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Udea ruckdescheli sp. n. from Crete and its phylogenetic relationships (Pyraloidea, Crambidae, Spilomelinae)

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Abstract. DNA barcode data reveal a distinct group of *Udea* specimens collected on Crete and previously misidentified as *Udea fulvalis* (Hübner, 1809) and *U. languidalis* ab. *veneralis* (Staudinger, 1870). Morphological examination of the specimens corroborates their status as a distinct species which is described as *Udea ruckdescheli* **sp. n.** Images of the adults and the genitalia of both sexes, as well as the DNA barcode sequences are presented. A phylogenetic analysis using molecular (*COI*, *wingless*) and morphological data indicates that the new species belongs to the *Udea numeralis* (Hübner, 1796) species group and is sister to the *Udea fimbriatralis* (Duponchel, 1833) species complex.

Introduction

Udea Guenée (in Duponchel), 1845 is the most species-rich genus of Spilomelinae, comprising 214 described species (Nuss et al. 2003–2016). *Udea* species inhabit every continent except Antarctica, but their main diversity is found in temperate regions and on oceanic islands (Munroe 1966). A number of *Udea* species such as *U. ferrugalis* (Hübner, 1796), *U. decrepitalis* (Herrich-Schäffer, 1848) and *U. costalis* (Eversmann, 1852) are widely distributed, while many others, e.g. *U. accolalis* (Zeller, 1867), *U. carniolica* Huemer and Tarmann, 1989, *U. cretacea* (Filipjev, 1925) and the species of oceanic islands have a much narrower distribution or are even endemic to a small region.

With 38 species occurring in Europe, *Udea* constitutes almost 40 percent of the European Spilomelinae diversity (Nuss et al. 2003–2016). Even though the European pyraloid fauna is relatively well studied in comparison to other regions of the Earth, a considerable number of *Udea* species have been described in the past few decades (Huemer and Tarmann 1989; Leraut 1996; Meyer et al. 1997; Slamka 2013; Tautel 2014).

Taxonomic and systematic research in *Udea* is impeded by the morphological homogeneity of the species: the uniform wing pattern between closely related species differs only slightly in colouration and maculation, and genitalia of both sexes provide only minor structural differences (Munroe 1966). In a phylogenetic analysis on the genus with a focus on European species, Mally and Nuss (2011) proposed four species groups supported by apomorphic characters of the wings

and genitalia. Nevertheless, taxonomic problems still persist, e.g. in the *U. fimbriatralis* complex, the *U. numeralis* complex, the *U. itysalis* (Walker, 1859b) species group and in *U. rhododendronalis* (Duponchel, 1834) (Munroe 1966; Leraut 1996; Slamka 2013). The increasing availability of molecular data enables a re-investigation of such taxa. Easily amplifiable gene sequences such as the DNA barcode (Hebert et al. 2003) allow quick and efficient screening of large numbers of specimens for overlooked and cryptic species (e.g. Huemer and Hebert 2011; Mutanen et al. 2012).

Combining morphological and molecular data in taxonomic studies not only increases the amount of information, but also allows for a comparison of the outcome of the different data sets against each other (Schlick-Steiner et al. 2010). This integrative approach is used to evaluate *Udea* specimens from Crete.

Material and methods

DNA barcodes were either obtained via sending a leg per specimen to the Barcode of Life Facilities in Guelph, Canada, or via DNA extraction and amplification from the abdomen according to the procedure of Knölke et al. (2005): the abdomen was detached from the dried specimen and DNA was extracted using the DNeasy Blood & Tissue kit (Qiagen) according to the manufacturer's protocol. The mitochondrial *COI* gene was amplified using the primers HybLCO (forward) and HybNancy (reverse) (Folmer et al. 1994; Wahlberg and Wheat 2008). For the nuclear *wingless* gene we used the primers HybLepWg1 (forward) and HybLepWg2 (reverse) (Wahlberg and Wheat 2008). Both primer pairs contained a 5' tail of the universal sequencing primers T7 (forward) or T3 (reverse), denoted by the 'Hyb' in the primer names. The 25 µl reactions contained 400 nM of forward and reverse primer, 0.75u *TaKaRa Ex Taq* Hot Start DNA Polymerase, 2.5 µl *Ex Taq* buffer (incl. $MgCl_2$), 800 µM dNTP mix and 2µl of DNA of concentration as extracted. PCR results were examined via gel electrophoresis on a 1% agarose gel and GelRed as dying agent. Successful PCR samples were cleaned with Exonuclease I (Exo) and Shrimp Alkaline Phosphatase (SAP). For the Sanger-sequencing PCR reactions we used 0.25–3.0 µl PCR sample, depending on the thickness of the respective agarose gel band, 160 nM of the sequencing primers T7 and T3, 0.5 µl BigDye, 1.0 µl sequencing buffer, and added up with distilled water to the 10 µl reaction volume. Sequencing was conducted at the sequencing facility of the University of Bergen, Department of Molecular Biology. PCR and sequencing PCR were performed on a Bio-Rad C1000 thermal cycler, ExoSAP clean-up was done with an MJ Research PTC-200 thermal cycler. Sequences were aligned using PhyDE version 0.9971 (Müller et al. 2008).

Dissection of genitalia was performed according to Robinson (1976). Morphological structures were investigated using a Leica M125 stereomicroscope. Photographic documentation of imagines was done with a Canon EOS 60D in combination with a Canon EF 100mm 1:2,8 Macrolens and Canon EOS Utility Version 2.10.2.0 on a Windows PC. A Leica CTR6000 Microscope in combination with a Leica DFC420 camera and Leica Application Suite programme, version 3.8.0 on a Windows PC was used for documentation of the genitalia.

The Bayesian inference of the combined molecular and morphological data was conducted using MrBayes 3.2.5 (Ronquist et al. 2012). We used the dataset published by Mally and Nuss (2011) and added the information for the six specimens of *U. ruckdescheli* for which we had molecular data available (see Table 1). The phylogenetic analysis of Mally and Nuss (2011) found a clade containing *Deana hybreasalis* (Walker, 1859a), *Mnesictena marmarina* Meyrick, 1884 and *Ude-*

oides muscosalis (Hampson, 1913) as sister to *Udea*, therefore we used this sister clade as outgroup in our analysis. This taxon sampling resulted in the morphological character 17, "Uncus – apex with bulbous thickening: absent (0); present (1)", being constant, therefore we excluded it from the dataset.

The data were divided into three partitions: *COI* (1459 bp), *wingless* (363 bp) and the morphological data (23 characters). We applied the GTR+G model for the gene partitions and the Mk model (Lewis 2001) with gamma rate variation for the morphological partition. The parameters for gamma shape, proportion of invariable sites, character state frequencies and GTR substitution rates were unlinked for the three partitions, and the overall rate was allowed to vary across partitions. The analysis was run for two million generations with four simultaneous analyses, sampling of the Markov chain at every 1,000th cycle and a burn-in of 25%. Effective sampling sizes and degree of convergence of the analyses were evaluated in Tracer (Rambaut et al. 2014). The final consensus tree was annotated using TreeGraph 2.9.2 (Stöver and Müller 2010), with all branches with posterior probabilities < 0.90 collapsed.

Abbreviations

BC	Barcode
bp	base pairs
COI	cytochrome oxidase subunit I
DNA	desoxyribonucleic acid
EBI	European Bioinformatics Institute, Saffron Walden, Great Britain
MTD	Senckenberg Museum of Zoology („Museum für Tierkunde") Dresden, Germany
NHMO	Natural History Museum Oslo, Norway
PCR	polymerase chain reaction
prep.	preparation
TLMF	Tiroler Landesmuseum Ferdinandeum, Innsbruck, Austria
ZMHB	Zoological Museum, Humboldt University, Berlin, Germany
ZMBN	Zoological Museum Bergen, Norway
ZSM	Zoological State Collections Munich, Germany

Results

The analysis of DNA Barcodes of *Udea* specimens from Crete resulted in three clusters: *U. ferrugalis*, *U. numeralis* and one unknown cluster. The latter remained unknown when analysing these sequences together with the data set of Mally and Nuss (2011), covering most of the European *Udea* species, revealing no congruence with any known species. Eventually, the specimens of the unknown cluster were morphologically compared against the known *Udea* species, which showed evidence that the specimens in question represent a still undescribed species. This new species belongs to *Udea* based on its forewing pattern with both cellular stigmata well developed and the postmedian line with a characteristic loop below the distal cellular stigma. Further diagnostic characters that place the new species in *Udea* are the narrow, elongate valvae and the bulbous, dorsally setose uncus head in the male genitalia as well as the elongate, lanceolate signum in the corpus bursae of the female genitalia.

Udea ruckdescheli sp. n.

http://zoobank.org/883EB672-9EA7-4ABA-957F-71DAC41484EA

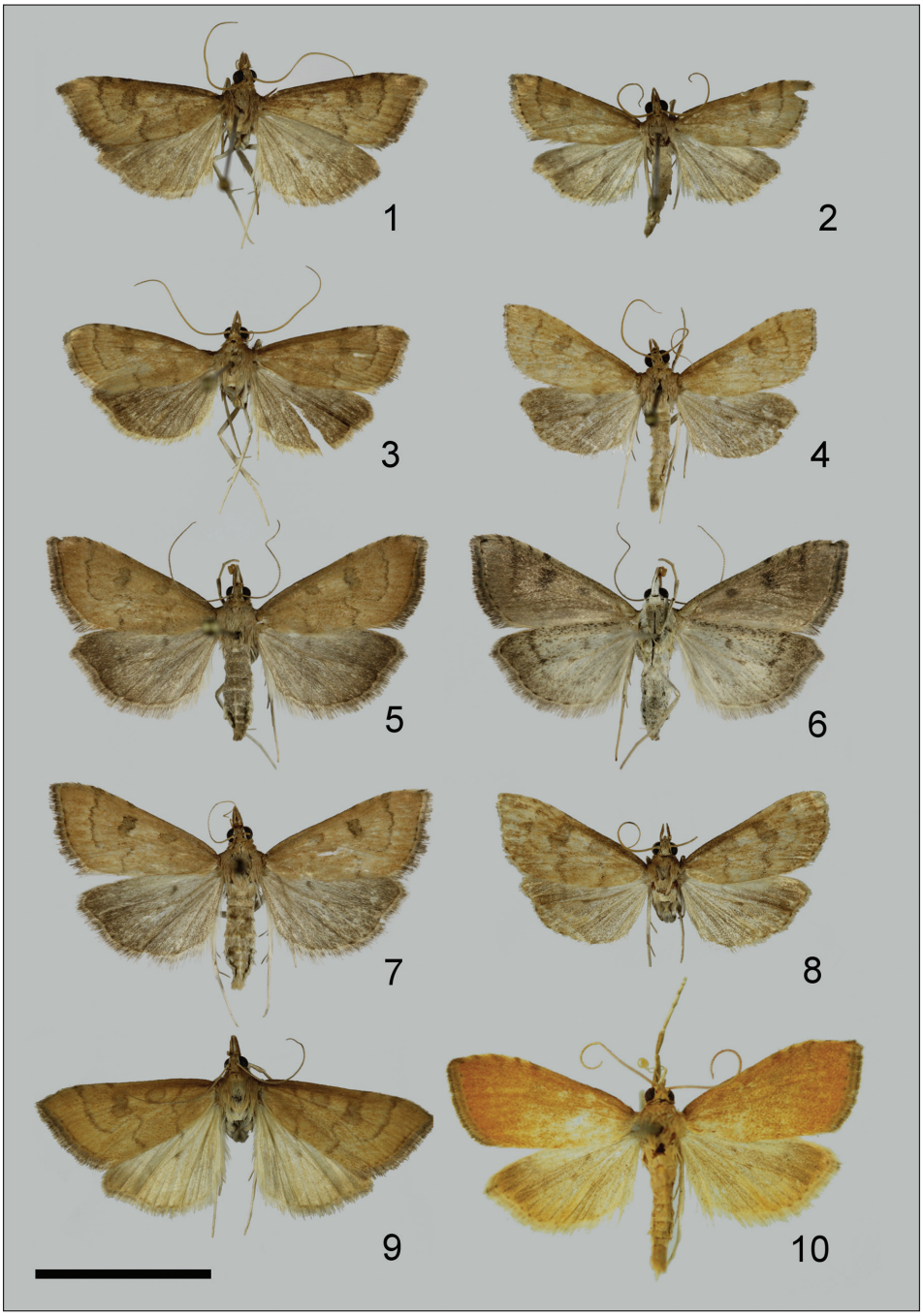
Figs 1–7, 11–15, 20–21

Type locality. Greece, Crete, Lasithi, near Moni Kapsa monastery, Perivolakia gorge, 10 m, 35.021555°N 26.050902°E.

Material examined. Holotype: ♂ "Perivolakia-Schl. 10m | M.Kapsa, N.Lassithi | KRETA/GRAECIA | (Tagf.T F - Lwd./BL) | leg. W. Ruckdeschel | [transverse, handwritten] 20.5.2000", [yellow label] "86509:ZSM | coll. W. Ruckdeschel | Udea | ruckdescheli | det. Segerer", [mint green label] " BC ZSM Lep 61775", [yellow label] "DNA voucher | Lepidoptera | ZMBN 2015 | [transverse] no. 087", "Mally prep. no. | [handwritten] 872 ♂" (ZSM). **Paratypes:** 1♂ as HT, but "86508" on yellow label, plus [orange label] "DNA voucher | Lepidoptera | ZMBN 2015 | [transverse] no. 129" and "Mally prep. no. | [handwritten] 932 ♂" (ZSM); 1♂ as HT, but "86510" on yellow label, [orange label] "DNA voucher | Lepidoptera | ZMBN 2014 | [transverse] no. 086", and "Mally prep. no. | [handwritten] 863 ♂"; 1♂ "Ano Saktouria | N. Rethymnon, 400m | KRETA/GRAECIA | (Leuchtturm SL+BL) | leg. W. Ruckdeschel | [transverse, handwritten] 18.5.2000", [yellow label] "86529:ZSM | coll. W. Ruckdeschel | Udea | ruckdescheli | det. Segerer", [mint green label] "BC ZSM Lep 61774", [orange label] "DNA voucher | Lepidoptera | MTD 2013 | [transverse] no. 1590", "Mally prep. no. | [handwritten] 663 ♂"; 1♂ "GREECE Crete, | Chania Prov.: Imbros | 35S KU 4170 0122 | 570 m. 11. vi. 2013 | leg. Leif Aarvik", [yellow label] "DNA voucher | Lepidoptera | ZMBN 2015 | [transverse] no. 152", "Mally prep. no. | [handwritten] 982 ♂" (NHMO); 1♀ "GREECE Crete, | Chania Prov.: Imbros | 35S KU 4170 0122 | 570 m. 15. vi. 2014 | leg. Leif Aarvik", [yellow label] "DNA voucher | Lepidoptera | ZMBN 2015 | [transverse] no. 151", "Mally prep. no. | [handwritten] 981 ♀" (NHMO); 1♀ same data except for "20. vi. 2014", [yellow label] "DNA voucher | Lepidoptera | ZMBN 2015 | [transverse] no. 150", "Mally prep. no. | [handwritten] 980 ♀" (NHMO). – **Additional material. GREECE.** 1♂ "GREECE Crete, | Chania Prov.: | Hora Sfakion | 35S KU 4031 9864 | 9-21. vi. 2014 | leg. Leif Aarvik"; 1♀ "GREECE Crete, | Chania Prov.: Imbros | 35S KU 4170 0122 | 570 m. 11. vi. 2013 | leg. Leif Aarvik"; 2♀ same data except for "20. vi. 2014" (NHMO).

Diagnosis. In wing pattern elements, *Udea ruckdescheli* is similar to *U. accolalis* (Zeller, 1867), *U. afghanalis* (Amsel, 1970), *U. ardekanalis* Amsel, 1961, *U. ferrugalis* (Hübner, 1796), *U. fimbriatralis*, *U. fulvalis*, *U. languidalis* (Eversmann, 1842), *U. praefulvalis* (Amsel, 1970) and *U. rubigalis* (Guenée, 1854). *Udea accolalis*, *U. ferrugalis* and *U. rubigalis* belong to the *Udea ferrugalis* species group, whose members differ by features of male and female genitalia (Mally and Nuss 2011).

The other similar species mentioned above belong to the *Udea numeralis* species group according to the presence of a longitudinal split posteriorly in the sclerotized section of the phallus, an autapomorphic character for this species group (Mally and Nuss 2011). In *Udea afghanalis* and *U. praefulvalis* the postmedian line forms an evenly arched line parallel to the termen, with the loop below the distal cellular stigma more accentuated and finger-shaped with parallel sides, whereas in *U. ruckdescheli* the loop is usually more angled, and anterior and posterior sections of the postmedian line are not aligned, i.e. the postmedian line's posterior section is further away from the termen than the anterior section. The valvae of *U. afghanalis* and *U. ardekanalis* are narrower, particularly in *U. ardekanalis* where they taper off into a narrow tip. The distal phallus apodeme of *U. afghanalis*, *U. fulvalis* and *U. praefulvalis* lacks the elongate dentate crests of *U. ruckdescheli* (Figs 12–15), and the apodeme is shorter in *U. fulvalis* (Fig. 17) and *U. praefulvalis*. In wing pattern elements, *U. ruckdescheli* cannot be distinguished from *U. fulvalis* (Fig. 8), but differs in male genitalia in the characters mentioned above as well as by the smaller vinculum saccus and the shorter fibulae (compare Fig. 11 with Fig. 16 of *U. fulvalis*). In the female genitalia,



Figures 1–10. Adult specimens. **1–7.** *Udea ruckdescheli*. **1.** Holotype ♂ (ZSM), Crete, Lasithi; **2.** Paratype ♂ (ZSM), Crete, Lasithi; **3.** Paratype ♂ (ZSM), Crete, Lasithi; **4.** Paratype ♂ (NHMO), Crete, Imbros; **5–6.** Paratype ♀ (NHMO), Crete, Imbros, dorsal (5) and ventral (6) aspect; **7.** Paratype ♀ (NHMO), Crete, Imbros. **8.** *U. fulvalis* ♂, Germany, Brandenburg. **9.** *U. languidalis* ♀, Iran, Golestan. **10.** *U. fimbriatralis* ab. *veneralis*, original specimen ♂ (ZMHB), Greece, Naxos. Scale bar represents 1 cm.

U. ruckdescheli (Figs 20–21) is distinguished from *U. fulvalis* by the conical antrum (tubular in *U. fulvalis*, see Fig. 22).

U. ruckdescheli is different from its sister species *U. fimbriatralis* and *U. languidalis* (Fig. 9) as the forewings are dorsally brownish with a diffuse ground colour, without a dark brown fringe, and the hindwings are brownish-grey dorsally (Figs 1–5, 7); *U. fimbriatralis* and *U. languidalis* have an orange, more homogenous forewing ground colour and a contrasting brown fringe as well as a whitish hindwing colour. The new species cannot be reliably distinguished from *U. fimbriatralis* and *U. languidalis* (Figs 18–19) in the male genitalia. In the female genitalia, *U. ruckdescheli* (Figs 20–21) is distinguished from *U. fimbriatralis* and *U. languidalis* by the sclerotisation of the posterior end of the ductus bursae being shorter than the colliculum (as long as or longer than colliculum in *U. fimbriatralis* and *U. languidalis*, see Fig. 23).

The DNA barcode (Table 1) of *U. ruckdescheli* is unique and does not match any other species barcoded so far. Intraspecific Barcode variation among the six sequenced specimens ranges from 0.00% to 0.65% (p-distance). The nearest neighbour is *U. languidalis*, with a p-distance of 1.94% to 2.26%.

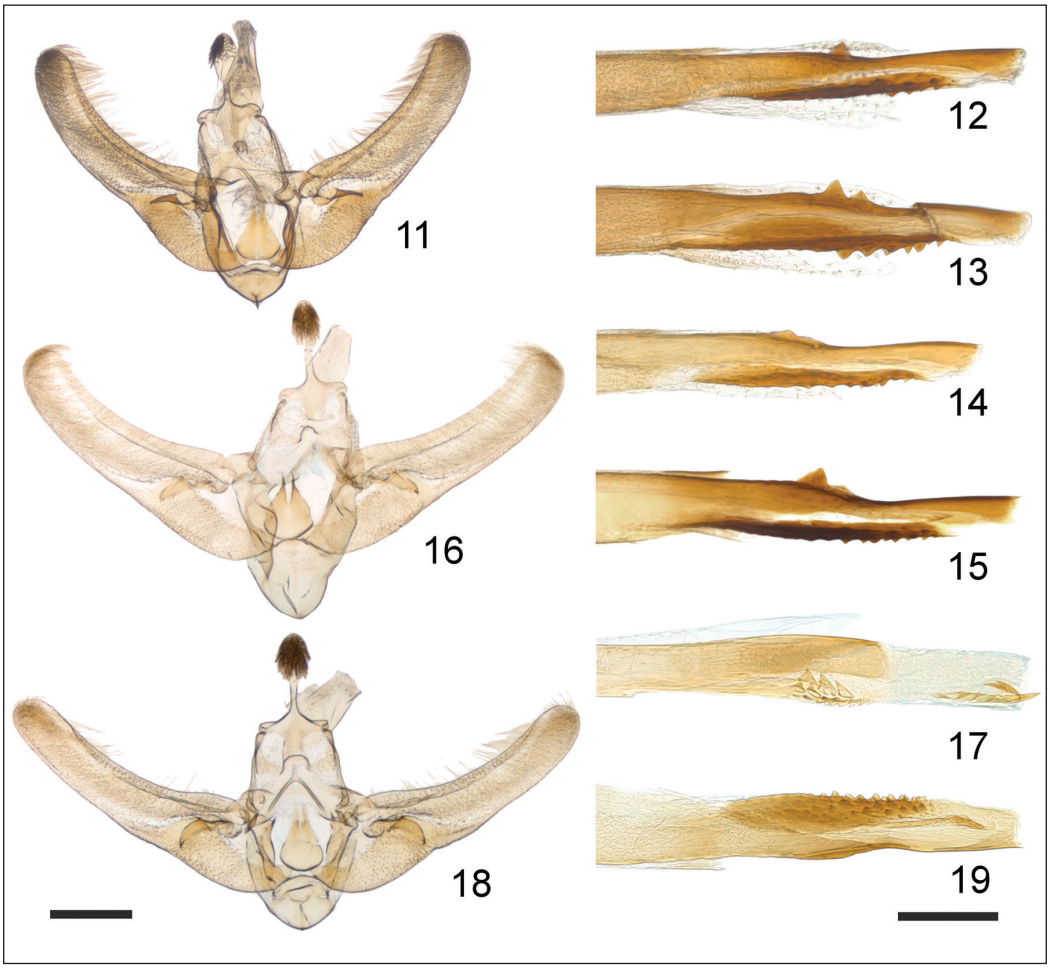
Description of adults. Head: Head greyish to light brown; frons slightly bulged; labial palps porrect, brownish, 1st segment and ventral side of 2nd segment white, 3rd segment in females approximately twice the length compared to males; maxillary palps well developed, with whitish scales; haustellum well developed, with whitish scales on base; eyes large, hemispherical; ocelli present; antennae ciliate, light brown, cilia in males dense and shorter than 1/4 of antennal diameter, ciliation in females shorter than in males; vertex with light brown spatulate scales; chaetosemata absent.

Thorax: Dorsal side light brown; ventral side cream to whitish; forelegs light brown, mid- and hindlegs cream to whitish; tibial spurs on fore-, mid-, hindleg: 0, 2, 4, on hindlegs anterior outer spur minute while inner spur almost reaching base of posterior pair of spurs.

Wings: Forewing ground colour diffuse light brown to orange-brown; diffuse dark brown antemedian line running obliquely distad, after half of length bending and running more or less orthogonally towards dorsum; proximal cellular stigma circular, distal cellular stigma 8-shaped, both stigmata bordered dark brown; postmedian line dark brown, running from costa parallel to termen, at half of length bending proximad, running below distal cellular stigma, then turning in semicircle towards lower end of termen and then half that way approaching dorsum orthogonally; postmedian line distally framed by lighter diffuse band; subterminal band with dark brown spots where it meets with wing veins; fringe dark brown; costa slightly darker than ground colour, with dark spots at ends of costal veins. Hindwings with one frenular bristle in males and two in females, without subcostal retinaculum on forewing, but with basal tuft of filiform scales reaching over the frenular bristle; ground colour brownish-grey, cell with a proximal and a distal brown spot, both often faint; postmedian line brown, clear to diffuse; continuous brown subterminal line with dark spots where it meets with veins; fringe dark brown. Undersides (Fig. 6) pale brown; forewings with prominent dark spots at the vein ends on costa and termen, distal cellular stigma and postmedian line visible as diffuse fuscous patterns; hindwings with the two central spots and postmedian line relatively clear.

Abdomen: Light brown, underside somewhat lighter.

Male genitalia: (Figs 11–15) Uncus base broad, constricted at lateral juncture with tegumen, uncus neck thin, head ovate, ventrally densely studded with bifurcate, anteriad setae. Tegumen

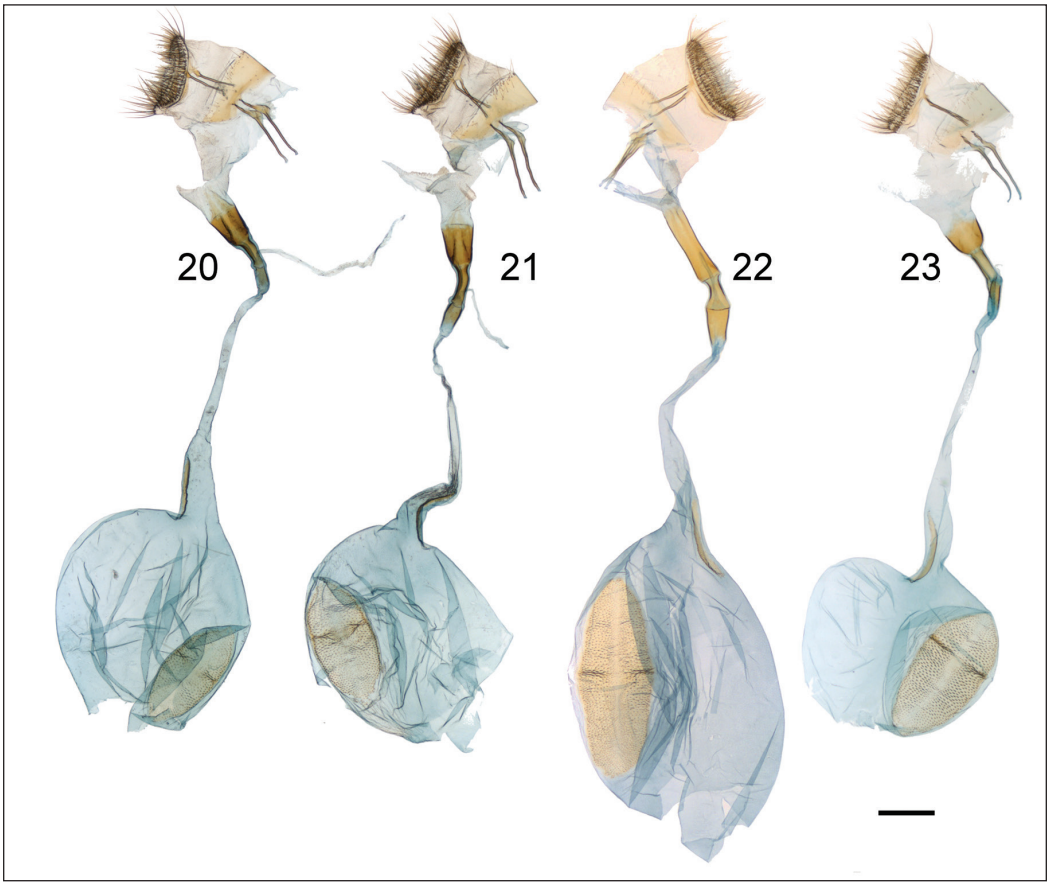


Figures 11–19. Male genitalia. **11–15.** *Udea ruckdescheli*. **11–12.** Holotype, Greece, Crete, N-Lasithi (Mally prep. no. 872; ZSM), male genital (11) and posterior phallus (12); **13.** Paratype, Crete, Ano Saktouria (Mally prep. no. 663; ZSM), posterior phallus (posterior section fractured); **14.** Paratype, Crete, N-Lasithi (Mally prep. no. 863; ZSM), posterior phallus; **15.** Crete, Imbros (Mally prep. No. 982; NHMO); posterior phallus. **16–17.** *U. fulvalis*, Romania, Orşova (Mally prep. no. 132; MTD), male genital (16) and posterior phallus (17). **18–19.** *U. languidalis*, Iran, Golestan, NP Golestan, Tange Gol (Mally prep. no. 163; TLMF), male genital (18) and posterior phallus (19). Left scale bar represents 500 µm for male genitalia, right scale bar represents 200 µm for posterior phalli.

rectangular, posteriomesally with a short dorsad, bulged pseudognathos. Vinculum roughly rectangular, with evenly rounded, ventrally keeled saccus. Juxta drop-shaped to elongated triangular, dorsal part tapered and deeply split, apices pointed. Valvae elongate, apex evenly rounded, costa proximally somewhat inflated, ventral edge straight to convex, but slightly concave near distal sacculus; sacculus roughly triangular, reaching distal end of fibula base; fibula elongate, triangular to claw-shaped, straight or slightly curved, posterioventrally directed, with small apical tooth. Transtilla arms short, triangular. Phallus tubular, slightly curved dorsad, without coecum; posterior

Table 1. Molecular data used in this study. GenSeq nomenclature after Chakrabarty et al. (2013).

Origin	Collection	DNA collection number	COI GenBank/ EBI access number; BOLD Barcode number	Wingless GenBank/ EBI access number	GenSeq nomencl.
Greece, Crete, Lasithi, near Moni Kapsa monastery, Perivolakia gorge, 35.021555°N, 26.050902°E, 10 m	ZSM (holotype ♂)	ZMBN Lep087	KX422253; BC ZSM Lep 61775	–	genseq-1
Greece, Crete, Rethymnon, Ano Saktouria, 35.121994°N, 24.614528°E, 400 m	ZSM (paratype ♂)	MTD Lep1590	KX422252; BC ZSM Lep 61774	–	genseq-2
Greece, Crete, Lasithi, near Moni Kapsa monastery, Perivolakia gorge, 35.021555°N 26.050902°E, 10 m	ZSM (paratype ♂)	ZMBN Lep086	LT595884	–	genseq-2
Greece, Crete, Chania Province, Imbros, 35.220867°N, 24.161978°E, 570 m	NHMO (paratype ♀)	ZMBN Lep150	LT595885	LT595888	genseq-2
Greece, Crete, Chania Province, Imbros, 35.220867°N, 24.161978°E, 570 m	NHMO (paratype ♀)	ZMBN Lep151	LT595886	LT595889	genseq-2
Greece, Crete, Chania Province, Imbros, 35.220867°N, 24.161978°E, 570 m	NHMO (paratype ♂)	ZMBN Lep152	LT595887	LT595890	genseq-2



Figures 20–23. Female genitalia. **20–21.** *Udea ruckdeschelli*. **20.** Paratype, Greece, Crete, locality (Mally prep. no. 980; NHMO); **21.** Paratype, Greece, Crete, locality (Mally prep. no. 981; NHMO). **22.** *U. fulvalis*, Romania, Orşova (Mally prep. no. 020; MTD). **23.** *U. languidalis*, Iran, Golestan, NP Golestan, Tange Gol (Mally prep. no. 104; TLMF). Scale bar represents 500 µm.

apodeme dorsally with a short sub-posterior ridge bearing one to three more or less prominent triangular teeth, and a simple stout posterior ending; ventrally with weakly sclerotised strip encircling a strongly sclerotised, longitudinal, dentate sclerite; four to seven small, conical cornuti present.

Female genitalia. (Figs 20–21) Corpus bursae globular to ovoid, membranous, with a lentiform, denticulate (main) signum bearing transverse ridge of larger denticles posterior to its centre. Ductus bursae emerging from posterior centre of corpus bursae, narrowing to thin tube; anterior part of ductus bursae with slim longitudinal accessory signum of approximately half of length of main signum stretching posteriad from junction with corpus bursae; posterior part of ductus bursae slightly widened, with short sclerotized section of approximately half of length of tubular, slightly bent colliculum. Ductus seminalis emerging from short membranous intersection between posterior part of ductus bursae and colliculum. Antrum conically widening posteriad, with central channel flanked by diffuse sclerotisations stretching posteriad into the otherwise membranous ostium bursae; posterior sclerotisation of ductus bursae, colliculum and anterior part of antrum with thickened mesocuticula. Apophyses anteriores slightly angled at broadened section at one third of their length; apophyses posteriores simple, approximately half the length of apophyses anteriores. Papillae anales simple, ventrally and dorsally connected to each other, with long, simple setae.

Immature stages and food plants. Unknown.

Distribution. So far only known from the Greek island of Crete, and potentially endemic. The altitudinal distribution ranges from 10 m to 570 m.

Etymology. The species is named after Walter Ruckdeschel, the collector of the initial part of the type material.

Phylogenetic placement. The morphological investigation of external and genital characters of the adult moths of *U. ruckdescheli* resulted in the following morphomatrix coding based on the characters proposed by Mally and Nuss (2011): (1) 0; (2) 1; (3) 1; (4) 0; (5) 0; (6) 1; (7) 1; (8) 0; (9) ?; (10) 0; (11) ?; (12) 0; (13) 1; (14) 0; (15) 1; (16) 1; (17) 1; (18) 0; (19) 1; (20) 1; (21) 0; (22) 0; (23) 0; (24) 0.

The phylogenetic analysis of the combined data resulted in the well-supported placement of *U. ruckdescheli* in the *U. numeralis* species group, where it is sister to the species pair *U. languidalis–U. fimbriatralis* (Fig. 24). This placement is in concordance with the autapomorphic longitudinal strip of the praephallus proposed by Mally and Nuss (2011) for the *U. numeralis* species group.

Remarks. The original specimen of *Botys fimbriatalis* [sic] ab. *veneralis* Staudinger, 1870 at ZMBH (Fig. 10) is not conspecific with the specimens discussed and depicted in Slamka (2013: 76, Pl. 15 Figs 107o–r, Pl. 22 Fig. 107d, Pl. 86 Fig. 107d) as *Udea languidalis* ab. *veneralis*. Instead, the specimens and genitalia depicted in Slamka (2013) are conspecific with *Udea ruckdescheli* sp. n.

Discussion

Udea ruckdescheli was found to co-occur spatially and temporally with its closest look-alike *U. fulvalis* (leg. L. Aarvik, NHMO). Therefore, collection vouchers identified as *U. fulvalis* should be re-identified. This is a pre-requisite to elucidate the geographical distribution, which according to current knowledge would be restricted to arid habitats of the southern part of Crete from elevations between 10 m and 570 m. In addition, further collecting in the entire eastern Mediterranean would help to shed light on the geographic distribution pattern of *U. ruckdescheli*.

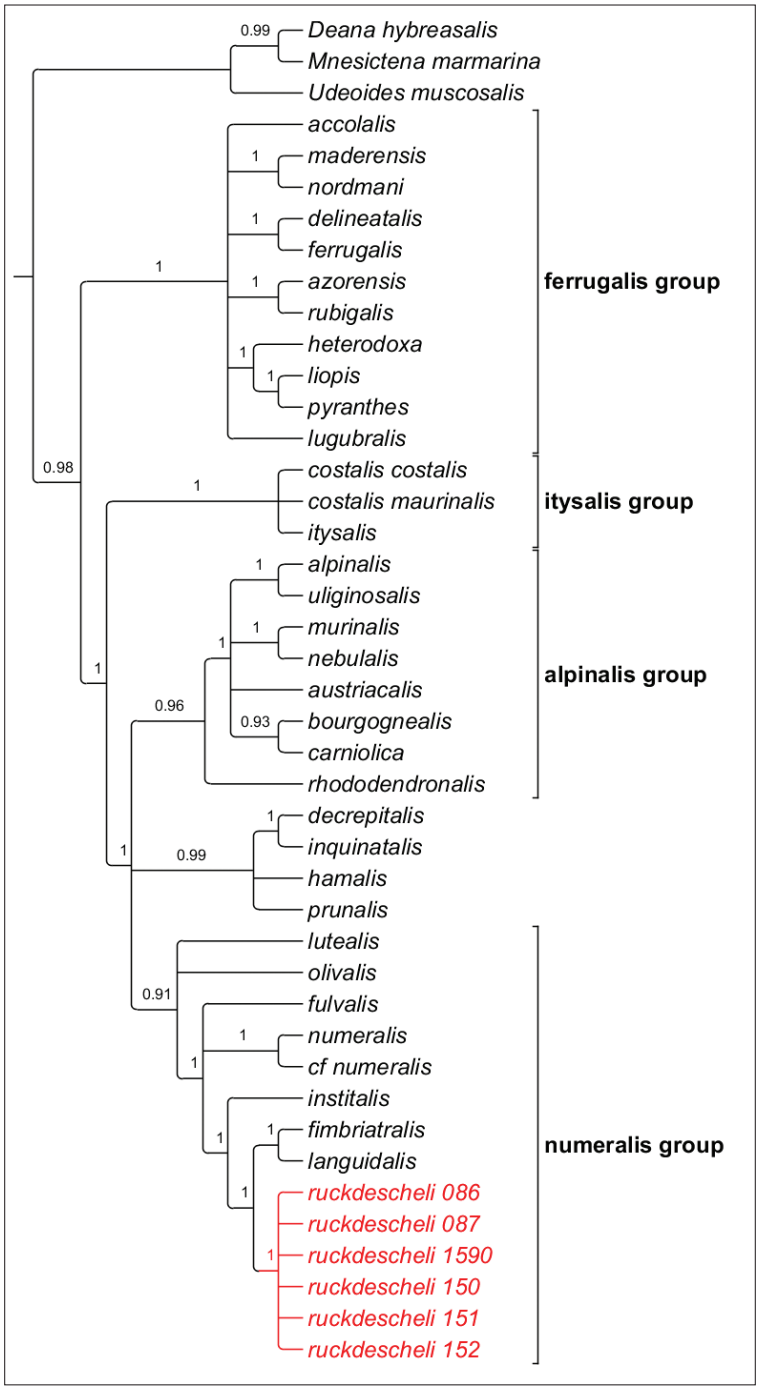


Figure 24. Bayesian inference phylogeny of European *Udea* species including *U. ruckdescheli*, sp .n. (red clade, numbers correspond to DNA collection numbers in Table 1), based on *COI*, *wingless*, and morphological data analysed with MrBayes 3.2.5. Numbers at the nodes represent posterior probabilities ≥ 0.90, nodes with posterior probabilities < 0.90 are collapsed.

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