A review of the genus *Mecistorhabdia* (Lepidoptera: Erebidae: Arctiinae: Syntomini) with a description of a new species from the Central African Republic

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**Abstract.** The genus *Mecistorhabdia* Kiriakoff, 1953 is reviewed and one new species *M. sulaki* sp. n. from the Central African Republic and Cameroon (Afrotropical region) described. The holotype female of the type species *M. haematoessa* (Holland, 1893) is matched with a conspecific male using a molecular technique. *M. burgessi* Kiriakoff, 1957 is removed from the synonymy as it is considered to be a valid species. Habitus and male genitalia of all three species are illustrated along with the female genitalia of *M. haematoessa*. A key for identification of species based on the structure of male genitalia and a map of their distribution are provided. The results of a study of the genetic diversity of the three species of *Mecistorhabdia*, based on cytochrome c oxidase subunit I gene, are presented. Relationships between species are briefly discussed.

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**INTRODUCTION**

For a long time the thyretines were thought to be a separate monophyletic lineage and treated as a separate family, the Thyretidae (Kiriakoff, 1949). Following morphological and molecular studies of the entire Noctuoidea it was downgraded to tribal rank by Jacobson & Weller (2002) and finally treated as a subtribe Thyretina of Syntomini (Zahiri et al., 2011). Recently a comprehensive molecular study revealed that the Thyretina is not monophyletic and male genitalia structures as intraspecific variability. The same misinterpretation was repeated by Przybyłowicz et al., 2019. As a result, it was formally synonymized with Syntomini. The group was revised by Przybyłowicz (2009), but since then very few papers have been published. Among these, Durante & Potenza (2014) listed the species of the genus *Balacra* Hampson, 1914 recorded in Gabon and Durante & Zangrilli (2016) revised the subgenus *Daphaenisca* Kiriakoff, 1953 and described three new species.

Until recently the genus *Mecistorhabdia* included only a single valid species, *M. haematoessa*, which was originally placed by Holland (1893) in the genus *Metarctia* Walker, 1855. This species was described based on a single female without description of its reproductive organs. Kiriakoff (1953) revised the status of this taxon and proposed a new genus *Mecistorhabdia*. The diagnosis of the new genus was based on significant differences in the newly described male genitalia in comparison with the genus *Elsa* (now *Rhipidarctia* Kiriakoff, 1953) with which *Mecistorhabdia* was compared in the original description. He provided the description of male genitalia supplemented by rather schematic drawings, but did not describe the female genitalia. Later Kiriakoff (1957) described one additional species, *M. burgessi*, from Uganda based on a single male. This new taxon was subsequently synonymized with *M. haematoessa* by Przybyłowicz & Kühne (2008). These authors wrongly treated the small differences in colouration and male genitalia structures as intraspecific variability. The same misinterpretation was repeated by Przybyłowicz (2009) in his catalogue of Thyretini.

The study of type specimens of both taxa and additional material from adjacent territories has made it possible to study this genus in more detail and as a consequence to describe another new taxon. Using molecular techniques, we managed to associate correctly the female holotype of *M. haematoessa* with known males and prove the morphological distinctiveness of taxa by using molecular and morphological approach. We verify the distribution of species...
and provide high-quality illustrations of the reproductive organs enabling an easier separation of species.

MATERIALS AND METHODS

In this study we follow the systematic account of Przybyłowicz et al. (2019) for the higher taxonomic levels. Specimens of the genus Mecistorhabdia were collected in Uganda (July 2011 by Harald Sulak), Central African Republic (September 2000 by local collector) and Republic of the Congo (January to March 1997 by Viktor Siniaev and Vladimir Murzin) and stored in the MWM collection. Additional material from the RMCA and ISEAPAS collections was used for comparison.

The abdomens were removed and placed in cold 5% KOH solution overnight after which the abdominal cuticle was opened by a right lateral cut to the genitalia, which were removed and stained in Evans Blue. The aedeagus was pulled out caudally. Images of genitalia were taken using a Leica DFC450 camera.

Forewing length was measured from the base to the apex of the wings, parallel to the wing costa. Forewing width was measured perpendicularly from the costa to the tornus.

Morphological terms for genitalia are those used by Klots (1970).

Abbreviations: FW – forewing; GP – genitium slide; HW – hindwing; CMNH – Carnegie Museum of Natural History, Pittsburgh, USA; ISEAPAS – Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Kraków, Poland; NMUK – Natural History Museum, London, UK; RBINS – Royal Belgian Centre of Natural Sciences, Brussels, Belgium; RMCA – Royal Museum for Central Africa, Tervuren, Belgium; ZSM – Zoologisches Staatliches Museum, Munich, Germany.

Molecular analysis

Total genomic DNA was extracted from leg muscle tissue of dried specimens or specimens preserved in pure ethanol using the GeneMATRIX Bio-Trace DNA Purification kit (EURx, Poland, following the standard protocol for tissue). The cytochrome c oxidase subunit I gene (COI) was amplified by polymerase chain reaction (PCR) using the primers LCO1490 (5’-GGT CAA CAA ATC ATA AAG ATA TTG G-3’) and HCO2198 (5’-TAA ACT TCA GGG TGA CCA AAA AAT CA-3’) (Folmer et al., 1994). In case of failure of sequencing with these primers, additional PCR reactions were carried out to recover amplicons using primers ZBJ-ArtF1c (5’-AGA TAT TGG AAC WTT ATA TTT TAT TTG G-3’) and ZBJ-ArtR2c (5’-WAC TAA TCA ATT WCC AAA TCC TCC-3’) (Zeale et al., 2011). This combination was necessary with the old female holotype of M. haematoessa (specimen No. 18.4.6), which is more than 100 years older than the other material. If one of these reactions was successful, an effort was made to obtain a barcode compliant record (>650 bp) by amplifying shorter regions of COI. PCR were performed in 25 µl reaction volume using 2× Phanta Max Master Mix (Vazyme Biotech Co., Ltd, China), 10 mM dNTP Mix, 10 µM of each primer and 4 µl of the genomic DNA. The PCR profile consisted of an initial denaturation step at 94°C for 3 min, followed by 36 cycles at 94°C for 1 min, 48°C for 1 min, and 72°C for 2 min and a final extension step of 7 min at 72°C. Successful PCR products were purified using the GeneMATRIX PCR/DNA Clean-Up Purification kit (EURx, Poland, following the standard protocol) and sequenced in both directions. All sequences were deposited in GenBank under the accession numbers MN441758 and MN441760–MN441768 (Table 1). The sequence of Mecistorhabdia burgessi from the GenBank database was also included in the analysis (Accession Number MK158553). Arctica caja (Linnaeus, 1758) and Lithosia quadra (Linnaeus, 1758) in the tribe Arctiini and Lithosiini, respectively (both in subfamily Arctiinae), were chosen as outgroup for analysis and the sequences were also taken from the GenBank database (Accession Numbers: HM873709 and KJ547685, respectively).

The obtained nucleotide sequences were edited and assembled into contigs in CodonCode Aligner (CodonCode Corporation). Sequences were also checked for protein-coding frame shifts to detect pseudogenes using MEGA X (Kumar et al., 2018) and compared with sequences from GenBank using a BLAST search. Best-fit models for Bayesian (BI) and maximum likelihood (ML) analyses were calculated in MrModeltest (Nylander, 2004) using the Akaike information criterion (AIC). ML analyses were carried out in IQTree (Nguyen et al., 2015). Bootstrap support was calculated using 1000 replicates. BI analyses were performed in MrBayes (Ronquist & Huelsenbeck, 2003) with four independent runs, each having three heated and one cold chain. Analyses were run for 6 million generations with trees sampled every 1000 generations. The first 25% of each run was discarded as burn-in. Convergence among the runs was assessed using Tracer (Bambaut et al., 2018). All trees were visualized using FigTree with a midpoint rooting option (Rambaut & Drummond, 2012).

Pairwise sequence divergences were calculated separately for intraspecific as well as interspecific comparisons with MEGA X using Kimura’s two parameter (K2P) distance model. Species delimitation method Automatic Barcode Gap Discovery, ABGD (Puillandre et al., 2012), is an automatic procedure that considers the sequences as hypothetical species based on the barcoding gap. The model first calculates a range of prior intraspecific diver-

Table 1. Taxonomic information and GenBank COI accession numbers of the taxa included in this study. (*) indicates the female holotype of M. haematoessa.

| Species                  | Specimen        | Origin           | GenBank COI Acc. No. | References               |
|--------------------------|-----------------|------------------|----------------------|--------------------------|
| Mecistorhabdia haematoessa | 18.4.1          | Africa: Angola, Cuanza Prov. | MN441768            | This study               |
|                          | 18.4.2          | Africa: Cameroon, Mt. Cameroon | MN441764            | This study               |
|                          | 18.4.3          | Africa: Cameroon, Mt. Cameroon | MN441763            | This study               |
|                          | 18.4.4          | Africa: Cameroon, Mt. Cameroon | MN441765            | This study               |
|                          | 18.4.5          | Africa: Cameroon, Mt. Cameroon | MN441766            | This study               |
|                          | 18.4.6(*)       | Africa: Gabon, Ogooué River | MN441767            | This study               |
| Mecistorhabdia burgessi  | LN051           | Africa: Uganda, Kibale NP | MK158553            | Przybyłowicz et al., 2019 |
|                          | N126            | Africa: DR Congo, Salonga NP | MN44441762         | This study               |
|                          | C10_II          | Africa: Uganda, Kibale NP | MN441761            | This study               |
|                          | B10_1           | Africa: Uganda, Kibale NP | MN441760            | This study               |
| Mecistorhabdia sulaki    | 22.5            | Africa: Cameroon, Ebogo | MN441758            | This study               |
| Arctica caja             | aca             | Finland           | HM873709            | Unpublished              |
| Lithosia quadra          | Iqu             | South Korea: Jeju | KJ547685            | Lee et al. (unpubl.)     |
gence to obtain the maximum limit of the intraspecific diversity and then partitions the data on the basis of the first significant gap beyond this limit, which is a potential limit between intra- and interspecific diversity. The data set was submitted to the ABGD online website (https://wwwabi.snv.jussieu.fr/public/abgd/) and analysed using the following settings: P (prior intraspecific divergence) set from 0.001 (Pmin) to 0.08 (Pmax) and Steps set to 10; X (minimum relative gap width) set to 1; Nb bins (for distance distribution) set to 20 and Kimura (K80) model and TS/TV set to 2.0 were selected.

RESULTS

Genus Mecistorhabdia Kiriakoff, 1953

Kiriakoff, 1953: 29; Przybyłowicz, 2009: 16, 56.

Type species: Metarctica haematoessa Holland, 1893: 396 (original designation).

Mecistorhabdia haematoessa (Holland, 1893)

(Figs 1, 2, 7, 8, 9, 12, 13, 15)

Metarctica haematoessa Holland, 1893: 396.
Mecistorhabdia haematoessa (Holland, 1893): Kiriakoff, 1953: 29; 1957: 97; Przybyłowicz & Kühne, 2008: 150; Przybyłowicz, 2009: 56.

Diagnosis. Habitus is quite similar to M. burgessi but distinctly differs from it in the male having a larger wing-span – 30–35 mm and 28–30 mm respectively. The structure of male genitalia should be used for safe identification, so in contrast to M. burgessi costal process of valva C-curved, the length of saccular process of valva is longer or equal in length to costal process. Vesica bears minute but distinct cornutus. It is also noteworthy that the coloura-
tion of *M. haematoessa* is much less orange than that of *M. burgessi.*

**Male** (Fig. 2). Wingspan: 30–35 mm; FW length: 18 mm, width: 8 mm, ratio 2.3:1; HW length: 11 mm, width: 7 mm, ratio 1.6:1. Antenna bipectinate, bright yellow. Head and patagia pale brown, tegula, thorax covered by dirty orange and yellow elongate scales. Abdomen dorsally light orange, ventrally pale brown. Forewing pale orange grey, with pale orange costal margin and blurs of dark yellow scales on postbasal, discal, postdiscal areas. Marginal edge of forewing mainly yellow. Hindwing pale-yellow.

**Female** (Fig. 1). Wingspan: 40–45 mm; FW length: 25 mm, width: 12 mm, ratio 2.1:1; HW length: 11 mm, width: 9 mm, ratio 1.2:1. Antenna bipectinate, yellow. Head, patagia and thorax covered with elongate grey scales. Abdomen dorsally dirty orange. Forewing grey with inclusions of dirty orange scales on costal margin and discal area; basal area bears two distinct dirty orange spots, post basal area has three dirty orange spots. Marginal edge of forewing mainly grey. Hindwing dark yellow.

**Male genitalia** (Figs 7, 9). Uncus coracoid shaped, extended in medial part; dorsally and laterally covered by elongate setae. Tagmen ribbon-shaped. Valvae symmetrical, divided in to two elongated and slightly curved processes: saccular process, which are the same length or longer than the costal process, covered by setae abdominally; costal process narrows towards top, dorsal edge and tip covered by elongate setae. At the base valvae bear basal appendage, which is almost half the size of costal process, curved dorsally and tip well covered with sclerotized elongate setae. Juxta well developed, almost X-shaped. Saccus rounded at top. Aedeagus tubular, narrow in basal part. Vesica divided in to two lobes – elongate dorsal with field of small sclerotizations on the base and an abdominal one with one or two small cornuti.

**Female genitalia** (Fig. 8). Papillae anales rounded and covered with setae; apophyses posteriors well developed; VIII segment strongly connected with vaginal plate, which is well developed and forms two bumps on the side of ostium; apophyses anteriores very small, almost three times shorter than apophyses posterior; corpus bursae oviform shape; ductus bursae, ductus seminalis and corpus bursae not sclerotized, without signum.

**Type material examined.** Holotype ♀, Gabon, Valley of the Ogooué River, Fangwé, leg. A.C. Good (Africa) [CMNH] (genitalia rotten).

**Other material examined.** Cameroon. 5♂, Mt Cameroon, SW slope, Elephant Camp, 1850 m, N 4.1453330 E 9.0870000, 2017-02-17, leg. P. Potocky, R. Tropek, J. Mertens, S. Janecek [NECUJ]; 1♂, Mt Cameroon, SW slope, Planty Camp, 1100 m, N 4.1175000 E 9.0709440, 2016-01-29, leg. V. Maicher, Sz. Safian, S. Janecek, R. Tropek, [NECUJ]; 1♂ as above but 2016-01-31; 1♂ as above but 2016-02-03, 1♀, RTE. Edea-Douala 12-1991, Th. Bouyer, NI GP 0.006 [RMCA], 1♂, Mann’s Spring 13.02.1989, 1800 m, trap on Dr Edwards, tree plot. Montane forest dom, trees Schefflera Nuxia ground vegetation Piper. NI GP 0.007 [RMCA], 1♂, as above but NI GP 0.008 [RMCA], 1♂, Zamakoé res. For. 4/5-7-1992, Th. Bouyer NI GP 0.011 [RMCA]. DR Congo. 1♂, Uele, Paulis, 1959.10.20, [RMCA], 1♂, as above but VII.1958, leg. Dr M. Fontaine, NI GP 0.002 [RMCA], 1♂, as above but 3.IV.1960, NI GP 0.004 [RMCA]. 1♀, as above but 1.XII.1956, 1♀, as above but 30.VII.1959, 1♀, as above but V-1957, NI GP 0.009 [RMCA]. 1♀, Eala X-1935, leg. J. Chesnérière NI GP 0.010 [RMCA]. Congo. 1♂, Lefini reserve bivallations near Mpo, 1964-01-10, leg. Endrody-Younga, [ISEAPAS]. 1♀, Odzala Nat. Park., H: 400–500 m, 0°23´N, 14°50´E, 29.01–03.03.1997, leg. Sinaev & Murzin. GP No. 36.294 [RMCA]. 1♀, Eala X-1935, leg. J. Chesnérière NI GP 0.010 [RMCA].

**Type locality.** Gabon, Valley of the Ogooué River, Lambarene.

**Distribution** (Fig. 12). Cameroon, Equatorial Guinea, Gabon, Republic of the Congo, Democratic Republic of the Congo, Angola.

**Remarks.** *M. haematoessa* was described based on a single female specimen. Unfortunately, genitalia of holo-
type specimen are destroyed so it is not possible to complete the analysis. Detection of a new taxon with unknown females sympatrically distributed with *haematoessa* raised the question about the real identity of the sexes ascribed until now to already known taxa. Due to the overall similarity of all three *Mecistorhabdia* species, scarcity of females and significant difference in size between males and females it was not obvious if the female type of *haematoessa* should be associated with the male morphotypes proposed by Kiriakoff (1953) or with those of the newly discovered new taxon. The only reliable and convincing answer for this question was the analysis and comparison of molecular characters of both male morphotypes and the female holotype of *M. haematoessa*.

**Mecistorhabdia burgessi** Kiriakoff, 1957, sp. rev.
(Figs 3, 10, 12, 13, 15)

*Mecistorhabdia burgessi* Kiriakoff, 1957: 96.
Mecistorhabdia burgessi Kiriakoff, 1957; Przybyłowicz & Kühne 2008: 150; Przybyłowicz 2009: 56.

Diagnosis. This species differs from others in external view of adult, which has a more intensive orange and dark-grey colouration on forewing and pale orange hindwing. Specimens of this species are frequently mixed together with M. haematoessa in collections of Lepidoptera. It differs from the latter taxon by smaller wingspan of male – 28–30 mm compared to 30–35 mm in M. haematoessa. The structure of male genitalia should be used for safe identification, so in contrast to M. haematoessa saccular process of valvae is distinctly shorter than costal process and vesica has no distinct cornutus (only tiny sclerotizations). It should also be noted that the costal process of valvae is almost straight in comparison with those of M. haematoessa. We removed the taxon burgessi from the synonymy of M. haematoessa in view of the distinct differences in structures of male genitalia.

Male (Figs 3, 4). Antenna bipectinate, bright yellow. Head and patagia dark brown, tegula, thorax covered by dirty orange and brown elongate scales. Abdomen dorsally dirty orange, ventrally pale brown. Wingspan 28–30 mm. Forewing dirty orange dark-grey, with intense orange costal margin and blurs of orange scales on postbasal, discal, postdiscal areas. Marginal edge of forewing mainly dirty orange. Hindwing pale-orange with grey scales on marginal edge.

Female. Unknown.

Male genitalia (Fig. 10). Uncus of coracid shape, extended in medial part; dorsally and laterally covered by elongate scales. Tegumen ribbon-shaped. Valvae symmetrical, divided into two elongated and slightly curved processes: saccular process, which is distinctly shorter than costal process, slightly curved, covered by setae abdominally; costal process narrows towards top, dorsal edge and tip covered by elongate setae. At the base valvae bear a basal appendage, which is almost half the size of costal process, curved dorsally and tip well covered with sclerotized elongate setae. Juxta well developed, almost X-shaped. Saccus rounded at top. Aedeagus tubular, narrows towards top. Vesica divided in to two lobes – elongated abdomen with field of tiny scrobilations at the base and laterally, which is much shorter and without cornuti.

Type material examined. Holotype: ♂, S.W. Uganda, Kigezi Distr., Impenetrable Forest, Kanungu, 4500 ft., May 1952 (J.A. Burgess) [NHMUK].

Other material examined. Uganda. 1♂, Kalinzu Forest, [..]65.01.7–10, leg. J. Scheven, [ZSM]; 1♂, Kibale Forest NP., Makerere Univ. Field Station, 1590 m, 0°34´11”N 30°22´29”E,
Mecistorhabdia sulaki sp. n.

(Figs 5, 6, 11, 12, 13, 15)

ZooBank taxon LSID: 4DA10EF3-74D9-42B6-BF5A-80B506BD1D0A

**Diagnosis.** This species differs from others in its smaller size – wingspan 27 mm, colouration of the forewing, which is distinctly brighter. The structure of male genitalia should be used for safe identification, because in contrast to *M. haematoessa* and *M. burgessi* the valvae have no basal appendage, basal part of the aedeagus is distinctly narrow, vesica has one area of tiny sclerotizations and two flattened round cornuti.

**Male** (Figs 5, 6). Antenna bipectinate, bright yellow. Head, patagia and thorax covered by dirty orange elongate scales. Abdomen dorsally orange, with elongate pale-yellow scales on tip. Wingspan 23–27 mm. Forewing bright orange yellow with deep orange costal margin and blurs of grey scales on postbasal, discal and postdiscal areas. Marginal edge of forewing mainly yellow. Hindwing pale-yellow.

**Female.** Unknown.

**Male genitalia** (Fig. 11). Uncus apparently extends to middle part and bears a small sharpened appendage on the tip; dorsally and laterally covered by elongate scales. Tegumen ribbon-shaped. Valvae symmetrical, divided in two elongated and slightly curved processes: costal process long, slightly extended, rounded and bears setae on distal part; saccular process half the length of costal process, with slightly rounded tip, ventrally covered by elongate setae. Juxta well developed and elongated. Saccus with rounded top. Aedeagus tubular, narrows and slightly curved basal part. Vesica divided in two lobes – elongate dorsal with area of minute sclerotizations and abdominal with two flat rounded cornuti.

**Type material.** Holotype ♂, Africa, Central African Republic, Bangui N 4°20' / E 18°32', 20 Sept. 2000, 350 m, leg. local collector, ex coll. Th. Greifenstein, Thomas Witt Stiftung, GP No. 26.861 [MWM]. Paratypes (4♂): 1♂, Cameroun: Nyazanga, 5/8-09-1992, Th. Bouyer, NI GP 0.005 [RMCA]; 2♂, Africa, Central African Republic, Bangui, N 4°20' / E 18°32', 20 Sept. 2000, 350 m, leg. local collector, ex coll. Th. Greifenstein, Thomas Witt Stiftung [MWM]; 1♂, Cameroun, Ebogo, 04.IV–16.IV.2013, Piotr Kowalski leg. [ISEAPAS].

**Type locality.** SW Uganda, Kanungu.

**Distribution** (Fig. 12). Democratic Republic of the Congo, Uganda, Kenya, Tanzania.
Results of molecular studies

There were no indels and stop codons in the 613 bp of COI. The MrModeltest indicated that the SYM + G (gamma distribution shape parameter G = 0.7231) as the best model of DNA substitution. The phylogenetic trees calculated using different methods had identical topologies, so only the Bayesian tree is shown (Fig. 13). The Bayesian posterior probability values for the nodes were generally higher than the bootstrap values. In the genus Mecistorhabdia species were clearly separated and formed a monophyletic group. The phylogenetic analysis divided the genus into three lineages in which Mecistorhabdia sulaki was a sister species to M. haematoessa + M. burgessi.

The K2P distances of the COI gene (barcoding region) between different Mecistorhabdia specimens ranged from 0 to 6% (Table 2). The maximum distance between the specimens of M. haematoessa was 0.3%. The oldest representative of M. haematoessa (the female holotype, specimen No. 18.4.6) was similar to the rest of the specimens of this species. The genetic divergence values between specimens of M. burgessi ranged from 0 to 0.99%. Average distance between M. burgessi and M. sulaki included in the analysis was 6%.

The ABGD method revealed gap between intra- and interspecific distance variation in the barcoding (Fig. 14). Hence, ABGD tree also clustered the COI sequences into three Mecistorhabdia groups (putative species) (Fig. 15), which are congruent with the phylogenetic tree (Fig. 13).

DISCUSSION

Mecistorhabdia is one of the smallest genera of Synthomini. However, the thorough investigation based on both morphological and molecular characters revealed hidden diversity within until now a monotypic genus. The previous study of the single types of M. haematoessa (female) and M. burgessi (male) led to the incorrect assumption that they represent a single taxon (Przybyłowicz & Kühne, 2008). This was due to the uniformity of both taxa in terms of pattern, colouration and male genitalia.

It is likely that careful reexamination of material (both existing in collections and new) of several other monotypic genera of Arctiinae from a wide area, including a morphogenetic analysis, would reveal the existence of further undescribed taxa. Such discoveries are already reported for Cacoethes Hübner, 1816 (de Freina, 2014) and Neophemula Kiriakoff, 1957 (Ochs, 2017).

Our study once again proves that old museum material can be used in molecular procedures to solve long-lasting taxonomic problems such as matching opposite sexes, detecting the molecular characters of unique types or ascribing incomplete types to particular taxa (Strutzenberger et al., 2012; Prosser et al., 2016). This last aspect is especially important when the genitalia are damaged due to mechanical (crushing, tearing) or biological (fungi, pests) factors. In such cases, COI sequences can be extracted from even small fragments of highly degraded DNA and provide crucial information on the taxonomic identity of the specimen analyzed.

Based on the above taxonomic treatment further studies can now be carried out on the genus Mecistorhabdia. In terms of morphology future studies should concentrate on collecting the so far undiscovered females of M. burgessi and M. sulaki. This fresh material will help in defining the distributions of the sympatric M. haematoessa and M. sulaki. The question of the intraspecific genetic variation of each species should be studied using freshly collected

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**Fig. 15.** Neighbour-joining phylogenetic tree showing the groups (hypothetical species) revealed by the ABGD analysis. (*) indicates the female holotype of M. haematoessa.
specimens. *M. burgessi* seems to be the typical representative of an East African fauna with the western border of its range in Ruwenzori Mountains. However, this hypothesis should be confirmed by extensive collecting in the eastern part of the Congo basin.

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