: *E. turcosyrca* (8: Syntype, [Turkey], Taurus c. Marasch, g.prep. 5576; 9: [Turkey], Aksehir, g.prep. 1324/2022 D. Wanke; 10: [Turkey], Taurus c. Marasch, g.prep. 1319/2022 D. Wanke; 11: Syntype, [Turkey], Taurus c. Marasch, g.prep. 1318/2022 D. Wanke); 12–15: *E. hoeferi* (12: Holotype, [Turkey], Malatya-Tecde, g.prep. 5570; 13: Paratype, [Turkey], Malatya-Tecde, g.prep. NHMUK 010317504; 14: Iran, Fars, Fort Sine-Sefid, g.prep. NHMUK 010317503; 15: Paratype [Turkey], Malatya-Tecde, g.prep. 1317/2022 D. Wanke); 16: *E. rajaeii* **sp. nov.** Wanke & Shirvani (Iran, Kerman, Dalfard, g.prep. 1321/2022 D. Wanke). a = upperside; b = underside. Scale-bar 1 cm.



FIGURES 17–21. Male genitalia of *Eumera* species. 17: *E. regina* (Griechenland, Fokida Nom, Chrisso, g.prep. 1328/2022 D. Wanke); 18: *E. turcosyrica* ([Turkey], Taurus c. Marasch, g.prep. 1319/2022 D. Wanke); 19–20: *E. hoeferi* (3: Paratype, [Turkey], Malatya-Tecde, g.prep. NHMUK 010317504; 4: Iran, Fars, Fort Sine-Sefid, g.prep. NHMUK 010317503); 21: *E. rajaeii* **sp. nov.** Wanke & Shirvani (Iran, Kerman, Dalfard, g.prep. 1321/2022 D. Wanke). a = genitalia capsule; b = aedeagus. Scale-bar 1 mm.

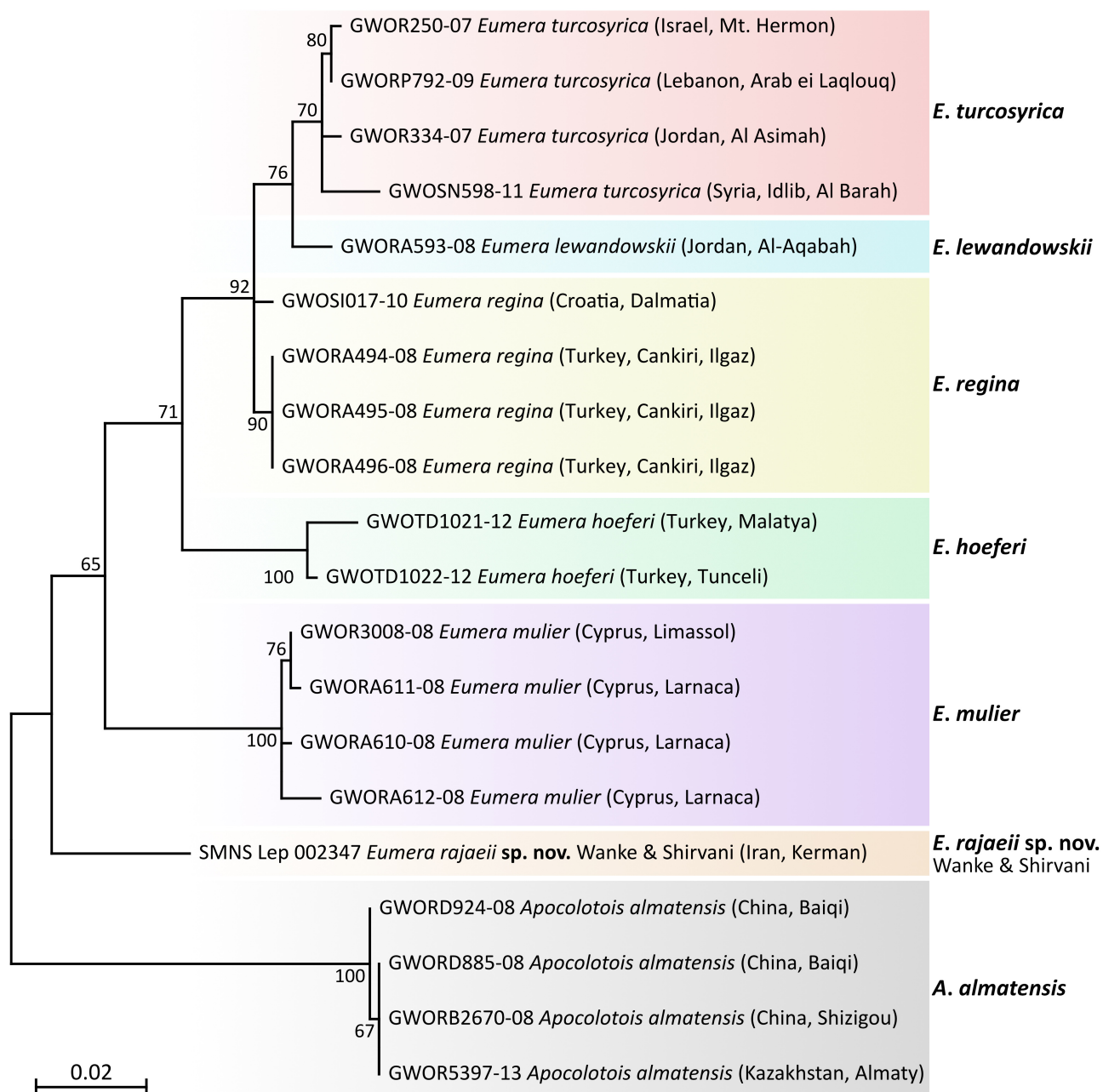


FIGURE 22. Maximum likelihood analysis including all known *Eumera* species and *Apocolotois almatensis* based on COI 5' sequences (built with MEGA X; Kimura 2-parameter model; bootstrap method, 1000 replications).

Distribution. Only known from the southern Iranian province Kerman (fig. 23)

DNA barcoding. The new species shows more than 6 % genetic p-distance from all other *Eumera* species. The genetically nearest species is *E. hoeferi* with 6.12 % difference (fig. 22, tab. 1).

Etymology. The new species is dedicated to our friend and mentor of the first author, Hossein Rajaei (SMNS, Germany), for his encouraging and always enjoyable collaboration and his exceptional contribution to the knowledge of Iranian Lepidoptera.

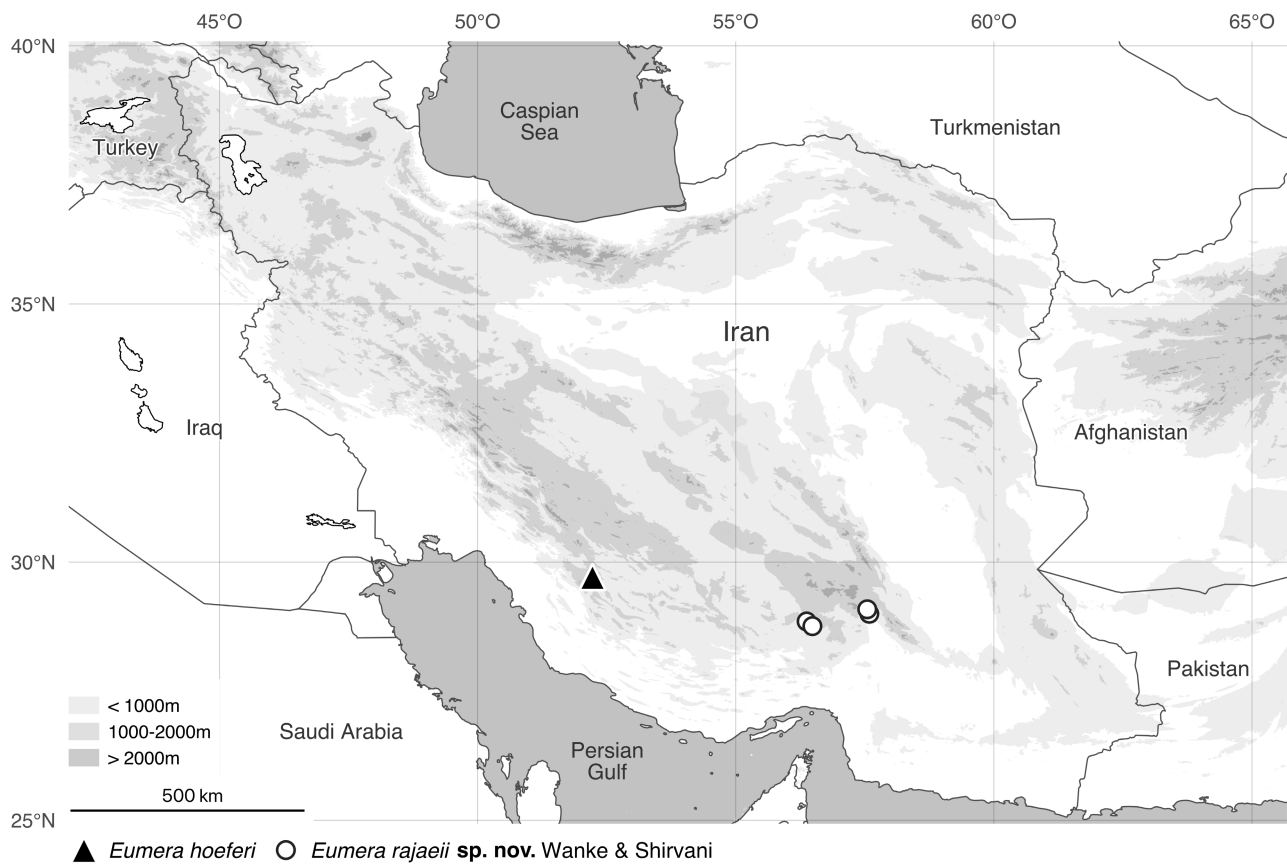


FIGURE 23. Distribution map of *Eumera* species in Iran.

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