

Contribution to the Knowledge of the Afrotropical Spilomelinae (Lepidoptera, Crambidae): A New Genus in the Tribe Nomophilini Kuznetzov & Stekolnikov 1979 Based on Morphology and DNA Barcoding

Michael Seizmair* 

Department of Entomology, Section Lepidoptera, SNSB Bavarian State Collection of Zoology Munich, Munich, Germany

Email: michael.seizmair@gmx.net

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Abstract

The new genus *Parathrausta* **gen.n.** in the subfamily Spilomelinae (Lepidoptera, Crambidae) is erected based on a series of specimens collected in the Afrotropical region of Saudi Arabia. The new genus is monotypical, with *Parathrausta internervalis* **sp.n.** its type species. The adults of the type species, the male genitalia, the female genitalia and the tympanal organs are described and figured. The new genus is recognized as related by characters in the male and female genitalia with genera in the tribes Steniini Guinée, 1854 and Nomophilini Kuznetzov & Stekolnikov, 1979, namely with *Bradina* Lederer, 1863, *Perisyntrocha* Meyrick, 1894, *Diathrausta* Lederer, 1863, *Diasemiopsis* Munroe, 1957, *Diasemiodes* Munroe, 1957 and with the genera in the *Duponchelia* Zeller, 1847 group comprising *Duponchelia* Zeller, 1847, *Penestola* Möschler, 1890, *Tatobotys* Butler, 1880 and *Hymenoptychis* Zeller, 1852. The character states differentiating the new genus from the comparative genera are discussed. Potential autapomorphies of the new genus are listed. The tribal assignment of the new genus to the Nomophilini Kuznetzov & Stekolnikov, 1979 based on morphological characters is discussed. The support of the tribal and cladistic assignment of the new genus as a sister clade to *Diathrausta* Lederer, 1863 based phylogenetic analyses (NJ, MP and ML) is shown. An unusually strong genetic divergence of the genus in the COI segment of the mt-DNA based on the Tamura-Nei distance measure from the morphologically related genera is recognized and addressed.

*Associated Independent Scientist.

Keywords

Pyraloidea, Taxonomy, Morphology, COI, New Genus, New Species, Arabian Peninsula

1. Introduction

The subfamily Spilomelinae has a worldwide distribution and is known as the most diverse subfamily in the Pyraloidea, currently comprising a total of 4100 valid species, 338 genera and 12 tribes [1] [2]. Mally *et al.* presented the first comprehensive revision of the subfamily at tribal level [1]. In this study, a synapomorphy has been recognized for the first time for the Spilomelinae based on morphological and phylogenetic data in the tympanal organs, namely the fornix tympani projecting in the ventral direction from the tympanic frame. Further characters recognized for the subfamily include a bilobed praecinctorium, the absence of a gnathos and the presence of ventral processes (fibulae) in the valva, and weak to absent sclerotization in the corpus bursae of the female genitalia [3] [4].

The subfamily has been extensively studied for the Palearctic, Neotropical and Oriental zones. Recent faunistic and taxonomic revisions have been reported in [5] [6] [7] [8]. For the Afrotropical zone, however, recent studies have been confined to South Africa, West Africa and the Malagasy Islands [9]-[14]. The potential for endemic taxa on specific and generic level in the Spilomelinae has to date been little explored. Shaffer & Munroe and Maes presented recent advances [14] [15]. In these studies, a total of ten genera known to date as endemic to Africa were described.

The Afrotropical zone of the Arabian Peninsula, which spans the southwestern province Dhofar of the Sultanate of Oman, Yemen and the south-western Saudi Arabia has been little explored for the Spilomelinae to date. The faunistic records have been based prevalently on historical data. The first comprehensive survey on literature and research status is given in Seizmair [16]. Studies by Hacker and Hausmann showed the endemic potential for several superfamilies including the Noctuoidea and Geometroidea of the mountain chains of the southern Arabian Peninsula spanning from the Hedjaz mountains in Saudi Arabia to the Saravat mountain chains along the Red Sea into the south of Yemen [17] [18].

In this study, a new genus *Parathrausta* **gen.n.**, of the subfamily is erected based on a series of crambid moths which came to the attention of the author when evaluating samples collected in the Fayfa Mountains in southwestern Saudi Arabia. The specimens were found to be related in internal morphology to genera in the tribes Steniini Guinée, 1854 and Nomophilini Kuznetsov & Stekolnikov, 1979. The tribal assignment to the Nomophilini Kuznetsov & Stekolnikov, 1979 and the cladistic placement of the new genus is discussed on the basis of morphological and molecular genetic data.

2. Materials and Methods

2.1. Sampling

The specimens ($n = 5$) presented in this paper belong to a moth sample collected in a research expedition to the Fayfa Mountains in the south-western province Jizan of the Kingdom of Saudi Arabia in March 2023. The material was captured by night using light traps equipped with UV-Power-LEDs spanning a wavelength spectrum of 365 nm - 385 nm. The trapping technique is described in Brehm [19].

2.2. Macro-Preparation, Dissection and Digital Image Processing

The adults were photographed after relaxation and subsequent preparation with a CANON EOS M6 Mark II under an MP-E-65 mm zoom. To examine the genitalia and tympanal organs, dissection and slide-mounting techniques were applied to the specimens according to the protocols described in Robinson and Maes [20] [21]. The preparation of the tympanal organs and of the genitalia was done under a Motic stereomicroscope (SMZ-171). The slides were photographed with a ToupCam c-mount camera (ToupTek Inc., Zhejiang, China). The images were processed using the imaging software Adobe Photoshop PS, Version 21.0.2.

2.3. Morphological Analyses and Comparisons

Analyses of wing pattern characters and morphological structures in the specimens of the sample were done on the images. Structural ratios in external characters, genitalia and tympanal organs were calculated on the images by means of the imaging software ToupView, Version 1.0 (ToupTek Inc., Zhejiang, China).

The specimens in the sample were compared with genitalia figures of morphologically related taxa [5] [14] [22] [23] [24] [25] [26].

2.4. Phylogenetic Analysis

2.4.1. DNA Extraction

From two specimens of the type series legs were separated for DNA extraction. Genomic DNA (658 base-pairs) was extracted using the GenElute Mammalian Genomic DNA (Sigma-Aldrich, USA). The DNA extraction was done by the staff of the Biotechnical Faculty, University of Ljubljana, Slovenia. The DNA extracts are deposited in the Zoological collection of this institute. Amplification was done on mitochondrial DNA—the Cytochrome c oxidase subunit I (COI) using standard primers (LCO1490 and HCO2198) and PCR amplification protocols. PCR products were purified using Exonuclease I and FastAP (Thermo Fisher Scientific Inc., USA) according to the manufacturer's instructions, and sequenced in both directions by Macrogen Europe (Amsterdam, The Netherlands). The resulting chromatograms were assembled and edited using Geneious 8.1.9. (Biomatters, New Zealand), with ambiguous bases coded using IUPAC nucleotide ambiguity characters.

2.4.2. Data Set Compilation

The DNA sequences of two type specimens and of taxa morphologically related to the two type specimens from the tribes Steniini Guinée, 1854 and Nomophilini Kuznetsov & Stekolnikov, 1979 were compiled into a data set in FASTA format. The DNA sequences (n = 19) of the comparative taxa were downloaded from the BOLD database [27]. The comparative material is listed in **Table 1**.

The taxa *Prophantis androstigmata* (Hampson, 1918) and *Trichaea pilicornis* (Herrich-Schäffer, 1866) were used as outgroups. Both taxa are attributed to the tribe Trichaeini Mally, Hayden, Neinhuis, Jordal & Nuss, 2019. The latter tribe was shown to be closely related to Steniini and Nomophilini [1].

2.4.3. Phylogenetic Tree Inference

The DNA sequences were aligned using the MUSCLE algorithm. The alignment was subsequently cured of potential alignment errors, strongly divergent and ambiguous regions using the software Gblocks 0.91b [28]. These two algorithms were applied using the portal Phylogeny.fr [29].

Table 1. Comparative material in the data set used for phylogenetic analysis identified by taxon names, BOLD ID, GenBank Access ID and Sample ID.

Taxon	BOLD ID	GenBank Access ID	Sample ID
<i>Penestola bufalis</i>	BBLOB1224-11.COI5P	-	BIOUG01416-G12
<i>Penestola bufalis</i>	BBLOB516-11.COI5P	-	BIOUG01397-D05
<i>Duponchelia fovealis</i>	EHL177-12. COI5P	-	C090901A1Jan2009
<i>Duponchelia fovealis</i>	FBLMU001-09. COI5P	HQ955198	BC ZSM Lep 25511
<i>Hymenoptychis sordida</i>	ANICN520-10. COI5P	HQ952790	10ANIC-10516
<i>Tatobotys biannulalis</i>	ANIC517-10.COI5P	HQ952787	10ANIC-10513
<i>Tatobotys vibrata</i>	PMAML4578-15. COI5P	-	USNM ENT 01068264
<i>Diathrausta harlequinialis</i>	LOFLC268-06.COI5P	-	06-FLOR-2148
<i>Diathrausta reconditalis</i>	LMIS071-06.COI5P	-	05-ONMIS-0071
<i>Diathrausta picata</i>	ANIC575-06. COI5P	-	ANIC Gen No. 000767
<i>Diathrausta ochreipennis</i>	ANICB104-06. COI5P	-	ANIC Gen No. 001236
<i>Diasemiopsis ramburialis</i>	ANICB702-07. COI5P	-	ANIC Gen No. 001670
<i>Diasemiopsis leodocusalis</i>	BLPED803-11.COI5P	-	11-SRNP-104405
<i>Diasemiodes eudamidasalis</i>	BLPCD772-08.COI5P	JQ560611	07-SRNP-108197
<i>Perisyntrocha sp.</i>	WALPD011-15. COI5P	-	BIOUG21481-D10
<i>Perisyntrocha sp.</i>	ANICN219-10. COI5P	HQ9528008	10ANIC-10215
<i>Bradina atopalis</i>	GBMIN18017-13. COI5P	KC135909	KC135909
<i>Bradina admixtalis</i>	ANICN210-10. COI5P	HQ952604	10ANIC-10206
<i>Bradina diagonalis</i>	MAMTL561-12. COI5P	KX862027	BIOUG02380-F07
<i>Prophantis androstigmata</i>	ANIC522-06.COI-5P	-	ANIC Gen No. 000714
<i>Trichaea pilicornis</i>	ASARD847-11.COI-5P	-	INB0004208564

For inferring a first phylogenetic hypothesis on the cladistic placement of the new genus MP- and ML-trees were computed. An NJ tree was computed to assess the genetic distances between the new genus and the morphologically related genera in the dataset. Furthermore, average genetic distances within and between the genera were computed. These computations were done using the software MEGA, Version 11.0.13 [30]. For the construction of the MP and NJ trees and of the genetic distance matrices a list of best fitting substitution models was computed based on the Bayesian Information Criterion (BIC) [31] using the same software. The Tamura-Nei model was selected [32]. For both approaches the branch supports were assessed by 5000 bootstrap replicates.

2.5. Terminology and Abbreviations

The denotations of veins follow the terminology of Shaffer & Munroe [14]. The descriptions of wing pattern characters, genitalia and tympanal organs follow the terminology of Maes [21]. Abbreviations: ML = Maximum Likelihood, MP = Maximum Parsimony, NJ = Neighbour Joining, n = length of a sample, slide no. = slide number, ZSM = Zoological State Collection Munich.

3. Results and Discussion

Parathrausta gen.n.

Zoobank ID:

urn:lsid:zoobank.org:act:F06E2514-930D-4389-AE64-93F4237F5A0A

Type species: *Parathrausta internervalis* sp.n.

External characters (Figure 1): Head: Antenna filiform ciliate, bipectinate. Frons flattened. Labial palpus porrect, slightly slanted and broadly scaled in segments 1 and 2, segment 3 vertically upturned, protruding from segment 2, spatulate. Maxillary palpus upright, filiform, unscaled. The proboscis is well developed. Wing venation: Forewing Sc half as long as the costal border. R1 develops from the posterior fifth of the cell, R2 and R3 + 4, R5 develop from the anterior angle of the cell. R1 and R2 are equal in length, widely spaced, terminating far below the costal border. R2 is free, closely apposed to R3 + 4, running straight to the termen. R3 + 4 is paralleled with R2 up to the posterior fourth of the wing then diverging towards the termen. R5 is basally approximated to R3 + 4, running parallel with the costa. M1 is basally approximated with R5, running quasi straight into the termen. M2, M3 and CuA1 develop from the posterior angle of the cell, basally closely approximated. CuA2 develops from the posterior fourth of the cubitus. The cell is equal in length to one-third of the costa. Retinaculum bristle present, marked as a small pad of long hairs. Hindwing Sc + R1 and Rs long stalked for half of the total wing length. Sc + R1 convex in the anterior fifth. M1 anastomosed with Sc + R1, running straight to the termen. M2, M3 and CuA1 develop from the posterior angle of the cell and are basally closely approximated. CuA2 develops from the middle of the cubitus. Origins of CuP and 1A + 2A closely approximated. 1A + 2A and 3A running parallel into the termen. Number of frenula: four spines.

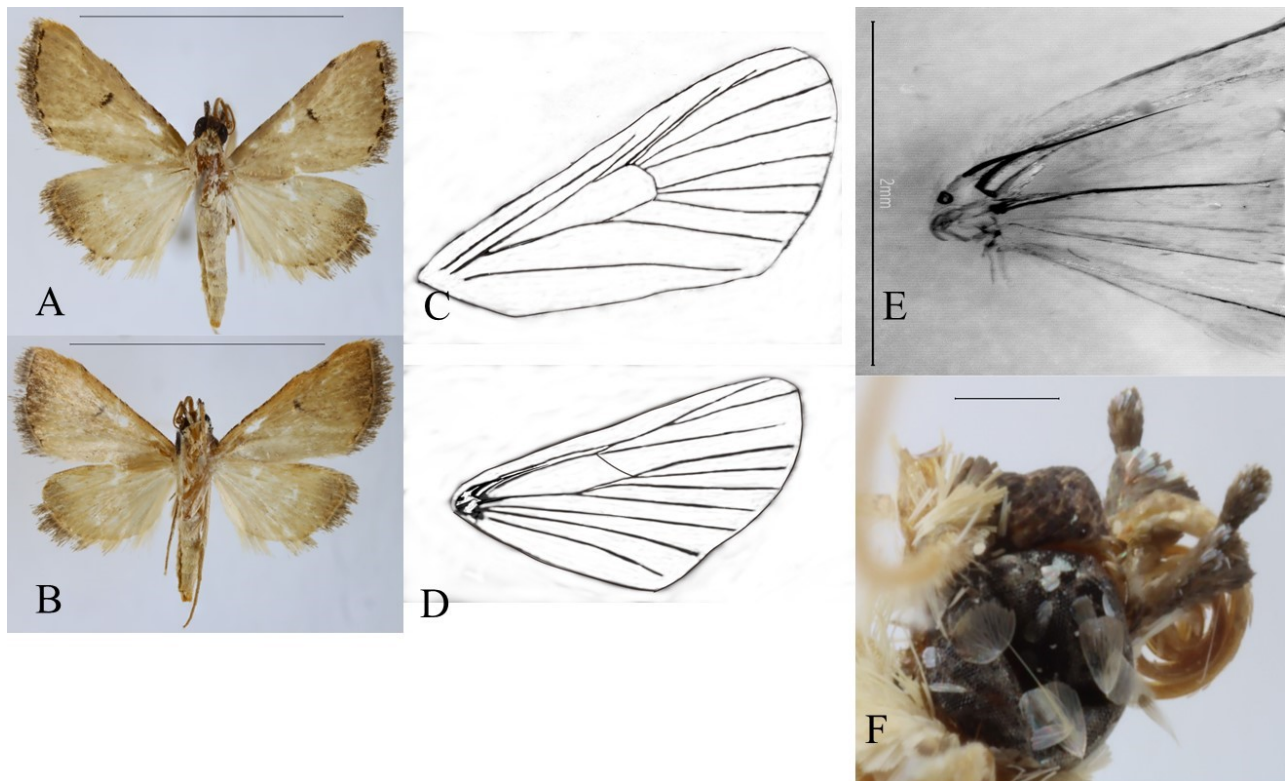


Figure 1. *Parathrausta internervalis* gen.n., sp.n.—external characters. A, B: Holotype, slide no. 23GP042, ♀. A: dorsal view, B: ventral view. C-F: Paratype, ♂, slide no. 23GP032. C: Forewing venation, D: Hindwing venation, E: close-up, frenulae. F: head profile. Scale bars A, B, E = 10 mm, F = 0.5 mm.

Male genitalia (Figure 2): Uncus lobar, apex ovate with bifid chaetae laterally and dorsally, neck relatively short, length relative to the width of the valva 0.4, with oblong chaetae laterally, scaphium absent, transition to the tegumen smooth, from a broad basis to an equally broad tegumen. Tegumen ridges concave, interconnected medially, forming an H-shaped structure. Transtilla of trapezoid shape, basally broadened, medially connected. Juxta digitiform, unsplit, laterally sclerotized. Vinculum broadened, with androconia present. Saccus v-shaped, relatively broad, width relative to length 0.8. Valva double as long as wide, costa straight, sclerotized, bare from inflation, with an elongate anterior-directed sub-costal process. Apex obliquely rounded towards the costa, with a tuft of short chaetae. Ventral border concave. Basal valva with three fibulae, two of which are short, equal in length, with their length relative to the length of the valva 0.17, laterally fanning out into multi-furcate structures. The third fibula is deciduous, oblong, three times as long as the two short ones, convex at the basis, thus forming a j-shape. A fourth rod-shaped sclerotization is present, however developing wide-spaced from the basis, distally fanning out into a multi-setose structure. Each of the fibulae is longitudinally oriented, running parallel to the ventral border and wide-spaced from the sacculus. Basal sacculus broad, acuminate. Phallus with stroke-shaped sclerites in the medial and posterior areas, vesica bare from cornuti, coecum present, with the anterior end narrowed and rounded at the tip, ductus ejaculatorius inserted laterally at the coecum.

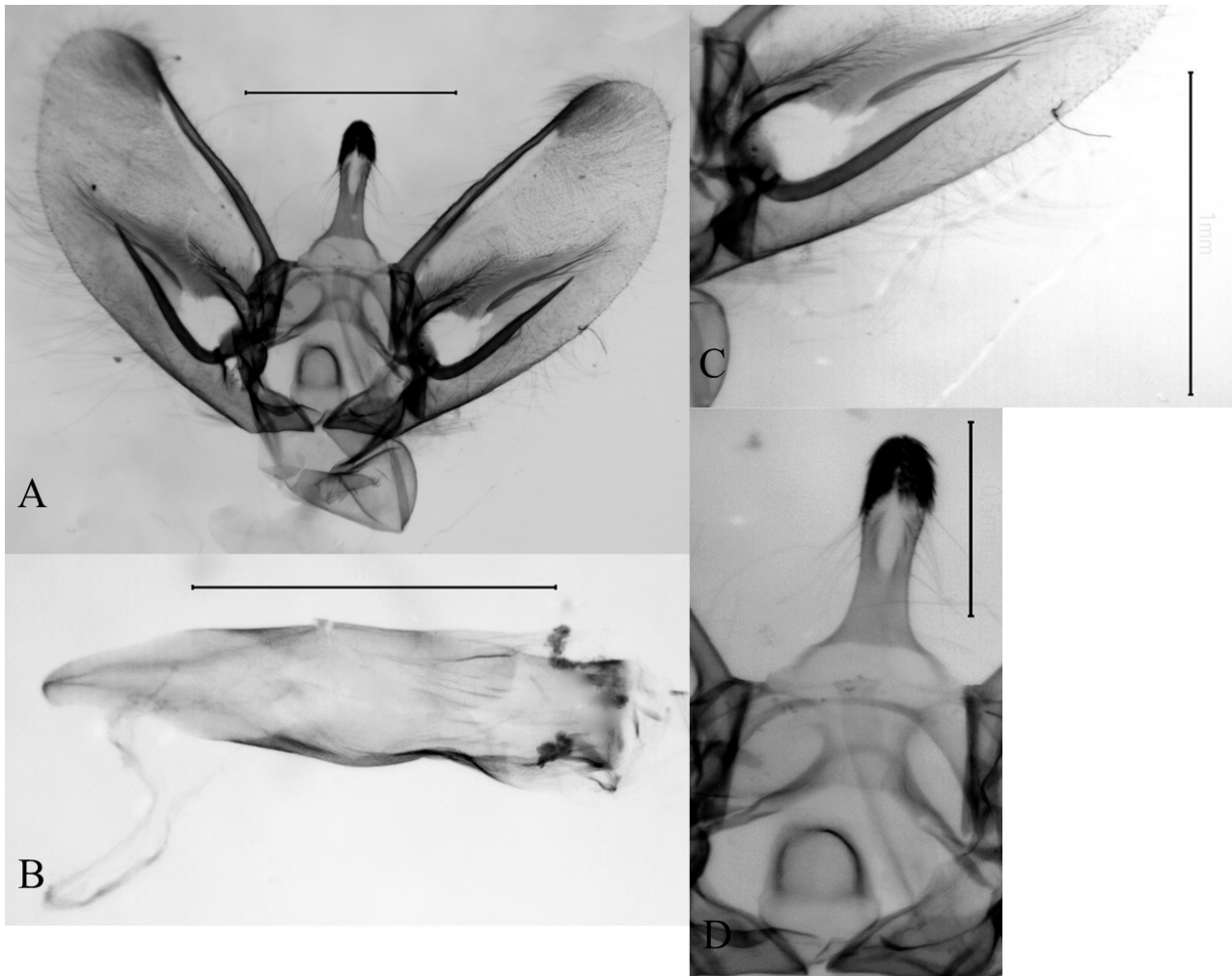


Figure 2. *Parathrausta internervalis* gen.n., sp.n., male genitalia, paratype, slide no. 23GP043. A: genitalia capsule, phallus omitted. B: phallus. C: Close-up, fibulae. D: Close-up, uncus, tegumen, juxta. Scale bars = 1 mm.

Female genitalia (Figure 3A, Figure 3B): Papilla analis ovate, strongly chaetose. Anterior apophyses medially dilated, 1.4 times as long as the posterior apophyses. Ostium membranous, bare from sclerotization. Antrum strongly broadened, barrel-shaped, membranous. Colliculum strongly sclerotized, broadened, bare from medial membranous strip. Ductus bursae broadened and strongly sclerotized at the posterior end, transition to the corpus bursae smooth, to a narrowed posterior corpus bursae. Corpus bursae ovate, wall with a transversally oriented, u-shaped, toothed signum, which is constant in width.

Tympanal organs (Figure 3C): Rami tympani medially connected. Bulla tympani closed. Pons tympani with a short, broadened basis, lobes short. Processi tympani present, basally broad, of sub-triangular shape. Fornix tympani narrow. Tergo-sternal sclerite, slender, thorn-shaped, shortened. The lobes of the praecinctorium differ in length and shape. The shorter lobe is sickle-shaped, with a right-angled curvature. The longer lobe is straight, acuminate, and strongly tapered in the anterior half.



Figure 3. *Parathrausta internervalis* gen.n., sp.n. A, B: female genitalia, holotype, slide no. 23GP042. A: Genitalia capsule, global view. B: Close-up, signum. C: tympanal organs, paratype, slide no. 23GP042. Scale bars = 1 mm.

Diagnosis: The new genus is morphologically related in the presence of an arch-shaped, serrate signum in the corpus bursae wall with the genera *Bradina* Lederer, 1863, *Perisyntrocha* Meyrick, 1894, *Diathrausta* Lederer, 1863, *Diasemiopsis* Munroe, 1957 and *Diasemiodes* Munroe, 1957. *Bradina* Lederer, 1893 is attributed to the Steniini, and the other genera are attributed to the Nymphilini [1] [2].

The new genus is differentiated from *Bradina* in the anastomosing of the R2 on the R3 + 4 stem in the forewing. In *Bradina* the R2 is anastomosed with the R3 + 4, in the new genus the R2 is free, however, closely apposed to R3 + 4 [1] [33]. The new genus is furthermore differentiated in the male genitalia from each of the comparative genera by the number and directedness of the fibulae.

In each of the comparative genera, the number of fibulae is ≤ 1 —zero in *Diasemiodes* Munroe, 1957, one in each of the other comparative genera. The fib-

ula is transversally directed towards the sacculus and develops from below the costa in each of the comparative genera. In the new genus the fibulae are longitudinally directed, running parallel with the sacculus and develop either medially from the basal valva or immediately above the basal sacculus. Furthermore, the vesica is armed with cornuti in each of the comparative genera. In the new genus, the vesica is unarmed. The saccus in the new genus is strongly protuberant, elongate and v-shaped, strongly shortened and u-shaped in the comparative genera *Diasemiodes*, *Diasemiopsis*, *Diathrausta* and *Perisyntrocha*. The costa of the valva is straight in the new genus, convex in the comparative genera.

The longitudinal directedness of the fibula(e) is also shared with the genus *Diasemiodes* Munroe, 1957 and with the genera in the *Duponchelia* Zeller, 1847 group, which comprises *Duponchelia* Zeller, 1847, *Penestola* Möscher, 1890, *Tatobotys* Butler, 1880 and *Hymenoptychis* Zeller, 1852 [26]. The *Duponchelia* group is attributed to the Steniini Guinée, 1854 [1] [2].

In the *Duponchelia* group the forewing R2 is anastomosed on R3 + 4 as in *Bradina* and the corpus bursae wall is bare from signa [1] [26]. The presence of a signum in the corpus bursae wall is viewed as exceptional for the Steniini [1]. Furthermore, the new genus and *Perisyntrocha*, *Diathrausta*, *Diasemiodes*, *Diasemiopsis* are distinguished from *Bradina* in the shape of the signum. In *Bradina* the signum is medially dilated, in *Perisyntrocha*, *Diathrausta*, *Diasemiodes*, *Diasemiopsis* and in the new genus, however, the signum is of constant width. With *Diathrausta* and *Diasemiodes* the new genus is furthermore related in the lobar shape of the uncus and the strongly sclerotized antrum.

The new genus is thus placed closest to the genera *Perisyntrocha*, *Diathrausta*, *Diasemiodes* and *Diasemiopsis* in the Nomophilini. However, the presence of several fibulae and their longitudinal directedness from the medial basis of the valva is exceptional for the Nomophilini [1]. The male genitalia of the known genera of this tribe are characterized by one or zero fibulae in the valva. If present, the fibula develops transversally from below the costa. Further potential apomorphies of the new genus are the H-shaped structure formed by the medially connected tegumen ridges and the presence of multi-furcate fibulae.

Phylogenetic placement (Figure 4, Figure 5; Table 2, Table 3): The new genus *Parathrausta* **gen.n.** is strongly supported by an unusually strong genetic divergence from the morphologically related genera in the tribes Steniini and Nomophilini, as shown in the original NJ tree. The new genus is genetically closest to *Diathrausta* (Figure 4, Figure 5). The average genetic distance between the haplotypes of the new genus and those of *Diathrausta* in the current dataset is 0.65, while the average genetic distances between the new genus and *Bradina*, *Perisyntrocha*, the *Diasemiodes* + *Diasemiopsis* clade and the *Duponchelia* group range between 0.68 and 0.73 (Table 2) in the present analysis. The average genetic distances within *Parathrausta*, and *Diathrausta* are respectively 0.01 and 0.08. The genetic distances within the other groups range between 0.02 and 0.10 (Table 3).

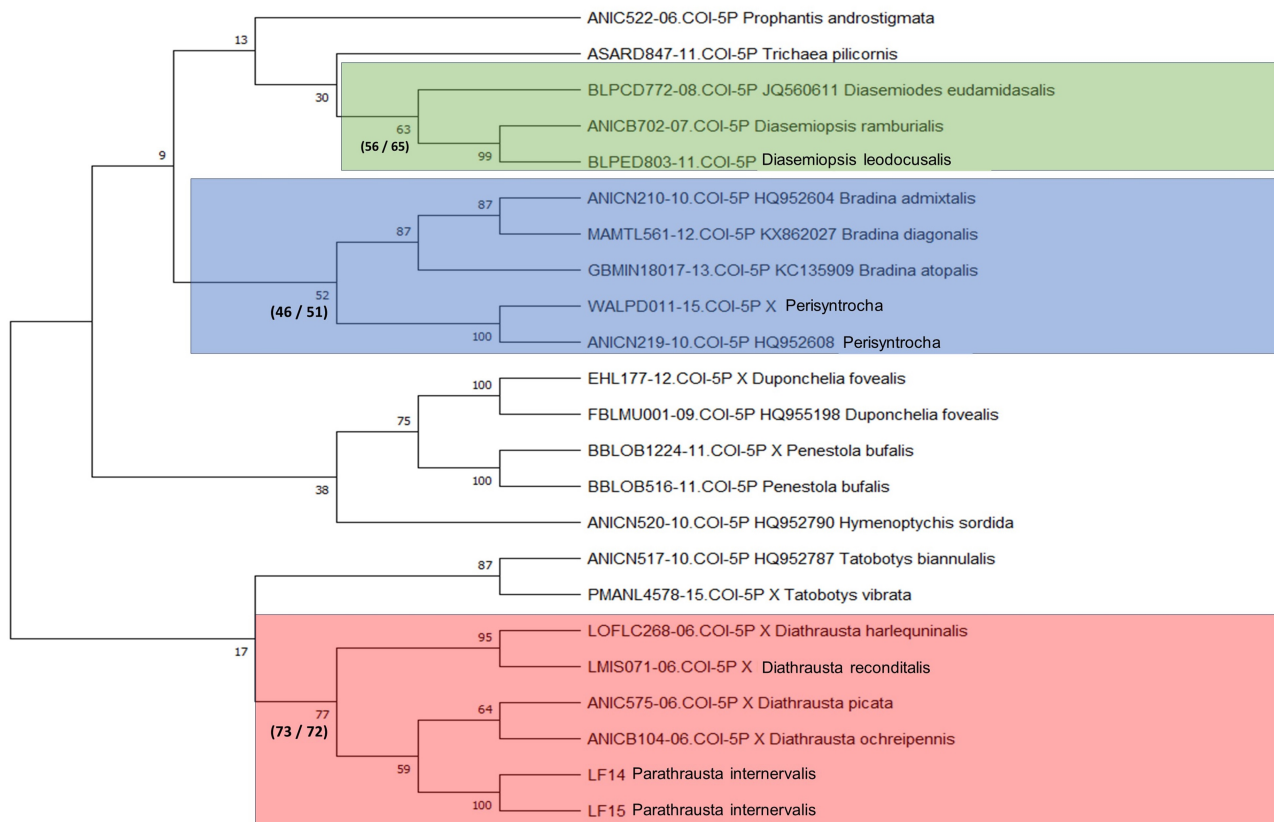


Figure 4. Phylogenetic hypothesis on the placement of the new genus, inferred from ML-Bootstrap Consensus Tree. The values on the branches are the BS values. The BS values from the MP- and NJ Bootstrap Consensus Trees for the clades Parathrausta + Diathrausta, Bradina + Perisyntrocha, Diasemiodes + Diasemiopsis are given in brackets below the ML-Bootstrap values.

Table 2. Average genetic distances between the genera/genus groups based on the Tamura-Nei distance model.

	Outgroup	Bradina	Duponchelia-group	Diathrausta	Perisyntrocha	Diasemiodes + Diasemiopsis	Parathrausta
Bradina	0.09						
Duponchelia-group	0.10	0.10					
Diathrausta	0.10	0.11	0.12				
Perisyntrocha	0.10	0.09	0.13	0.12			
Diasemiodes + Diasemiopsis	0.08	0.09	0.11	0.10	0.11		
Parathrausta	0.69	0.68	0.69	0.65	0.73	0.67	

Table 3. Average genetic distances within the genera/genus groups.

outgroup	0.08
Bradina	0.05
Duponchelia group	0.1
Diathrausta	0.08
Perisyntrocha	0.02
Diasemiodes + Diasemiopsis	0.05
Parathrausta	0.01

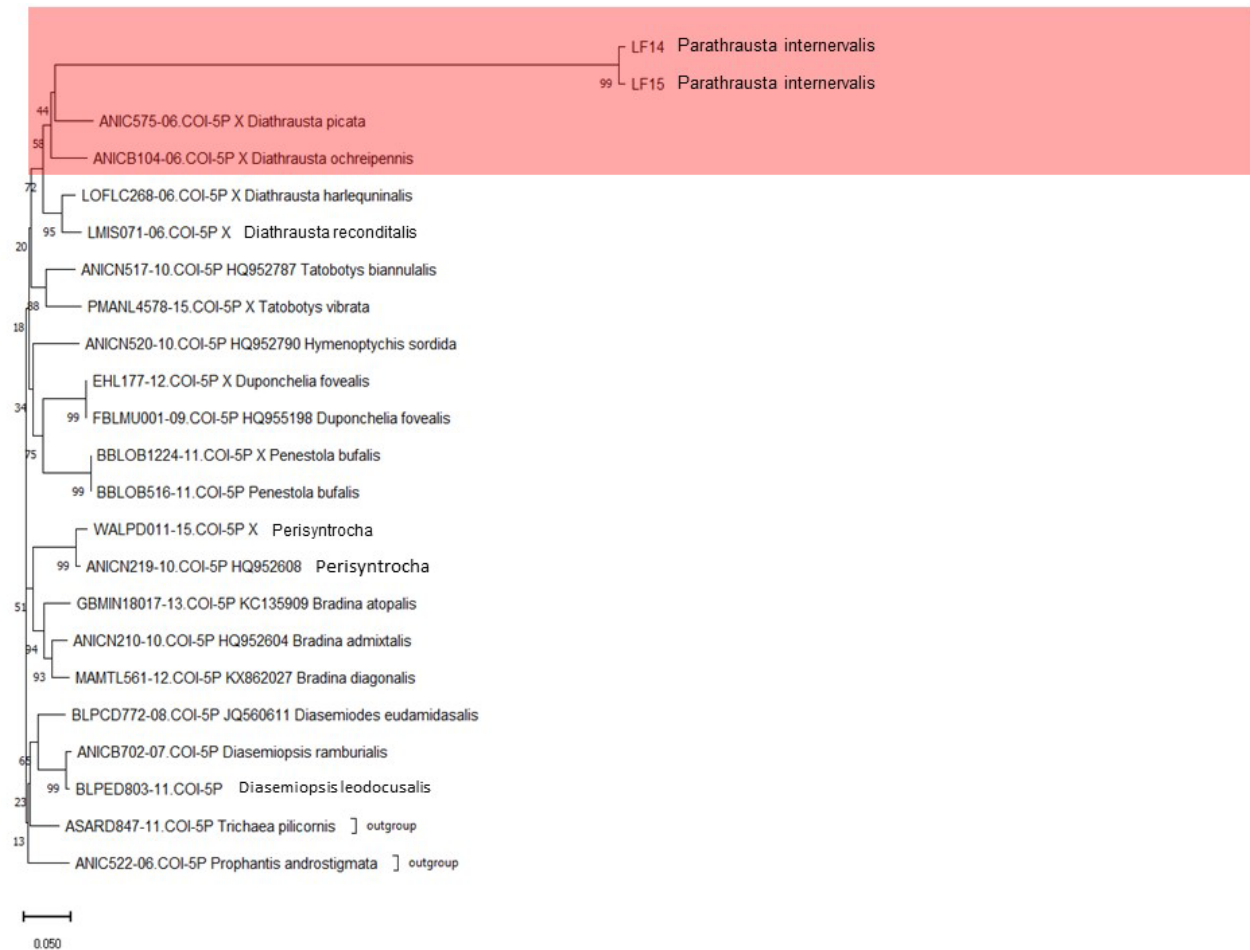


Figure 5. NJ-Tree, Original Tree showing the genetic divergence of the new genus from the morphologically related taxa. The BS values are given beside the branches.

In the MP-, ML- and NJ-bootstrap consensus trees inferred from the current dataset, the new genus appears as a sister of sub-clades under *Diathrausta*. The pertaining branch is substantially supported with BS values between 72 and 77. However, a clade formed by the genera related by the presence of an arch-shaped transversal signum cannot be confirmed by any of the analyses in the current dataset. These genera are distributed over several clades according to the present analysis: Weak to moderate branch support is given to *Diasemiopsis* + *Diasemiodes*, with BS values between 56 and 65. *Bradina* + *Perisyntrocha* is weakly supported, with BS values between 46 and 52.

Diversity and distribution: The genus is monotypical. The distribution is Afrotropical, at present only known from south-western Saudi Arabia.

Etymology: The generic name refers to the hypothetical cladistic position derived from the present dataset as sister to *Diathrausta*. It is composed of the prefix *para-* (greek: besides, next to) and the suffix *-thrausta*. The gender of the genus is feminine.

***Parathrausta internervalis* sp.n.**

Zoobank ID:

urn:lsid:zoobank.org:act:86CFDC11-1351-46A5-A721-E6E4CB74B321

Material: Holotype: ♀, Saudi Arabia, Prov. Jizan, Fayfa Mts., Al Kasha, 17°14'30.21"N, 43°3'40.00"E, 640 m, 22.-23.III.2923, slide no. 23GP042, leg. et prep. M. Seizmair, coll. ZSM. Paratypes: 2 ♂, 2 ♀, same collection data as for the holotype, slide no. 23GP032, 23GP043, 23GP053, 23GP054, leg., prep, coll. M. Seizmair.

External characters (Figure 1A, Figure 1B, Figure 1F): Wingspan: 12.2 mm - 13.2 mm. Length of forewing: 6.2 mm - 7.6 mm. Head: Antenna yellowish in the flagellum, ciliae greyish-white. Frons, vertex and tegula greyish-white. Basal scales of the proboscis yellowish. Labial palpus brownish scaled, sporadically interspersed with greyish scales, length relative to the diameter of the eye 60%. Maxillary palpus equal in length to one-fifth of the diameter of the eye. Thorax: Venter and dorsum grey scaled. Legs greyish-white scaled in the femur, tibia and tarsi yellowish-brown. Length of the inner relative to the outer metathoracic spurs 60%. Forewing double as long as broad, costal and dorsal borders straight. Apex acuminate, upturned. Termen medially concave. Tornus edged. Upper side ground yellowish-brown, bare from lines. Costal border interspersed with darkish brown scales over 3/4 of its length. Discocellular spot darkish-brown, claviform. Termen with darkish-brown interneural spots. Fringe darkish-brown. Underside with darkish-brown postmedial fasciae ranging from R5 to M3. Retinaculum bristle marked as a pad of elongate yellowish-grey hairs. Hindwing 1.2 times as long as broad, costal border straight, apex and tornus rounded. Upper side ground yellowish-grey, with darkish-brown postmedial fasciae ranging from Sc + R1 to M2. Termen with darkish-brown interneural spots ranging from M1 to 1A + 2A. No further maculation is present. The underside is identical to the upper side. Abdomen: elongate, dorsum greyish-white scaled, venter yellowish-grey in the female, dorsum yellowish-brown, venter yellowish-grey in the male.

Male genitalia: As for the genus.

Female genitalia: As for the genus.

Tympanal organs: As for the genus.

Bionomics: The type specimens were captured on grassy terraces interspersed with shrubs on the verge of a tropical rainforest. The premature stages, larval food plant and habitat choice are unknown at present.

Distribution: Currently known only from its type locality in south-western Saudi Arabia, near the Yemen border.

Etymology: The epitheton refers to one of the external character states of the species, namely the interneural spots in the fore- and hindwing termen.

4. Conclusions

In this paper a new monotypical genus *Parathrausta* **gen.n.** was erected with the type species *Parathrausta internervalis* **sp.n.**. The attribution of the material to a new genus in the subfamily Spilomelinae is phylogenetically strongly supported

by the unusually great genetic divergence of 0.65 from morphologically related genera in the *Duponchelia* group, *Bradina*, *Perisyntrocha*, *Diathrausta*, *Diasemiodes*, *Diasemiopsis*. The genetic divergence is seen to be in accordance with the morphological differences of the new genus from the comparative genera. These morphological differential characters were shown to be the anastomosing of the forewing R2, the number of fibulae, the shape and directedness of the fibulae, the shape of the saccus and of the costa. The medial connectedness of the tegumen arms and the presence of multi-furcate fibulae are valued as potential autapomorphies of the genus. Furthermore, the results of the present phylogenetic analyses are valued as a first indication of the placement of the new genus in the Nomophilini as a sister to *Diathrausta*. Morphological characters shared with *Diathrausta* are the lobar shape of the uncus and the strongly sclerotized antrum. However, a full understanding of the unusual genetic divergence of the haplotypes of the new genus from those of the morphologically related genera is not possible by the currently available data. Sequences of Afrotropical species of *Bradina*, *Diathrausta*, and *Diasemiopsis* are currently unavailable. In particular, the exceptionally strong genetic divergence from *Diathrausta* may be relativized when data from other parts of the genomes of the new genus and its relatives become known. The sister relation to *Diathrausta* may be in need of revision when molecular data of Afrotropical species become known.

Further study is necessary for understanding the relatedness of the new genus and the genera of the Nomophilini related by the transversal, arch-shaped signum. The latter character as a potential homology could not be supported by the presently available molecular genetic data.

Distribution, abundance, reproduction and ecology of the new genus are unknown at present and are subject to further research.

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Conflicts of Interest

The author declares no conflicts of interest regarding the publication of this paper.

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