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African bats in the collection of the National Museum, Prague (Chiroptera). III. Bats from Kenya in the collections of the Natural History Museum, Vienna, and National Museum, Prague

Petr BENDA[1,2], Friederike SPITZENBERGER[3], Marek UVIZL[1,2],
Peter VALLO[4] & Jaroslav ČERVENÝ[5]

[1] Department of Zoology, National Museum (Natural History), Václavské nám. 68,
CZ–115 79 Praha 1, Czech Republic; petr.benda@nm.cz
[2] Department of Zoology, Faculty of Science, Charles University in Prague, Viničná 7,
CZ–128 44 Praha 2, Czech Republic
[3] BatLife Österreich, Wien, Austria
[4] Institute of Vertebrate Biology, Czech Academy of Sciences, Květná 8, CZ–603 65 Brno, Czech Republic
[5] Department of Game Management and Wildlife Biology, Czech University of Life Sciences,
Kamýcká 1176, CZ–165 21 Praha 6, Czech Republic

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Abstract. A list of 711 specimens of bats belonging to 55 species of 11 families originating from Kenya, housed in the collections of the Natural History Museum, Vienna, Austria (494 specimens / 39 species / 9 families), and the National Museum, Prague, Czech Republic (217 / 34 / 9), is presented in a systematic review. The species lists are complemented by comments on distribution, morphometric data, and in some species, also on the phylogenetic affinities. The specimens originate from 64 localities that cover almost completely the territory of Kenya (33 NMW localities, 35 NMP localities) and represent 188 new records (species vs. locality). The NMP collection contains one species new for the Kenyan fauna confirmed by the molecular genetic approach, *Neoromicia capensis*, and the bat fauna of Kenya now comprises 110 species in total. In *Cardioderma cor*, *Coleura afra*, *Platymops setiger*, *Vansonia rueppellii*, *Neoromicia zuluensis*, *Pseudoromicia nyanza*, *Afropipistrellus grandidieri*, *Scotophilus nux*, and *Miniopterus mossambicus*, the collection specimens represent significant distribution records, making their occurrence ranges in Kenya more precise. A discrepancy between the morphotype and genotype was observed in the genus *Epomophorus*; three species of this genus were identified based on their morphological traits, while their mtDNA sequences only partly agreed with this identification, and showed presence of the genome of *E. gambianus* in Kenya, where it was not identified by the morphological approach. These results suggest broad sharing of the mitochondrial genome among fruit bat species. The morphometric comparisons of *Rhinolophus acrotis* from Kenya revealed an extraordinarily small-sized morphotype of its Mount Elgon populations. However, this morphotype seems to represent just a local montane ecomorph without taxonomic relevance. Syntopic occurrence of deeply separated mitochondrial lineages of *Coleura afra* (genetic distances 3.4–3.8%) suggests rather a complex phylogenetic history of the species than a taxonomic relevance of this lineage separation. The sequence obtained from the Kenyan *Taphozous perforatus* did not differ substantially from the haplotypes of this species available from other populations from Africa and the Middle East, all samples created a single lineage. This result shows the formerly suggested separate taxonomic position of *T. perforatus* populations from eastern Africa to be unjustified, and thus, we suggest the name *haedinus* Thomas to be considered a junior synonym of *perforatus* Geoffroy. The sequences of *Taphozous*

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hildegardeae, evaluated for the first time, represented a single lineage that formed a separated branch within the genus *Taphozous*, in a sister position to the lineage comprising the Oriental *T. melanopogon*. The taxonomic assessment of the populations of the *Scotophilus dinganii* morphotype of eastern Africa, assigned to two separate species, *S. andrewreborii* and *S. ejetai*, did not corroborate such division. We suggest the prior name *Scotophilus colias* to be used for these populations and the names *andrewreborii* Brooks et Bickham and *ejetai* Brooks et Bickham to be considered junior synonyms of *colias* Thomas. The revision of the type locality of *Miniopterus minor* Peters, 1867 indicates that it lies on Zanzibar Island instead of the Zanzibar Coast of mainland Tanzania, as it was mentioned previously.

Key words. Museum collection, catalogue, bats, distribution, taxonomy, East Africa, Afrotropics.

INTRODUCTION

Kenya is a large country of East Africa (580,367 square kilometres) situated astride the equator. It contains geographically, geologically, and ecologically very diverse environments, such as the coastal plains along the Indian Ocean in the east that are covered by a mosaic of humid coastal forests, high plateaus covered mainly by various shapes of the Somali-Masai savanna, and by a patchwork of rainforest-savanna habitats in the west, as well as islands of high mountains with Afromontane forests, the dominant geological feature is the Great Rift Valley with its lakes which crosses the country from north to south (Burgess et al. 2004, Happold & Lock 2013). In comparison with the faunas of many other African countries, the bat fauna of Kenya is well known and studied for a long time. Already Harrison (1961) mentioned 74 species of bats from this country, Aggundey & Schlitter (1984) listed 95 species, and recently, at the time of immense taxonomic changes in the African mammal fauna, Monadjem et al. (2024) reported the occurrence of 109 bat species from Kenya (Table 1).

Bat specimens from Kenya are scattered over many collections; Aggundey & Schlitter (1984) extracted data on bats from 15 museum collections throughout Europe and North America, plus from the National Museum of Kenya, Nairobi, Van Cakenberghe & Seamark

Table 1. Composition of the bat fauna of Kenya according to four subsequent reviews and species composition of the bat collections of the Natural History Museum, Vienna (NMW) and National Museum, Prague (NMP)

family	Harrison 1961	Aggundey & Schlitter 1984	Musila et. al. 2019	Monadjem et al. 2024	NMW+NMP
Pteropodidae	9	11	10	10	7
Rhinopomatidae	1	1	1	1	1
Megadermatidae	2	2	2	2	2
Rhinolophidae	6	7	7	7	5
Rhinonycteridae	2	2	2	3	1
Hipposideridae	5	6	7	8	6
Emballonuridae	5	7	7	7	3
Nycteridae	6	6	7	7	2
Molossidae	10	14	19	19	6
Vespertilionidae	25	34	36	39	18
Miniopteridae	3	5	6	6	4
total	74	95	104	109	55

(2022) listed 16,022 specimens of Kenyan bats in total, scattered over 55 collections. The most diverse material and presumably also the richest in specimens of Kenyan bats, ordered by the species diversity, are the collections housed in the Royal Ontario Museum (Toronto, Canada), Field Museum of Natural History (Chicago, USA), Natural History Museum (London, UK), Smithsonian National Museum of Natural History (Washington, USA), National Museum of Kenya (Nairobi, Kenya), Museum of Comparative Zoology, Harvard University (Cambridge, USA), American Museum of Natural History (New York, USA), and Museum and Research Institute Senckenberg (Frankfurt am Main, Germany). Of this material, Monadjem et al. (2024)

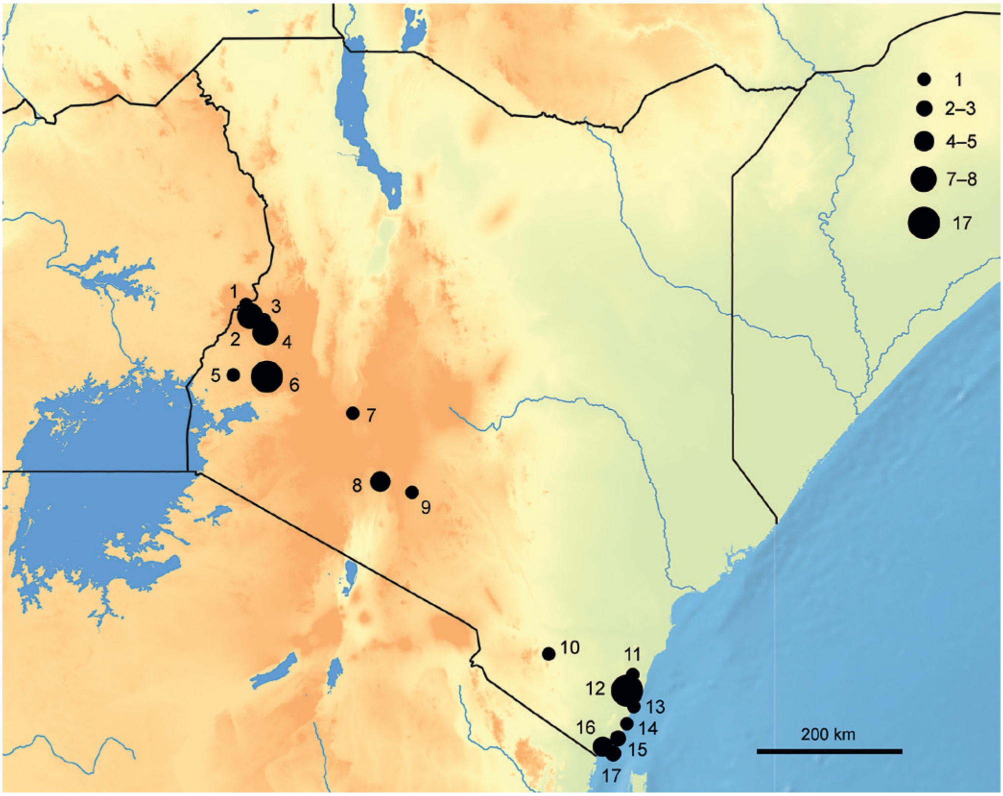


Fig. 1. Map of Kenya with the localities of recorded bat specimens housed in the collection of the Natural History Museum, Vienna, Austria (NMW); the size of the circle corresponds with the number of species collected (see legend in top right corner of the map), some circles represent more than one locality (total number of localities is 33). Legend: 1 – Mount Elgon Reserve North, Khybe Sawmill Cave, 2 – Mount Elgon NP, caves and Rongai Camp, 3 – Saboti, Kapkulkul Caves, 4 – Kiminini, caves, 5 – Sabatia, 6 – North Nandi Forest, Chomisia, 7 – Nakuru, Menengai Caves, 8 – Suswa, Suswa Cave, 9 – Nairobi, 10 – Tsavo East NP, Voi Gate, 11 – Chasimba, 12 – Pangani, Belfry and Lwandani Caves, 13 – Mombasa, Shimola Tewa, 14 – Ukunda, Diani, 15 – Msambweni, Msambweni Caves, 16 – Shimoni, Main Well Cave, 17 – Shimoni, Road Side Cave.

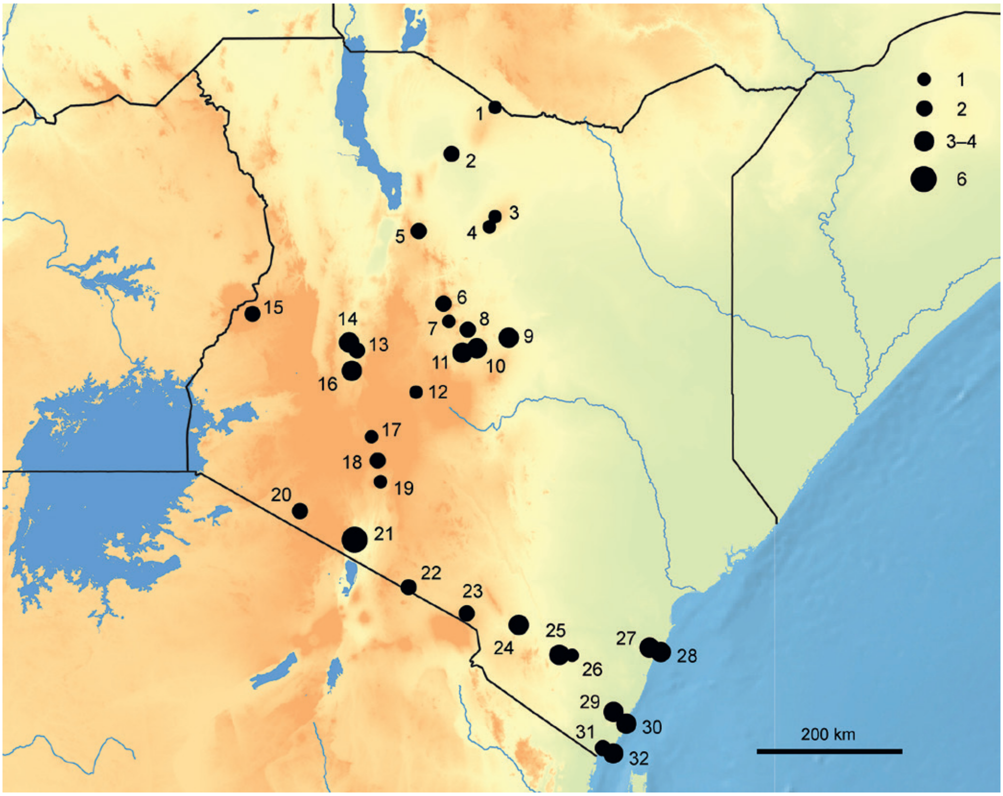


Fig. 2. Map of Kenya with the localities of recorded bat specimens housed in the collection of the National Museum, Prague, Czech Republic (NMP); the size of the circle corresponds with the number of species collected (see legend in top right corner of the map), some circles represent more than one locality (total number of localities is 35). Legend: 1 – Forolle, 2 – Kalacha, 3 – Marsabit NP, Gof Sokorete Gudha, 4 – Karare, 5 – South Horr, 6 – Engilae, 7 – Wamba, 8 – Ololokwe, 9 – Gotu Falls, 10 – Archers Post, Buffalo Springs Reserve, Simba Lodge, 11 – Archers Post, Samburu Reserve, King Lion Camp, 12 – Ol Pejeta, 13 – Lake Baringo, Lesukut Island, 14 – Kampi Ya Samaki, 15 – Mount Elgon NP, Rongai Camp, 16 – Loboi, 17 – Gilgil, 18 – Hells Gate NP, Naiburta Camp, 19 – Suswa, Suswa Cave, 20 – Ewangan, 21 – Ol Kirimatian, 22 – Namanga, 23 – Kimana, 24 – Tsavo West NP, Ngulia Lodge, 25 – Tsavo East NP, Sentrim Camp, 26 – Tsavo East NP, Aruba Ashnil Lodge, 27 – Watamu, Mida Creek Camp, 28 – Watamu, Kaboga Cave, 29 – Shimba Hills NP, Shimba Hills Lodge, 30 – Ukunda, Diani, 31 – Fikirini, Mbenyenye Cave, 32 – Shimoni, Slave Cave.

extracted more than 1,200 record localities of bats (species/site) from Kenya based either on museum specimens or on published sequences, both presumably with a revised species identification. Collections of bats from Kenya are also housed in the Natural History Museum, Vienna, Austria (NMW) and National Museum, Prague, Czech Republic (NMP), see Table 1. These two bat collections were created by different ways. The large bat collection of the NMW was gathered mainly during two expeditions focused on the south-western and south-eastern parts of the country made by the staff of the NMW mammal department between November 1979 and January 1980, and in January 1981, the collection contains also few additional bat specimens (<10) collected rather randomly by several donors of the NMW collection (in 1903 and 1978). The medium-sized collection of the Kenyan bats in the NMP comprises mostly specimens gathered by the staff and students of several academic institutions of the Czech Republic during various research projects focused on the diversity of small mammal fauna of East Africa (see e.g., Bryja et al. 2014, 2018, 2019, 2024, Mizerovská et al. 2019, etc.), and additionally by the staff and supporters of the NMP; the additions to the Kenyan bats have been made recently during several research trips in the period 2004–2023.

The NMW series of Kenyan bats contains 494 specimens belonging to 39 species of nine families. These bats originate from 33 localities situated mainly in the south-western and south-eastern corners of the country (Fig. 1) and represent 114 records (species vs. locality). A minority of these records were published briefly by Aggundey & Schlitter (1984), and in the case of fruit bats by Claessen & De Vree (1991) and Bergmans (1994, 1997), but most of the collection has remained unpublished. The NMP collection of bats from Kenya comprises 217 specimens representing 34 species of nine families. These specimens came from 35 localities covering almost the entire country (except the extreme north-west and a large part of the east, see Fig. 2) and gave 79 new records. Concerning the information potential, these collections, containing more than 700 specimens in total, have a certain value for zoological research and the knowledge of the East African bat fauna. In this catalogue, we describe the NMW and NMP collections of Kenyan bats mainly in the context of the most recent review of bats of sub-Saharan Africa by Monadjem et al. (2024). We intend this contribution as the third part of a catalogue series of African bats housed in the NMP collection (see Benda et al. 2022, 2023), this time in combination with a more extensive specimen set kept in the NMW collection.

METHODS

The lists of specimens from the collections of the Natural History Museum, Vienna, Austria (NMW) and National Museum, Prague, Czech Republic (NMP) are arranged in alphabetical order (according to the collection locality name) and then, in chronological order (according to collection date), for each species. The lists include, for each item, the following information: (1) indication of sex, (2) NMW / NMP collection ID, (3) preparation type (see Abbreviations below), (4) name of the locality (primarily listed by the name of the closest settlement, protected area, or notable physical feature), (5) date of collection, and (6) collector name/s. For names of the first-level administrative divisions and geographic coordinates of the localities see gazetteer (Appendix 1; in alphabetical order). The lists of specimens of particular species are complemented by a list of references reporting the particular specimen/s or the finding/s, and in some cases, also additional data concerning the specimens. The term East Africa is here used in its historical sense, covering the territories of the contemporary states of Uganda, Kenya, Rwanda, Burundi, and Tanzania. For other and not quite strict geographical meanings, we use the term 'eastern Africa'.

Basic biometric data taken from the NMW and NMP specimens are presented in Tables 2–12, and 14–23, only the data on adult specimens are included. The specimens were measured in a standard way with the use of mechanical calliper. Horizontal dental dimensions were taken on cingulum margins.

Molecular genetic examinations

Selected series of the NMP specimens were subjected to molecular genetic analyses, while the constitution of the NMW specimens did not allow their genetic examination. For details concerning DNA sequencing of particular African bat taxa see Vallo et al. (2008, 2013, 2015), Benda & Vallo (2012), Uvizl et al.

(2019), and Benda et al. (2022, 2023). Sequences were edited and aligned using the MAFFT plugin (Katoh & Standley 2013) in Geneious 11.0.5 (https://www.geneious.com), and subsequently manually edited. The sequences were translated to amino acids to check for the presence of stop codons, which would indicate pseudogenes have been amplified. Basic Local Alignment Search Tool (BLAST; Altschul et al. 1990) was used to search for the most related sequences and confirmed the species identification in some samples that were just tentative based on morphological examination. The GenBank Accession Numbers of the newly defined haplotypes are listed in Appendix 2. Sequences of comparative haplotypes of the family Emballonuridae and Hipposideridae were extracted from previously published studies (Goodman et al. 2006, 2012, Vallo et al. 2008, 2018, Ruedi et al. 2012, Çoraman et al. 2013, Monadjem et al. 2013a, Arai et al. 2019, Demos et al. 2019b, Lutz et al. 2019, Uvizl et al. 2019, Patterson et al. 2020, Furey et al. 2021, Benda et al. 2022, Wu et al. 2023).

Phylogenetic analyses were conducted using maximum likelihood (ML) based on the cytochrome *b* gene dataset. The most appropriate nucleotide substitution model (TVM+F+I+G4 for the family Emballonuridae, HKY+F+G4 for the genus *Epomophorus*, and TPM2u+F+G4 for the genus *Hipposideros*) was selected using the Bayesian information criterion (BIC) in ModelFinder (Kalyaanamoorthy et al. 2017). The ML tree was inferred with the selected substitution model using IQ-TREE (Nguyen et al. 2015). The best-scoring ML was identified through the use of the ultrafast bootstrap (UFBoot; Hoang et al. 2018), employing 1,000 bootstrap replicates and 1,000 topology replicates. The ML analysis was carried out on the IQtree web server (Trifinopoulos et al. 2016).

Abbreviations

Dimensions. LAt = forearm length; – LCr = greatest length of skull (including praemaxilla); – LOc = occipitocanine length; – LCb = condylobasal length; – LCc = condylocanine length; – LaZ = zygomatic width; – LaI = width of interorbital constriction; – LaP = width of postorbital constriction; – LaInf = infraorbital width; – LaN = neurocranium width; – LaM = mastoidal width; – ANc = neurocranium height; – LBT = largest horizontal length of tympanic bulla; – CC = rostral width between labial margins of canines; – M^1M^1 = rostral width between labial margins of first upper molars; – M^2M^2 = rostral width between labial margins of second upper molars; – M^3M^3 = rostral width between labial margins of third upper molars; – CM^1 = length of upper tooth-row between mesial margin of canine and distal margin of first molar; – CM^2 = length of upper tooth-row between mesial margin of canine and distal margin of second molar; – CM^3 = length of upper tooth-row between mesial margin of canine and distal margin of third molar; – LMd = condylar length of mandible; – ACo = height of coronoid process; – CM_2 = length of lower tooth-row between mesial margin of canine and distal margin of second molar; – CM_3 = length of lower tooth-row between mesial margin of canine and distal margin of third molar.

Collections. BCSU = Biological Collection, Sana'a University, Sana'a, Yemen; – BMNH = Natural History Museum, London, UK; – CM = Carnegie Museum, Pittsburgh, USA; – DM = Durban Natural Science Museum, Durban, South Africa; – FMNH = Field Museum of Natural History, Chicago, USA; – HNHM = Hungarian Natural History Museum, Budapest, Hungary; – HZM = Harrison Zoological Museum, Sevenoaks, UK; – MHNG = Natural History Museum, Geneva, Switzerland; – MNHN = National Museum of Natural History, Paris, France; – MSNG = Natural History Museum Giacomo Doria, Genoa, Italy; – MZUF = Natural History Museum, Zoology Section "La Specola", Florence, Italy; – NMB = National Museum, Bloemfontein, South Africa; – NMK = National Museum of Kenya, Nairobi, Kenya; – NMP = National Museum (Natural History), Prague, Czech Republic; – NMW = Natural History Museum, Vienna, Austria; – SMF = Museum and Research Institute Senckenberg, Frankfurt am Main, Germany; – TM = Ditsong National Museum of Natural History, Pretoria, South Africa; – ZFMK = Zoological Institute and Museum Alexander Koenig, Bonn, Germany; – ZMB = Natural History Museum, Humboldt University, Berlin, Germany; – ZMMU = Zoological Museum, Moscow State University, Moscow, Russia.

Others. A = alcohol specimen; – B = skin (balg); – leg. = legit [presented, bequeathed, sent]; – M = mean; – max., min. = dimension range margins; – NP = National Park; – S = skull; – SD = standard deviation; – Sk = skeleton.

ANNOTATED LIST OF SPECIMENS

Pteropodidae

***Eidolon helvum* (Kerr, 1792)**

NMW Material (1). 1 ♀ (NMW 50264 [S+B]), Sabatia, 24 May 1978, leg. H. Schifter.

Eidolon helvum is the most widespread fruit bat species of sub-Saharan Africa, it was recorded in all habitats and regions between Mauritania and Senegal in the west, the Sudan, Ethiopia and Kenya in the east, and South Africa and Mozambique in the south (Hayman & Hill 1971, Bergmans 1990, Thomas & Henry 2013). In East Africa, its occurrence is limited to the south-west of the region, the north-eastern limits of the distribution range of *E. helvum* go through central and south-eastern Kenya (Kingdon 1974, Bergmans 1990, Monadjem et al. 2024); around twenty localities of this bat are known from the southern part of the country (Bergmans 1990, Monadjem et al. 2024). The site Sabatia from where the NMW specimen originates, is among those already reported for *E. helvum* from Kenya (Kock 1978); it is situated ca. 45 km north-west of Nakuru (0°02'S, 35°45'E sensu Aggundey & Schlitter 1984). However, the NMW specimen originates rather from the city of Sabatia in the Kakamega County (00°14'N,

Table 2. Biometric data on the NMW and NMP specimens of *Eidolon helvum*, *Rhinopoma macinnesi*, *Hipposideros megalotis*, *Doryrhina cyclops*, *Nycteris macrotis*, and *Platymops setiger* from Kenya. For abbreviations see Methods

dimension	*Eidolon helvum*	*Rhinopoma macinnesi* 97912	*Rhinopoma macinnesi* 97913	*Hipposideros megalotis*	*Doryrhina cyclops*	*Nycteris macrotis* 32246	*Nycteris macrotis* 32247	*Platymops setiger*
LAt	123.4	50.5	48.9	38.1	71.1	47.3	42.4	32.4
LCr	53.35	16.82	15.99	–	–	21.16	18.96	–
LOc	–	16.35	15.55	14.63	30.37	21.15	18.82	–
LCb	51.61	15.18	14.36	–	–	18.83	16.68	–
LCc	–	14.42	13.73	12.64	26.08	18.54	16.48	–
LaZ	31.62	9.19	9.21	7.16	16.63	12.43	10.66	–
LaI	9.15	2.45	2.34	2.44	3.56	5.88	4.81	3.74
LaP	6.05	–	–	–	–	4.71	4.92	–
LaInf	12.05	4.49	4.41	3.83	9.18	5.38	4.63	4.38
LaN	21.33	6.92	6.84	6.56	12.28	9.37	8.32	–
LaM	–	8.35	8.27	7.43	13.07	9.08	8.02	–
ANc	15.02	5.58	5.33	4.88	9.24	7.74	6.61	–
LBT	–	4.53	4.14	3.47	4.08	3.68	2.98	–
CC	9.53	3.76	3.65	3.24	7.83	5.82	4.62	4.08
M^3M^3	–	6.77	6.94	4.97	11.67	8.35	6.92	7.08
CM^2	19.76	–	–	–	–	–	–	–
CM^3	–	5.48	5.08	4.67	10.67	7.46	6.47	5.88
LMd	42.21	10.78	10.33	8.58	19.88	13.93	11.88	11.79
ACo	18.75	3.92	3.66	2.34	6.02	4.94	3.78	4.37
CM_3	–	5.82	5.45	5.02	11.71	7.93	6.88	6.28

Table 3. Biometric data on the NMW and NMP specimens of *Rousettus aegyptiacus* and *Stenonycteris lanosus* from Kenya (only adult specimens are included). For abbreviations see Methods

dimension	*Rousettus aegyptiacus* (♂♂)					*Rousettus aegyptiacus* (♀♀)					*Stenonycteris lanosus* (♂♀)				
	n	**M**	min	max	SD	*n*	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*6*	**92.32**	86.3	96.1	3.600	*9*	**91.69**	88.2	96.0	2.829	*6*	**87.40**	86.4	90.5	1.553
LCr	*6*	**42.98**	41.91	44.82	1.009	*9*	**41.17**	40.02	42.93	1.103	*5*	**42.21**	41.34	43.31	0.706
LCb	*6*	**41.26**	39.47	43.02	1.245	*9*	**39.44**	38.43	41.43	1.020	*5*	**39.74**	39.06	40.94	0.718
LaZ	*6*	**26.50**	25.29	27.63	0.774	*9*	**24.89**	23.91	25.37	0.472	*6*	**24.35**	23.83	25.47	0.640
LaI	*6*	**8.22**	7.98	8.44	0.183	*9*	**7.92**	7.18	8.39	0.393	*6*	**7.69**	7.47	8.02	0.192
LaP	*6*	**8.34**	7.45	8.98	0.542	*9*	**8.59**	7.76	9.32	0.608	*6*	**9.72**	8.98	10.81	0.799
LaInf	*6*	**10.14**	9.68	10.72	0.459	*9*	**9.98**	9.52	10.67	0.355	*5*	**10.00**	9.54	10.35	0.301
LaN	*6*	**17.37**	16.86	17.88	0.417	*9*	**16.78**	15.53	17.48	0.617	*6*	**17.48**	16.83	18.02	0.454
LaM	*6*	**16.07**	15.53	16.53	0.440	*9*	**15.40**	14.65	15.92	0.441	*6*	**15.51**	15.04	15.81	0.274
ANc	*6*	**13.00**	12.35	13.66	0.452	*9*	**12.39**	11.67	12.91	0.372	*6*	**12.79**	12.34	13.60	0.445
LBT	*6*	**4.34**	4.08	4.65	0.184	*9*	**4.25**	3.93	4.59	0.229	*6*	**4.45**	4.20	4.74	0.211
CC	*6*	**8.85**	8.38	9.77	0.506	*9*	**8.37**	7.78	8.67	0.272	*6*	**8.67**	8.34	8.85	0.203
M^2M^2	*6*	**12.86**	11.88	13.97	0.768	*9*	**12.50**	12.08	12.78	0.213	*6*	**12.09**	11.78	12.38	0.221
CM^2	*6*	**16.46**	15.88	17.08	0.475	*9*	**15.83**	15.18	16.41	0.417	*6*	**14.58**	14.09	14.93	0.288
LMd	*6*	**33.80**	32.48	35.47	1.036	*9*	**32.27**	31.21	33.18	0.811	*6*	**31.83**	31.09	32.84	0.592
ACo	*6*	**13.92**	13.28	15.22	0.673	*9*	**13.51**	12.74	13.82	0.321	*6*	**11.48**	10.75	12.27	0.609
CM_3	*5*	**17.94**	17.27	18.63	0.558	*9*	**17.38**	16.64	18.31	0.556	*6*	**16.24**	15.48	16.68	0.455

34°31'E; 25 km WSW of Kakamega), still within the known range of this bat in Kenya. The dimensions of the NMW specimen of *E. helvum* from Kenya are shown in Table 2.

Rousettus aegyptiacus **(Geoffroy, 1810)**

NMW Material (18). 4 ♂♂, 3 ♀♀ (NMW 32164–32170 [S+B]), Chasimba, 13 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

4 ♂♂, 7 ♀♀ (NMW 32153–32163 [S+B]), Mount Elgon National Park, Kitum Cave, 25 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

NMP Material (2). 1 ♂, 1 ♀ (NMP 98062 [S+A], 98061 [A]), Mount Elgon National Park, Rongai Camp, 21 July 2010, leg. A. Konečný, J. S. Mbau & R. Šumbera.

References. Aggundey & Schlitter (1984), Bergmans (1994).

Rousettus aegyptiacus is the species with the most extensive distribution range among the African fruit bats, it covers almost the whole sub-Saharan Africa, except the most arid areas, from Senegal to northern Eritrea and eastern Ethiopia, and to south-western Angola and southernmost Cape, but also the north-eastern corner of Africa (Sudan, Egypt) and a large part of the Middle East and southern Pakistan (Hayman & Hill 1971, Bergmans 1994, Benda et al. 2011a, 2019, Monadjem et al. 2020, 2024). In East Africa, *R. aegyptiacus* is a frequent and widespread bat across most of the region, it is missingt only in southern and western Tanzania and north-eastern Kenya (Kulzer 1959, Kingdon 1974, Bergmans 1994, Monadjem et al. 2024). The NMW and NMP specimens originate from western and south-eastern Kenya, i.e., from the areas where this bat is common (Harrison 1961, Aggundey & Schlitter 1984, Bergmans 1994). Moreover, both localities and the NMW specimens were already published by Bergmans (1994). The dimensions of the adult NMW and NMP specimens of *R. aegyptiacus* are shown in Table 3.

Stenonycteris lanosus (Thomas, 1906)

NMW Material (8). 1 ♂, 2 ♀♀ (NMW 32171–32173 [S+B]), Mount Elgon National Park, Makingeny Cave, 26 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
3 ♂♂, 2 ♀♀ (NMW 32174–32178 [S+B]), Nakuru, Menengai Cave, 3 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Reference. Bergmans (1994).

Stenonycteris lanosus is an endemic of eastern Africa, its distribution range stretches from south-western Ethiopia and south-eastern South Sudan to eastern Tanzania, northern Malawi and eastern DR Congo (Bergmans 1994, Monadjem et al. 2024). In East Africa, the most abundant records are available from the areas adjacent to the Western Rift Valley of Uganda, Rwanda and DR Congo, while in Kenya just a few localities of *S. lanosus* are known only in the south-western quarter of the country (Aggundey & Schlitter 1984, Bergmans 1994), where also the NMW specimens were collected. The NMW specimens from both sites were mentioned by Bergmans (1994), although these localities were sampled for this bat previously, see the reviews by Aggundey & Schlitter (1984) and Bergmans (1994). The dimensions of the adult NMW specimens of *S. lanosus* are shown in Table 3.

Myonycteris angolensis (du Bocage, 1898)

NMW Material (23). 1 ♂, 4 ♀♀ (NMW 32187–32191 [S+B]), Kiminini, Chepkelele Cave, 31 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂, 3 ♀♀ (NMW 32179–32181 [S+B], 32182 [A]), Kiminini, Kipsiryori Cave, 29 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂, 1 ♀ (NMW 32185, 32186 [S+B]), Kiminini, Nabongo Cave, 30 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♀♀ (NMW 32183, 32184 [S+B]), Kiminini, Nyungu ya Mawe Cave, 30 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♀ (NMW 32686 [S+B]), North Nandi Forest, 3 km W of Chomisia, 22 November 1979, leg. F. Spitzenberger;
1 ♀ (NMW 32687 [S+B]), North Nandi Forest, 3 km W of Chomisia, 5 December 1979, leg. F. Spitzenberger;
1 ♂ (NMW 32192 [S+B]), Pangani, near the Lwandani Cave, 9 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂, 4 ♀♀ (NMW 32193–32197 [S+B]), Pangani, near the Lwandani Cave, 11 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♂♂ (NMW 32198, 32199 [S+B]), Pangani, near the Lwandani Cave, 12 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Reference. Bergmans (1997).

Myonycteris angolensis is a fruit bat widely distributed throughout the tropical zone of Africa, its range stretches across the forest belt from the Gambia and Guinea-Bissau to central Ethiopia, west-central Angola and central Mozambique (Hayman & Hill 1971, Bergmans 1997,

Table 4. Biometric data on the NMW and NMP specimens of *Myonycteris angolensis* and *Epomophorus wahlbergi* from Kenya (only adult specimens are included). For abbreviations see Methods

dimension	*Myonycteris angolensis* (♂♀)					*Epomophorus wahlbergi* (♂♂)					*Epomophorus wahlbergi* (♀♀)				
	n	**M**	min	max	SD	*n*	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*14*	**77.31**	74.9	79.8	1.345	*7*	**81.67**	79.0	84.5	2.107	*9*	**77.50**	73.7	80.7	2.487
LCr	*13*	**40.91**	39.43	42.74	0.893	*5*	**50.25**	49.35	51.42	0.811	*7*	**44.29**	43.18	45.28	0.749
LCb	*13*	**40.04**	38.61	41.91	0.884	*5*	**50.46**	49.45	51.81	0.891	*7*	**44.04**	43.12	44.97	0.689
LaZ	*14*	**24.07**	22.68	25.41	0.669	*6*	**26.68**	25.61	27.53	0.705	*6*	**24.61**	23.07	25.41	0.802
LaI	*14*	**6.67**	6.13	7.57	0.462	*6*	**8.70**	8.28	9.26	0.360	*7*	**7.90**	7.11	8.74	0.579
LaP	*14*	**7.72**	6.47	8.92	0.696	*5*	**9.59**	8.57	10.45	0.679	*7*	**9.28**	9.07	9.86	0.271
LaInf	*14*	**9.56**	8.93	10.41	0.406	*6*	**11.71**	10.98	12.67	0.593	*7*	**11.12**	10.83	11.68	0.306
LaN	*14*	**15.34**	14.28	16.38	0.506	*6*	**17.13**	16.56	17.68	0.468	*7*	**16.18**	15.44	16.57	0.388
LaM	*14*	**14.47**	13.88	15.09	0.341	*6*	**17.49**	16.96	18.44	0.542	*7*	**16.23**	15.54	17.02	0.454
ANc	*14*	**11.38**	10.74	11.83	0.342	*6*	**10.97**	10.48	11.31	0.316	*7*	**10.51**	10.09	10.73	0.225
LBT	*13*	**4.34**	3.88	4.67	0.212	*6*	**4.60**	4.42	4.89	0.167	*7*	**4.49**	4.41	4.58	0.058
CC	*14*	**8.00**	7.64	8.56	0.277	*6*	**10.14**	9.75	10.71	0.356	*7*	**9.01**	8.57	9.33	0.271
M^1M^1	–	–	–	–	–	*6*	**14.31**	13.87	14.98	0.534	*6*	**13.04**	12.45	13.53	0.379
M^2M^2	*12*	**12.86**	12.02	14.39	0.631	–	–	–	–	–	–	–	–	–	–
CM^1	–	–	–	–	–	*6*	**17.23**	16.75	17.84	0.437	*7*	**15.49**	14.73	16.17	0.514
CM^2	*13*	**15.57**	15.13	16.16	0.369	–	–	–	–	–	–	–	–	–	–
LMd	*14*	**32.02**	31.18	33.31	0.604	*6*	**40.13**	39.08	41.53	0.833	*7*	**34.73**	33.66	35.88	0.687
ACo	*14*	**13.64**	12.88	14.41	0.461	*6*	**16.53**	15.88	17.29	0.472	*7*	**14.58**	14.12	15.63	0.558
CM_2	–	–	–	–	–	*6*	**19.58**	18.79	20.88	0.782	*7*	**17.47**	16.72	18.36	0.566
CM_3	*13*	**17.18**	16.58	17.86	0.443	–	–	–	–	–	–	–	–	–	–

Monadjem et al. 2020, 2024). In East Africa, this bat is most abundant in the forested western parts of the region adjacent to the Western Rift Valley and to Lake Victoria, in Uganda, Rwanda and eastern DR Congo; in the eastern savanna parts of East Africa, patchily distributed records of *M. angolensis* are known from the northern part of Tanzania and from southern Kenya (Kingdon 1974, Bergmans 1997, Monadjem et al. 2024). The NMW specimens come from three localities of southern Kenya, in all of them this bat species was reported to occur already before: caves at Kiminini (Mount Elgon region), North Nandi Forest, and the Pangani caves near Mombasa (Aggundey & Schlitter 1984, Bergmans 1997). The NMW specimens from the Kiminini caves were mentioned by Bergmans (1997), and the forests near Kamamega and the Mount Elgon region are traditional sites of the *M. angolensis* collections (Harrison 1961, Aggundey & Schlitter 1984). The dimensions of the adult NMW specimens of *M. angolensis* are shown in Table 4.

Epomophorus wahlbergi (Sundevall, 1846)

NMW Material (5). 4 ♀♀ (NMW 53297–53300 [S+A]), Mombasa, Shimola Tewa, 3 April 1980, leg. K. Magnus;

1 ♀ (NMW 32689 [S+Sk+B]), North Nandi Forest, 4 km SW of Chomisia, 4 December 1979, leg. F. Spitzenberger.

NMP Material (24). 3 ♀♀ (NMP 97940 [A], 97941, 97942 [S]), Ewangan, Oldarpoi Camp, 8 December 2021, leg. P. Benda, L. Bufka & J. Červený;
2 ♂♂, 2 ♀♀ (NMP 97952, 97953 [S+A], 97954, 97955 [A]), Kimana, 18 August 2022, leg. P. Benda & J. Červený;
3 ♂♂, 1 ♀ (NMP 98023, 98024, 98026 [S+A], 98025 [A]), Kwale, Shimba Hills National Park, Shimba Hills Lodge, 4 July 2023, leg. P. Benda & J. Červený;
1 ♂, 1 ♀ (NMP 98057, 98058 [S+A]), Namanga, 27 June 2010, leg. J. Bryja, J. S. Mbau & R. Šumbera;
1 ♂ (NMP 97946 [A]), Ol Kirimatian, Nyiro River Camp, 16 August 2022, leg. P. Benda & J. Červený;
1 ♂, 1 ♀ (NMP 98034, 98035 [S+A]), Ukunda, Diani, Diani Marine Lodge, 6 July 2023, leg. P. Benda & J. Červený;
1 ♂, 3 ♀♀ (NMP 97969 [S+A], 97968, 97970, 97971 [A]), Ukunda, Diani, Leisure Lodge, 21 August 2022, leg. P. Benda & J. Červený;
1 ♀ (NMP 97990 [S+A]), Ukunda, Diani, Leisure Lodge, 23 August 2022, leg. P. Benda & J. Červený;
1 ♂, 2 ♀♀ (NMP 98005 [S+A], 98006, 98007 [A]), Watamu, Mida Creek Camp, 2 July 2023, leg. P. Benda & J. Červený.

Epomophorus wahlbergi is a widespread bat of the central and south-eastern parts of Africa, between Gabon, Uganda, and Somalia in the north, and Angola and southernmost Cape in the south (Hayman & Hill 1971, Bergmans 1988). It is one of the most common fruit bat species of East Africa and the most frequent fruit bat in Kenya, where it occurs only in the southern two

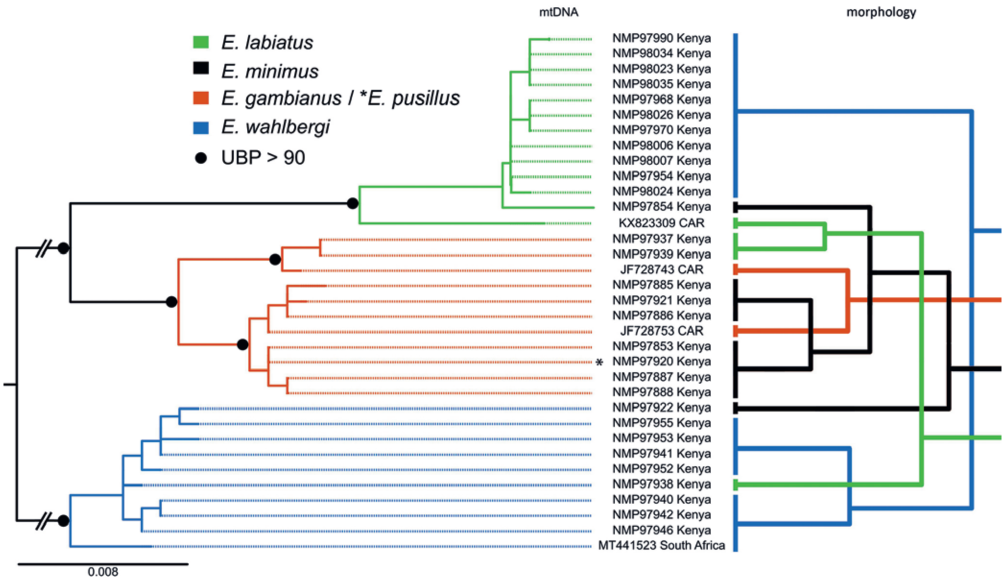


Fig. 3. Comparison of results from two approaches used for identification of the NMP specimens of the genus *Epomophorus* from Kenya. On the left, maximum likelihood tree depicting the phylogenetic relationships among specimens reconstructed using a cytochrome *b* dataset; black dots on the nodes indicate branch support values ≥90% UFBoot. On the right, cladograms of four *Epomophorus* species based on the morphological examinations of the specimens used in the genetic analysis.

Table 5. Biometric data on the NMW and NMP specimens of *Epomophorus labiatus* and *E. minimus* from Kenya (only adult specimens are included). For abbreviations see Methods

dimension	*Epomophorus labiatus* (♀♀)					*Epomophorus minimus* (♂♂)					*Epomophorus minimus* (♀♀)				
	n	**M**	min	max	SD	*n*	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*4*	**68.38**	66.5	70.3	1.565	*5*	**62.02**	61.0	64.1	1.355	*10*	**60.57**	57.6	63.1	1.745
LCr	2	**42.61**	42.44	42.78	0.240	*4*	**35.48**	35.08	35.74	0.301	*8*	**33.00**	30.98	34.45	1.115
LCb	*2*	**41.99**	41.84	42.14	0.212	*4*	**34.36**	33.77	34.75	0.416	*8*	**31.91**	29.72	33.22	1.130
LaZ	*3*	**21.74**	20.82	22.40	0.823	*4*	**19.95**	19.48	20.29	0.373	*9*	**19.03**	18.14	19.75	0.527
LaI	*3*	**6.51**	5.93	6.83	0.506	*4*	**6.15**	5.73	6.52	0.356	*9*	**5.99**	5.53	6.22	0.235
LaP	*3*	**8.71**	8.41	8.89	0.264	*4*	**8.27**	7.93	8.59	0.364	*9*	**8.26**	7.85	8.63	0.221
LaInf	*3*	**9.85**	9.28	10.35	0.538	*4*	**8.61**	8.49	8.73	0.113	*9*	**8.11**	7.76	8.41	0.227
LaN	*3*	**14.97**	14.18	15.48	0.696	*4*	**13.39**	13.16	13.64	0.238	*9*	**13.30**	12.83	14.31	0.418
LaM	*2*	**15.80**	15.67	15.93	0.184	*4*	**13.98**	13.38	14.35	0.439	*9*	**13.42**	12.69	14.21	0.449
ANc	*2*	**10.58**	10.48	10.67	0.134	*4*	**10.03**	9.85	10.26	0.204	*9*	**9.84**	9.43	10.23	0.295
LBT	*2*	**4.32**	4.26	4.38	0.085	*4*	**3.61**	3.45	3.84	0.206	*7*	**3.55**	3.33	4.41	0.382
CC	*3*	**7.95**	7.64	8.33	0.350	*4*	**6.92**	6.68	7.23	0.231	*9*	**6.51**	6.18	6.84	0.230
M^1M^1	*3*	**11.85**	11.44	12.09	0.359	*4*	**10.31**	10.03	10.76	0.321	*8*	**10.00**	9.63	10.48	0.334
CM^2	*3*	**14.42**	14.04	14.64	0.333	*4*	**12.10**	11.79	12.26	0.217	*9*	**11.25**	10.65	11.72	0.414
LMd	*3*	**32.28**	30.09	33.44	1.898	*4*	**26.94**	26.33	27.17	0.405	*9*	**25.15**	23.91	26.34	0.846
ACo	*3*	**12.50**	11.91	12.92	0.526	*4*	**11.73**	10.98	12.20	0.567	*9*	**10.61**	8.57	11.43	0.857
CM_2	*3*	**15.87**	15.19	16.37	0.612	*4*	**13.18**	12.95	13.68	0.339	*8*	**12.32**	11.26	13.16	0.699

thirds of the country area, reaching the northern margin of the species distribution range there (Kulzer 1959, Kingdon 1974, Aggundey & Schlitter 1984, Bergmans 1988, Monadjem et al. 2024). The nine localities of the NMW and NMP specimens of *E. wahlbergi* are distributed regularly along the whole southern border of Kenya and conform to the distribution pattern of this bat as given in detail by Bergmans (1988: 135, Fig. 11). Thus, they do not represent unusual records.

The dimensions of the adult NMW and NMP specimens of *E. wahlbergi* are shown in Table 4. The examined mitochondrial gene (cytochrome *b*) was sequenced for 18 specimens (82% of the NMP specimens); in seven of them (39%, NMP 97940–97942, 97946, 97952, 97953, 97955) the obtained haplotypes were in concord by 99.0–99.3% with the haplotype MT441523 of *E. wahlbergi* from South Africa (Moir, unpubl.), while in eleven specimens (61%, NMP 97954, 97968, 97970, 97990, 98006, 98007, 98023, 98024, 98026, 98034, 98035) they agreed in 98.4% with the haplotype KX823309 of *E. labiatus* from Djibouti (Hassanin et al. 2016, 2020), see Fig. 3. This genetic separation has a clear geographical pattern, the mtDNA of *E. wahlbergi* was found in populations of the western part of the sampled transect across southern Kenya (sites 20, 21, and 23 in Fig. 2) and the mtDNA of *E. labiatus* in the eastern section of this transect line (sites 23, 27, 29, and 30); in Kimana (23), both haplotype types were present syntopically (all specimens were netted during one netting session into the same net).

Since the identification of *E. wahlbergi* based on morphology (body and skull size, palatal ridges) is unmistakable, these results suggest sharing of the mitochondrial genome among fruit bat species rather than a misidentification of several specimens (Fig. 3). Anyway, such sharing of mitochondrial genomes between species within the genus *Epomophorus* Bennet, 1836 was already observed and described (see Nesi et al. 2011).

Although the existence of two distinct mitochondrial lineages with an apparent geographical pattern could indicate a phylogenetic division of lowland and highland populations of *E. wahlbergi* in Kenya (cf. Kulzer 1959, see the discussion by Bergmans 1988: 132–134), the syntopic occurrence of the two lineages does not support such hypothesis. Additional sampling of haplotypes at a large geographical scale is necessary to understand a possible phylogenetic relevance of the genetic variation in *E. wahlbergi*.

***Epomophorus labiatus* (Temminck, 1837)**

NMW Material (1). 1 ♀ (NMW 32688 [S+Sk]), North Nandi Forest, 4 km SW of Chomisia, 29 November 1979, leg. F. Spitzeneberger.

NMP Material (4). 3 ♀♀ (NMP 97937 [A], 97938, 97939 [S]; Fig. 4), Ewangan, Oldarpoi Camp, 8 December 2021, leg. P. Benda, L. Bufka & J. Červený;
1 ♀ (NMP 97945 [A]), Ol Kirimatian, Nyiro River Camp, 16 August 2022, leg. P. Benda & J. Červený.

Reference. Claessen & De Vree (1991).

Epomophorus labiatus is distributed in the central and eastern parts of Africa, from north-eastern Nigeria, eastern Sudan, and Eritrea in the north, to western Congo (B.), Zambia, and Malawi in the south, it also occurs in south-western Arabia (Bergmans 1988, Benda et al. 2011b, Monadjem et al. 2024). In East Africa, *E. labiatus* is the most common fruit bat, however, its occurrence is concentrated mainly in the area in between the Rift Valleys (Bergmans 1988, Monadjem et al. 2024). It is by far the most abundant fruit bat in Uganda, while in Tanzania and Kenya, it belongs to medium frequent fruit bat species. In Kenya, the records are scattered

Figs. 4, 5. Portraits of fruit bats from Kenya in the NMP collection. 4 – a female of *Epomophorus labiatus* collected at the Oldarpoi Camp, Ewangan, on 8 December 2021. 5 – a female of *Epomophorus minimus* from the Simba Lodge, Buffalo Springs Reserve, collected on 24 November 2021. All photos by J. Červený.

sparsely over most of the country area; Monadjem et al. (2024) reported the number of records of *E. labiatus* from Kenya representing just a half of that of *E. wahlbergi*. The three localities of the NMW and NMP specimens lie within the range of abundant occurrence of *E. labiatus* in Kenya (cf. Bergmans 1988).

The dimensions of the adult NMW and NMP specimens of *E. labiatus* are shown in Table 5. The metric data conform to those given for this species by Bergmans (1988) and Claessen & De Vree (1991). The examined mitochondrial gene (cytochrome *b*) was sequenced for three specimens of *E. labiatus* from Ewangan; in two of them (NMP 97937, 97939) the obtained haplotypes agreed in 99.7% with the haplotype JF728743 of *E. gambianus* (Ogilby, 1835) from near Bangui, Central African Republic (Nesi et al. 2011), while the sequence of the remaining specimen (NMP 97938) concurred in 99.3% with the haplotype MT441523 of *E. wahlbergi* from Mnceba, South Africa (Moir, unpubl.). This record resembles the evidence obtained from the examined Kenyan specimens of *E. wahlbergi* (see above), however, none of the examined specimens of *E. labiatus* showed the haplotype assigned previously to this bat, but haplotypes of two other species (Fig. 3), moreover, one of them (*E. gambianus*) does not occur in Kenya and the closest part of its range lies ca. 675 km from Ewangan sensu Bergmans (1988) and ca. 885 km sensu Monadjem et al. (2024). Again, we have to stress that only additional sampling of haplotypes at a large geographical scale could help to understand a possible phylogenetic relevance of the mitochondrial genetic variation in the *Epomophorus* bats.

Epomophorus minimus Claessen et De Vree, 1991

NMW Material (1). 1 ♀ (NMW 32200 [S]), Pangani, near the Lwandani Cave, 10 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

NMP Material (17). 2 ♀♀ (NMP 97853, 97854 [S+A]; Fig. 5), Archers Post, Buffalo Springs Reserve, Simba Lodge, 24 November 2021, leg. P. Benda, L. Bufka & J. Červený;
2 ♂♂, 9 ♀♀ (NMP 97885–97891 [S+A], 97892–97895 [A]), Kampi Ya Samaki, Soi Safari Lodge, 2 December 2021, leg. P. Benda, L. Bufka & J. Červený;
3 ♂♂ (NMP 97920, 97921 [S+A], 97922 [A]), Loboi, Zakayos Camp, 3 December 2021, leg. P. Benda, L. Bufka & J. Červený;
1 ♂ (NMP 98060 [S+A]), Wamba, 1 July 2010, leg. J. Bryja, J. S. Mbau & R. Šumbera.

Reference. Claessen & De Vree (1991).

Epomophorus minimus is an endemic of north-eastern Africa, its limited range stretches from central and eastern Ethiopia in the north to eastern Uganda, northern Tanzania, eastern Kenya, and southern Somalia in the south (Claessen & De Vree 1991, Happold 2013a, Benda et al. 2019). All the NMP specimens of *E. minimus* originate from the areas of common occurrence of this bat in Kenya (Aggundey & Schlitter 1984, Claessen & De Vree 1991), from the central regions of the country. On the other hand, the locality of the NMW specimen, Pangani near Mombasa, lies south of the range margin of *E. minimus* as designated by Claessen & De Vree (1991) and Monadjem et al. (2024) at 03°51'S and represents a prolongation of the distribution range of this bat by ca. 190 km southwards. The southernmost localities of the described range are Patta Island (02°07'S) and Shompole (02°05'S; Aggundey & Schlitter 1984, Monadjem et al. 2024).

The dimensions of the adult NMW and NMP specimens of *E. minimus* are shown in Table 5. The metric data conform to those given for this species by Claessen & De Vree (1991). Interestingly, the specimen NMW 32200 was identified as an immature individual of *E. labiatus* by Claessen & De Vree (1991: 222); however, our re-examination of this bat and its comparison with the available samples of both *E. labiatus* and *E. minimus* from Kenya showed the concerned NMW specimen to be referred to as *E. minimus*. Although it really is a bat of the subadult age, it is fully grown (with fully developed last molars, but not completely ossified intersphenoidal suture), enough to be correctly identified (LAt 61.0 mm, LCr 32.56 mm, CM^3 11.60 mm); moreover, the signs of the subadult age (unossified intersphenoidal suture, not fully grown last molars) are frequently present in the adult (reproducing) females of (various species of) fruit bats, in the pregnant or lactating stages. We thus consider the specimen NMW 32200 to be a young adult female of *E. minimus*, rather than a juvenile of *E. labiatus*.

The mitochondrial gene for cytochrome *b* was examined in nine specimens of *E. minimus* (47% of the NMP specimens). None of the sequences obtained from them were unique for *E. minimus*, all of them were affiliated with the haplotypes of four other *Epomophorus* species (Fig. 3). The largest number, six specimens (NMP 97853, 97885–97888, 97921) from all three sampled sites (Archers Post, Kampi Ya Samaki, and Loboi), were in concord with the mitochodrial genome of a species that does not occur in Kenya, their haplotypes agreed by 99.7–99.9% with the haplotype JF728753 of *E. gambianus* from Bangui, Central African Republic (Nesi et al. 2011). One specimen/sequence (NMP 97922 from Loboi) agreed in 99.0% with the haplotype MT441523 of *E. wahlbergi* from Mnceba, South Africa (Moir, unpubl.), one specimen/sequence (NMP 97854 from Archers Post) in 98.3% with the haplotype KX823309 of *E. labiatus* from Djibouti (Hassanin et al. 2016, 2020), and the last specimen/sequence (NMP 97920 from Loboi) agreed in 99.8% with the haplotype JF728708 of *E. pusillus* Peters, 1868 from Bangui, Central African Republic (Nesi et al. 2011). *Epomophorus pusillus* is a very rare bat in Kenya, it was documented only in the westernmost regions of the country and not in or nearby Loboi at Lake Bogoria (Bergmans 1989, Monadjem et al. 2024). In Loboi, the highest haplotype diversity was found, the mitochondrial DNA of three other species (*E. gambianus*, *E. wahlbergi*, *E. pusillus*) was detected in three specimens of *E. minimus*, while in the Buffalo Springs Reserve near Archers Post, the mtDNA of two species was found (*E. gambianus*, *E. labiatus*). This evidence resembles the situation found in *E. labiatus* (see above), in which none of the three examined specimens had the mtDNA of this species but instead they possessed the mtDNA of two other species. In *E. mimimus*, this was documented at an even larger scale, none of the nine examined specimens had the mtDNA of this bat species, but they showed the mtDNA of four (!) other morphologically distinct species of the genus (Fig. 3).

Rhinopomatidae

Rhinopoma macinnesi Hayman, 1937

NMP Material (2). 1 ♂, 1 ♀ (NMP 97912, 97913 [S+A]; Figs. 6, 7), Lake Baringo, Lesukut Island, 3 December 2021, leg. P. Benda, L. Bufka & J. Červený.

Rhinopoma macinnesi is an endemic of arid regions of north-eastern Africa, it occurs in a limited and disjunct range composed of two parts, a north-eastern part in Eritrea and northern Somalia, and a south-western part in north-western Kenya and south-easternmost South Sudan (Van Cakenberghe & De Vree 1994). Nine localities are known from Kenya (Aggundey & Schlitter 1984, Monadjem et al. 2024), it is the highest concentration of records of this bat from a country (only two sites are known from Eritrea and single localities are reported from two other countries; Van Cakenberghe & De Vree 1994, Monadjem et al. 2024). All Kenyan sites but one (Lodwar) are adjacent to the Eastern Rift Valley and are directly associated with

Figs. 6, 7. *Rhinopoma macinnesi* from Kenya in the NMP collection. 6 – a small colony in a cave on the Lesukut Island, Lake Baringo, 3 December 2021. 7 – a male collected from the colony.

two large rift lakes, Lake Turkana and Lake Baringo, and five localities of *R. macinnesi* are situated in the islands of these lakes. The Lesukut Island is the southernmost locality within the whole range of this bat; besides the NMP specimens, *R. macinnesi* was documented from this island already by Kock (1969) and Aggundey & Schlitter (1984). It was only the second documented site of this species after the type locality (Bat Island, Lake Rudolf [= Lake Turkana]; Hayman 1937), even though later this bat was found elsewhere.

The dimensions of the NMP specimens of *R. macinnesi* from Kenya are shown in Table 2, these values as well as the skull (rostrum) shapes of these bats conform to those defined for this species by Van Cakenberghe & De Vree (1994). This bat is the only species of the family Rhinopomatidae that has not yet been studied by means of the molecular genetic approach (see Hulva et al. 2007, Benda et al. 2012, 2019). The phylogenetic relationship of *R. macinnesi* thus remains to be re-examined with the help of a genetic analysis with respect to the morphometric evidence (see Van Cakenberghe & De Vree 1994). However, this problem should be a part of a further study comprising the whole family Rhinopomatidae.

Megadermatidae

***Lavia frons* (Geoffroy, 1810)**

NMP Material (4). 1 ♂, 1 ♀ (NMP 97914, 97915 [S+A]; Figs. 8, 9), Loboi, Zakayos Camp, 3 December 2021, leg. P. Benda, L. Bufka & J. Červený;
1 ♂ (NMP 97947 [S+A]), Ol Kirimatian, Nyiro River Camp, 16 August 2022, leg. P. Benda & J. Červený;
1 ♀ (NMP 98064 [S+A]), Ol Kirimatian, Shompole Conservancy, 12 August 2013, leg. J. Červený.

Lavia frons is a bat widely distributed across the tropical zone of Africa, its range stretches through the woodland savanna belt from Senegal and Guinea-Bissau to central Sudan, northern

Table 6. Biometric data on the NMP specimens of *Lavia frons* and *Cardioderma cor* from Kenya. For abbreviations see Methods

dimension			*Lavia frons*					*Cardioderma cor*		
	n	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*4*	**60.50**	57.0	63.3	2.642	*25*	**55.94**	53.3	60.5	1.837
LOc	*4*	**25.40**	24.37	26.36	0.908	*21*	**26.26**	24.28	27.19	0.711
LCc	*4*	**22.16**	21.19	22.78	0.722	*21*	**23.03**	21.61	23.84	0.585
LaZ	*4*	**14.93**	14.18	15.48	0.636	*22*	**15.61**	14.88	16.42	0.442
LaI	*4*	**7.52**	6.92	8.09	0.480	*22*	**6.08**	5.39	6.48	0.253
LaP	*4*	**3.07**	2.93	3.31	0.171	*22*	**2.87**	2.26	3.71	0.387
LaInf	*4*	**5.75**	5.32	6.25	0.383	*22*	**5.48**	4.98	5.74	0.176
LaN	*4*	**10.51**	10.02	11.28	0.553	*22*	**10.80**	10.02	11.22	0.275
LaM	*4*	**12.10**	11.77	12.32	0.252	*22*	**11.60**	11.18	12.01	0.250
ANc	*4*	**8.22**	8.07	8.44	0.184	*22*	**8.89**	8.19	9.48	0.317
LBT	*4*	**4.76**	4.67	4.92	0.113	*22*	**4.92**	4.22	5.21	0.259
CC	*4*	**6.13**	5.88	6.42	0.264	*22*	**5.82**	5.35	6.12	0.186
M^3M^3	*4*	**8.92**	8.55	9.41	0.398	*22*	**9.09**	8.28	9.61	0.310
CM^3	*4*	**9.38**	9.29	9.52	0.113	*22*	**9.79**	9.16	10.18	0.305
LMd	*4*	**16.93**	15.94	17.68	0.747	*22*	**18.02**	17.09	18.93	0.545
ACo	*4*	**5.14**	4.82	5.43	0.251	*22*	**5.90**	5.52	6.41	0.210
CM_3	*4*	**10.48**	10.29	10.64	0.148	*22*	**11.05**	10.39	11.51	0.345

Figs. 8, 9. Portraits of *Lavia frons* from Kenya in the NMP collection; a specimen collected at the Zakayos Camp, Loboi, on 3 December 2021.

Eritrea, and southern Somalia, and to Gabon, western DR Congo, central Zambia, and eastern Tanzania (Kock 1969, Hayman & Hill 1971, Vonhof & Kalcounis 1999, Happold 2013d, Monadjem et al. 2020, 2024). In East Africa, *L. frons* is a widespread and abundant bat in most of the region, it is missing only in southern Tanzania (Kulzer 1959, Kingdon 1974, Monadjem et al. 2024). In Kenya, it is a very common species, the western part of the country represents an area of the highest concentration of records of *L. frons* in its whole distribution range (Kock 1969, Monadjem et al. 2024). All the NMP specimens originate from western Kenya, from the Ol Kirimatian and Lake Bogoria regions (Berger 1910, Kollmann 1914, Aggundey & Schlitter 1984). The dimensions of the NMP specimens of *L. frons* from Kenya are shown in Table 6.

Cardioderma cor (Peters, 1872)

NMP Material (26). 1 ♀ (NMP 97865 [S+A]; Fig. 10), Archers Post, Samburu Reserve, King Lion Camp, 25 November 2021, leg. P. Benda, L. Bufka & J. Červený;
1 ♀ (NMP 97868 [S+A]), Archers Post, Samburu Reserve, King Lion Camp, 26 November 2021, leg. P. Benda, L. Bufka & J. Červený;
1 ♂ (NMP 98048 [S+A]), Forolle, 13 September 2004, leg. D. Modrý;
1 ♂, 1 ♀ (NMP 97870, 97871 [S+A]), Gotu Falls, Sempire Camp, 27 November 2021, leg. P. Benda, L. Bufka & J. Červený;
6 ♀♀ (NMP 98050–98054 [S+A], 98049 [A]), Kalacha, 18 September 2004, leg. D. Modrý;
3 ♂♂, 1 ♀ (NMP 97916, 97917, 97919 [S+A], 97918 [A]), Loboi, Zakayos Camp, 3 December 2021, leg. P. Benda, L. Bufka & J. Červený;
1 ♀ (NMP 97948 [S+A]), Ol Kirimatian, Nyiro River Camp, 16 August 2022, leg. P. Benda & J. Červený;
1 ♂, 1 ♀ (NMP 97974 [S+A], 97975 [A]; Fig. 11), Shimoni, Slave Cave, 22 August 2022, leg. P. Benda & J. Červený;
1 ♀ (NMP 98352 [S+A]), South Horr, 1 October 2004, leg. D. Modrý;

Figs. 10, 11. *Cardioderma cor* from Kenya in the NMP collection. 10 – portrait of a female collected at the King Lion Camp, Samburu Reserve, on 25 November 2021. 11 – a group roosting in the Slave Cave, Shimoni, 22 August 2022.

1 ♂, 3 ♀♀ (NMP 97999–98002 [S+A], Voi, Tsavo East National Park, Aruba Ashnil Lodge, 29 June 2023, leg. P. Benda & J. Červený;
2 ♀♀ (NMP 98003 [S+A], 98004 [A]), Voi, Tsavo East National Park, Aruba Ashnil Lodge, 30 June 2023, leg. P. Benda & J. Červený;
1 ♂ (NMP 98008 [S+A]), Watamu, Mida Creek Camp, 2 July 2023, leg. P. Benda & J. Červený.

Cardioderma cor is an endemic of eastern Africa, its distribution range stretches from eastern Sudan, Eritrea, Djibouti, and eastern Somalia in the north, to western Uganda, central Tanzania, and Zanzibar in the south (Hayman & Hill 1971, Csada 1996, Happold 2013c, Monadjem et al. 2024). In East Africa, it occurs in the northern parts of Uganda and Tanzania and in the whole Kenya (Kulzer 1959, Kingdon 1974, Monadjem et al. 2024). It is the latter country from which the highest number of records of *C. cor* within its whole distribution range has been published (Monadjem et al. 2024). The numerous localities of the NMP specimens are scattered all over the territory of Kenya, except the extreme north-west and north-east; several of the NMP sites were already published as the localities of this bat (Hollister 1918, De Beaux 1923, Harrison 1961, Aggundey & Schlitter 1984). On the other hand, the NMP specimens of *C. cor* from Forolle, Kalacha, and South Horr represent the first records of this bat from the northern Chalbi Desert at the border with Ethiopia. The dimensions of the NMP specimens of *C. cor* from Kenya are shown in Table 6.

Rhinolophidae

Rhinolophus acrotis von Heuglin, 1861

NMW Material (33). 2 ♂♂ (NMW 32269, 32270 [S+B]), Kiminini, Chepkelele Cave, 31 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♀♀ (NMW 32267 [S+B], 32268 [A]), Kiminini, Nyungu ya Mawe Cave, 30 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
4 ♂♂, 3 ♀♀ (NMW 32248–32254 [S+B]), Mount Elgon National Park, Chepnyalil Cave, 24 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂ (NMW 32261 [S+Sk]), Mount Elgon National Park, Rongai Camp, 24 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♀ (NMW 32266 [S+Sk]), Mount Elgon National Park, Rongai Camp, 27 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
3 ♂♂, 1 ♀ (NMW 32255–32258 [S+B]), Mount Elgon National Park, Kitum Cave, 24 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂ (NMW 32265 [S+B]), Mount Elgon National Park, Kol Cave, 27 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♂♂ (NMW 32259, 32260 [S+B]), Mount Elgon National Park, Makingeny Cave, 24 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♂♂ (NMW 32262, 32263 [S+B]), Mount Elgon National Park, Makingeny Cave, 26 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂ (NMW 32264 [S+B]), Mount Elgon Reserve North, Khybe Sawmill Cave, 27 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
4 ♂♂, 6 ♀♀ (NMW 32271–32280 [S+B]), Saboti, Kapkulkul Caves, 2 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Reference. Benda et al. (2024).

Rhinolophus acrotis is a locally abundant bat throughout eastern and southern Africa, occurring in a long belt stretching from the north-eastern Sudan to the south-western Cape (Uvizl et al.

Table 7. Biometric data on the NMW specimens of *Rhinolophus acrotis*, *R. hildebrandtii*, and *R. eloquens* from Kenya. For abbreviations see Methods

dimension	*Rhinolophus acrotis*					*Rhinolophus hildebrandtii*					*Rhinolophus eloquens*				
	n	**M**	min	max	SD	*n*	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*33*	**51.77**	49.9	54.7	1.199	*16*	**61.14**	58.0	63.6	1.628	*11*	**57.51**	56.0	58.8	1.094
LCr	*31*	**21.70**	21.07	22.23	0.281	*13*	**28.22**	26.76	29.18	0.728	*7*	**26.25**	25.58	26.66	0.380
LOc	*32*	**21.34**	20.85	21.93	0.259	*16*	**26.88**	25.64	27.68	0.543	*10*	**25.35**	24.84	25.69	0.282
LCc	*32*	**18.62**	18.15	19.04	0.229	*16*	**24.03**	22.61	24.92	0.685	*10*	**22.41**	21.96	22.71	0.253
LaZ	*31*	**11.16**	10.69	11.52	0.171	*16*	**13.75**	12.82	14.31	0.382	*10*	**13.01**	12.75	13.27	0.179
LaI	*32*	**2.50**	2.21	2.78	0.134	*16*	**2.86**	2.63	3.36	0.200	*10*	**2.76**	2.48	3.21	0.215
LaInf	*32*	**5.37**	5.18	5.54	0.096	*16*	**7.10**	6.82	7.37	0.180	*10*	**6.92**	6.58	7.23	0.182
LaN	*32*	**9.03**	8.67	9.61	0.183	*16*	**10.95**	10.34	11.18	0.232	*10*	**10.22**	9.81	10.82	0.284
LaM	*32*	**9.92**	9.68	10.23	0.134	*16*	**12.44**	11.75	12.83	0.287	*10*	**11.78**	11.37	12.20	0.256
ANc	*32*	**6.70**	6.24	7.08	0.172	*16*	**7.78**	7.33	8.13	0.234	*10*	**7.46**	6.67	7.98	0.390
LBT	*32*	**2.99**	2.68	3.22	0.119	*15*	**4.62**	4.31	5.03	0.234	*10*	**4.23**	3.98	4.47	0.139
CC	*31*	**5.75**	5.53	5.93	0.109	*16*	**7.13**	6.88	7.53	0.170	*10*	**6.96**	6.73	7.19	0.159
M^3M^3	*32*	**7.88**	7.63	8.12	0.120	*15*	**9.61**	9.16	9.93	0.201	*10*	**9.41**	8.95	9.76	0.243
CM^3	*32*	**7.63**	7.28	7.83	0.114	*16*	**9.90**	9.32	10.62	0.299	*13*	**9.22**	8.68	9.54	0.232
LMd	*31*	**13.93**	13.51	14.28	0.191	*16*	**18.51**	17.42	19.16	0.506	*10*	**17.36**	17.06	17.74	0.198
ACo	*32*	**3.42**	3.28	3.63	0.090	*16*	**5.22**	4.34	5.48	0.318	*10*	**4.52**	4.18	5.02	0.221
CM_3	*32*	**8.21**	7.93	8.54	0.124	*16*	**10.46**	9.74	10.95	0.292	*10*	**9.84**	9.64	10.06	0.149

2024, cf. Hayman & Hill 1971, Csorba et al. 2003, Monadjem et al. 2020, 2024). In East Africa, *R. acrotis* is not a rare species in the upland areas of Rwanda, Uganda, and western Kenya, it sparsely occurs also in Burundi, northern Tanzania, and south-eastern Kenya (Kulzer 1959, Aggundey & Schlitter 1984, Monadjem et al. 2024). The NMW series of specimens originates from a very limited region of Mount Elgon and adjacent areas of western Kenya (Fig. 1), where this bat was recorded frequently and repeatedly (Ruxton 1926, Theodor 1957, 1968, Harrison 1961, Koopman 1966, Đulić & Mutere 1974, Aggundey & Schlitter 1984, Demos et al. 2019a, etc.).

The dimensions of the NMW specimens of *R. acrotis* from Kenya are shown in Table 7. According to the revision by Uvizl et al. (2024), this bat is represented by two basic phylogenetic lineages in Africa, co-identified with two subspecies, *R. a. acrotis* from Ethiopia, Sudan, Eritrea, and Somalia, and *R. a. augur* Andersen, 1904, occurring in eastern and southern Africa between southern South Sudan and southern South Africa. These two lineages/taxa are characterised by morphotypes that are more or less clearly distinct from each other in body and skull size (Benda et al. 2024: 241, Table 1), *R. a. acrotis* is small-sized (LAt 45.9–53.2 mm, LCc 17.4–18.8 mm, CM^3 7.3–7.8 mm, n=13), and *R. a. augur* is large-sized (LAt 50.4–57.4 mm, LCc 18.6–20.6 mm, CM^3 7.6–8.8 mm, n=45); only few specimens were positioned in the zone of metric overlap of these two size categories (Benda et al. 2024: 243, Fig. 1). With respect to this size-trait distribution, the Kenyan samples – represented by the NMW series (plus two SMF specimens) from Mount Elgon – are in a medium position (Fig. 12), according to their metric characters, they cannot be attributed to either of the two morphotypes but stay in between, in their overlap zone. Such a peculiar morphotype has not been found in any other part of the *R. acrotis* distribution range.

On the other hand, as demonstrated by Demos et al. (2019a) and Uvizl et al. (2024), both the mtDNA and nucDNA haplotypes from bats of the Mount Elgon populations are an integral part of the eastern African haplogroup of *R. a. augur*, and do not show a phylogenetic separation. The extraordinary small-sized morphotype of the Mount Elgon populations of *R. acrotis augur* thus most probably represents just a local form, perhaps an ecomorph that evolved in the mountain conditions of the Great Rift region of East Africa. The taxon *Rhinolophus keniensis* Hollister, 1916, described as a small-sized form of the '*Rhinolophus augur* group' (Hollister 1916: 2) based on a specimen from Mount Kenya, currently considered a synonym of *R. a. augur* (see Uvizl et al. 2024), fits in its size the dimension range of *R. acrotis* from eastern and southern Africa (LAt 52.0 mm, LCc 20.4 mm, CM^3 8.6 mm; Hollister 1916: 2) and does not match the size range of the Mount Elgon population.

Comparative material (53). **Eritrea** [2]: 1 ♂ (MSNG 44312 [S+A]), Assab, July 1893, leg. G. Pestalozza; – 1 ♂ (MSNG 27583 [S+B]), Assab, Dancalia, February 1929, leg. S. Patrizi. – **Ethiopia** [11]: 1 ♂ (NMP 95891 [S+A]), Aksum, King Basen's Tomb, 1 November 2012, leg. P. Benda; – 1 ♀ (NMP 95913 [S+A], Aman Amba, Simien National Park, 5 November 2012, leg. P. Benda; – 1 ♂ (NMP 95962 [S+A]), Chara, 15 km E of Bonga, 26 November 2012, leg. P. Benda; – 3 ♀♀ (NMP 95937–95939 [S+A]), Dangola Washa Caves, 5 km SW of Kesa, 12 November 2012, leg. P. Benda; – 1 ♂ (MZUF 6029 [S]),

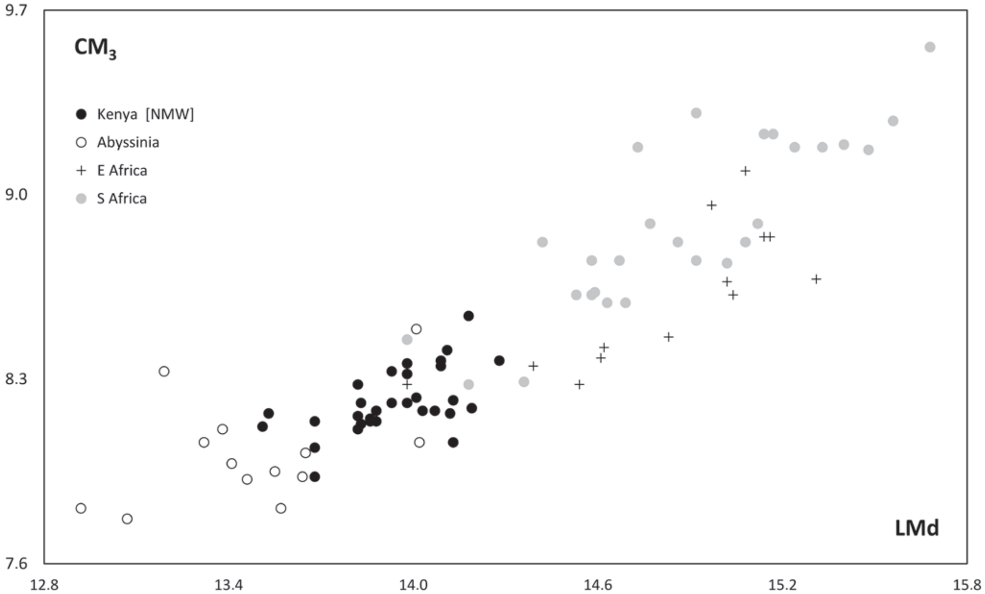


Fig. 12. Bivariate plot of the Kenyan and comparative samples of *Rhinolophus acrotis*: mandible length (LMd) against the length of lower tooth-row (CM_3). For comparative material see text. Legend of the geographical specification of the comparative sets: Abyssinia = Eritrea, Ethiopia, and the Sudan; E Africa = Rwanda, Uganda, Tanzania, Malawi, and Kenya (other than the NMW series); S Africa = South Africa and Mozambique.

Gorgora, Lago Tana, 1828 m, 13 March 1937, leg. G. Dainelli; – 1 ♀ (MSNG 18243 [S+B]), Harrar, date unlisted, leg. P. Felter; – 2 ♀♀ (MSNG 45630a, 45630b [S+A]), Harrar, 1893, leg. Salimbeni; – 1 ♂ (MZUF 5649 [S]), Lago Tana, 1937, leg. G. Dainelli. – **Kenya** [2]: 1 ♂, 1 ♀ (SMF 39427, 39431 [S]), Naibei's Great Cave, Kapasakwany, Süd Seite des Mt. Elgon, 13 December 1970, leg. Dr. Mutuku. – **Malawi** [4]: 1 ♂ (BMNH 97.10.1.18. [S+B], holotype of *Rhinolophus augur zambesiensis* Andersen, 1904), Fort Hill, N. Nyasa, July 1896, leg. A. Whyba; – 1 ♂, 2 ♀♀ (NMP mw199, mw231, mw232 [S+A]), Ntchisi Forest Reserve, 8–9 July 2008, leg. J. Šklíba. – **Mozambique** [1]: 1 ♀ (MSNG 18316 [S+B]), Quelimane, 5 November 1908, collector unlisted. – **Rwanda** [1]: 1 ind. (SMF 92961 [S+Sk]), Lava-Höhle Ubuvumo, 11 December 2004, leg. Laumanns. – **South Africa** [26]: 1 ♀ (SMF 55037 [S+B]), Doornhoek, Pietermaritzburg, Natal, 27 March 1976, leg. I. W. Espie; – 1 ♂, 2 ♀♀ (DM 8373–8375 [S+A]), Fort Yolland Farm, Eshowe-Melmoth, Entumeni Dist., KwaZulu-Natal, 14 May 2005, leg. P. J. Taylor; – 4 ♂♂, 3 ♀♀ (NMW 26126–26132 [S+B]), Guano Cave, Tsitsikama, Coastal National Park, Cape Prov., 4 December 1975, leg. F. Spitzenberger & B. Herzig; – 1 ♂ (TM 46882 [S+A]), Haffenden Heights, Limpopo, 3 November 2002, leg. L. Cohen; – 1 ♀ (BMNH 4.5.1.8. [S+B], holotype of *Rhinolophus augur zuluensis* Andersen, 1904), Jususic Valley, 20 mi NW of Eshowe, Zululand, 17 November 1903, leg. C. H. B. Grant; – 1 ♂ (TM 47619 [S+A]), Kaalrug, Mpumalanga, 25 October 2004, leg. L. Cohen; – 1 ♂ (MSNG 44467 [S+A]), Kenilworth, soborgo della Citta del Capo, 15 March 1906, leg. W. L. Sclater; – 2 ♂♂ (NMB 11072, 11075 [S+B]), Koegelbeen Cave, Hay (Griekwastad), Northern Cape, 22 February 1997, leg. N. Avenant; – 1 ♂ (BMNH 4.10.1.1. [S+B], holotype of *Rhinolophus augur* Andersen, 1904), Kuruman, Bechuana, 19 April 1904, leg. R. B. Woosnam; – 3 ♂♂, 1 ♀ (DM 8376–8379 [S+A]), Melmoth, Woodlands Estate, KwaZulu-Natal, 15 May 2005, leg. P. J. Taylor; – 1 ♀ (NMB 10638 [S+B]), Merrimetzie, Winburg Dist., Free State, 6 February 1996, coll. J. P. Eksteen & N. Avenant; – 1 ♂ (SMF 44809 [S+A]), Rhin. Z., Transvaal, 27 December 1952, leg. Zumpt; – 1 ♀ (TM 46643 [S+A]), Sudwala Caves, Mpumalanga, 18 December 2008, leg. H. C. Schoeman & S. Stoffberg; – 1 ♀ (SMF 19557 [S]), Uitkoms, Transvaal, 19 January 1958, leg. J. Meester. – **Sudan** [1]: 1 ♀ (MSNG 46965 [S+A]), Port Sudan, Mar Rosso, January 1908, leg. G. Nicolosi. – **Tanzania** [4]: 2 ♂♂ (SMF 91227, 91228 [S+A]), Amani-Sigi Forest Reserve, E Usambara Mts., Tanga Reg., 14 March 1999, leg. Frontier; – 1 ♂ (SMF 92505 [S+A]), Nilo Forest Reserve, 3 August 2000, leg. Frontier; – 1 ♀ (NMW 19822 [S]), Ugano, Ruvumq Prov., 1935–1936, leg. H. Zerny. – **Uganda** [1]: 1 ♀ (SMF 44092 [S+A]), Kisoro, Kigezi Dist., 30 October 1975, leg. A. B. C. Killango.

Rhinolophus hildebrandtii Peters, 1878

NMW Material (16). 8 ♂♂, 3 ♀♀ (NMW 32294–32304 [S+B]), Pangani, near the Lwandani Cave, 9 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
3 ♂♂, 1 ♀ (NMW 32305–32308 [S+B]), Pangani, near the Lwandani Cave, 11 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♀ (NMW 32309 [S+B]), Pangani, near the Lwandani Cave, 12 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Reference. Aggundey & Schlitter (1984).

Rhinolophus hildebrandtii, as a bat species re-described by Taylor et al. (2012), is an endemic of eastern Africa, where it occurs in the savanna belt stretching from central Tanzania and Burundi to the north-eastern DR Congo and the southern parts of South Sudan and Ethiopia (Monadjem et al. 2024). The majority of its records are known from Kenya, in the southern and south-eastern parts of the country *R. hildebrandtii* ranks among rather common bats (Kulzer 1959, O'Shea & Vaughan 1980, Aggundey & Schlitter 1984, Monadjem et al. 2024). The locality of collection of the NMW series of *R. hildebrandtii* was published already by Aggundey & Schlitter (1984), the dimensions of these specimens are shown in Table 7.

Rhinolophus eloquens Andersen, 1905

NMW Material (14). 1 ♀ (NMW 32283 [S+B]), Kiminini, 2 km NE of Hanson's farm, 2 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂ (NMW 32282 [S+B]), Kiminini, Chepkelele Cave, 31 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂ (NMW 32281 [S+B]), Mount Elgon National Park, Makingeny Cave, 24 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂ (NMW 32692 [S+Sk+B]), North Nandi Forest, 7 km NE of Chomisia, 11 December 1979, leg. F. Spitzenberger;
2 ♂♂ (NMW 32292, 32293 [S+B]), Suswa, Suswa Cave, 17 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♂♂ (NMW 32284, 32285 [S+B]), Pangani, Lwandani Cave, 9 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
3 ♀♀ (NMW 32286–32288 [S+B]), Pangani, near the Lwandani Cave, 9 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♀ (NMW 32289 [S+B]), Pangani, near the Lwandani Cave, 10 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂, 1 ♀ (NMW 32290, 32291 [S+B]), Pangani, near the Lwandani Cave, 11 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Reference. Aggundey & Schlitter (1984).

Rhinolophus eloquens is an endemic of eastern Africa, its distribution range stretches from the north-eastern DR Congo, South Sudan, southern Ethiopia, and Somalia, to Rwanda and northern Tanzania, including Pemba and Zanzibar islands (Koopman 1975, 1994, Csorba et al. 2003, Simmons 2005, Lanza et al. 2015, Monadjem et al. 2024). The Kenyan records are the most abundant across the whole range, 22 localities are known from the south-western and south-eastern parts of the country (Aggundey & Schlitter 1984). The localities of the NMW specimens were mostly reported by Aggundey & Schlitter (1984); namely the Liwandi Cave at Pangani (as 'Ribe') and 'Mt. Elgon' were mentioned directly as the sites of the NMW material, and a record of this bat from the Kiminini Caves was published previously by Simpson et al. (1968). Only the Suswa Cave represents a new Kenyan locality of *R. eloquens*, although still within the known distribution range of the species (Monadjem et al. 2024). The dimensions of the NMW specimens of *R. eloquens* from Kenya are shown in Table 7.

Rhinolophus simulator Andersen, 1904

NMW Material (7). 2 ♂♂ (NMW 32314, 32315 [S+B]), Kiminini, Kipsiryori Cave, 29 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
5 ♀♀ (NMW 32316–32320 [S+B]), Kiminini, Nabongo Cave, 30 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Reference. Aggundey & Schlitter (1984).

Rhinolophus simulator is a bat distributed in savannas of eastern and southern Africa, from central Ethiopia and South Sudan in the north to southern Botswana and Natal in the south (Csorba et al. 2003, Simmons 2005, Monadjem et al. 2020, 2024). In East Africa, it is a rare but widely distributed bat across the central and eastern parts of the region, it still remains unreported from Uganda, Rwanda, and Burundi (Monadjem et al. 2024). The broader area of Mount Elgon, from where the NMW specimens originated, is the westernmost known locality of *R. simulator* in East Africa, and the only area of its slightly abundant occurrence in the region (Aggundey & Schlitter 1984, Monadjem et al. 2024). Aggundey & Schlitter (1984) reported the NMW series from the Kipsiryori Cave, while that from the close Nabongo Cave remained unpublished until now. The dimensions of the NMW specimens of *R. simulator* from Kenya are shown in Table 8.

Rhinolophus webalai Patterson, Dick, Bartonjo et Demos, 2024

NMW Material (4). 1 ♀ (NMW 32310 [S+B]), Pangani, near the Lwandani Cave, 9 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂ (NMW 32311 [S+B]), Pangani, near the Lwandani Cave, 12 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂ (NMW 32312 [S+B]), Suswa, Suswa Cave, 16 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂ (NMW 32313 [A]), Suswa, Suswa Cave, 17 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Rhinolophus webalai is a very recently recognised endemic bat of eastern Africa (Patterson et al. 2024), one of the species that was distinguished from the broad rank of *R. landeri* Martin, 1838 s.l., formerly considered to be a bat distributed widely across the savanna zones of almost the entire Afrotropics, from the Gambia and Guinea-Conakry in the west, to Ethiopia and Somalia in the east, and southern Mozambique in the south (Hayman & Hill 1971, Kingdon 1974, Koopman 1994, Simmons 2005). The distribution range of *R. webalai*, confirmed by the results of molecular genetic analysis by Patterson et al. (2024), comprises eleven localities spread across

Table 8. Biometric data on the NMW specimens of *Rhinolophus simulator* and *R. webalai* from Kenya. For abbreviations see Methods

dimension		*Rhinolophus simulator*					*Rhinolophus webalai*			
	n	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*7*	**45.54**	41.6	47.0	1.840	*4*	**42.70**	40.8	44.4	1.474
LCr	*7*	**19.31**	18.84	19.63	0.269	*2*	**18.56**	18.37	18.74	0.262
LOc	*7*	**18.75**	18.24	19.02	0.254	*3*	**17.82**	17.66	17.98	0.160
LCc	*7*	**16.56**	16.14	16.81	0.227	*3*	**15.73**	15.58	15.93	0.180
LaZ	*7*	**9.09**	8.85	9.28	0.145	*3*	**8.93**	8.54	9.42	0.448
LaI	*7*	**2.16**	2.06	2.33	0.096	*3*	**2.20**	2.11	2.31	0.103
LaInf	*7*	**4.54**	4.48	4.63	0.056	*3*	**4.66**	4.53	4.74	0.116
LaN	*7*	**8.16**	7.91	8.32	0.143	*3*	**7.85**	7.74	7.93	0.098
LaM	*7*	**9.04**	8.81	9.28	0.149	*3*	**8.80**	8.68	8.93	0.125
ANc	*7*	**5.56**	5.32	5.76	0.154	*3*	**5.43**	5.18	5.74	0.284
LBT	*6*	**3.12**	2.96	3.31	0.128	*3*	**2.92**	2.84	2.98	0.072
CC	*7*	**4.34**	4.21	4.42	0.073	*3*	**4.66**	4.48	5.02	0.312
M^3M^3	*7*	**6.39**	6.18	6.48	0.107	*3*	**6.51**	6.24	6.94	0.376
CM^3	*7*	**6.56**	6.46	6.75	0.104	*3*	**6.47**	6.38	6.58	0.103
LMd	*7*	**11.93**	11.64	12.12	0.181	*3*	**11.40**	11.09	11.67	0.291
ACo	*7*	**2.58**	2.48	2.68	0.079	*3*	**2.50**	2.43	2.64	0.121
CM_3	*7*	**6.81**	6.69	6.96	0.091	*3*	**6.85**	6.62	7.09	0.235

most of Kenya and four sites in southernmost South Sudan. However, the authors expected the presence of this species also in adjacent parts of Uganda and northern Tanzania, and perhaps also in Somalia, where *R. landeri* s.l. was reported to occur (Swynnerton & Hayman 1951, Csorba et al. 2003, Thorn & Kerbis Peterhans 2009, Lanza et al. 2015). Most probably, the occurrence of *R. webalai* in Kenya corresponds with most of the records of *R. landeri* reported by Aggundey & Schlitter (1984) and *R. lobatus* Peters, 1852 by Monadjem et al. (2024), respectively. Although not confirmed by the molecular genetic approach, we consider the here reported NMW specimens to belong to *R. webalai*. The dimensions of the NMW specimens (Table 8) conform to those published for this bat by Patterson et al. (2024) and the two localities of origin of these specimens lie within the range depicted by the latter authors (both sites were published as of *R. landeri* by Aggundey & Schlitter 1984).

Rhinonycteridae

Triaenops afer **Peters, 1877**

NMW Material (16). 6 ♂♂, 2 ♀♀ (NMW 32355–32362 [S+B]), Pangani, Lwandani Cave, 9 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♂♂ (NMW 32363 [S+A], 32364 [S+Sk]), Pangani, near the Lwandani Cave, 9 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂ (NMW 32365 [S+B]), Pangani, near the Lwandani Cave, 11 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
3 ♂♂ (NMW 32366–32368 [S+B]), Pangani, near the Lwandani Cave, 12 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♂♂ (NMW 32353, 32354 [S+B]), Shimoni, Main Well Cave, 7 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Triaenops afer occurs disjunctly in two range parts in sub-Saharan Africa, a large part covers the savanna belt of eastern Africa from Djibouti, northern Ethiopia, and western Central African Republic in the north, to eastern Zimbabwe and central Mozambique in the south; and a small part includes few localities in the south-western Congo (B.) and north-western Angola (Benda & Vallo 2009, Bates et al. 2013, Monadjem et al. 2024). In East Africa, *T. afer* represents a rather frequent species, numerous localities are available from eastern Tanzania (including islands), Kenya, and few records come also from Uganda (Monadjem et al. 2024). Most records were reported from Kenya, where more than twenty sites scattered across the whole country are known, including the northern and eastern parts (Aggundey & Schlitter 1984, Rossoni et al. 2021).

The series of the NMW specimens of *T. afer* originates from two areas of south-eastern Kenya adjacent to the sea coast, at least a third of the Kenyan records of this bat was made from this region rich in karst phenomena (Aggundey & Schlitter 1984, Rossoni et al. 2021), where also the type locality of this bat is situated (Mombaça; Peters 1877). The NMW material of *T. afer* thus does not represent an unusual collection.

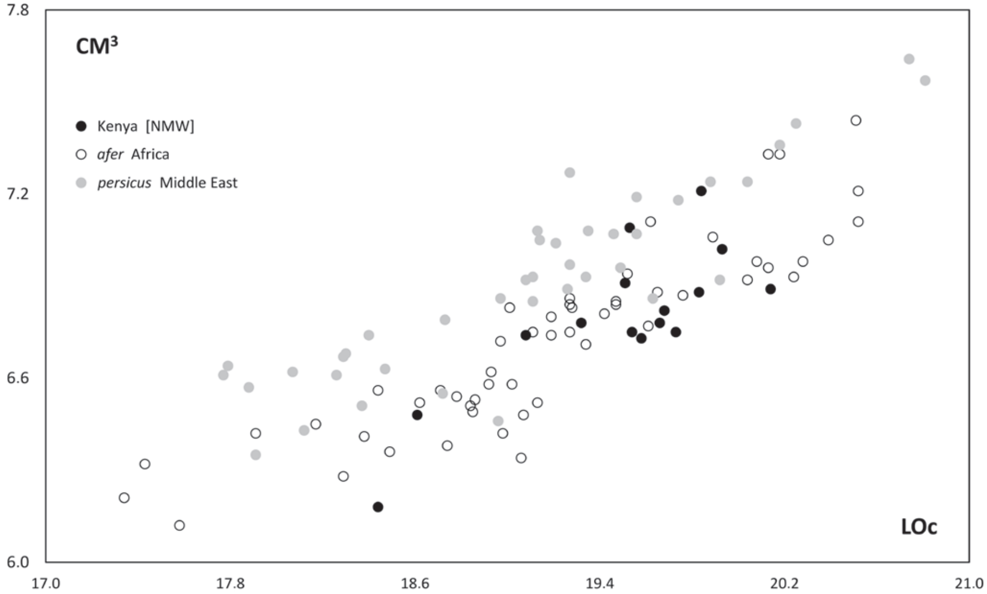
In their revision of the genus *Trianeops* Dobson, 1871 based on the results of morphometric and molecular genetic analyses, Benda & Vallo (2009) suggested that all populations of this genus occurring in continental Africa have to be referred to *T. afer*, and not to *T. persicus* Dobson, 1871. The latter species was formerly a single recognised species within the whole Afro-Asian continental range of the genus, while Benda & Vallo (2009) suggested to restrict its occurrence only to the Middle East. However, based on the additional genetic analysis by

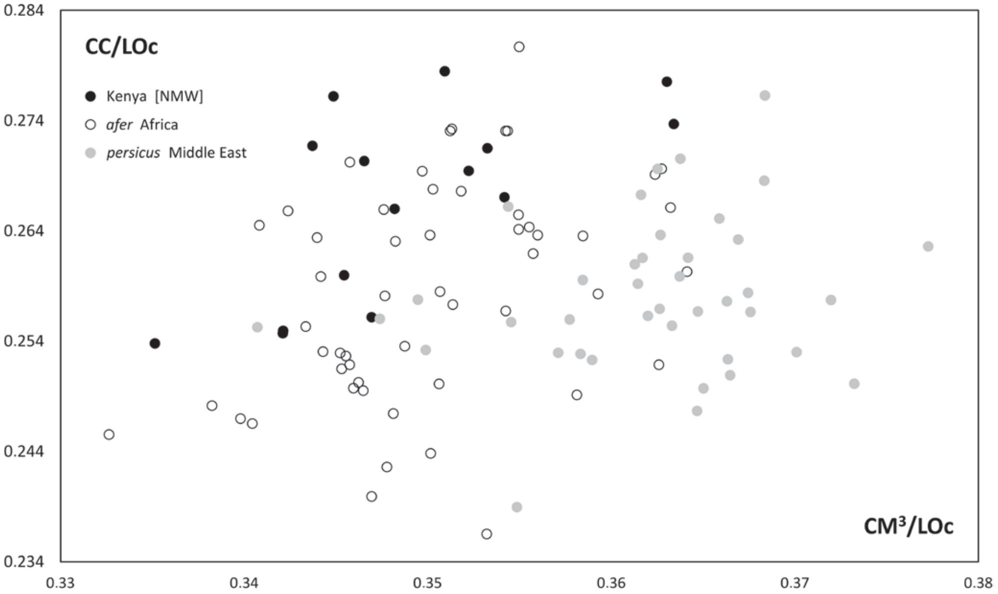
Table 9. Biometric data on the NMW specimens of *Triaenops afer* from Kenya, and on comparative samples of the genus *Triaenops* from Africa and the Middle East. For abbreviations see Methods

dimension	*Triaenops afer*					*Triaenops afer*					*Triaenops persicus*				
	Kenya (NMW)					Africa					Middle East				
	n	**M**	min	max	SD	*n*	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*16*	**52.81**	50.9	55.40	1.452	*43*	**54.59**	49.3	59.1	2.508	*38*	**52.35**	48.0	57.3	2.216
LCr	*14*	**19.89**	18.74	20.54	0.512	*49*	**19.72**	17.75	21.05	0.816	*36*	**19.78**	18.38	21.76	0.888
LOc	*15*	**19.49**	18.44	20.14	0.468	*53*	**19.21**	17.34	20.52	0.771	*40*	**19.09**	17.77	20.81	0.785
LCc	*15*	**16.93**	16.02	17.54	0.429	*53*	**16.75**	14.97	18.13	0.727	*40*	**16.71**	15.47	18.27	0.717
LaZ	*15*	**9.16**	8.63	9.37	0.214	*52*	**8.99**	8.12	9.72	0.358	*40*	**8.90**	8.28	9.84	0.361
LaI	*15*	**2.69**	2.34	3.02	0.184	*53*	**2.73**	2.34	3.23	0.186	*40*	**2.64**	2.32	2.91	0.144
LaInf	*15*	**6.79**	6.32	7.02	0.208	*53*	**6.64**	5.86	7.22	0.316	*39*	**6.39**	6.01	6.69	0.205
LaN	*15*	**7.39**	7.25	7.62	0.105	*53*	**7.39**	6.82	7.85	0.228	*40*	**7.46**	7.02	8.11	0.223
LaM	*15*	**8.80**	8.58	9.08	0.145	*53*	**8.71**	7.97	9.33	0.303	*40*	**8.71**	8.14	9.42	0.276
ANc	*15*	**6.93**	6.62	7.46	0.213	*53*	**6.74**	6.04	7.41	0.303	*40*	**6.81**	6.36	7.37	0.298
LBT	*15*	**2.98**	2.78	3.16	0.116	*53*	**3.05**	2.68	3.41	0.163	*40*	**3.00**	2.62	3.97	0.240
CC	*15*	**5.20**	4.68	5.43	0.214	*53*	**4.97**	4.32	5.53	0.304	*40*	**4.93**	4.33	5.73	0.295
M^3M^3	*15*	**6.83**	6.54	7.21	0.165	*53*	**6.66**	6.19	7.34	0.268	*40*	**6.75**	6.18	7.54	0.280
CM^3	*15*	**6.80**	6.18	7.21	0.243	*53*	**6.72**	6.12	7.44	0.298	*40*	**6.91**	6.35	7.64	0.313
LMd	*15*	**12.05**	11.38	12.62	0.343	*53*	**11.92**	10.67	12.98	0.559	*40*	**12.04**	10.97	13.46	0.577
ACo	*15*	**2.82**	2.63	2.98	0.102	*53*	**2.77**	2.38	3.18	0.189	*40*	**2.68**	2.42	3.13	0.185
CM_3	*15*	**7.32**	6.67	7.74	0.267	*53*	**7.21**	6.54	7.96	0.348	*40*	**7.44**	6.91	8.17	0.333

Rossoni et al. (2021), comprising a more representative series of African samples than that by Benda & Vallo (2009), *T. persicus* has been recently confirmed to occur also in Kenya, besides its Middle Eastern range, along with the more widely distributed *T. afer*. The occurrence of the former species is known from three sites in western Kenya, adjacent to the Eastern Rift Valley, while no evidence of this bat is available from the coastal areas of the country (Rossoni et al. 2021), from where the NMW series originates.

The dimensions of the NMW specimens of *T. afer* from Kenya are shown in Table 9. Compared to the dimensions of African and Middle Eastern samples (including all type specimens, Table 9, Figs. 13, 14), most of the NMW specimens conform in their dimensions to the morphotype of *T. afer* as redefined by Benda & Vallo (2009). The two geographical groups of populations / species differ in their body and skull size and skull shape from each other; *T. afer* (African morphotype) is on average large and has a relatively short and wide rostrum and relatively and absolutely large tympanic bullae, while *T. persicus* (Middle Eastern morphotype) is rather small with a relatively long and narrow rostrum and small tympanic bullae. Although the values of these size and shape characters overlap in certain specimens of the two population groups, most of the specimens are ordered in accordance with these morphotype characteristics and geographical affiliation. In the NMW series of specimens, this overlap is rather insignificant and most specimens lie out of the overlap zone (Fig. 13); all specimens seem to pertain to a single morphotype representing *T. afer*. On the other hand, the minority of African specimens deeply overlapping with those from the Middle East (and vice versa) exhibits an existence of morphotype variability in both population groups and eventually, they might indeed represent





Figs. 13, 14. Bivariate plots of the Kenyan and comparative samples of *Triaenops afer* and *T. persicus*. For comparative material see text. 13 – occipitocanine length of skull (LOc) against the length of upper tooth-row (CM^3). 14 – relative length of rostrum (CM^3/LOc) against the relative width of rostrum (CC/LOc).

a mixture of several lineages/taxa. However, such a hypothesis requires a parallel molecular genetic evidence.

Comparative material (93). *Triaenops afer*: **Central African Republic** [3]: 2 ♂♂, 1 ♀ (MNHN 1985-1198, 1199, 1985-1366 [S+A]), La Maboké, date unlisted, leg. R. Pujol. – **Congo (Brazzaville)** [9]: 5 ♂♂, 2 ♀♀ (MNHN 1968-412, 1985-1348a, 1348b, 1349, 1985-1497, MNHG 1074.041–045 [S+A], holotype and paratypes of *Triaenops persicus majusculus* Aellen et Brosset, 1968), Grotte de Doumboula, Loudima (Kouilou), 19 June 1964, leg. J. P. Adam; – 2 ♀♀ (MNHN 1985-1350, 1985-1351 [S+A], paratypes of *Triaenops persicus majusculus* Aellen et Brosset, 1968), Grotte de Meya-Nzouari (Kouilou), 22 November 1966, leg. J. P. Adam. – **Ethiopia** [20]: 1 ♂, 1 ♀ (ZMMU S-189632, S-189634 [S+B]), Bermil, 10 & 11 April 2010, leg. D. A. Vasen′kov; – 2 ♂♂ (ZMMU S-189613, S-189628 [S+B]), Gelego, 22 March & 27 March 2010, leg. D. A. Vasen′kov; – 1 ♂ (MZUF 6031 [S+A]), Lago di Tana, 5 March 1937, leg. Dainelli; – 1 ♂ (ZMMU S-168986 [S+B), between Mazante-Feri and Tepi, 12 October 2000, leg. L. A. Lavrenčenko & P. N. Morozov; – 1 ♂ (NMP 95925 [S+A]), Megenagna, Alatish National Park, 8 November 2012, leg. P. Benda; – 1 ♂, 3 ♀♀ (ZMMU S-181707, S-181709, S-181710, S-181717 [S+B]), Majanger zone, 10 km W of Meti, Lake Bishan-Wak'a vicinity, 2 April, 10 April, 11 April & 18 April 2007, leg. S. V. Kruskop, L. A. Lavrenčenko & P. N. Morozov; – 6 ♂♂, 3 ♀♀ (NMP 92150–92152, 92161, 92163–92167 [S+A]), Sof Omar Caves, 2 May & 3 May 2003, leg. P. Benda & J. Obuch. – **Kenya** [2]: 1 ♀ (MZUF 4361 [S+A]), Kilifi, 3 November 1968, leg. B. Lanza; – 1 ♂ (ZMB 5074 [S+A], holotype of *Triaenops afer* Peters, 1877), Mombaca, date unlisted, leg. J. M. Hildebrandt. – **Somalia** [13]: 1 ♂ (MZUF 7863 [S+A]), Galgalo, Migiurtinia, 8 October 1973, leg. R. Barazzano; – 1 ♂ (NMP pb7759 [S+A]), Laas Ciide, 22 November 2023, leg. P. Benda; – 1 ♀ (MZUF 2233 [S+A]), Pozzi di Mahas, 9 August 1959, leg. A. Sammicheli; – 6 ♂♂, 4 ♀♀ (MZUF 13074, 13086, 13088, 15719, 15721, 15723, 15725–15727, 15729 [S+A]), Showli Berdi, Bardera, 14–15 March 1984, 24–25 November 1985, leg. L. Chelazzi & G. Messana, H. Boni & H. Poggesi. – **Tanzania** [6]: 6 inds. (MNHN 1911-730/3–5, 8, 10, 1981-1359 [S+A]), Tanga, Grotte de Kulumuzi, 1909, leg. M. Alluaud.
Triaenops persicus: **Iran** [3]: 1 ♂, 2 ♀♀ (BMNH 76.3.10.3., ZMB 4370/1–2 [S+A], syntypes of *Triaenops persicus* Dobson, 1871), Shiraz, Persia, date & collector unlisted. – **Oman** [17]: 3 ♀♀ (NMP 92717–92719 [S+A]), Ain Jarziz, 27 October 2009, leg. P. Benda, A. Reiter & M. Uhrin; – 1 ♀ (NMP 92703 [S+A]),

Figs. 15, 16. Portraits of a female of *Hipposideros megalotis* (NMP 97943) collected at the Naiburta Camp, Hells Gate National Park, Kenya, on 14 August 2022.

Hagarir, 25 October 2009, leg. P. Benda, A. Reiter & M. Uhrin; – 5 ♂♂, 3 ♀♀ (NMP 93800–93807 [S+A]), 5 km W of Rawdah, 10 April 2011, leg. P. Benda, A. Reiter & M. Uhrin; – 3 ♂♂ (NMP 92758–92760 [S+A]), Taiq, 30 October 2009, leg. P. Benda, A. Reiter & M. Uhrin; – 1 ♂ (NMP 94065 [S+A]), Wadi Hannah, 30 March 2012, leg. P. Benda, A. Reiter & M. Uhrin; – 1 ♀ (NMP 97064 [S+A]), Wadi Shaith, 16 km WNW of Raysut, leg. P. Benda, A. Reiter & M. Uhrin. – **United Arab Emirates** [1]: 1 ♂ (BMNH 67.1227 [S+B], holotype of *Triaenops persicus macdonaldi* Harrison, 1955), El Ain, Buraimi Oasis, 4 September 1953, leg. D. L. Harrison. – **Yemen** [19]: 1 ♂, 1 ♀ (NMP 92271, 92273 [S+A]), Damqawt, 16 October 2005, leg. P. Benda; – 7 ♂♂, 5 ♀♀ (NMP 92253, 92254, 92256–92262, 92266 [S+A], 92255, 92263 [A], BCSU pb3037, pb3038 [S+A]), Hawf, 12 October, 14 October & 15 October 2005, leg. P. Benda; – 2 ♂♂, 1 ♀ (NMP 92275, 92276 [S+A], BCSU pb3123 [S+A]), Jebel Bura, W of Riqab, 30 October 2005, leg. P. Benda; – 1 ♀ (NMP 92277 [S+A]), Wadi Tuban, Kadamat al'Abali, 24 October 2007, leg. P. Benda & A. Reiter; – 1 ♂ (NMP 92279 [S+A]), Wadi Zabid, ca. 10 km SE of Al Mawkir, 30 October 2007, leg. P. Benda & A. Reiter.

Hipposideridae

Hipposideros megalotis (von Heuglin, 1861)

NMP Material (1). 1 ♀ (NMP 97943 [S+A]; Figs. 15, 16), Kwa Muhia, Hells Gate National Park, Naiburta Camp, 14 August 2022, leg. P. Benda & J. Červený.

Hipposideros megalotis is a rare bat, an endemic of the north-eastern Afrotropics (Kingdon 1974, Monadjem et al. 2024). Its distribution range is composed of two parts, northern and southern, interrupted by the Turkana arid region; the northern part comprises Eritrea, central Ethiopia, Djibouti, western Saudi Arabia, and southern Somalia, the southern part includes the savannas of central Kenya (Largen et al. 1974, Legendre 1982, Aggundey & Schlitter 1984, Gaucher & Brosset 1990, Lanza et al. 2015). While only few sites are known from the northern range, including the type locality, Bogos-Land (= Keren region, Eritrea; von Heuglin 1861), numerous records of *H. megalotis* are available from the Kenyan distribution spot, representing a belt of savanna habitats stretching between Lake Baringo in the north and Mount Suswa in the south (Harrison 1961, Largen et al. 1974, Kock et al. 1975, Aggundey & Schlitter 1984, Monadjem et al. 2024). The NMP specimen originates from the Hells Gate National Park in the southern part of the Kenyan range section, it is the second southernmost locality within the whole species range. The dimensions of the NMP specimen of *H. megalotis* from Kenya are shown in Table 2.

Hipposideros tephrus Cabrera, 1906

NMW Material (1). 1 ♂ (NMW 32327 [S+B]), Tsavo East National Park, Voi Gate, 3 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

NMP Material (12). 2 ♂♂, 3 ♀♀ (NMP 97928–97931 [S+A], 97932 [A]; Fig. 17), Gilgil, Oasis Camp, 6 December 2021, leg. P. Benda, L. Bufka & J. Červený;
2 ♂♂ (NMP 97872, 97873 [S+A] ; Fig. 18), Gotu Falls, Sempire Camp, 27 November 2021, leg. P. Benda, L. Bufka & J. Červený;
4 ♂♂, 1 ♀ (NMP 97896–97899 [S+A], 97900 [A]), Kampi Ya Samaki, Soi Safari Lodge, 2 December 2021, leg. P. Benda, L. Bufka & J. Červený.

Hipposideros tephrus is a bat whose species rank has been suggested just recently (Vallo et al. 2008, Monadjem et al. 2013a), formerly it was considered to represent a subspecies of *H.*

caffer s.l. (Hayman & Hill 1971, Koopman 1975, 1994, Simmons 2005). The distribution range of *H. tephrus*, as indicated by Vallo et al. (2008), comprises the Maghreb and the Sahel zone of the northern Afrotropics from Senegal to Yemen. Later, Patterson et al. (2020) demonstrated this lineage to occur also in East Africa, in Uganda and western and southern Kenya, and Baldwin et al. (2021) added the records from the coastal savanna zone of West Africa (Ghana). A question arose whether the name *tephrus* Cabrera should stay the prior name for this species in such extensive range and no other name within the *H. caffer* group is appropriate instead (e.g. *Phyllorrhina bicornis* von Heuglin, 1861). However, this point still remains to be studied. The localities of the NMW and NMP specimens do not represent important additions to the knowledge of the distribution of *H. tephrus* in Kenya, all of them are situated within the known distribution range of this species (as of *H. caffer* s.l. by Aggundey & Schlitter 1984 and Monadjem et al. 2024).

The dimensions of the NMW and NMP specimens of *H. tephrus* from Kenya are shown in Table 10. Sequences of the cytochrome *b* gene obtained from the NMP specimens from Kenya were affiliated with the East African (mitochondrial) haplogroups of *H. tephrus*, haplogroups *caffer* 1 and *caffer* 3 (corresponding to the nuclear haplogroup *caffer* 1–3) sensu Patterson et al. (2020), and the lineage A2 sensu Vallo et al. (2008), see Fig. 19. The specimens from Lake Baringo (NMP 97896, 97897, 97899) and from Lake Elmenteita (NMP 97928–97930) agreed in 100% with the haplotype MT149743 (*caffer* 1) from the specimen FMNH 215444 collected from the Lion Hill Cave in the Lake Nakuru NP, west-central Kenya. The sequence from Gotu Falls (NMP 97872) corresponded by 99.6% with the haplotype MT149757 (*caffer* 3) obtained from the specimen FMNH 234022 from Mwingi, central Kenya, and the bat NMP 97873 from the same site was congruent by 99.4% with the haplotype MT149765 (*caffer* 3) from the specimen NMK 184287 from the Marsabit NP, northern Kenya.

Figs. 17, 18. Portraits of *Hipposideros tephrus* from Kenya in the NMP collection. 17 – a male collected at the Oasis Camp near Gilgil on 6 December 2021. 18 – a male from the Sempire Camp, Gotu Falls, collected on 27 November 2021.

Table 10. Biometric data on the NMW and NMP specimens of *Hipposideros tephrus*, and of *H. ruber* and *H.* aff. *ruber* from Kenya. For abbreviations see Methods

dimension		*Hipposideros tephrus*					*Hipposideros ruber* & *H.* aff. *ruber*			
	n	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*13*	**48.21**	42.0	52.6	2.983	*10*	**49.97**	48.5	52.5	1.161
LCr	*11*	**17.17**	16.59	17.63	0.334	*7*	**18.49**	18.21	18.78	0.225
LOc	*11*	**17.02**	16.36	17.66	0.371	*7*	**18.42**	18.19	18.68	0.197
LCc	*11*	**14.55**	13.97	15.16	0.333	*7*	**15.85**	15.68	16.05	0.141
LaZ	*11*	**8.98**	8.47	9.41	0.238	*7*	**10.07**	9.56	10.39	0.316
LaI	*11*	**2.66**	2.44	2.84	0.139	*7*	**2.93**	2.79	3.36	0.197
LaInf	*11*	**4.43**	4.12	4.54	0.123	*7*	**4.76**	4.61	5.07	0.164
LaN	*11*	**7.73**	7.57	7.93	0.127	*7*	**8.39**	8.31	8.51	0.071
LaM	*11*	**9.14**	8.91	9.41	0.173	*7*	**9.76**	9.64	9.84	0.074
ANc	*11*	**5.51**	5.18	5.88	0.216	*7*	**5.90**	5.41	6.28	0.280
LBT	*11*	**3.13**	2.93	3.41	0.148	*7*	**3.27**	3.12	3.51	0.135
CC	*11*	**3.83**	3.68	4.24	0.157	*7*	**4.52**	4.26	4.75	0.195
M^3M^3	*11*	**5.93**	5.71	6.06	0.101	*7*	**6.90**	6.68	7.17	0.184
CM^3	*11*	**5.78**	5.58	5.93	0.112	*7*	**6.65**	6.48	6.76	0.125
LMd	*11*	**10.37**	10.02	10.89	0.259	*7*	**11.56**	11.06	11.93	0.356
ACo	*11*	**2.45**	2.27	2.68	0.121	*7*	**2.61**	2.51	2.76	0.088
CM_3	*11*	**6.22**	5.94	6.49	0.170	*7*	**7.15**	6.84	7.36	0.208

Hipposideros ruber **(Noack, 1893) and *H.*** aff. ***ruber***

NMW Material (6). 3 ♂♂ (NMW 32322, 32323 [S+B], 32321 [A]), Mount Elgon National Park, Kol Cave, 27 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

1 ♂ (NMW 32326 [S+B]), Pangani, near the Lwandani Cave, 12 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

2 ♂♂ (NMW 32324, 32325 [A]), Shimoni, Main Well Cave, 7 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

NMP Material (5). 5 ♂♂ (NMP 98028, 98030–98032 [S+A], 98029 [A]; Figs. 20, 21), Kwale, Shimba Hills National Park, Shimba Hills Lodge, 5 July 2023, leg. P. Benda & J. Červený.

Hipposideros ruber s.l. is a parataxon comprising several separate genetic lineages/species, defined by morphological similarities within the *H. caffer* group sensu Koopman (1975); the *ruber* morphotype was defined as the large-sized form of the group with the condylocanine length of skull larger than 15.5 mm (see also Vallo et al. 2008). This parataxon is distributed broadly across the forest and woodland savanna zones of sub-Saharan Africa, from Senegal and the Gambia in the west, to the southern Sudan and northern Ethiopia in the east, and southern Angola and central Mozambique in the south, plus islands of the Gulf of Guinea and the Zanzibar Archipelago (Hayman & Hill 1971, Koopman 1994, Monadjem et al. 2024). In East Africa, this morphotype is known to occur sparsely in all countries south of the central parts of Uganda and Kenya (Kingdon 1974, Monadjem et al. 2024); in the latter country, limited records are available from its western part (Mount Elgon region), south-eastern part (Mombasa region), and central part (Nairobi), see Aggundey & Schlitter (1984). The NMW and NMP

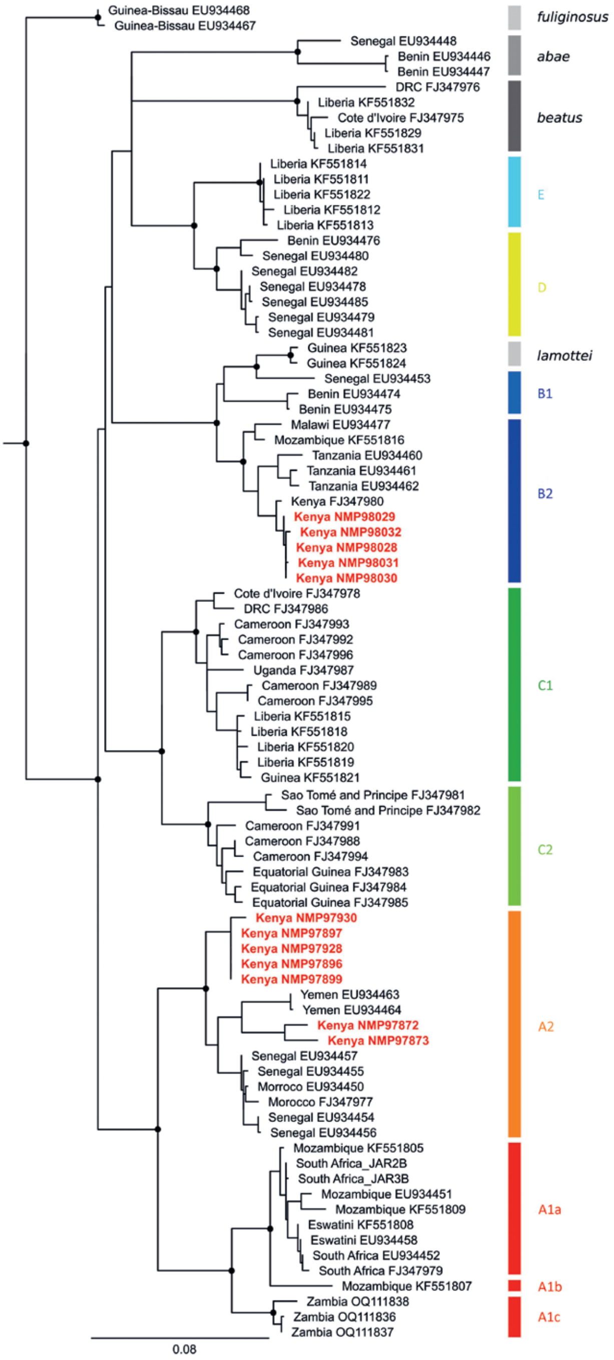
→
Fig. 19. Maximum likelihood tree of reconstructed phylogenetic relations of the *Hipposideros caffer* complex (cf. Vallo et al. 2008, Monadjem et al. 2013a) and *H. fuliginosus* (Temminck, 1853) as an outgroup, based on the cytochrome *b* sequences (the labelling of the lineages sensu Vallo et al. 2008). See Vallo et al. (2008), Monadjem et al. (2013a) and Benda et al. (2022) for the published haplotypes, the new sequences from the NMP specimens from Kenya are in red (see Appendix 2). Black dots on the nodes denote high branch support of these these nodes (e.g., SH-aLRT ≥80%, aBayes ≥0.95, UFBoot ≥90%).

specimens originate from the two former parts of the country, thus, their records do not represent a significant addition to the occurrence picture of this morphotype in Kenya.

The dimensions of the NMW and NMP specimens of *H. ruber* s.l. from Kenya are shown in Table 10. Sequences of the cytochrome *b* gene obtained from the NMP specimens from the Shimba Hills NP in south-eastern Kenya conformed to the haplotypes extracted from bats collected in the coastal parts of the country; the sequences from the specimens NMP 98028, 98029, and 98032 were congruent by 99.8–99.9% with the haplotype MN064732 from the specimen FMNH 220177 collected in the Pare Cave near Fikirini in southernmost Kenya, and the sequences of the specimens NMP 98030 and 98031 agreed in 99.9% and 100%, respectively, with the haplotype MT149778 from the specimen NMK 187202 collected in a cave near Watamu, south-eastern Kenya. These haplotypes fall into the mitochondrial haplogroup *caffer* 5 (= nuclear haplogroup '*caffer* 5–8+*ruber* 1') sensu Patterson et al. (2020) and the lineage B2 sensu Vallo et al. (2008), respectively (see Fig. 19).

This lineage (comprising both the mtDNA and nucDNA evidence) includes samples from south-eastern Kenya (Kilifi and Kwale Counties), Tanzania (including Zanzibar), Malawi, Mozambique, and also from the Murchison Falls NP in north-western Uganda (although other

Figs. 20, 21. *Hipposideros ruber* from Kenya in the NMP collection. 20 – a group roosting in a room of the Shimba Hills Lodge near Kwale, Shimba Hills National Park. 21 – portrait of a male collected from this group on 5 July 2023.


Guinea-Bissau EU934468
Guinea-Bissau EU934467
Senegal EU934448
Benin EU934446
Benin EU934447
DRC FJ347976
Liberia KF551832
Cote d'Ivoire FJ347975
Liberia KF551829
Liberia KF551831
Liberia KF551814
Liberia KF551811
Liberia KF551822
Liberia KF551812
Liberia KF551813
Benin EU934476
Senegal EU934480
Senegal EU934482
Senegal EU934478
Senegal EU934485
Senegal EU934479
Senegal EU934481
Guinea KF551823
Guinea KF551824
Senegal EU934453
Benin EU934474
Benin EU934475
Malawi EU934477
Mozambique KF551816
Tanzania EU934460
Tanzania EU934461
Tanzania EU934462
Kenya FJ347980
Kenya NMP98029
Kenya NMP98032
Kenya NMP98028
Kenya NMP98031
Kenya NMP98030
Cote d'Ivoire FJ347978
DRC FJ347986
Cameroon FJ347993
Cameroon FJ347992
Cameroon FJ347996
Uganda FJ347987
Cameroon FJ347989
Cameroon FJ347995
Liberia KF551815
Liberia KF551818
Liberia KF551820
Liberia KF551819
Guinea KF551821
Sao Tomé and Principe FJ347981
Sao Tomé and Principe FJ347982
Cameroon FJ347991
Cameroon FJ347988
Cameroon FJ347994
Equatorial Guinea FJ347983
Equatorial Guinea FJ347984
Equatorial Guinea FJ347985
Kenya NMP97930
Kenya NMP97897
Kenya NMP97928
Kenya NMP97896
Kenya NMP97899
Yemen EU934463
Yemen EU934464
Kenya NMP97872
Kenya NMP97873
Senegal EU934457
Senegal EU934455
Morroco EU934450
Morocco FJ347977
Senegal EU934454
Senegal EU934456
Mozambique KF551805
South Africa_JAR2B
South Africa_JAR3B
Mozambique EU934451
Mozambique KF551809
Eswatini KF551808
Eswatini EU934458
South Africa EU934452
South Africa FJ347979
Mozambique KF551807
Zambia OQ111838
Zambia OQ111836
Zambia OQ111837
0.08
fuliginosus
abae
beatus
E
D
lamottei
B1
B2
C1
C2
A2
A1a
A1b
A1c

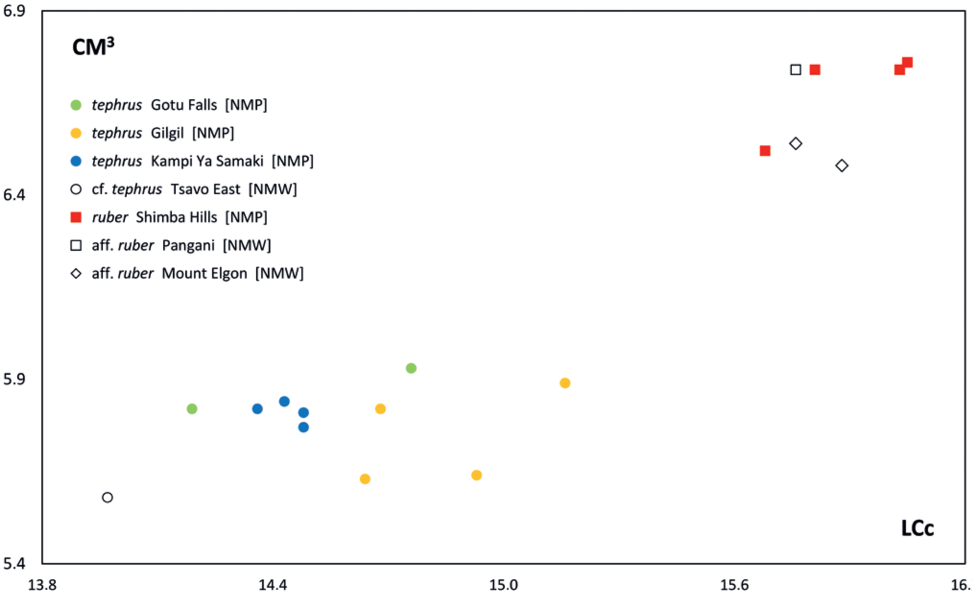


Fig. 22. Bivariate plot of the NMW and NMP samples of bats of the *Hipposideros caffer* group from Kenya: condylocanine length of skull (LCc) against the length of upper tooth-row (CM³). Closed symbols denote specimens examined by the molecular genetic approach, open symbols denote specimens examined only by morphometry.

Ugandan, as well as western Kenyan, DR Congolese, and Rwandan samples fall into other lineages), see Vallo et al. (2008) and Patterson et al. (2020). With the exception of the Ugandan locality, these samples represent a continuous range across eastern Africa, from south-eastern Kenya to central Mozambique. Moreover, no other lineage of *H. ruber* s.l. was detected in the depicted area (see Vallo et al. 2008 and Patterson et al. 2020). The genetic characters suggest that these populations represent a single phylogenetic unit that is geographically rather well defined, just the Ugandan population remains in question.

Morphologically, the specimens of this lineage lie on the transition between the two basic size-defined morphotypes, and comprise bats of both the small-sized *caffer* morphotype (its large representatives) and the large-sized *ruber* morphotype (its small representatives) and in fact, constitute the third, medium-sized morphotype (LCc 15.0–16.4 mm, vs. whole size range of the *caffer* group, LCc 13.8–17.5 mm; comp. Fig. 22 and Vallo et al. 2008: 197, Fig. 2). Bats of this lineage seem to represent a well size-defined morphotype (overlapping in size range margins with both classical morphotypes) that conforms to the description of *Phyllorhina rubra* Noack, 1893 (= *Hipposideros ruber*), defined by Noack (1893: 587) as follows: LAt 52 mm, LCr 18 mm, LaZ 11 mm (comp. the data in Table 10). The holotype of this name originates from the "Lugerrunjere-Fluss" (= Ngerengere River) in eastern Tanzania, i.e., from the centre of the above delimited distribution range of the lineage. Unfortunately, a detailed examination of the type skull (ZMB 89571) is not possible, since only the alcoholic specimen of the holotype without skull is available in the ZMB collection (Turni & Kock 2008), however, for the basic comparison the data given by Noack (1893) seem to be sufficient.

The mitochondrial and nuclear haplogroups *caffer* 5–8 sensu Patterson et al. (2020) and the mitochondrial lineage B2 sensu Vallo et al. (2008), respectively, seem to represent a real, genetically, morphologically, and geographically well defined phylogenetic unit, deserving a full species position (see Vallo et al. 2008, Monadjem et al. 2013a). We do not see any variance in naming this unit *H. ruber* [s.str.], although any additional evidence will certainly be useful for confirmation of this conclusion. Monadjem et al. (2024) considered (probably) only the haplogroup *caffer* 7 sensu Patterson et al. (2020) to represent *H. ruber* s.str., to which they attributed bats from central Mozambique, Malawi, and central and southern Tanzania. However, such a narrow conception does not consider the evidence given by the nuclear genome analysis, showing this bat to be a more widespread faunal element of eastern Africa. On the other hand, due to the dimensional overlap with the small-sized morphotype occurring in sympatry with *H. ruber* in south-eastern Africa (at least) and representing *H. caffer* s.str. (Vallo et al. 2008, Monadjem et al. 2013a, Benda et al. 2022), the simple size-based identification of individuals of these two species ceased for the moment. The morphological definition and possible differences useful for determination of these two species in the zones of their sympatric occurrence remain to be discovered.

Simultaneously, a "nomenclatural" problem arose, since the real *ruber* morphotype is the medium-sized form. The large-sized morphotype of the *caffer* group sensu Koopman (1975), until now named the *ruber* morphotype or *H. ruber* s.l., has to be renamed with an appropriate name. Here we tentatively use *H.* aff. *ruber*, in accordance with Vallo et al. (2011a).

Unfortunately, the NMW material of *H.* aff. *ruber* cannot be attributed to a clade/lineage; although the Shimoni and Pangani series of specimens came from the areas where only the lineages *caffer* 5–8 sensu Patterson et al. (2020) have been documented (and we can affiliate them with *H. ruber* s.str.), the Mount Elgon series originated from a region where the lineages *ruber* 1 and 2 sensu Patterson et al. (2020) were recorded. The NMW set thus may represent a mixture of several lineages/species, only sharing the large-sized morphotype of the *caffer* group. Hence, we keep these specimens preliminarily under the parataxon *H.* aff. *ruber*.

***Macronycteris vittata* (Peters, 1852)**

NMW Material (20). 8 ♂♂, 4 ♀♀ (NMW 32328–32339 [S+B]), Shimoni, Road Side Cave, 6 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♂♂, 6 ♀♀ (NMW 32340, 32341, 3243–32348 [S+B]), Shimoni, Road Side Cave, 7 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

NMP Material (7). 2 ♂♂, 2 ♀♀ (NMP 97982–97985 [S+A]), Fikirini, Mbenyenye Cave, 22 August 2022, leg. P. Benda & J. Červený;
1 ♂ (NMP 97973 [S+A]; Fig. 24), Shimoni, Slave Cave, 22 August 2022, leg. P. Benda & J. Červený;
2 ♂♂ (NMP 98015, 98016 [S+A]; Fig. 24), Watamu, Kaboga Cave, 3 July 2023, leg. P. Benda & J. Červený.

The limits of the distribution range of *Macronycteris vittata* are still a subject of research. However, this bat is not rare in the central and north-eastern parts of Africa according to Monadjem et al. (2024). Its records are scattered from South Sudan and central Ethiopia in the north, to central Namibia and northern South Africa in the south, while the distribution in West Africa remains controversial. In East Africa, it belongs among rather infrequent bats, the

Figs. 23, 24. *Macronycteris vittata* from Kenya in the NMP collection. 23 – portrait of a male collected from the Slave Cave, Shimoni, on 22 August 2022. 24 – a colony of ca. 800 individuals in the Kaboga Cave at Watamu, observed on 3 July 2023.

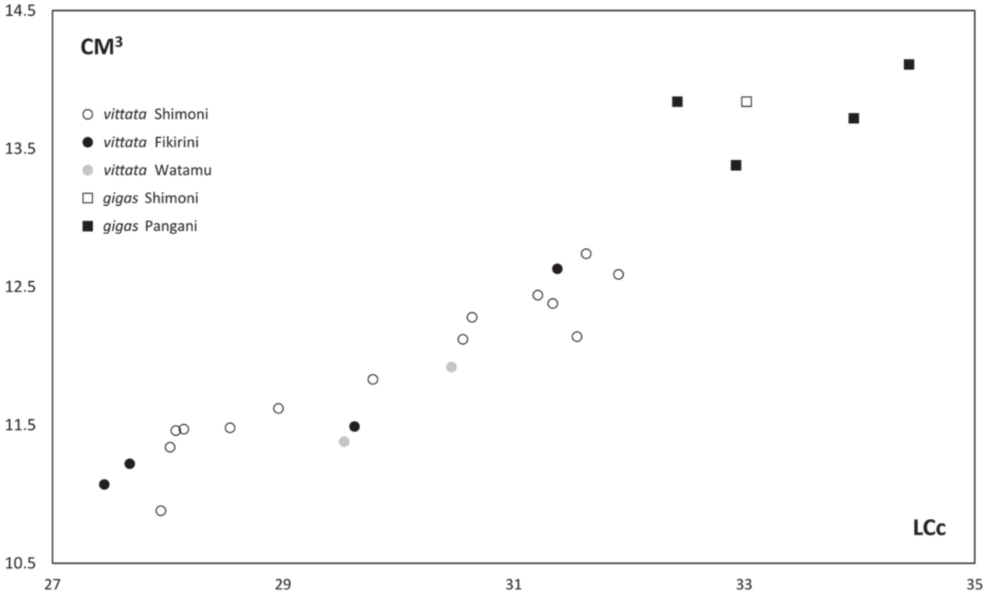


Fig. 25. Bivariate plot of the NMW and NMP samples of bats of the genus *Macronycteris* from Kenya: condylocanine length of skull (LCc) against the length of upper tooth-row (CM^3). Only adult specimens are included.

Table 11. Biometric data on the NMW and NMP specimens of *Macronycteris vittata* and *M. gigas* from Kenya. For abbreviations see Methods

dimension	*Macronycteris vittata*					*Macronycteris gigas*				
	n	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*20*	**95.55**	86.7	103.4	5.506	*5*	**105.04**	98.9	109.6	4.717
LCr	*20*	**34.25**	30.93	36.84	2.096	*5*	**38.13**	37.34	40.38	1.308
LOc	*20*	**34.48**	31.17	37.46	2.255	*5*	**38.20**	37.31	40.83	1.514
LCb	*20*	**30.39**	28.02	32.44	1.521	*5*	**33.94**	33.23	35.16	0.736
LCc	*20*	**29.72**	27.45	31.91	1.524	*5*	**33.35**	32.42	34.43	0.818
LaZ	*20*	**19.08**	17.11	20.64	1.281	*5*	**20.97**	20.24	22.58	0.923
LaI	*19*	**3.46**	3.18	3.67	0.139	*5*	**3.81**	3.41	4.13	0.295
LaInf	*20*	**9.74**	8.87	10.73	0.531	*5*	**11.12**	10.77	11.68	0.347
LaN	*20*	**12.62**	11.34	14.57	0.665	*5*	**14.20**	13.88	14.62	0.289
LaM	*20*	**16.53**	14.79	18.18	1.327	*5*	**17.17**	16.53	18.68	0.861
ANc	*20*	**12.07**	9.35	14.57	1.858	*5*	**12.90**	11.94	15.24	1.351
LBT	*20*	**4.15**	3.67	5.56	0.429	*5*	**4.41**	4.18	4.65	0.193
CC	*20*	**9.53**	8.61	10.37	0.630	*5*	**10.97**	10.38	11.47	0.463
M^3M^3	*20*	**12.00**	10.98	12.62	0.435	*5*	**14.07**	13.43	14.47	0.419
CM^3	*20*	**11.82**	10.88	12.74	0.560	*5*	**13.78**	13.38	14.11	0.264
LMd	*20*	**23.14**	21.14	24.93	1.260	*5*	**26.28**	25.77	27.46	0.698
ACo	*20*	**7.70**	6.68	8.64	0.517	*5*	**8.73**	8.41	9.34	0.370
CM_3	*20*	**13.40**	12.45	14.39	0.704	*5*	**15.70**	15.18	16.43	0.456

confirmed records of *M. vittata* are known from Burundi and the eastern parts of Kenya and Tanzania, including Zanzibar and Pemba (Monadjem et al. 2024). The localities of the NMW and NMP specimens rank among those already published by various authors, see the reviews by Aggundey & Schlitter (1984) and Monadjem et al. (2024).

The dimensions of the adult NMW and NMP specimens of *M. vittata* from Kenya are shown in Table 11 (see also Fig. 25). Sequences of cytochrome *b* gene extracted from two NMP specimens (NMP 97973, 97982) agreed in 100% with the haplotype MT149882 extracted from the specimen FMNH 192801 (Pemba Island, Tanzania), and from two other NMP specimens (NMP 98015, 98016) in 100% with the haplotype MT149876 from the specimen FMNH 215952 (Arabuko Sokoke Reserve, Kenya; Patterson et al. 2020).

Macronycteris gigas (Wagner, 1845)

NMW Material (5). 1 ♀ (NMW 32349 [S+B]), Pangani, near the Lwandani Cave, 10 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

2 ♀♀ (NMW 32350 [S+B], 32351 [S+Sk]), Pangani, near the Lwandani Cave, 11 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

1 ♂ (NMW 32352 [S+B]), Pangani, near the Lwandani Cave, 12 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

1 ♀ (NMW 32342 [S+B]), Shimoni, Road Side Cave, 6 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Reference. Aggundey & Schlitter (1984).

Similarly as in the previous bat species, the distribution range of *Macronycteris gigas* is still insufficiently defined. It is considered to be a predominantly West African species, distributed continually in the forest zone from the Gambia and Guinea-Bissau to the Central African Republic, western Angola, central DR Congo, and western Uganda (Monadjem et al. 2024). In East Africa, besides the single locality in westernmost Uganda connecting the continual West African range (Rwanasenge; Thorn & Kerbis Peterhans 2009), *M. gigas* is known to occur only in the coastal areas of south-eastern Kenya and eastern Tanzania (Happold 2013b, Monadjem et al. 2024). The two localities of the NMW specimens that have been published already by Aggundey & Schlitter (1984) are also situated in the latter region.

The dimensions of the NMW specimens of *M. gigas* from Kenya are shown in Table 11. While the ranges of the forearm length of *M. gigas* and *M. vittata* from the NMW and NMP collections were overlapping (Table 11), the large skull measurements (LCr, LCc, LaInf, CM^3, LMd, CM_3) clearly separated the specimens of these two species from south-eastern Kenya, i.e. from the region of their sympatric and syntopic occurrence (Table 11, see Fig. 25). Without doubts, the occurrence of *M. gigas* in south-eastern Kenya was confirmed by the results of genetic analysis by Patterson et al. (2020); these results also indirectly confirmed the applicability of the traditional size characters for distinguishing between these two species (cf. Andersen 1906, Thorn & Kerbis Peterhans 2009, Happold 2013b).

Doryrhina cyclops (Temminck, 1853)

NMW Material (1). 1 ♂ (NMW 32691 [S+Sk+B]), North Nandi Forest, 3 km W of Chomisia, 6 December 1979, leg. F. Spitzenberger.

Doryrhina cyclops is a forest dwelling bat, its distribution range stretches in a belt across the rainforest zone from the Gambia and Senegal to South Sudan, southern Kenya and central Tanzania, including Bioko Island (Hayman & Hill 1971, Decher & Fahr 2005, Monadjem et al. 2024). Only few records are available from East Africa, and just four sites are known from Kenya (Aggundey & Schlitter 1984, Schlitter et al. 1986, Cockle et al. 1998, Monadjem et al. 2024). One locality of *D. cyclops*, Shimba Hills NP, was reported from the south-eastern part of the country (Schlitter et al. 1986), the remaining records were made in the forest patches of western Kenya. The NMW specimen of this bat came from the latter area.

The dimensions of the NMW specimen of *D. cyclops* from Kenya are shown in Table 2. Although this male specimen is large, its dimensions still lie within the range margins of this species as given by Hill (1963) and Decher & Fahr (2005) and mostly do not reach those of *D. camerunensis* Eisentraut, 1956, which is also known to occur in western Kenya (Patterson et al. 2020, Monadjem et al. 2024).

Emballonuridae

Coleura afra (Peters, 1852)

NMW Material (25). 6 ♂♂, 7 ♀♀ (NMW 32201–32203, 32207, 32209, 32212 [S+B], 32208 [S], 32204–32206, 32210, 32211, 32213 [A]), Msambweni, Msambweni Caves, 7 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

2 ♂♂, 4 ♀♀ (NMW 32216–32219 [S+B], 32220 [S+Sk], 32215 [A]), Pangani, Lwandani Cave, 9 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

2 ♂♂, 2 ♀♀, 1 ind. (NMW 27655–27658 [S+A], 27659 [S+Sk]), Ukunda, Diani, July 1978, leg. K. Kollnberger;
1 ♀ (NMW 32214 [A]), Ukunda, Diani, Leisure Lodge, 8 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

NMP Material (8). 1 ♀ (NMP 98038 [S+A]), Engilae, 1 September 2004, leg. D. Modrý;
1 ♂, 3 ♀♀ (NMP 97986–97988 [S+A], 97989 [A]; Figs. 26, 27), Fikirini, Mbenyenye Cave, 22 August 2022, leg. P. Benda & J. Červený;
1 ♂ (NMP 97991 [S+A]), Ukunda, Diani, Leisure Lodge, 23 August 2022, leg. P. Benda & J. Červený;
1 ♂, 1 ♀ (NMP 98022 [S+A], 98021 [A]), Watamu, Kaboga Cave, 3 July 2023, leg. P. Benda & J. Červený.

References. Vallo et al. (2018), Uvizl et al. (2019).

Coleura afra is a widespread bat in the savanna belt of the African tropical zone, its records are distributed patchily from Guinea-Bissau and Guinea-Conakry to the southern Sudan, southern Somalia, western Angola, and central Mozambique (Kock 1969, Dunlop 1997, Uvizl et al. 2019). In East Africa, the occurrence of *C. afra* is the most abundant of the whole continent and nearly continuous from the southern Sudan and eastern DR Congo to southern Kenya and north-eastern Tanzania (Kulzer 1959, Kingdon 1974, Aggundey & Schlitter 1984, Webala et al. 2009, Monadjem et al. 2024). Most of the NMW and NMP specimens originate from localities in the coastal areas of Kenya, where this species is a common bat and these records do not represent a significant addition to its distribution pattern (see Peters 1879, Kulzer 1959, Harrison 1961, Kingdon 1974, Aggundey & Schlitter 1984, Musila et al. 2020). The NMP specimen from Engilae in central Kenya is more important since *C. afra* is a rather infrequent bat there. This record interconnects the previously documented localities at Lake Turkana, Lake Baringo, and near Mwidi (Kingdon 1974, Aggundey & Schlitter 1984, Webala et al. 2009, Vallo et al. 2018).

Figs. 26, 27. *Coleura afra* from Kenya in the NMP collection. 26 – an individual roosting in the Mbenyenye Cave near Fikirini. 27 – a female collected from this cave on 22 August 2022.

Table 12. Biometric data on the NMW and NMP specimens of *Coleura afra*, *Taphozous hildegardeae*, and *Nycteris thebaica* from Kenya. For abbreviations see Methods

dimension	*Coleura afra*					*Taphozus hildegardeae*					*Nycteris thebaica*				
	n	**M**	min	max	SD	*n*	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*27*	**49.13**	45.9	51.4	1.478	*24*	**65.08**	63.2	68.0	1.325	*11*	**42.95**	39.4	45.2	1.765
LCr	*16*	**18.07**	17.57	18.48	0.258	*14*	**20.91**	20.61	21.53	0.270	*11*	**18.81**	17.98	19.48	0.555
LOc	*21*	**17.83**	17.32	18.32	0.261	*23*	**21.39**	20.93	22.09	0.300	*11*	**18.85**	18.22	19.42	0.458
LCb	*15*	**16.67**	16.19	16.98	0.224	*14*	**19.98**	19.54	20.83	0.315	*10*	**16.61**	15.80	17.41	0.602
LCc	*22*	**16.18**	15.62	16.81	0.263	*23*	**19.86**	19.54	20.63	0.291	*9*	**16.54**	15.81	17.11	0.463
LaZ	*22*	**10.29**	9.94	10.84	0.219	*24*	**12.60**	12.34	13.21	0.215	*11*	**10.87**	10.27	11.41	0.391
LaI	*22*	**5.31**	4.91	5.81	0.221	*24*	**5.88**	5.03	6.37	0.232	*11*	**4.76**	4.61	5.03	0.126
LaP	*22*	**3.05**	2.71	3.27	0.146	*24*	**4.95**	4.82	5.18	0.081	*11*	**4.19**	3.92	4.76	0.267
LaInf	*22*	**4.99**	4.51	5.33	0.223	*24*	**5.83**	5.63	6.03	0.111	*11*	**4.57**	4.43	4.74	0.103
LaN	*22*	**7.86**	7.49	8.34	0.190	*24*	**9.82**	5.16	10.38	1.005	*11*	**8.39**	7.97	8.66	0.209
LaM	*21*	**9.33**	8.84	9.74	0.231	*24*	**11.23**	11.02	11.73	0.156	*10*	**8.31**	8.08	8.63	0.180
ANc	*22*	**6.35**	5.93	6.71	0.189	*24*	**7.90**	7.68	8.14	0.146	*10*	**6.50**	6.28	6.76	0.165
LBT	*21*	**3.70**	3.47	4.14	0.156	*21*	**4.80**	4.52	5.02	0.126	*11*	**3.25**	2.98	3.51	0.151
CC	*20*	**4.28**	3.97	4.49	0.132	*24*	**4.04**	3.93	4.27	0.082	*11*	**4.57**	4.31	4.98	0.208
M^3M^3	*21*	**8.12**	7.79	8.82	0.233	*24*	**8.80**	8.61	9.17	0.153	*11*	**6.95**	6.71	7.38	0.205
CM^3	*23*	**7.31**	7.04	7.73	0.156	*24*	**8.92**	8.61	9.26	0.159	*11*	**6.39**	6.13	6.74	0.210
LMd	*23*	**12.62**	12.03	13.22	0.272	*24*	**15.47**	15.02	16.08	0.293	*11*	**12.00**	11.35	12.38	0.362
ACo	*23*	**3.51**	3.24	3.76	0.135	*24*	**5.57**	5.31	5.85	0.116	*11*	**3.78**	3.48	4.03	0.183
CM_3	*23*	**7.39**	7.12	7.87	0.173	*24*	**9.71**	9.47	10.31	0.191	*11*	**6.88**	6.56	7.21	0.220

For this study, we newly generated 11 sequences of the cytochrome *b* gene of three emballonurid species from Kenya from the NMP collection (four for *Coleura afra*, one for *Taphozous perforatus*, and six for *T. hildegardeae*; the specimen of *C. afra* NMP 98038 was sequenced already by Vallo et al. 2018). These sequences were supplemented with GenBank sequences of available Old World emballonurids as well as of nycterid bats as an outgroup, resulting in a final dataset comprising 233 sequences (Fig. 28, Appendix 2). The 1,140 bp long dataset contained 587 parsimony informative positions (51.5% of the total length).

The sequences of *C. afra* clustered into four lineages similarly as in the previous studies (Vallo et al. 2018, Uvizl et al. 2019) and the new Kenyan sequences grouped with two previously reconstructed lineages, the first one (East Africa 1, EA1; Fig. 28) formed with other samples from Kenya and from Pemba Island of Tanzania (Ruedi et al. 2012), the other one (EA2) with the samples from mainland Tanzania (Amboni Caves at Tanga; Goodman et al. 2012). Other two lineages of *C. afra* were formed with samples from Ghana and Gabon (cf. Vallo et al. 2018), but the relationships among these lineages has not yet been satisfactorily resolved, including this study. Similarly, the relationships are not yet resolved within the entire genus *Coleura*, containing three other species. The only supported node was found between two species of the Indian Ocean islands, *C. kibomalandy* from Madagascar and *C. seychellensis* from the Seychelles. The genetic distances among the four mitochondrial lineages of *C. afra* are rather large (3.39–5.72%; Table 13, Uvizl et al. 2019), enough to give a basis for taxonomic splitting (see e.g. Baker & Bradley 2006). However, the sympatric and even syntopic occurrence of the lineages containing the Kenyan bats (East Africa 1 and 2) in the Mbenyenye Cave in southernmost Kenya (own data, Demos et al. 2019b), combined with a lack of any morphological distinctness (all Kenyan specimens share the identical morphotype, Fig. 29, see also data by Vallo et al. 2018), suggests a complex phylogenetic history of the species rather than a taxonomic relevance of these mitochondrial lineage separations. Without doubts, these findings

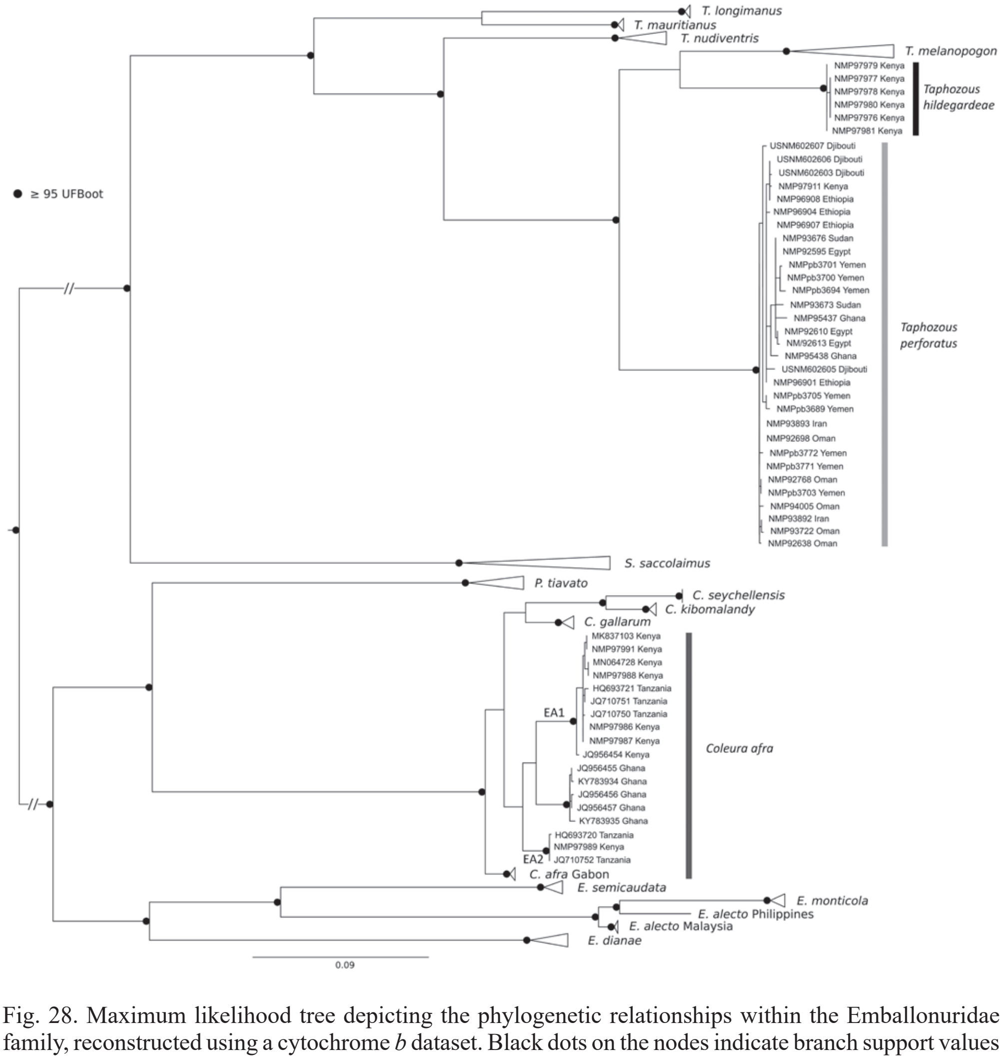


Fig. 28. Maximum likelihood tree depicting the phylogenetic relationships within the Emballonuridae family, reconstructed using a cytochrome *b* dataset. Black dots on the nodes indicate branch support values ≥90% UFBoot. See Vallo et al. (2018) and Uvizl et al. (2019) for the published haplotypes, for new haplotypes from Kenya and Ethiopia see Appendix 2; abbreviations of the genus names: *T.* – *Taphozous*, *S.* – *Saccolaimus*, *P.* – *Paremballonura*, *C.* – *Coleura*, *E.* – *Emballonura*.

Table 13. Percent pairwise uncorrected genetic distances among and within the reconstructed emballonurid genera *Taphozous* and *Saccolaimus*, and *Coleura* based on the cytochrome *b* sequences

Taphozous	*longimanus*	*mauritianus*	*nudiventris*	*melanopogon*	*hildegardeae*	*perforatus*	*saccolaimus*
longimanus	26.00						
mauritianus	12.0–12.4	0.1–0.3					
nudiventris	16.4–17.8	14.8–16.4	0.0–4.4				
melanopogon	19.0–19.7	16.5–18.5	15.0–18.9	0.0–7.3			
hildegardeae	17.4–18.4	17.5–17.9	15.1–16.5	11.3–13.0	0.0–0.2		
perforatus	18.6–19.4	17.5–18.4	16.4–18.5	11.7–13.0	11.7–12.9	0.0–1.4	
saccolaimus	20.3–21.4	19.4–19.8	18.7–21.6	20.7–22.1	21.0–22.1	19.9–21.9	0.5–9.7
Coleura	*seychellensis*	*kibomalandy*	*gallarum*	*afra* EA1	*afra* Ghana	*afra* EA2	*afra* Gabon
seychellensis	0.00						
kibomalandy	5.18–5.53	5.80					
gallarum	8.20–8.76	6.78–7.40	0.00–1.14				
afra East Africa 1	8.48–9.25	8.00–8.96	5.03–6.39	0.00–0.76			
afra Ghana	8.68–8.77	7.48–8.16	5.37–5.80	3.58–4.19	0.09–0.44		
afra East Africa 2	8.51–8.65	7.19–7.59	4.67–5.00	3.39–3.81	3.42–3.71	0.00–0.09	
afra Gabon	8.25–8.51	6.90–7.81	4.41–5.17	4.82–5.72	4.65–5.09	4.11–4.50	0.09–0.35

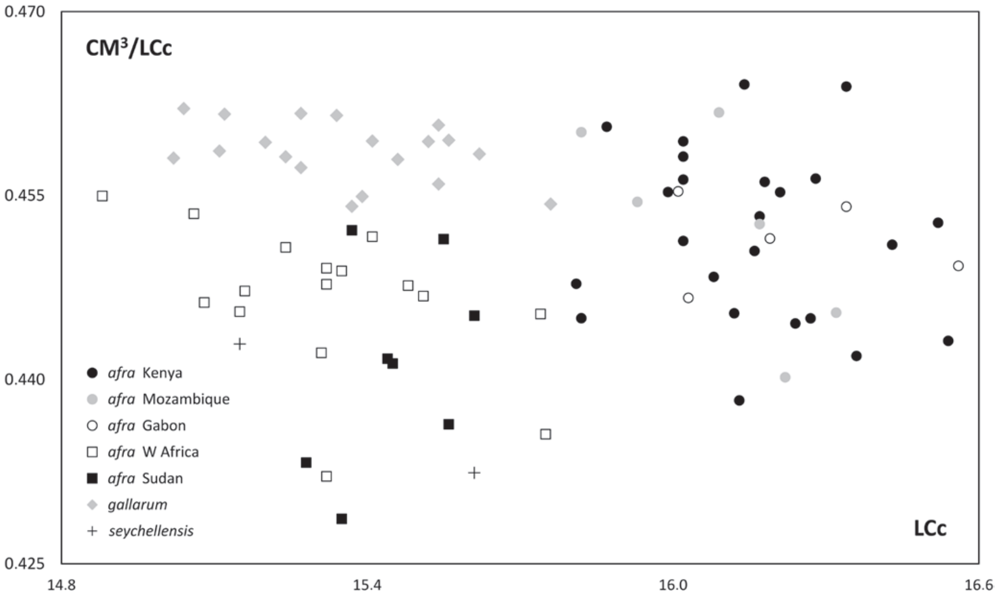


Fig. 29. Bivariate plot of the examined Kenyan and comparative samples of the genus *Coleura*: condylocanine length of skull (LMd) against the relative length of rostrum (CM_3/LCc). For comparative material see text. Legend of the geographical specification of the comparative sets: W Africa = Ghana, Guinea-Conakry, and Guinea-Bissau; Sudan = Kordofan and South Sudan; *gallarum* = Oman, Yemen, and the Sudan (Suakin); *seychellensis* = Seychelles.

deserve a deep attention and profound research with a broad sampling of *Coleura* across its range and combined molecular genetic revision with the use of both mitochondrial and nuclear markers to define convincingly the species limits of *C. afra* and other species of the genus. The dimensions of the NMW and NMP specimens of *C. afra* from Kenya are shown in Table 12.

Comparative material (60). *Coleura afra*: **Gabon** [5]: 2 ♂♂, 3 ♀♀ (NMP GB84, GB86, GB130–132 [S+A], Belinga, date unlisted, leg. P. Vallo. – **Guinea-Conakry** [12]: 10 ♂♂, 1 ♀, 1 ind. (ZMMU S-129899–129910, S-174445 [S]), Kindia, January 1981, leg. Konstantinov. – **Guinea-Bissau** [1]: 1 ♀ (MHNG 1326.3 [S+A], syntype of *Coleura kummeri* Monard, 1939), Madina Boé, 5 March 1938, leg. A. Monard. – **Ghana** [3]: 1 ♂ (NMP pv44 [S+A]), Buoyem, date unlisted, leg. P. Vallo; – 1 ♂, 1 ♀ (NMP G12/287, G12/288 [S+A]), Tongo, 8 November 2012, leg. P. Vallo. – **Kenya** [2]: 2 inds. (MHNG 1717.6, 1717.7 [S]), grotte a Coleura, Leisure Lodge, Diani Beach, 26 km S of Mombasa, 29 September 1975, leg. P. Strinati & V. Aellen. – **Mozambique** [6]: 2 ♂♂, 2 ♀♀, 2 inds. (ZMB 571[a, b], 54845, 67559, 67562, 67651 [S+A], type series of *Emballonura afra* Peters, 1852), Tete, 1843–1847, leg. W. Peters. – **South Sudan** [3]: 2 ♀♀ (ZFMK 183, 186 [S+B]), Gebel Zeraf (Bahr el Zeraf), 14 March 1913, leg. H. Freiherr von Geyr & O. le Roi; – 1 ♂ (ZFMK 187 [S+B]), Taufikia (Bahr el Abiad), 17 March 1913, leg. H. Freiherr von Geyr & O. le Roi. – **Sudan** [5]: 3 ♂♂, 2 ♀♀ (ZMMU S-101617, S-101619–101622 [S+A]), 2 km NE of Kadugli, 6 January 1965, leg. D. Kock.

Coleura gallarum: **Oman** [7]: 7 ♀♀ (NMP 94041–94047 [S+A]), Ain Hamran Cave, 28 March 2012, leg. P. Benda, A. Reiter & M. Uhrin. – **Sudan** [2]: 2 ♂♂ (MHNG 913.005, 1047.081 [S+A]), Suakin, 16 February 1956, leg. P. Strinati. – **Yemen** [12]: 1 ♂, 1 ♀ (MSNG 44397[a, b] [S+A]), presso di Aden, 1893, leg. A. Pogliani; – 5 ♂♂, 5 ♀♀ (NMP pb3773, 3774, 3776–3781 [S+A], pb3775, 3782 [A]), Shuhayr, 6 November 2007, leg. P. Benda & A. Reiter.

Coleura seychellensis: **Seychelles** [2]: 1 ♂, 1 ♀ (ZMB 3470[a, b] [S+A], syntypes of *Coleura seychellensis* Peters, 1868), Seychelles, date unlisted, leg. E. P. Wright.

Taphozous perforatus **Geoffroy, 1818**

NMP Material (1). 1 ♂ (NMP 97911 [S+A]; Fig. 30), Lake Baringo, Lesukut Island, 3 December 2021, leg. P. Benda, L. Bufka & J. Červený.

Taphozous perforatus is a widespread inhabitant of dry open habitats of south-western Asia and a large part of Africa (Bonaccorso 2019); in Asia, it occurs in the belt stretching from the Levant and southern Arabia to western and southern India, its African range comprises the north-eastern section of the Sahara and a belt of savannas of the sub-Saharan part of the continent, from Senegal and Guinea-Bissau to the Sudan, Djibouti, and Somalia, and from South Sudan and Ethiopia to northern Botswana and eastern South Africa (Kock 1969, Kingdon 1974, Harrison & Bates 1991, Pearch et al. 2001, Bonaccorso 2019, Monadjem et al. 2024). With the exception of the areas broadly associated with the Nile river, *T. perforatus* is a rather rare bat in its African range. In East Africa, a limited number of records is scattered over most of the region, altogether ten localities are known from Kenya, mainly from the more arid areas of the central and eastern parts of the country (Kingdon 1974, Aggundey & Schlitter 1984, Webala et al. 2009, Monadjem et al. 2024). The NMP specimen from the Lesukut Island in Lake Baringo represents the westernmost record from Kenya along with the record from the Central Island of Lake Turkana, situated some 320 km northwards (Aggundey & Schlitter 1984).

However, the new NMP specimen of *T. perforatus* from Kenya contributed to the understanding of the phylogenetic relations among populations of this bat and its intraspecific taxonomy. The intraspecific taxonomic arrangement of this bat is rather controversial, several poorly defined subspecies have been recognised (Thomas 1915, Allen 1939, Harrison 1958, 1962, Kock

Fig. 30. Portrait of a male of *Taphozous perforatus* (NMP 97911) collected from a small cave on the Lesukut Island, Lake Baringo, Kenya, on 3 December 2021.

1969, Hayman & Hill 1971, Hill & Morris 1971, Koopman 1975, 1994). Most recently, Simmons (2005), Taylor (2013), and Bonaccorso (2019) agreed with the existence of four subspecies of *T. perforatus*. The nominotypical form in Egypt and northern Sudan, *T. p. haedinus* Thomas, 1915 in the Asian range and in eastern Africa, *T. p. senegalensis* Desmarest, 1820 in West Africa from Senegal to Nigeria, and *T. p. sudani* Thomas, 1915 from the southern Sudan to South Africa. However, the molecular genetic analysis by Uvizl et al. (2019) did not find support for such a diversified intraspecific arrangement in this bat. The haplotypes of *T. perforatus* from the Middle East (Iran, Oman, Yemen), north-eastern Africa (Egypt, Sudan, Djibouti), and West Africa (Ghana) created a single lineage, both for mitochondrial and nuclear markers, with a very shallow genetic diversity – among 41 haplotypes of the gene for cytochrome *b*, an average genetic distance was 0.6%. This result suggested that the populations of western Asia and western and north-eastern Africa represent a single taxon, and since *T. perforatus* was described based on the specimens from Upper Egypt (type locality: Kom Ombo and Thebes; see Benda & Ševčík 2020) whose populations were included into the analysis, all the sampled populations should belong to the nominotypical form. However, this analysis did not solve the validity of particular subspecies, only broadened the range of the nominotypical one.

The description of the dark coloured East African subspecies *T. p. haedinus*, which was formerly considered to occur also in the Middle East (Thomas 1915, Kock 1969) and in a more extreme view also in the whole Asian distribution range of *T. perforatus* (Koopman 1994, Taylor 2013, Bonaccorso 2019), was based on a single male from Chanler Falls, Eusso Nyiro, British East Africa (= Gotu Falls, Ewaso Nyiro, Kenya; Thomas 1915). The type locality lies

223 km east of the Lesukut Island, from where the NMP specimen originates. Both localities are situated in central Kenya and most likely, they are inhabited by an identical population. The NMP specimen of *T. perforatus* was subjected to a molecular genetic analysis (see details under *Coleura afra* above) and compared with numerous haplotypes available for this species from other countries. The Kenyan haplotype aligned well with all other compared haplotypes, both African and Middle Eastern ones (sensu Uvizl et al. 2019, plus samples from Ethiopia), forming a single lineage (the genetic distance among 31 haplotypes of the cytochrome *b* gene was in the range of 0.00–1.41%; see Table 13), in a sister position to the lineages comprising *Taphozous hildegardeae* and *T. melanopogon* Temminck, 1841 (Fig. 28). Otherwise, the topology of the genus *Taphozous* is in accordance with the previous study by Uvizl et al. (2019).

This result showed that the populations of *T. perforatus* from eastern Africa (Kenya, Ethiopia, Djibouti) represent an identical phylogenetic unit with the populations of this bat from the Palaearctic range (Egypt, northern Sudan, Arabia, Iran) and from West Africa. The recognition of the subspecies *T. p. haedinus* is thus obviously unjustified. This view is also supported by the morphometric comparison, no apparent difference in metric traits was observed among the populations examined parallelly by the molecular genetic approach (Fig. 31, Table 14); in Table 14 see also the dimensions of the NMP specimen of *T. perforatus* from Kenya.

The dark colouration of the pelage in this alleged subspecies seems to represent just a (local) ecomorph which is not reflected in the phylogenetic structure of the species (cf. Corbet 1978). We suggest to consider the name *haedinus* Thomas a junior synonym of *perforatus* Geoffroy and without a taxonomic relevance, and the same applies for the name *swirae* Harrison, 1958

Table 14. Biometric data on the NMP specimen of *Taphozous perforatus* from Kenya, and on comparative samples of this species from Africa and Arabia. For abbreviations see Methods

dimension	Kenya	Ghana		NE Africa					Arabia				
	97911	95437	95438	*n*	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	62.9	62.5	61.0	*39*	**63.26**	59.8	66.5	1.578	*37*	**62.52**	60.3	65.00	1.200
LCr	20.44	–	19.53	*13*	**20.05**	19.47	21.06	0.459	*29*	**20.09**	19.43	20.83	0.374
LOc	21.03	20.68	20.44	*19*	**20.63**	19.48	21.48	0.569	*29*	**20.63**	19.72	21.29	0.438
LCc	19.58	19.18	18.93	*19*	**19.32**	18.68	19.92	0.401	*29*	**19.14**	18.32	19.98	0.313
LaZ	12.02	11.58	11.76	*19*	**11.81**	11.28	12.24	0.270	*29*	**11.79**	11.59	12.23	0.145
LaI	5.84	5.32	5.76	*18*	**5.67**	5.34	6.12	0.190	*29*	**5.60**	5.38	6.03	0.156
LaP	4.39	4.54	4.41	*20*	**4.43**	4.18	4.79	0.161	*29*	**4.25**	4.02	4.53	0.141
LaInf	5.46	5.13	5.56	*20*	**5.44**	5.04	5.83	0.181	*29*	**5.45**	5.26	5.63	0.103
LaN	9.53	9.41	9.58	*19*	**9.49**	9.23	9.83	0.166	*29*	**9.32**	8.92	9.67	0.163
LaM	10.48	10.34	10.39	*20*	**10.52**	10.27	10.75	0.123	*29*	**10.38**	10.08	10.61	0.135
ANc	7.54	7.46	7.71	*19*	**7.51**	7.09	7.85	0.198	*29*	**7.33**	6.98	7.62	0.145
LBT	4.64	4.44	4.31	*19*	**4.58**	4.42	4.84	0.131	*29*	**4.52**	4.34	4.74	0.106
CC	3.81	3.69	3.73	*20*	**3.76**	3.52	3.98	0.136	*29*	**3.77**	3.55	3.93	0.088
M^3M^3	8.33	8.14	8.27	*21*	**8.27**	8.04	8.63	0.162	*29*	**8.32**	7.94	8.63	0.159
CM^3	8.64	8.61	8.47	*21*	**8.67**	8.38	8.98	0.192	*29*	**8.67**	8.39	9.02	0.134
LMd	15.28	14.86	14.59	*19*	**15.13**	14.66	15.83	0.341	*29*	**15.09**	14.54	15.49	0.209
ACo	5.38	5.44	5.37	*20*	**5.42**	5.04	5.72	0.198	*29*	**5.47**	5.23	5.71	0.127
CM_3	9.52	9.43	9.48	*20*	**9.29**	5.32	9.88	0.958	*29*	**9.53**	9.14	10.18	0.208

described based on specimens from north-western Nigeria (Harrison 1958), considering the phylogenetic position of the Ghanaian samples of *T. perforatus* (Fig. 28). The other two subspecies names of the species rank of *T. perforatus* that are considered valid (see above), *T. p. senegalensis* and *T. p. sudani* (incl. *rhodesiae* Harrison, 1964), remain to be examined with the help of molecular genetic analysis of samples from Senegal/Mauritania, South Sudan, and southern Africa. Taxonomic revision is needed also in the case of position of the Indian populations of this bat.

Comparative material (82). **Egypt** [16]: 3 ♂♂, 1 ♀, 1 ind. (ZFMK 59.272, 59.273 [S+B], 59.310, 59.311 [A], 59.266 [B]), Abruawash, 15 April 1959, leg. H. Roer; – 1 ♂ (ZFMK 77.1071 [S+A]), Assuan, 5 February 1910, leg. O. le Roi; – 1 ♂ (NMP 92595 [S+A]), El A'aqab, 25 January 2010, leg. P. Benda, R. Lučan & I. Horáček; – 4 ♀♀ (ZFMK 81.247–81.250 [A]), Karnak, Niltal, Tal der Könige (Privatgräber), 31 December 1980, leg. H.-E. Back & F. Klees; – 2 ♂♂, 3 ♀♀ (NMP 92609–92613 [S+A]), Luksor, 27 January 2010, leg. P. Benda, R. Lučan & I. Horáček. – **Ethiopia** [12]: 8 ♂♂, 4 ♀♀ (NMP 96901–96910 [S+A], 96899, 96900 [A]), Mille, 29 September 2019, leg. P. Benda. – **Ghana** [2]: 1 ♂ (NMP 95438 [S+A]), Nakbanduri, 12 November 2012, leg. P. Vallo; – 1 ♀ (NMP 95437 [S+A]), Tongo, 8 November 2012, leg. P. Vallo. – **Oman** [21]: 2 ♂♂ (NMP 92715, 92716 [S+A]), Ain Jarziz, 27 October 2009, leg. P. Benda, A. Reiter & M. Uhrin; – 1 ♂ (NMP 92638 [A]), At Tabaqah, 19 October 2009, leg. P. Benda, A. Reiter & M. Uhrin; – 1 ♂ (NMP 94005 [S+A]), Hanah, 23 March 2012, leg. P. Benda,

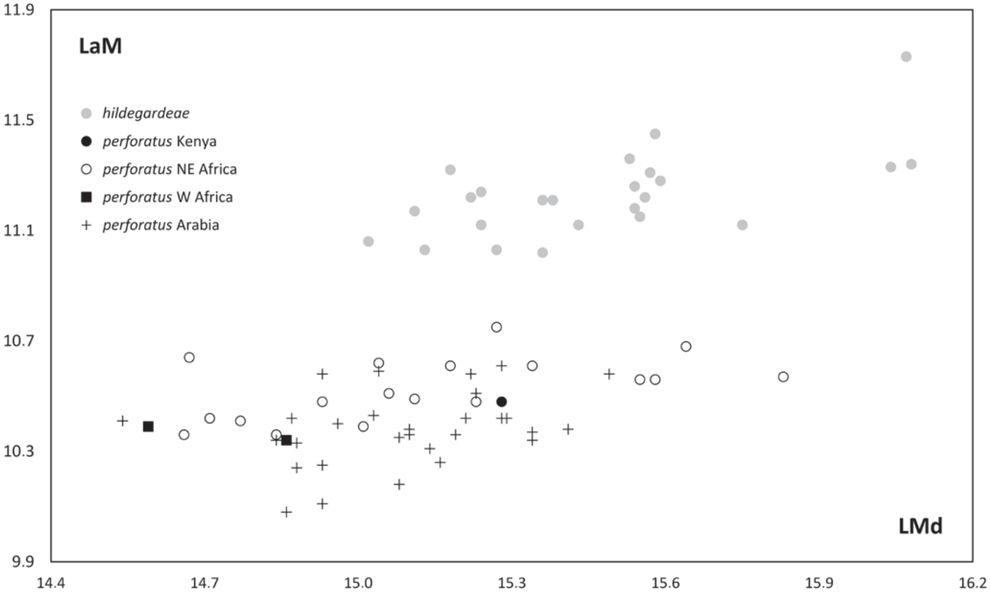


Fig. 31. Bivariate plot of the Kenyan and comparative samples of the genus *Taphozous*: mandible length (LMd) against the mastoidal width (LaM). For comparative material see text. Legend of the geographical specification of the comparative sets: *hildegardeae* = Kenya (NMW & NMP); NE Africa = Egypt, Ethiopia, Somalia, and the Sudan; W Africa = Ghana; Arabia = Oman and Yemen.

A. Reiter & M. Uhrin; – 8 ♂♂, 4 ♀♀ (NMP 92763, 92764, 92766–92768, 93721, 93722 [S+A], 92765 [A]), Jaalan Bani Bu Ali, 1 November 2009, 2 April 2011, leg. P. Benda, A. Reiter & M. Uhrin; – 1 ♂, 5 ♀♀ (NMP 92697–92699 [S+A], 92700–92702 [A]), wadi 2 km to W of Rakhyut, 25 October 2009, leg. P. Benda, A. Reiter & M. Uhrin; – 1 ♂ (NMP 94072 [S+A]), wadi 1 km E of Sadah, 31 March 2012, leg. P. Benda, A. Reiter & M. Uhrin; – 1 ♀ (NMP 92734 [S+A]), Taqah, 28 October 2009, leg. P. Benda, A. Reiter & M. Uhrin; – 1 ♂ (NMP 97091 [S+A]), Wadi Al Ajal, 2 November 2019, leg. P. Benda, A. Reiter & M. Uhrin. – **Somalia** [5]: 1 ♂, 4 ♀♀ (MZUF 2313–2317 [S+A]), Chisimaio, Grotte di Chisimaio, 25 August 1959, leg. Missione Biologica Somalia 1959. – **South Sudan** [2]: 2 ♂♂ (ZFMK 77.1077, 77.1078 [A]), Djebel Zeraf, 14 March 1913, leg. H. Freiherr von Geyr & O. le Roi; – **Sudan** [4]: 2 ♂♂, ♀♀ (NMP 93673–93675 [S+A], 93676 [A]), Quikkah, 9 December 2010, leg. P. Benda & J. Šmíd. – **Yemen** [20]: 1 ♂, 1 ♀ (NMP pb3771, 3772 [S+A]), Shuhayr, 6 November 2007, leg. P. Benda & A. Reiter; – 6 ♂♂, 12 ♀♀ (NMP pb3690–3695, 3700, 3701, 3703–3706 [S+A], pb3689, 3696–3699, 3702, 3704 [A]), Zabid, citadel, 30 October 2007, leg. P. Benda & A. Reiter.

Taphozous hildegardeae Thomas, 1909

NMW Material (20). 1 ♀ (NMW 32240 [S+Sk]), Pangani, Belfry Cave, 11 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♂♂, 2 ♀♀ (NMW 32236–32239 [S+B]), Pangani, Lwandani Cave, 9 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂, 4 ♀♀ (NMW 32235 [S+B], 32232, 32234 [S+A], 32231, 32233 [S+Sk]), Shimoni, Main Well Cave, 7 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
4 ♂♂, 6 ♀♀ (NMW 32221–32223, 32225–32230 [S+B], 32224 [S+Sk]), Shimoni, Road Side Cave, 6 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

NMP Material (8). 3 ♂♂, 3 ♀♀ (NMP 97977–97871 [S+A], 97976 [A]; Fig. 32, 33), Shimoni, Slave Cave, 22 August 2022, leg. P. Benda & J. Červený;
2 ♀♀ (NMP 98036, 98037 [S+A]; Fig. 33), Shimoni, Slave Cave, 7 July 2023, leg. P. Benda & J. Červený.

Reference. Aggundey & Schlitter (1984).

Taphozous hildegardeae is an endemic of East Africa, its range covers a relatively small area, some 450 km long line of the sea coast of Kenya and north-eastern Tanzania, between Manda Island in the north and Tonga in the south (Thomas 1909, Kulzer 1959, Kock 1974, Aggundey & Schlitter 1984, Cockle et al. 1998, Monadjem et al. 2024). Two additional records were reported from arid steppes of the Kenyan inland (Harrison 1961, Hayman & Hill 1971, Aggundey & Schlitter 1984), but their correct species identification was questioned (Kock 1974, Colket & Wilson 1998, Bonaccorso 2019) and recently, they were assigned to *T. perforatus* (Monadjem et al. 2024). The localities of the NMW and NMP specimens belong to the known occurrence areas of *T. hildegardeae*. The coastal settlement Shimoni was mentioned as a locality of this bat already by Thomas (1909) in his paper containing the species description, although the type locality is Rabai, ca. 15 km north-west of Mombasa. Aggundey & Schlitter (1984: 125) attributed the NMW material from the two caves at Pangani to the type locality of *T. hildegardeae*, although these caves are situated ca. 15 km north-east of Rabai. Rabai and Pangani in Kenya, plus Kilulu in Tanzania (Cockle et al. 1998) represent the only confirmed sites of occurrence of *T. hildegardeae* situated inland of East Africa, although just 15–30 km from the sea shoreline.

The dimensions of the NMW and NMP specimens of *T. hildegardeae* from Kenya are shown in Table 12, see also Fig. 31 for metric comparison of this species with *T. perforatus*, showing a much broader braincase in *T. hildegardeae*, a character stressed already by Thomas (1915).

Figs. 32, 33. *Taphozous hildegardeae* from Kenya in the NMP collection. 32 – individuals roosting in the Slave Cave, Shimoni, observed on 7 July 2023. 33 – a male collected from this cave on 22 August 2022.

Similarly as the NMP series of the previous emballonurid bat species, the specimens of *T. hildegardeae* were analysed by a molecular genetic approach (see details under *Coleura afra* above). This species was subjected to a molecular study for the first time and the two haplotypes obtained from six specimens from Shimoni represented a single lineage that formed a separated, well-supported branch within the genus *Taphozous* (Fig. 28). This lineage was in a sister position to the lineage comprising haplotypes of *T. melanopogon*, a species morphologically very similar to *T. hildegardeae*, with a broad distribution in the Oriental region, in a range some 4000 km away from the East African coast (stretching from India and Ceylon to the Philippines, Moluccas, and Timor; Bonaccorso 2019). This result corresponds well with the morphological evidence, such a close relationship of these two species was presumed already by Thomas (1909, 1915) and Colket & Wilson (1998) based on similarities in the pelage colouration and body and skull size and skull shape. This close phylogenetic relationship and also biogeographical circumstances suggest the origin of *T. hildegardeae* in the Oriental region, with the ancestral population in India where it gave origin to *T. melanopogon*, arrived in East Africa (perhaps with the help of monsoon wind currents?) and gave origin to *T. hildegardeae* in a limited area of the East African shoreland. A similar phylogenetic/biogeographic scenario is expected also in the flying foxes of the genus *Pteropus* that colonised the offshore and other islands in the western Indian Ocean from the Oriental Region (see e.g. O'Brien et al. 2009).

Nycteridae

Nycteris thebaica Geoffroy, 1813

NMW Material (7). 2 ♂♂, 3 ♀♀ (NMW 32241–32245 [S+B]), Msambweni, Msambweni Caves, 7 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♀♀ (NMW 10323, 10324 [S+A]), Nairobi, 23 April 1903, leg. F. Steindachner;

NMP Material (4). 1 ♀ (NMP 97866 [S+A]), Archers Post, Samburu Reserve, King Lion Camp, 25 November 2021, leg. P. Benda, L. Bufka & J. Červený;
1 ♀ (NMP 98055 [S+A]), Kalacha, 18 September 2004, leg. D. Modrý;
1 ♂ (NMP 98027 [S+A]), Kwale, Shimba Hills National Park, Shimba Hills Lodge, 4 July 2023, leg. P. Benda & J. Červený;
1 ♂ (NMP 98033 [S+A]; Fig. 34), Kwale, Shimba Hills National Park, Shimba Hills Lodge, 5 July 2023, leg. P. Benda & J. Červený.

References. Aggundey & Schlitter (1984), Van Cakenberghe & De Vree (1998), Van Cakenberghe & Seamark (2022).

Nycteris thebaica is a common bat throughout Africa except the rainforest zone and a large part of the Sahara. It occurs also in the western and southern parts of Arabia (Hayman & Hill 1971, Kingdon 1974, Van Cakenberghe & De Vree 1998, Monadjem et al. 2024). In East Africa, it belongs to the most common and widespread bats; Monadjem et al. (2024) reported 50 record localities scattered all over the territory of Kenya except the north-east. The NMW and NMP specimens of *N. thebaica* originate from the areas of known occurrence of this bat in the

Fig. 34. Portrait of a male of *Nycteris thebaica* (NMP 98033) collected at the Shimba Hills Lodge near Kwale, Shimba Hills National Park, Kenya, on 5 July 2023.

country (see Harrison 1961, Nader & Kock 1983, Aggundey & Schlitter 1984) and do not represent an important addition to its distribution picture. Moreover, the NMW series from the Msambweni Caves was published already by Aggundey & Schlitter (1984) and Van Cakenberghe & De Vree (1998), and that from Nairobi by Van Cakenberghe & Seamark (2022).

The dimensions of the NMW and NMP specimens of *N. thebaica* from Kenya are shown in Table 12. The results of examination of the mitochondrial gene for cytochrome *b* of the three NMP specimens of *N. thebaica* affiliated them with two lineages sensu Demos et al. (2019b). The bats from the Shimba Hills (NMP 98027, 98033) belong to the lineage *thebaica* 4 (congruence of 99.8% and 100% with the haplotypes MK837295 and MK837289, respectively), which is distributed along the sea coast of Kenya (Demos et al. 2019b), but also in Zambia (Benda et al. 2022); both specimens that produced the two comparative haplotypes also came from the Shimba Hills (FMNH 220448, 220455; Demos et al. 2019b). The specimen NMP 97866 from the Samburu Reserve showed a congruence of 97.6% with the haplotype MK837101 of the lineage "cf. *thebaica* 2", till now known only from the Marsabit NP in northern Kenya (Demos et al. 2019b).

Nycteris macrotis Dobson, 1876

NMW Material (2). 2 ♂♂ (NMW 32246, 32247 [S+B]), Pangani, near the Lwandani Cave, 9 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Reference. Aggundey & Schlitter (1984).

Nycteris macrotis is a widely distributed bat, its range covers a large part of sub-Saharan Africa in several extensive patches from Senegal in the west to the Sudan and Somaliland in the east, and northern Botswana and central Mozambique in the south (Hayman & Hill 1971, Van Cakenberghe & De Vree 1985, Monadjem et al. 2024). In East Africa, the records are scattered all over the region, *N. macrotis* is widely distributed across the southern part of Kenya (Aggundey & Schlitter 1984, Van Cakenberghe & De Vree 1985). The locality of the NMW specimens is situated in the area of the most abundant records of this bat in Kenya, the Mombasa region (see Monadjem et al. 2024), and was reported already by Aggundey & Schlitter (1984), although under an erroneous site name, Ribe. The dimensions of the NMW specimens of *N. macrotis* from Kenya are shown in Table 2.

Molossidae

Platymops setiger (Peters, 1878)

NMP Material (1). 1 ♂ (NMP 98056 [S+A]), South Horr, 1 October 2004, leg. D. Modrý.

Platymops setiger is an endemic of eastern Africa, it occurs in a belt of dry savannas stretching from southern South Sudan and south-western Ethiopia to western, central, and southern Kenya (Kingdon 1974, Monadjem et al. 2024). The majority of records is available from Kenya, some 18 sites are known, most of them in the southern part of the country (O'Shea & Vaughan 1980, Aggundey & Schlitter 1984, Webala et al. 2004, Monadjem et al. 2024). The locality of the NMP specimen, South Horr, represents a new occurrence point in northern Kenya and a new easternmost limit of *P. setiger* in the northern part of its whole distribution range (north of the Ewaso Nyiro River in central Kenya). Only few available dimensions of the NMP specimen (because of a damaged skull) of *P. setiger* from Kenya are shown in Table 2.

Chaerephon pumilus (Cretzschmar, 1830)

NMP Material (16). 3 ♂♂, 7 ♀♀ (NMP 98039–98047 [S+A], 98351 [A]), Engilae, 1 September 2004, leg. D. Modrý;

4 ♀♀ (NMP 97877–97880 [S+A]; Fig. 35), Karare, Gof Bongolle, 29 November 2021, leg. P. Benda, L. Bufka & J. Červený;

1 ♀ (NMP 97951 [S+A]; Figs. 36), Kimana, 17 August 2022, leg. P. Benda & J. Červený;

1 ♀ (NMP 97950 [S+A]), Ol Kirimatian, Nyiro River Camp, 16 August 2022, leg. P. Benda & J. Červený.

Although some authors (see e.g. Van Cakenberghe & Seamark 2022, Monadjem et al. 2024) considered the genus *Chaerephon* Dobson, 1874 an inner group of the genus *Mops* Lesson, 1842 (based on the preliminary results of molecular genetic analyses, see Lamb et al. 2011, Ammerman et al. 2012, Shi & Rabosky 2015, Amador et al. 2018) and merged the taxonomic contents of both genera under the latter name, we still keep tentatively the traditional view (cf. Freeman 1981, Koopman 1993, 1994, Simmons 2005, Taylor 2019, Monadjem et al. 2020, etc.), until a final solution of this phylogenetic question is available (see also Gregorin & Cirrandello 2016).

Bats traditionally assigned to *Chaerephon pumilus* are currently considered a complex composed of several species (Goodman et al. 2010, Naidoo et al. 2016, Monadjem et al. 2020). However, the phylogenetic relations within the complex as well as its taxonomic arrangement still remain to be resolved. If the complex really comprises more species, the name *C. pumilus* is most probably not applicable for the populations from a big part of sub-Saharan Africa (Naidoo et al. 2016). Moreover, the status of East African populations has been examined only partially and almost without any context with the populations from other parts of Africa (Goodman

Figs. 35, 36. Portraits of *Chaerephon pumilus* from Kenya in the NMP collection. 35 – a female collected at Gof Bongolle near Karare, on 29 November 2021. 36 – a female netted in Kimana on 17 August 2022.

Table 15. Biometric data on the NMP specimens of *Chaerephon pumilus*, *Mops condylurus*, and *Nyctinomus aegyptiacus* from Kenya. For abbreviations see Methods

dimension	*Chaerephon pumilus*					*Mops condylurus*					*Nyctinomus aegyptiacus*				
	n	**M**	min	max	SD	*n*	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*16*	**38.19**	37.1	39.9	0.780	*5*	**47.08**	45.1	48.3	1.289	*3*	**49.47**	49.2	49.8	0.306
LCr	*15*	**17.34**	16.84	17.78	0.278	*4*	**21.26**	20.54	22.09	0.690	*3*	**20.46**	20.34	20.53	0.107
LCb	*15*	**16.23**	15.61	17.32	0.387	*4*	**18.83**	18.31	19.52	0.522	*3*	**19.91**	19.88	19.93	0.025
LaZ	*14*	**10.78**	10.43	11.10	0.177	*4*	**13.26**	12.89	13.59	0.330	*3*	**12.92**	12.74	13.18	0.232
LaI	*15*	**3.66**	3.47	3.96	0.137	*4*	**4.49**	4.44	4.58	0.066	*3*	**4.62**	4.57	4.67	0.050
LaInf	*15*	**4.74**	4.33	5.07	0.195	*4*	**5.84**	5.68	6.14	0.215	*3*	**5.34**	5.24	5.44	0.100
LaN	*15*	**8.60**	8.17	9.03	0.254	*4*	**10.65**	10.49	10.93	0.201	*3*	**10.27**	10.08	10.46	0.190
LaM	*15*	**10.02**	9.60	10.25	0.172	*4*	**12.10**	11.84	12.42	0.287	*3*	**11.88**	11.73	12.14	0.229
ANc	*15*	**6.04**	5.69	6.48	0.252	*4*	**7.73**	7.36	8.27	0.398	*3*	**6.67**	6.49	6.77	0.154
LBT	*15*	**3.61**	3.43	3.84	0.141	*4*	**3.72**	3.41	3.94	0.222	*3*	**4.45**	4.22	4.61	0.204
CC	*15*	**4.94**	4.61	5.22	0.186	*4*	**6.15**	5.81	6.62	0.372	*3*	**5.53**	5.27	5.68	0.226
M^3M^3	*15*	**7.90**	7.66	8.31	0.164	*4*	**9.32**	9.14	9.53	0.164	*3*	**8.99**	8.72	9.16	0.234
CM^3	*15*	**6.69**	6.41	6.84	0.111	*4*	**7.81**	7.68	7.96	0.146	*3*	**8.26**	8.03	8.52	0.246
LMd	*15*	**11.84**	11.51	12.26	0.223	*4*	**14.16**	13.68	14.68	0.462	*3*	**14.77**	14.62	14.96	0.172
ACo	*15*	**3.22**	3.07	3.39	0.104	*4*	**3.96**	3.79	4.22	0.195	*3*	**4.46**	4.42	4.52	0.051
CM_3	*15*	**7.07**	6.75	7.34	0.189	*4*	**8.63**	8.02	9.14	0.468	*3*	**8.81**	8.58	9.13	0.284

& Ratrimomanarivo 2007, Ratrimomanarivo et al. 2009, Taylor et al. 2009, Goodman et al. 2010, Naidoo et al. 2016).

The morphotype of *C. pumilus* s.l. ranks among the most common and widespread bat forms in the Afrotropics except the southern Sahara and the arid regions of south-western Africa (Hayman & Hill 1971, Bouchard 1998). In East Africa, it is a widespread and locally very common bat (e.g., in Rwanda, western and south-eastern Uganda, or central Kenya), distributed all over the region (Kingon 1974, Thorn & Kerbis Peterhans 2009, Monadjem et al. 2024). More than fifty record sites were reported from Kenya, this bat is the most frequently recorded representative of the molossid family from the country (Kulzer 1959, Harrison 1961, O'Shea & Vaughan 1980, Aggundey & Schlitter 1984, Webala et al. 2009, 2019, López-Baucells et al. 2017, Musila et al. 2020). The four localities of the NMP specimens are situated within the known range in Kenya and do not represent an important contribution to the distribution picture of this common bat.

The dimensions of the NMP specimens of *C. pumilus* s.l. from Kenya are shown in Table 15. All sequences of the cytochrome *b* gene obtained from the NMP specimens from all four Kenyan localities affiliated most closely with the haplotypes referred to *C. leucogaster* (Grandidier, 1869) from Pemba Island, Tanzania, i.e. to one of the candidate names for a possible separate species within the *C. pumilus* species complex (Naidoo et al. 2016). The sequences from the specimens NMP 97877–97880 from Karare and NMP 97950 from Ol Kirimatian showed congruence of 99.8% with the haplotype EU716003 extracted from the specimen FMNH 192886 (Ratrimomanarivo et al. 2009, Naidoo et al. 2016), a sequence from one examined bat of the series from Engilae (NMP 98045) was in 99.9% congruence with the latter Pemban FMNH specimen/haplotype; a sequence from the specimen NMP 97951 from Kimana showed congruence of 99.8% with the haplotype KF193638 from the specimen FMNH 192891, also from Pemba (Goodman et al. 2010).

Chaerephon bivittatus (von Heuglin, 1861)

NMW Material (2). 1 ♂, 1 ♀ (NMW 32508, 32509 [S+Sk]), Kiminini, Namino Cave, 30 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Chaerephon bivittatus occurs patchily in a long belt of savannas across the eastern part of Africa, stretching from Eritrea to Zimbabwe (Hayman & Harrison 1966, Eger & Peterson 1979, Monadjem et al. 2024). In East Africa, it was found abundantly in south-western and southern Kenya (25 record sites in total, it is the second most common molossid bat of the country), while only few records of *C. bivittatus* are available from eastern Uganda or central Tanzania (Kingdon 1974, Aggundey & Schlitter 1984, Monadjem et al. 2024). The NMW specimens of this bat originate from the broader area of Mount Elgon, a region where the occurrence of this bat was reported by previous authors (Hayman & Harrison 1966, Eger & Peterson 1979, Aggundey & Schlitter 1984). The dimensions of the NMW specimens of *C. bivittatus* from Kenya are shown in Table 16.

Mops condylurus (Smith, 1833)

NMP Material (5). 2 ♂♂, 3 ♀♀ (NMP 97923, 97924, 97925, 97927 [S+A], 97925 [A]; Fig. 37), Loboi, former Lake Bogoria Reserve headquarter, 4 December 2021, leg. P. Benda, L. Bufka & J. Červený.

Table 16. Biometric data on the NMW and NMP specimens of *Chaerephon bivittatus*, *Myotis welwitschii*, *Vansonia rueppellii*, *Neoromicia capensis*, *Pseudoromicia rendalli*, *Afropipistrellus grandidieri*, and *Mimetillus moloneyi* from Kenya. For abbreviations see Methods

dimension	*Chaerephon bivittatus* 32508	*Chaerephon bivittatus* 32509	*Myotis welwitschii*	*Vansonia rueppellii*	*Neoromicia capensis*	*Pseudoromicia rendalli*	*Afropipistrellus grandidieri*	*Mimetillus moloneyi*
LAt	47.5	–	58.8	34.8	33.1	32.6	33.4	–
LCr	19.18	19.96	19.65	13.41	13.69	12.64	13.32	13.82
LCb	18.18	18.55	18.88	12.59	13.43	12.21	12.81	13.74
LaZ	12.32	12.32	13.44	8.96	9.06	8.08	9.37	10.33
LaI	4.13	4.02	4.82	4.24	3.57	3.62	3.79	4.68
LaInf	5.07	5.38	6.18	4.27	4.44	3.83	4.55	5.36
LaN	9.93	10.24	9.56	7.56	6.61	6.48	6.43	7.96
LaM	11.46	11.48	10.36	7.83	7.84	7.32	7.98	9.23
ANc	7.33	7.68	7.28	5.63	4.47	4.57	5.28	4.64
LBT	–	–	3.88	–	–	3.11	2.76	3.43
CC	–	5.48	5.62	–	4.33	3.94	4.61	4.75
M^3M^3	8.98	9.33	8.69	–	5.88	–	6.34	6.95
CM^3	7.37	7.74	7.89	4.62	4.92	4.48	4.74	4.84
LMd	13.75	13.28	15.21	9.28	9.98	9.13	10.02	10.26
ACo	3.78	3.46	5.02	2.58	3.38	3.08	3.04	3.42
CM_3	–	8.38	8.61	4.93	5.18	4.81	5.27	5.14

Figs. 37, 38. Portraits of molossid bats from Kenya in the NMP collection. 37 – a male of *Mops condylurus* collected from a colony roosting in a building of the former Lake Bogoria Reserve headquarter, Loboi, 4 December 2021. 38 – a male of *Nyctinomus aegyptiacus* netted above a swimming pool of the Ngulia Lodge, Tsavo West National Park, on 20 August 2022.

Mops condylurus is one of the most common and widespread savanna bats of sub-Saharan Africa, distributed from Mauritania and Senegal to the Sudan, southern Somalia, and Natal, and absent only in south-western Africa (Hayman & Hill 1971, Happold 2013e, Monadjem et al. 2024). The central parts of East Africa belong to the regions with the most abundant records of this bat, in the southern part of Kenya, *M. condylurus* is a common bat (Harrison 1961, Kingdon 1974, O'Shea & Vaughan 1980, Aggundey & Schlitter 1984, Webala et al. 2004, 2009, Thorn & Kerbis Peterhans 2009, Monadjem et al. 2024). The series of the NMP specimens originating from the western bank of Lake Bogoria does not contribute significantly to the picture of *M. condylurus* distribution, although this locality lies in the area of less frequent occurrence of this bat.

The dimensions of the NMP specimens of *M. condylurus* from Kenya are shown in Table 15. Sequences obtained from four of these bats demonstrated the highest correspondence with the haplotypes obtained from the central African populations of *M. condylurus*. One haplotype, originating from the specimens NMP 97924 and 97927, showed 100% congruence with the haplotype MZ265562 from Mossaka, Congo (B.) (Seifert et al. 2022), another haplotype from the specimen NMP 97925 agreed in 99.8% with the haplotype JQ956445 from the Lobaye Province, Central African Republic (Maganga et al. 2014), and the last haplotype from the specimen NMP 97926 corresponded by 99.5% with the haplotype MK330941 extracted from an individual from the Taita Hills, southern Kenya (Forbes et al. 2019).

Nyctinomus aegyptiacus Geoffroy, 1818

NMP Material (3). 3 ♂♂ (NMP 97965–97967 [S+A]; Fig. 38), Tsavo West National Park, Ngulia Lodge, 20 August 2022, leg. P. Benda & J. Červený.

Nyctinomus aegyptiacus s.l. is the most widely distributed molossid bat of the Old World; it occurs patchily across the non-forested parts of Africa, from South Africa to Egypt and Morocco, in southern Arabia, Iran, and broadly in the Indian subcontinent, from Afghanistan to Bangladesh and Ceylon (Simmons 2005). In East Africa, the records of *N. aegyptiacus* s.l. are spread in a strip of areas stretching between north-eastern Uganda through central and southern Kenya to north-eastern Tanzania, the majority of East African records are known from Kenya (Aggundey & Schlitter 1984, Thorn & Kerbis Peterhans 2009, Monadjem et al. 2024). The locality of origin of the NMP specimens, Ngulia Lodge in the Tsavo West NP, is situated within this relatively narrow strip and does not represent an important addition to the distribution picture of this bat in Kenya.

Nyctinomus aegyptiacus is considered to be a complex composed of more than one species (Benda et al. 2012, Monadjem et al. 2020), particular populations differ from each other by their body and skull size and by genetic traits (Benda et al. 2012, Richards et al. 2023, own unpubl. data). The dimensions of the NMP specimens of *N. aegyptiacus* s.l. from Kenya are shown in Table 15; they suggest that these specimens belong to the large-sized morphotype of the complex, corresponding with the morphotype of *N. aegyptiacus* s.str., known to occur in North Africa and the Middle East (Benda et al. 2012).

Otomops harrisoni **Ralph, Richards, Taylor, Napier et Lamb, 2015**

NMW Material (29). 15 ♂♂, 14 ♀♀ (NMW 32479–32502, 32504–32506 [S+B], 32507 [S+Sk], 32503 [A]), Suswa, Suswa Cave 14, Paddington Station, 18 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

NMP Material (4). 2 ♂♂, 2 ♀♀ (NMP 97933, 97934, 97936 [S+A], 97935 [A]; Figs. 39, 40), Suswa, Suswa Cave, 7 December 2021, leg. P. Benda, L. Bufka & J. Červený.

Figs. 39, 40. *Otomops harrisoni* from Kenya in the NMP collection. 39 – a cluster roosting in the Suswa Cave, Mount Suswa, observed on 7 December 2021, a part of a large colony containing several thousand bats. 40 – portrait of a male collected from this colony.

Table 17. Biometric data on the NMW and NMP specimens of *Otomops harrisoni*, *Myotis tricolor*, and *Glauconycteris argentata* from Kenya. For abbreviations see Methods

dimension	*Otomops harrisoni*					*Myotis tricolor*					*Glauconycteris argentata*				
	n	**M**	min	max	SD	*n*	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*33*	**68.79**	65.5	72.2	1.790	*24*	**49.04**	46.8	52.2	1.460	*29*	**41.76**	37.7	44.4	1.248
LCr	*31*	**27.83**	26.52	28.93	0.763	*23*	**17.59**	17.06	18.01	0.225	*29*	**11.87**	11.54	12.21	0.177
LCb	*31*	**25.71**	24.38	27.21	0.823	*23*	**16.53**	15.93	17.08	0.263	*29*	**12.01**	11.61	12.34	0.187
LaZ	*30*	**14.19**	13.41	14.91	0.402	*23*	**11.42**	11.03	11.91	0.268	*29*	**9.40**	9.08	9.68	0.158
LaI	*31*	**5.37**	5.04	5.75	0.160	*23*	**4.30**	4.12	4.47	0.103	*29*	**4.67**	4.34	5.03	0.153
LaInf	*31*	**5.87**	5.32	6.34	0.333	*23*	**4.51**	4.27	4.76	0.114	*29*	**4.54**	4.21	4.81	0.129
LaN	*31*	**12.20**	11.68	12.67	0.267	*23*	**8.66**	8.41	9.08	0.152	*29*	**7.77**	7.48	8.14	0.155
LaM	*31*	**13.72**	13.22	14.34	0.316	*23*	**9.19**	8.85	9.42	0.159	*29*	**8.48**	8.11	8.71	0.141
ANc	*31*	**9.02**	8.52	9.41	0.196	*23*	**6.51**	6.27	6.67	0.098	*29*	**5.74**	5.42	6.12	0.158
LBT	*31*	**7.27**	6.98	7.68	0.201	*23*	**3.29**	3.21	3.45	0.074	*29*	**3.31**	2.98	3.48	0.120
CC	*31*	**5.95**	5.34	6.49	0.342	*23*	**4.64**	4.47	4.83	0.097	*29*	**4.44**	4.27	4.67	0.088
M^3M^3	*31*	**10.46**	9.86	11.23	0.321	*23*	**7.27**	6.94	7.52	0.157	*29*	**6.20**	5.92	6.43	0.137
CM^3	*31*	**10.61**	10.11	11.27	0.330	*23*	**6.73**	6.52	6.91	0.105	*29*	**4.23**	4.04	4.47	0.115
LMd	*31*	**18.65**	17.66	19.66	0.636	*23*	**12.82**	12.28	13.28	0.238	*29*	**8.89**	8.48	9.22	0.178
ACo	*31*	**3.57**	3.27	3.88	0.150	*23*	**3.97**	3.76	4.21	0.101	*29*	**2.78**	2.53	2.93	0.102
CM_3	*31*	**11.22**	10.56	11.98	0.432	*23*	**7.19**	6,98	7.43	0.112	*29*	**4.63**	4.46	4.83	0.114

Otomops harrisoni is a recently distinguished bat species, an endemic of the north-eastern Afrotropics, its records stretch from Rwanda, via central, western, and southern Kenya, south-eastern Ethiopia and Djibouti, to northern Eritrea and western Yemen (Hill & Morris 1971, Kock & Zinner 2004, Lamb et al. 2008, Benda et al. 2011b, Ralph et al. 2015, Patterson et al. 2018, Monadjem et al. 2024). The locality of the NMW and NMP series of this bat, the lava cave complex of Mount Suswa, belongs to the traditional sites of examination and/or collection of this bat, see the review by Aggundey & Schlitter (1984).

The dimensions of the NMW and NMP specimens of *O. harrisoni* from Kenya are shown in Table 17. Sequences of the cytochrome *b* gene extracted from the NMP specimens agreed in 99.9–100% with the haplotypes MH010731 and MH010741 from Mount Suswa, Kenya (extracted from the specimens FMNH 216757, 225589; Patterson et al. 2018), in 99.9% with the haplotype KJ509966 from Al Mahwit, Yemen (HZM 52.33977; Ralph et al. 2015), and in 99.8% with the haplotype EF216433 from Sof Omar Caves, Ethiopia (NMP 91202; Lamb et al. 2008).

Vespertilionidae

***Myotis tricolor* (Temminck, 1832)**

NMW Material (24). 1 ♂ (NMW 32382 [S+Sk]), Kiminini, Kauka Cave, 29 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

1 ♂, 2 ♀♀ (NMW 32383–32385 [S+B]), Kiminini, Kipsiryori Cave, 29 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

4 ♂♂ (NMW 32369, 32371, 32372 [S+B], 32370 [B]), Mount Elgon National Park, Chepnyalil Cave, 24 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

9 ♂♂ (NMW 32373–32381 [S+B]), Mount Elgon National Park, Chepnyalil Cave, 26 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
4 ♂♂, 1 ♀ (NMW 32387, 32388, 32390 [S+B], 32386, 32389 [S+Sk]), Saboti, Kapkulkul Caves, 2 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♀♀ (NMW 32391, 32392 [S+B]), Suswa, Suswa Cave 34, 17 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Reference. Aggundey & Schlitter (1984).

Myotis tricolor is a rather common bat of the eastern part of sub-Saharan Africa between northern Ethiopia and southernmost Cape (Hayman & Hill 1971, Monadjem et al. 2020, 2024), in West Africa it is a very rare bat with single records from Liberia, Nigeria, and western DR Congo (Koopman 1989, Monadjem et al. 2024). In East Africa, the records of *M. tricolor* are scattered in four spots, in north-western Rwanda, in eastern Tanzania, in northern Uganda, and in a rather extensive area covering eastern Uganda and western and central Kenya (Cockle et al. 1998, Van Cakenberghe & Seamark 2022, Monadjem et al. 2024). In Kenya, some twenty records of this bat are scattered across the south-western part of the country; the localities of the NMW specimens of *M. tricolor* originate from two regions where this bat was already collected before, Mount Elgon and Mount Suswa (see Aggundey & Schlitter 1984), in the former region this bat was collected most frequently in Kenya (see also Van Cakenberghe & Seamark 2022). The dimensions of the NMW specimens of *M. tricolor* from Kenya are shown in Table 17.

***Myotis welwitschii* (Gray, 1866)**

NMW Material (1). 1 ♀ (NMW 32690 [S+Sk+B]), North Nandi Forest, 4 km SW of Chomisia, 29 November 1979, leg. F. Spitzenberger.

References. Fahr & Ebigbo (2003), Van Cakenberghe & Seamark (2022).

Myotis welwitschii has a very broad but patchy distribution in sub-Saharan Africa, it occurs almost exclusively in upland areas and was documented from all main mountain ranges and highland plateaus of this region except for dry zones (Fahr & Ebigbo 2003, Sedláček et al. 2006). In East Africa, *M. welwitschii* was documented only in the western and southern upland parts (Monadjem et al. 2024), in Kenya the records are concentrated to a relatively small area adjacent to Mount Elgon and Lake Victoria in a range of medium altitudes of 1148–1892 m a. s. l. (Aggundey & Schlitter 1984, Webala et al. 2019, Monadjem et al. 2024). Fahr & Ebigbo (2003) reported five localities of *M. welwitschii* from Kenya, Webala et al. (2019) and Monadjem et al. (2024) added three sites, the Kakamega nad Kisere Forests, and Kisumu (see also Patterson et al. 2019). The NMW specimen coming from the North Nandi Forest near Chomisia was mentioned already by Fahr & Ebigbo (2003), this site represents the highest locality of the species in Kenya and the second southernmost site in the country, some 35 km north of Kisimu on the Lake Victoria bank, the southernmost record. The dimensions of the NMW specimen of *M. welwitschii* from Kenya are shown in Table 16.

***Glauconycteris argentata* (Dobson, 1875)**

NMW Material (29). 2 ♂♂ (NMW 32748, 32749 [S+A]), North Nandi Forest, 2 km W of Chomisia, 10 December 1979, leg. F. Spitzenberger;
1 ♂ (NMW 32750 [S+A]), North Nandi Forest, 2 km W of Chomisia, 11 December 1979, leg. F. Spitzenberger;

10 ♂♂, 1 ♀ (NMW 32736–32738 [S+B], 32739 [S+Sk+B], 32729–32735 [S+A]), North Nandi Forest, 4 km SW of Chomisia, 26 November 1979, leg. F. Spitzenberger;
3 ♂♂, 4 ♀♀ (NMW 32740–32744 [S+B], 32745, 32746 [S+A]), North Nandi Forest, 4 km SW of Chomisia, 29 November 1979, leg. F. Spitzenberger;
1 ♂ (NMW 32747 [S+B]), North Nandi Forest, 7 km NE of Chomisia, 4 December 1979, leg. F. Spitzenberger;
3 ♂♂, 4 ♀♀ (NMW 32751–32757 [S+A]), North Nandi Forest, 7 km NE of Chomisia, 11 December 1979, leg. F. Spitzenberger.

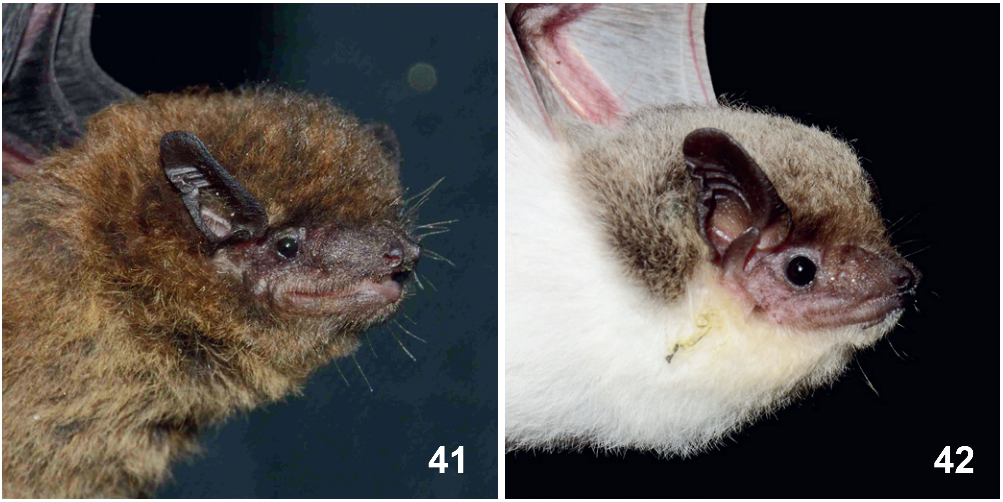
Glauconycteris argentata is a species distributed across the woodland savanna zone of central Africa, from Cameroon and north-western Angola to Uganda, Kenya, and northern Malawi (Hayman & Hill 1971, Kingdon 1974, Happold 2013f, Monadjem et al. 2024). In East Africa, it is a widespread bat in a belt stretching from Uganda and Rwanda to the southern part of Kenya and north-eastern Tanzania (Kingdon 1974, López-Baucells et al. 2017, Webala et al. 2019, Monadjem et al. 2024). The Nandi Forest, where the NMW series of *G. argentata* was collected, was listed among the Kenyan record sites of this bat already by Harrison (1961) and Aggundey & Schlitter (1984), although the NMW specimens have not yet been mentioned. The dimensions of the NMW specimens of *G. argentata* from Kenya are shown in Table 17.

***Pipistrellus hesperidus* (Temminck, 1840)**

NMW Material (27). 1 ♂ (NMW 32396 [S+B]), Mount Elgon National Park, Rongai Camp, 28 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂, 3 ♀♀ (NMW 32700–32703 [S+Sk+B]), North Nandi Forest, 2 km W of Chomisia, 10 December 1979, leg. F. Spitzenberger;
1 ♂ (NMW 32704 [S+Sk+B]), North Nandi Forest, 2 km W of Chomisia, 11 December 1979, leg. F. Spitzenberger;
1 ♀ (NMW 32693 [S+B]), North Nandi Forest, 3 km W of Chomisia, 20 November 1979, leg. F. Spitzenberger;
2 ♂♂, 1 ♀ (NMW 32695, 32721 [S+Sk+B], 32694 [S+A]), North Nandi Forest, 4 km SW of Chomisia, 26 November 1979, leg. F. Spitzenberger;
3 ♀♀ (NMW 32696, 32697 [S+B], 32722 [S+Sk+B]), North Nandi Forest, 4 km SW of Chomisia, 29 November 1979, leg. F. Spitzenberger;
1 ♀ (NMW 32723 [S+A]), North Nandi Forest, 4 km SW of Chomisia, 4 December 1979, leg. F. Spitzenberger;
1 ♀ (NMW 32699 [S+Sk+B]), North Nandi Forest, 4 km SW of Chomisia, 9 December 1979, leg. F. Spitzenberger;
2 ♀♀ (NMW 32724 [S+B], 32698 [S+Sk+B]), North Nandi Forest, 7 km NE of Chomisia, 4 December 1979, leg. F. Spitzenberger;
4 ♂♂, 6 ♀♀ (NMW 32705, 32706, 32709, 32710, 32713, 32725 [S+Sk+B], 32707, 32708, 32711, 32712 [S+A]), North Nandi Forest, 7 km NE of Chomisia, 11 December 1979, leg. F. Spitzenberger.

NMP Material (1). 1 ♂ (NMP 97876 [S+A]; Fig. 41), Marsabit National Park, Gof Sokorete Gudha, 28 November 2021, leg. P. Benda, L. Bufka & J. Červený.

Monadjem et al. (2020, 2021, 2024) considered *Pipistrellus hesperidus* to represent a bat species inhabiting savannas and woodlands of eastern Africa, distributed in their whole extent from Eritrea to South Africa (see also *P. kuhlii* (Kuhl, 1817) [s.l.] in Kingdon 1974). Although the *Pipistrellus* populations of West Africa, from Senegal to Cameroon, were also assigned to this



Figs. 41, 42. Portraits of pipistrelle bats from Kenya in the NMP collection. 41 – a male of *Pipistrellus hesperidus* (NMP 97876) collected at Gof Sokorete Gudha, Marsabit National Park, on 28 November 2021. 42 – a male of *Vansonia rueppellii* (NMP 97972) netted in garden of the Leisure Lodge, in Diani, Ukunda, on 21 August 2022.

bat (see Simmons 2005, Kearney 2013b, Burgin 2019), their affiliation with this species was doubted (see Koubínová et al. 2013, Monadjem et al. 2021), however, a reliable taxonomic solution is still missing. In East Africa and Ethiopia, *P. hesperidus* is widely distributed over the whole area (Largen et al. 1974, Thorn & Kerbis Peterhans 2009, Webala et al. 2009, Monadjem et al. 2024, own data), it is a very frequent faunal element namely in western, central, and southern Kenya (Aggundey & Schlitter 1984, López-Baucells et al. 2017). The localities of the NMW specimens, Nandi Forest and Mount Elgon NP, are not listed among the known occurrence sites of this bat (cf. Monadjem et al. 2021), on the other hand, numerous records of *P. hesperidus* are available from the close surrounding areas. The NMP specimen was collected in the forested part of the Marsabit NP, where, however, many specimens of this bat were recorded previously, see Monadjem et al. (2021).

The dimensions of the NMW and NMP specimens of *P. hesperidus* from Kenya are shown in Table 18. While the species identification of the NMP specimen from Marsabit was confirmed by the molecular genetic approach (the haplotype from the specimen NMP 97876 was in 99.9% congruence with the haplotype MT778008 extracted from the specimen FMNH 208058 from Mt. Meru, Tanzania; Monadjem et al. 2021), the NMW specimens were determined only based on a morphologic examination. However, the metric comparison of the NMW series from western Kenya with a sample set of more than sixty genetically identified specimens of *P. hesperidus* from Ethiopia did not reveal any substantial dimensional difference (see Table 18, Fig. 43). The description of the species was most probably based on specimens originating from central Ethiopia (see Kock 2001), originally “Les bords de la Mer rouge vers les côtés d’Abyssinie”

Table 18. Biometric data on the NMW and NMP specimens of *Pipistrellus hesperidus* from Kenya, on comparative samples of this species from Ethiopia, and on *Afronycteris nana* from Kenya. For abbreviations see Methods

dimension	*Pipistrellus hesperidus* Kenya					*Pipistrellus hesperidus* Ethiopia					*Afronycteris nana*				
	n	**M**	min	max	SD	*n*	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*28*	**33.97**	31.7	37.9	1.749	*63*	**34.48**	31.0	37.0	1.351	*12*	**30.38**	28.2	32.6	1.380
LCr	*27*	**12.96**	12.24	13.93	0.460	*62*	**12.98**	12.23	13.66	0.340	*12*	**11.42**	11.12	11.68	0.186
LCb	*28*	**12.48**	11.76	13.61	0.472	*62*	**12.52**	11.63	13.22	0.335	*12*	**10.73**	10.38	10.92	0.176
LaZ	*27*	**8.59**	8.03	9.42	0.352	*56*	**8.61**	8.09	9.02	0.199	*9*	**7.24**	7.04	7.68	0.203
LaI	*28*	**3.56**	3.23	3.98	0.186	*62*	**3.57**	3.12	4.04	0.166	*12*	**3.16**	2.95	3.38	0.123
LaInf	*28*	**4.22**	3.83	4.74	0.211	*62*	**4.21**	3.68	4.61	0.195	*12*	**3.15**	2.98	3.32	0.106
LaN	*28*	**6.72**	6.24	7.28	0.288	*62*	**6.75**	6.13	7.16	0.212	*12*	**5.95**	5.81	6.18	0.131
LaM	*28*	**7.50**	7.06	8.11	0.301	*62*	**7.53**	6.77	7.84	0.226	*12*	**6.58**	6.42	6.77	0.116
ANc	*28*	**4.71**	4.31	5.12	0.191	*62*	**4.71**	4.29	5.04	0.153	*12*	**4.20**	3.89	4.41	0.152
LBT	*28*	**2.93**	2.44	3.34	0.193	*60*	**2.93**	2.56	3.19	0.169	*12*	**2.57**	2.37	2.75	0.124
CC	*28*	**4.27**	3.91	4.71	0.230	*62*	**4.23**	3.75	4.54	0.178	*12*	**3.36**	3.24	3.47	0.067
M^3M^3	*28*	**5.73**	5.41	6.49	0.253	*62*	**5.74**	5.28	6.58	0.221	*12*	**4.62**	4.48	4.75	0.073
CM^3	*28*	**4.78**	4.48	5.25	0.192	*62*	**4.79**	4.44	5.09	0.139	*12*	**3.86**	3.74	4.04	0.094
LMd	*27*	**9.49**	8.92	10.35	0.356	*62*	**9.51**	8.94	10.09	0.260	*12*	**7.80**	7.48	8.12	0.204
ACo	*27*	**2.89**	2.61	3.14	0.137	*62*	**2.90**	2.54	3.24	0.145	*12*	**2.34**	2.21	2.48	0.094
CM_3	*27*	**5.10**	4.05	5.59	0.301	*62*	**5.10**	4.11	5.48	0.213	*12*	**4.11**	3.93	4.32	0.106

by Temminck (1840: 211), meaning the same populations in the broader geographical sense (sea coast of Eritrea).

Comparative material (65). **Ethiopia**: 1 ♂, 1 ♀ (NMP 94998, 94999 [S+A]), Bale National Park, 7 November 2012, leg. J. Bryja, P. Kaňuch, R. Šumbera & Yonas Meheretu; – 2 ♀♀ (NMP 92179, 92180 [S+A]), Baro River bridge, 15 km N of Masha, 9 May 2003, leg. P. Benda & J. Obuch; – 1 ♂ (NMP 95963 [S+A]), 15 km E of Bonga, 26 November 2012, leg. P. Benda; – 1 ♀ (ZMMU S-167221 [S+A]), Chismariet, March 1999, leg. L. A. Lavrenčenko & P. N. Morozov; – 3 ♂♂ (NMP 95885–95887 [S+A]), Desea Forest, 2 km E of Atsbi, 30 October 2012, leg. P. Benda; – 5 ♂♂ (NMP 92113–92116 [S+A], 92117 [A]), Goba, 1 May 2003, leg. P. Benda & J. Obuch; – 3 ♀♀ (NMP 95914–95916 [S+A]), Gondar, Royal Enclosure, 6 November 2012, leg. P. Benda; – 6 ♂♂, 5 ♀♀ (ZMMU S-168932–168936, S-168938, S-168939, S-168941–168943 [S+A], S-168940 [S]), 24 km by road SE of Hirna to Deder, 24 & 25 September 2000, leg. L. A. Lavrenčenko & P. N. Morozov; – 1 ♀ (NMP 95875 [S+A]), 4 km S of Korem, 28 October 2012, leg. P. Benda; – 1 ♂ (ZMMU S-181670 [S+A]), Majanger zone, 10 km W of Meti, Lake Bishan-Wak'a vicinity, 6 April 2007, leg. S. V. Kruskop; – 1 ♂, 2 ♀♀ (ZMMU S-168927, S-168928 [S+A], S-168926 [S]), between Mazante-Feri and Tepi, 12 & 13 October 2000, leg. L. A. Lavrenčenko & P. N. Morozov; – 1 ♂, 7 ♀♀ (NMP 92206–92212 [S+A], 92213 [A]), Metu, 10 May 2003, leg. P. Benda & J. Obuch; – 8 ♂♂, 2 ♀♀ (NMP 95906–95908, 95910–95912, ZMMU S-178471, S-178472, S-178763 [S+A], NMP 95909 [A]), Simien National Park, Sankaber Camp, 26 April, 30 April & 17 May 2005, 5 November 2012, leg. P. Benda, S. V. Kruskop & A. A. Varšavskij; – 1 ♀ (NMP 92226 [S+A]), Sor River, 1 km N of Sor, 11 May 2003, leg. P. Benda & J. Obuch; – 9 ♂♂, 4 ♀♀ (NMP 95861–95871, HNHM pb5480, 5481 [S+A]), Suba, Menagesha Forest, 25 October 2012, leg. P. Benda & P. Kaňuch.

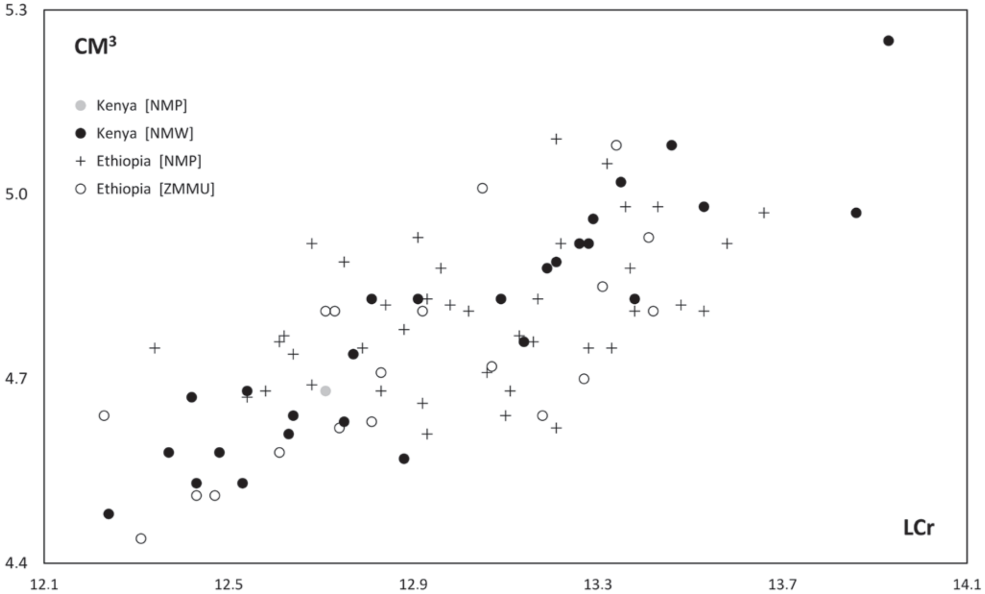


Fig. 43. Bivariate plot of the NMW and NMP specimens of *Pipistrellus hesperidus* from Kenya and comparative samples of this bat from Ethiopia: largest length of skull (LCr) against the length of upper tooth-row (CM^3). For comparative material see text.

Vansonia rueppellii (Fischer, 1829)

NMP Material (1). 1 ♂ (NMP 97972 [S+A]; Fig. 42), Ukunda, Diani, Leisure Lodge, 21 August 2022, leg. P. Benda & J. Červený.

Vansonia rueppellii is widely distributed over the whole Africa including its Palaearctic part and it reaches also the northern parts of Arabia (Hayman & Hill 1971, Harrison & Bates 1991, Kingdon 1974, Haggon et al. 2024, Monadjem et al. 2024). It inhabits mainly open habitats and in Africa, its records are scattered irregularly from Morocco, Tunisia, and Egypt in the north, to northern Namibia and northern South Africa in the south, Mauritania and Senegal in the west, and the Sudan, Ethiopia, and Tanzania in the east (Happold 2013h, Monadjem et al. 2024). In East Africa, *V. rueppellii* is known from two separated ranges, the western area is broadly adjacent to the Rift Valleys of Uganda, Tanzania, and Kenya (most records are associated with the region of Lake Victoria), the eastern area fringes the sea coast of Tanzania and Kenya, including Zanzibar (Monadjem et al. 2024); the latter island represents the type locality of the subspecies *V. r. pulcher* (Dobson, 1875), see Dobson (1875: 472). Both segments of the distribution range are present in Kenya, two sites are known from the western part of the country, Naivasha and Kisumu (Aggundey & Schlitter 1984, Monadjem et al. 2024), and two sites from the sea coast, the Arabuko-Sokoke Forest and near Watamu, both north of Mombasa (Musila et al. 2020). The NMP specimen of *V. rueppellii* originates from the southern part of the sea coast of Kenya, south of Mombasa, its locality interconnects the known Kenyan and Tanzanian coastal parts of the distribution range. The dimensions of the NMP specimen of *V. rueppellii* from Kenya are shown in Table 16.

Scotoecus hirundo **(de Winton, 1899)**

NMW Material (2). 1 ♂ (NMW 32727 [S+Sk+B]), North Nandi Forest, 4 km SW of Chomisia, 26 November 1979, leg. F. Spitzenberger;
1 ♂ (NMW 32728 [S+Sk+B]), North Nandi Forest, 4 km SW of Chomisia, 29 November 1979, leg. F. Spitzenberger.

NMP Material (6). 2 ♀♀ (NMP 97851, 97852 [S+A]), Archers Post, Buffalo Springs Reserve, Simba Lodge, 23 November 2021, leg. P. Benda, L. Bufka & J. Červený;
1 ♀ (NMP 97864 [S+A]), Archers Post, Buffalo Springs Reserve, Simba Lodge, 24 November 2021, leg. P. Benda, L. Bufka & J. Červený;
1 ♀ (NMP 97867 [S+A]; Fig. 44), Archers Post, Samburu Reserve, King Lion Camp, 25 November 2021, leg. P. Benda, L. Bufka & J. Červený;
2 ♀♀ (NMP 97995 [S+A], 97994 [A]; Fig. 45), Voi, Tsavo East National Park, Sentrim Camp, 25 August 2022, leg. P. Benda & J. Červený.

The taxonomy of the dark-winged species of the genus *Scotoecus* Thomas, 1901 remains unresolved, one to three species were suggested to exist in this group (Koopman 1993, 1994, Simmons 2005). The morphologic examinations of geographic variability showed small-sized bats to occur in the savanna belt from Senegal to Ethiopia and Uganda, medium-sized bats in eastern Africa, and large-sized bats in southern Africa, plus a marked sexual dimorphism

Figs. 44, 45. Portraits of *Scotoecus hirundo* from Kenya in the NMP collection. 44 – a female collected at the King Lion Camp, Samburu Reserve, on 25 November 2021. 45 – a female from the Sentrim Camp, Tsavo East National Park, netted on 25 August 2022.

Table 19. Biometric data on the NMW and NMP specimens of *Scotoecus hirundo* and *Neoromicia zuluensis* from Kenya. For abbreviations see Methods

dimension	*Scotoecus hirundo* (♀♀, NMP)					*Scotoecus hirundo* (♂♂, NMW)		*Neoromicia zuluensis*				
	n	**M**	min	max	SD			*n*	**M**	min	max	SD
LAt	*6*	**35.07**	33.6	36.3	1.129	36.2	38.0	*6*	**28.85**	27.5	29.7	1.013
LCr	*5*	**14.26**	13.98	14.54	0.207	15.44	15.28	*6*	**12.22**	11.62	12.63	0.339
LCb	*5*	**13.89**	13.52	14.18	0.242	15.14	15.06	*6*	**11.67**	11.04	12.14	0.375
LaZ	*5*	**10.76**	10.58	11.08	0.216	12.12	11.53	*6*	**7.67**	7.27	8.12	0.306
LaI	*5*	**4.67**	4.27	4.87	0.241	5.09	5.02	*6*	**2.97**	2.88	3.18	0.113
LaInf	*5*	**5.34**	5.14	5.52	0.143	5.98	6.18	*6*	**3.48**	3.34	3.79	0.156
LaN	*5*	**7.92**	7.58	8.35	0.280	8.31	8.23	*6*	**5.93**	5.71	6.18	0.186
LaM	*5*	**9.71**	9.57	9.98	0.165	10.61	10.08	*6*	**6.76**	6.47	7.13	0.251
ANc	*5*	**5.52**	5.37	5.65	0.121	5.98	5.71	*6*	**4.32**	4.04	4.45	0.143
LBT	*5*	**3.28**	3.03	3.48	0.171	3.62	3.58	*6*	**2.67**	2.58	2.75	0.062
CC	*5*	**5.19**	4.93	5.41	0.186	6.14	6.05	*6*	**3.62**	3.42	3.87	0.159
M^3M^3	*5*	**7.15**	6.94	7.41	0.185	7.75	7.64	*6*	**4.99**	4.83	5.28	0.154
CM^3	*5*	**5.60**	5.43	5.79	0.161	6.13	6.27	*6*	**4.32**	4.04	4.45	0.151
LMd	*5*	**11.03**	10.88	11.12	0.101	12.28	12.11	*6*	**8.59**	8.08	8.88	0.298
ACo	*5*	**3.58**	3.48	3.81	0.149	4.11	3.84	*6*	**2.76**	2.62	2.83	0.077
CM_3	*5*	**5.94**	5.79	6.08	0.127	6.74	6.71	*6*	**4.67**	4.39	4.82	0.151

with males being larger than females (Hill 1974, Robbins 1980, Taylor & van der Merwe 1998, Cotterill 2001, own data). These findings can indicate either an existence of several taxa within this genus or a cline of increasing body size from north to south within one taxon. Without employment of molecular genetic methods in a broad geographical scale, this problem will remain unresolved. Similarly to our first catalogue part (Benda et al. 2022), we temporarily assign the Kenyan specimens under a broadly defined taxon *Scotoecus hirundo* s.l. (cf. Hayman & Hill 1971, Koopman 1975, 1993, 1994, Happold 2013i, Moratelli 2019a).

This form is a widespread but uncommon savanna bat of sub-Saharan Africa (Happold 2013i, Moratelli 2019a). In East Africa, *S. hirundo* s.l. is a very common bat, the highest abundance of records within its whole range is known in central, western and south-eastern Kenya, Monadjem et al. (2024) reported 42 localities from the country in total. So, the NMW and NMP specimens do not represent an important contribution to the distribution picture of *S. hirundo* s.l. in Kenya.

The dimensions of the NMW and NMP specimens of *S. hirundo* s.l. from Kenya are shown in Table 19. The data indicate the existence of a conspicuous sexual dimorphism, the limited samples differ clearly in skull size, males are larger than females (LCr mean 15.36 mm and 14.26 mm, respectively), without an overlap in dimensional ranges (except neurocranium width, LaN). Since this size difference is well marked and the males and females originate from different habitats (forest vs. dry savanna), these two size categories could theoretically represent two species, females belonging to the small-sized *S. hirundo*, while males to the large-sized *S. hindei* Thomas, 1901; alternatively, the whole series of both sexes represents the large-sized

S. hindei (cf. Hill 1974). However, as stressed above, this problem is in need of a profound revision (see also Monadjem et al. 2020).

Afronycteris nana (Peters, 1852)

NMW Material (10). 1 ♂, 1 ♀ (NMW 32719 [S+Sk+B], 32720 [S+A]), North Nandi Forest, 2 km W of Chomisia, 11 December 1979, leg. F. Spitzenberger;
1 ♀ (NMW 32714 [S+B]), North Nandi Forest, 4 km SW of Chomisia, 26 November 1979, leg. F. Spitzenberger;
1 ♂ (NMW 32715 [S+A]), North Nandi Forest, 4 km SW of Chomisia, 29 November 1979, leg. F. Spitzenberger;
1 ♂ (NMW 32716 [S+Sk+B]), North Nandi Forest, 4 km SW of Chomisia, 4 December 1979, leg. F. Spitzenberger;
1 ♂ (NMW 32718 [S+Sk+B]), North Nandi Forest, 4 km SW of Chomisia, 9 December 1979, leg. F. Spitzenberger;
1 ♀ (NMW 32717 [S+Sk+B]), North Nandi Forest, 7 km NE of Chomisia, 4 December 1979, leg. F. Spitzenberger;
1 ♂, 1 ♀ (NMW 32393, 32394 [S+B]), Pangani, near the Lwandani Cave, 11 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂ (NMW 32395 [S+B]), Pangani, near the Lwandani Cave, 12 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

NMP Material (2). 1 ♂, 1 ♀ (NMP 97874, 97875 [S+A]; Fig. 46), Gotu Falls, Sempire Camp, 27 November 2021, leg. P. Benda, L. Bufka & J. Červený.

Figs. 46, 47. Portraits of pipistrelle bats from Kenya in the NMP collection. 46 – a male of *Afronycteris nana* (NMP 97874) collected at the Sempire Camp, Gotu Falls, on 27 November 2021. 47 – a female of *Neoromicia zuluensis* (NMP 97882) from the Sabache Camp at Ololokwe, netted on 30 November 2021.

Afronycteris nana is a bat commonly inhabiting most of the savanna and dry forest habitats of sub-Saharan Africa, from western Senegal, central Niger, and northern Eritrea, to central Namibia and eastern South Africa (Hayman & Hill 1971, Kingdon 1974, Monadjem et al. 2024). In East Africa, it is a very frequent bat, distributed evenly over the whole region, including the humid and arid parts of Kenya (Hollister 1918, Howel 1974, O'Shea & Vaughan 1980, Aggundey & Schlitter 1984, Webala et al. 2009, 2019, López-Baucells et al. 2017, Monadjem et al. 2024). The NMW and NMP specimens come from three areas of Kenya, representing three different habitat types, an upland forest in the west, coastal forest mosaic in the south-east, and semi-arid steppe in the centre of country. However, considering the broad distribution of *A. nana* in Kenya (Monadjem et al. 2024), these specimens do not bring an important addition to the occurrence picture of this bat.

The dimensions of the NMW and NMP specimens of *A. nana* from Kenya are shown in Table 18. Sequences of the examined mitochondrial gene for cytochrome *b* from two NMP specimens from Gotu Falls (a site where *A. nana* was recorded already by Aggundey & Schlitter 1984) agreed in 100% with the haplotype MT777956 from the specimen FMNH 234716 originating in southern Kenya (Mwingi, Kitui; Monadjem et al. 2021).

Neoromicia zuluensis (Roberts, 1924)

NMP Material (6). 1 ♂ (NMP 97869 [S+A]), Archers Post, Samburu Reserve, King Lion Camp, 26 November 2021, leg. P. Benda, L. Bufka & J. Červený;

1 ♂, 1 ♀ (NMP 97881, 97882 [S+A]; Fig. 47), Ololokwe, Sabache Camp, 30 November 2021, leg. P. Benda, L. Bufka & J. Červený;

2 ♂♂, 1 ♀ (NMP 97996–97998 [S+A]), Voi, Tsavo East National Park, Sentrim Camp, 25 August 2022, leg. P. Benda & J. Červený.

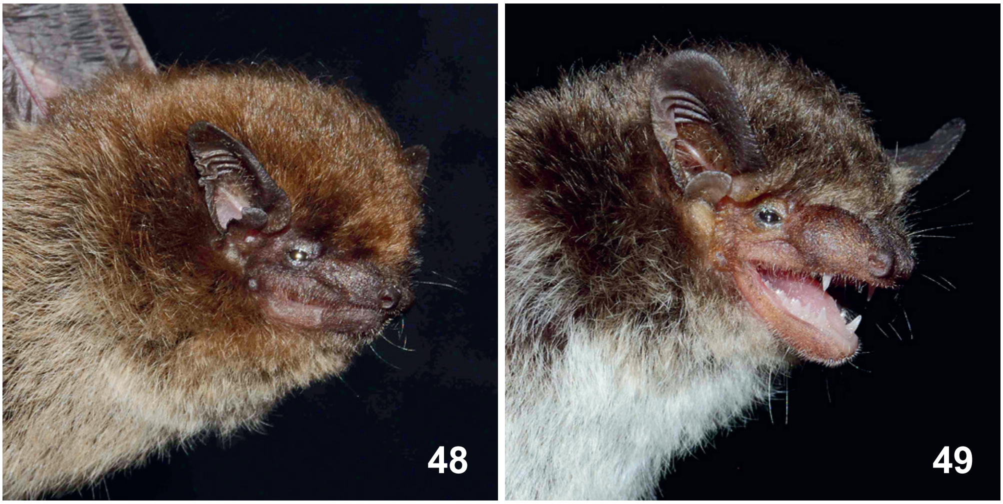
Neoromicia zuluensis is a bat that has been recognised as a full species relatively recently (Peterson et al. 1995, Kearney et al. 2002, Simmons 2005, Monadjem et al. 2010), while formerly, it was considered to represent a southern African subspecies of *N. somalica* (Koopman 1975, 1993, 1994, Hill & Harrison 1987). Simmons (2005) and Monadjem et al. (2010) reported the confirmed occurrence of *N. zuluensis* only from southern Africa, from central Namibia and northern South Africa to the northern parts of Angola and Zambia, and only uncertain occurrence from East Africa (Monadjem et al. 2010) and eastern Africa (Kenya, Ethiopia, and the Sudan; Simmons 2005), respectively. From eastern Africa (Ethiopia, southern South Sudan, eastern Uganda, and western Kenya), the occurrence of *N. zuluensis* is mentioned without doubts by Patterson & Webala (2012) or Van Cakenberghe et al. (2017). The molecular genetic revision by Monadjem et al. (2021) confirmed the presence of this bat species in East Africa, namely in the central and south-eastern parts of Kenya. Monadjem et al. (2024) reported nine localities of this bat from these areas of Kenya, and additionally two from Rwanda and one from central Tanzania. The localities of the NMP specimens generally conform to the distribution picture of *N. zuluensis* in Kenya given by Monadjem et al. (2024), the records from the Samburu Reserve and Tsavo East NP lie within the range of known localities. The latter site slightly prolongs the genetically confirmed range of the species distribution to the north, Ololokwe is situated 32 km north of the three camp sites in the Samburu Reserve with records of *N. zuluensis* (Vervet, Larsen's, King Lion; Monadjem et al. 2021, 2024, own data).

The dimensions of the NMP specimens of *N. zuluensis* from Kenya are shown in Table 19. Sequences of the cytochrome *b* gene from the NMP specimens were in concordance of 99.3–99.8% with the haplotypes of *N. zuluensis* from Kenya published by Monadjem et al. (2021). The bats NMP 97869, 97882, and 97996 (i.e., from all three sites) agreed in 99.5–99.8% with the haplotype MT778008 from the specimen FMNH 221023 collected at the Komboyo Campsite, Tsavo West NP. The haplotypes from the specimens NMP 97881, 97997, and 97998 conformed by 99.3–99.6% to the haplotype MT777993 from the specimen FMNH 234600 from the Ngelani Baobab in Mutha, south-central Kenya.

***Neoromicia somalica* (Thomas, 1901)**

NMP Material (3). 1 ♂ (NMP 98059 [S+A]), Namanga, 27 June 2010, leg. J. Bryja, J. S. Mbau & R. Šumbera;
1 ♀ (NMP 97884 [S+A]; Fig. 48), Nanyuki, Ol Pejeta Reserve, Stable, 1 December 2021, leg. P. Benda, L. Bufka & J. Červený;
1 ♂ (NMP 97949 [S+A]), Ol Kirimatian, Nyiro River Camp, 16 August 2022, leg. P. Benda & J. Červený.

Traditionally, *Neoromicia somalica* was considered to be a widely distributed bat in the dry savanna zone of the northern part of Africa (Simmons 2005, cf. Koopman 1993, 1994), from Guinea-Bissau and Senegal in the west, to the Sudan and Somalia in the east, and to DR Congo and Tanzania in the south. However, based on a molecular genetic analysis, Monadjem et al. (2021) suggested to restrict the range of *N. somalica* s.str. to eastern Africa, with confirmed records spread in a belt of savannas stretching from Somaliland via Kenya to central Tanzania, while the West African occurrence of this bat was doubted and the respective populations were assigned to a possible separate taxon (see also Koubínová et al. 2013). On the other hand,



Figs. 48, 49. Portraits of pipistrelle bats from Kenya in the NMP collection. 48 – a female of *Neoromicia somalica* (NMP 97884) collected in the Ol Pejeta Reserve near Nanyuki on 1 December 2021. 49 – a female of *Pseudoromicia nyanza* from the Soi Safari Lodge, Kampi Ya Samaki, Lake Baringo, netted on 2 December 2021.

Table 20. Biometric data on the NMP specimens of *Neoromicia somalica*, *Pseudoromicia nyanza*, and *Nycticeinops schlieffenii* from Kenya. For abbreviations see Methods

dimension	*Neoromicia somalica*					*Pseudoromicia nyanza*					*Nycticeinops schlieffenii*				
	n	**M**	min	max	SD	*n*	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*3*	**31.50**	30.3	33.4	1.664	*10*	**31.40**	29.8	34.3	1.237	*13*	**33.50**	31.0	34.9	1.129
LCr	*3*	**12.23**	11.71	12.94	0.638	*7*	**12.49**	12.17	13.09	0.330	*11*	**13.30**	12.78	13.65	0.237
LCb	*3*	**11.79**	11.24	12.57	0.694	*7*	**11.86**	11.61	12.45	0.296	*11*	**12.84**	12.31	13.18	0.251
LaZ	*3*	**7.91**	7.68	8.31	0.348	*7*	**8.26**	8.04	8.83	0.261	*10*	**9.11**	8.82	9.32	0.152
LaI	*3*	**3.20**	3.07	3.42	0.189	*7*	**3.49**	3.42	3.58	0.057	*11*	**3.71**	3.48	3.93	0.136
LaInf	*3*	**3.63**	3.48	3.78	0.150	*7*	**3.91**	3.72	4.14	0.124	*11*	**4.45**	4.21	4.61	0.107
LaN	*3*	**6.17**	6.11	6.22	0.056	*7*	**6.60**	6.37	6.73	0.121	*11*	**6.83**	6.62	7.08	0.137
LaM	*3*	**6.89**	6.68	7.08	0.201	*7*	**7.23**	7.11	7.48	0.147	*11*	**7.87**	7.68	8.28	0.176
ANc	*3*	**4.54**	4.41	4.73	0.168	*7*	**4.44**	4.31	4.71	0.144	*11*	**5.01**	4.84	5.22	0.146
LBT	*3*	**2.85**	2.74	2.93	0.098	*7*	**2.86**	2.65	3.02	0.143	*11*	**2.96**	2.74	3.23	0.138
CC	*3*	**3.84**	3.62	4.23	0.336	*7*	**4.02**	3.93	4.13	0.091	*11*	**4.23**	3.98	4.48	0.137
M^3M^3	*3*	**5.27**	5.03	5.68	0.354	*7*	**5.37**	5.11	5.94	0.265	*11*	**5.86**	5.56	6.07	0.161
CM^3	*3*	**4.42**	4.19	4.75	0.295	*7*	**4.25**	4.07	4.67	0.205	*11*	**4.80**	4.68	4.91	0.074
LMd	*3*	**8.58**	8.26	9.16	0.506	*7*	**8.95**	8.73	9.67	0.336	*11*	**9.66**	9.32	9.96	0.222
ACo	*3*	**2.84**	2.67	3.18	0.292	*7*	**2.83**	2.64	3.11	0.149	*11*	**3.35**	3.01	3.48	0.140
CM_3	*3*	**4.69**	4.31	5.02	0.358	*7*	**4.66**	4.52	5.11	0.205	*11*	**5.18**	5.04	5.40	0.109

Benda et al. (2022) and Monadjem et al. (2024) prolonged the known extent of the range of *N. somalica* southwards to Zambia and Malawi. However, in East Africa, this bat has been considered a common component of the fauna, covering by its occurrence widely and abundantly the whole region (Aggundey & Schlitter 1984, Thorn & Kerbis Peterhans 2009, Monadjem et al. 2021, 2024). Thus, three localities of the NMP specimens situated in central and southern Kenya do not represent a significant contribution to the distribution picture of *N. somalica* in the country.

The dimensions of the NMP specimens of *N. somalica* from Kenya are shown in Table 20. Sequences of the cytochrome *b* gene obtained from two NMP specimens were in high congruence with the haplotypes of *N. somalica* published by Monadjem et al. (2021). The specimen NMP 97884 showed an agreement of 100% with the haplotype MT777981 extracted from the specimen NMK 184639 from the Ol Jogi Conservancy in central Kenya; the bat NMP 97949 was in concordance of 99.6% with the haplotype MT777989 from the specimen FMNH 225624 originating from the Masai Mara NR, south-western Kenya.

***Neoromicia capensis* (Smith, 1829)**

NMP Material (1). 1 ♂ (NMP 97944 [S+A]), Kwa Muhia, Hells Gate National Park, Naiburta Camp, 14 August 2022, leg. P. Benda & J. Červený.

Traditionally, *Neoromicia capensis* was regarded as a widely distributed savanna bat of sub-Saharan Africa, from Senegal to the Sudan and South Africa, including most of East Africa (Hayman & Hill 1971, Corbet & Hill 1980, Patterson & Webala 2012, Kearney 2013a, Moratelli

2019b, etc.). However, based on the results of a molecular genetic analysis (Monadjem et al. 2021), the current distribution range of *N. capensis* has been restricted to the southern half of the continent, stretching from central DR Congo, Burundi, and central Tanzania to the Cape (Monadjem et al. 2024), while the populations of West Africa, from Guinea-Bissau to Cameroon, were assigned to *N.* cf. *capensis*. In East Africa, the accepted occurrence of *N. capensis* s.str. remained only in the southern part of Tanzania, plus a record in southern Burundi (Makamba, cf. Van Cakenberghe et al. 2017), being the northernmost African admitted occurrence site of this species (Monadjem et al. 2024). The records from Kenya attributed to *N. capensis* by Aggundey & Schlitter (1984), eleven localities in total (including those originally reported by Hollister 1918, Zimmerman 1972, and Kock 1981), were referred to *Laephotis kirinyaga* Monadjem, Patterson, Webala et Demos, 2021 by Monadjem et al. (2024). Therefore, *N. capensis* disappeared from the list of Kenyan bat fauna.

However, this disappearance has been only short-lived as the specimen NMP 97944 collected at the Naiburta Camp in the Hells Gate NP, south-central Kenya, was found to possess a haplotype that showed a congruence of 99.9% with the haplotype MT777881 extracted from the specimen of *N. capensis* FMNH 219120 collected in the Ruaha NP, southern Tanzania (Monadjem et al. 2021). This record indicates that the distribution of *N. capensis* extends further to the north than suggested by Monadjem et al. (2024) and the southern part of Kenya belongs to the distribution range of this bat. This record also suggests that at least some of the specimens/records arbitrarily affiliated with *L. kirinyaga* by Monadjem et al. (2024) might in fact represent *N. capensis* as it was reported originally. The dimensions of the NMP specimen of *N. capensis* from Kenya are shown in Table 16.

***Pseudoromicia rendalli* (Thomas, 1889)**

NMW Material (1). 1 ♀ (NMW 32397 [S+B]), Pangani, near the Lwandani Cave, 11 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Reference. Aggundey & Schlitter (1984).

Pseudoromicia rendalli is the most widespread species of the recently described Afrotropical bat genus *Pseudoromicia* Monadjem, Patterson, Webala et Demos, 2021, that contains at least ten species, mainly of the West African distribution (Monadjem et al. 2021, Grunwald et al. 2023, Juste et al. 2023). The range of *P. rendalli* stretches across the savanna zones from the Gambia and Sierra Leone in the west, to the Sudan in the east, and northern Botswana and eastern South Africa in the south (Hayman & Hill 1971, Moratelli R., 2019b, Monadjem et al. 2024). In East Africa, its distribution is limited to the northern part of the region, with single records in Rwanda, Uganda, and western Kenya, and with a higher abundance in central and south-eastern Kenya (Kingdon 1974, Aggundey & Schlitter 1984, Thorn & Kerbis Peterhans 2009, Musila et al. 2020). The NMW specimen from Pangani was published already by Aggundey & Schlitter (1984); although this report has not been accepted as a species evidence in the review of specimen-based records by Monadjem et al. (2024), the locality lies within the distribution limits in south-eastern Kenya as given by the latter authors.

The dimensions of the NMW specimen of *P. rendalli* from Kenya are shown in Table 16. The values of the skull metric data on this bat are slightly lower than those given for this species by Thorn & Kerbis Peterhans (2009), Monadjem et al. (2020), and Grunwald et al. (2023). However, these authors examined a material not sufficient to give real variation ranges of size parameters in this bat.

Pseudoromicia nyanza Monadjem, Patterson, Webala et Demos, 2021

NMP Material (10). 5 ♂♂, 4 ♀♀ (NMP 97902–97904, 97908–97910 [S+A], 97905–97907 [A]; Fig. 49), Kampi Ya Samaki, Soi Safari Lodge, 2 December 2021, leg. P. Benda, L. Bufka & J. Červený; 1 ♀ (NMP 98065 [S+A]), Ol Kirimatian, Shompole Conservancy, 12 August 2013, leg. J. Červený.

Pseudoromicia nyanza is a bat species that has been described recently based on a series of specimens from Kenya, its type locality is Kisumu on the eastern bank of Lake Victoria (Monadjem et al. 2021). Besides those from the type locality, specimens from four other Kenyan sites were assigned to the new species by Monadjem et al. (2021), all situated in the south-western corner of the country. Later, Monadjem et al. (2024) assigned almost all records (55 in total) from eastern Africa formerly referred to *P. tenuipinnis* (Peters, 1872) to *P. nyanza*, while the former species is now restricted to West and Central Africa. According to the latter authors, *P. nyanza* is distributed in a large part of eastern Africa, between north-western DR Congo, south-western Ethiopia, central Kenya, northern Tanzania, and western Burundi. Altogether 14 localities are reported from Kenya, scattered over the central and south-western parts of the country (Monadjem et al. 2024). The NMP series of *P. nyanza* from Kampi Ya Samaki represents a new record of the species from the region of Lake Baringo, where *P. tenuipinnis* s.l. was reported repeatedly (Kock 1981, Aggundey & Schlitter 1984, Monadjem et al. 2024). The locality of the other NMP specimen, Shompole Conservancy, represents a new occurrence point in Kenya and a shift of the species range margin to the south-east, ca. 125 km south of Lake Naivasha and 130 km west of the Masai Mara Reserve, the closest sites reported by Monadjem et al. (2024).

The dimensions of the NMP specimens of *P. nyanza* from Kenya are shown in Table 20. Sequences of the cytochrome *b* gene obtained from two NMP specimens from Kampi Ya Samaki, Lake Baringo, showed a congruence with other haplotypes of *P. nyanza* from south-western Kenya sensu Monadjem et al. (2021): the haplotype from the specimen NMP 97902 corresponded by 98.0% with the haplotype MT778048 from the specimen FMNH 225617 from the Masai Mara Reserve, and the specimen NMP 97903 corresponded by 98.2% with the haplotype MT778041 from the specimen FMNH 215659 originating from the Ruma National Park.

Afropipistrellus grandidieri (Dobson, 1876)

NMW Material (1). 1 ♀ (NMW 32398 [S+B]), Pangani, near the Lwandani Cave, 12 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Afropipistrellus grandidieri is a rare bat throughout its wide range covering the central parts of Africa between Cameroon, Uganda, south-eastern Kenya, central Mozambique, and Angola; less than thirty localities of this bat are available from this area (Hayman et al. 1966, Thorn et al. 2007, Monadjem et al. 2021, Benda et al. 2022). In East Africa, three occurrence ranges are known: central Uganda, western Burundi, and the sea coast areas of north-eastern Tanzania (including Zanzibar, the type locality of this bat; Dobson 1876) and south-eastern Kenya (Monadjem et al. 2024). It is a very rare bat in the latter country, documented there just recently (Thorn et al. 2007). Currently, five records of *A. grandidieri* from two areas are known, Watamu and Kwale (Thorn et al. 2007, Monadjem et al. 2021). The locality of the NMW specimen, near the Lwandani Cave, lies in between these two areas and interconnects the Kenyan occurrence range of this bat into a narrow belt along the sea coast. The dimensions of the NMW specimen of *A. grandidieri* from Kenya are shown in Table 16. By its body size (LAt

33.4 mm, LCr 13.32 mm, CM^3 4.74 mm), this specimen corresponds well with the dimensions of the small-sized East African nominotypical subspecies (Thorn et al. 2007).

Nycticeinops schlieffenii (Peters, 1859)

NMP Material (13). 1 ♂, 8 ♀♀ (NMP 97855–97857, 97860–97863 [S+A], 97858, 97859 [A]), Archers Post, Buffalo Springs Reserve, Simba Lodge, 24 November 2021, leg. P. Benda, L. Bufka & J. Červený;
1 ♀ (NMP 97901 [S+A]), Kampi Ya Samaki, Soi Safari Lodge, 2 December 2021, leg. P. Benda, L. Bufka & J. Červený;
1 ♂ (NMP 97883 [S+A]; Fig. 50), Ololokwe, Sabache Camp, 30 November 2021, leg. P. Benda, L. Bufka & J. Červený;
1 ♂ (NMP 97962 [S+A]; Fig. 51), Tsavo West National Park, Ngulia Lodge, 19 August 2022, leg. P. Benda & J. Červený;
1 ♂ (NMP 97963 [S+A]), Tsavo West National Park, Ngulia Lodge, 20 August 2022, leg. P. Benda & J. Červený.

Nycticeinops schlieffenii is a bat broadly distributed in dry savannas and arid steppes of sub-Saharan Africa, from western Mauritania and Senegal to the eastern Sudan, Somalia, central Namibia, and eastern South Africa (Kingdon 1974, Happold 2013g, Lanza et al. 2015, Monadjem et al. 2024). In East Africa, it is widespread over the whole region, although only moderately frequent, most of the records are available from Kenya, where they are scattered across the country except the north-east (Aggundey & Schlitter 1984, Monadjem et al. 2024). In the NMP collection of Kenyan bats, the specimens of *N. schlieffenii* are available from four localities, three in the central part and one in the southern part of the country, thus the NMP material originates from areas where the species was already reported, see Aggundey

Figs. 50, 51. Portraits of *Nycticeinops schlieffenii* from Kenya in the NMP collection. 50 – a male (NMP 97883) from the Sabache Camp at Ololokwe, netted on 30 November 2021. 51 – a male (NMP 97962) collected at the Ngulia Lodge, Tsavo West National Park, on 19 August 2022.

& Schlitter (1984). The dimensions of the NMP specimens of *N. schlieffenii* from Kenya are shown in Table 20.

Mimetillus moloneyi (Thomas, 1891)

NMW Material (1). 1 ♀ (NMW 32726 [S+Sk+B]), North Nandi Forest, 4 km SW of Chomisia, 29 November 1979, leg. F. Spitzenberger.

Mimetillus moloneyi is distributed in the forest zone of tropical Africa, from Sierra Leone and Guinea-Conakry to south-western Ethiopia, Angola, and southern Mozambique, including Bioko Island (Hayman & Hill 1971, Monadjem et al. 2024). In East Africa, this bat is distributed most abundantly in the north-western woodland and forested parts of the region (Kingdon 1974, Thorn & Kerbis Peterhans 2009, Monadjem et al. 2024), although records from central Kenya and the sea coast zone of Kenya and Tanzania also exist (Kingdon 1974, Aggundey & Schlitter 1984, Musila et al. 2020). The NMW specimen of *M. moloneyi* originates from the Nandi Forest in south-western Kenya, an area of relatively common occurrence of this species (Aggundey & Schlitter 1984); its dimensions are shown in Table 16.

Scotophilus colias Thomas, 1904

NMW Material (15). 1 ♀ (NMW 32792 [S+A]), North Nandi Forest, 2 km W of Chomisia, 10 December 1979, leg. F. Spitzenberger;
1 ♀ (NMW 32793 [S+Sk+B]), North Nandi Forest, 2 km W of Chomisia, 11 December 1979, leg. F. Spitzenberger;
2 ♀♀ (NMW 32783 [S+B], 32782 [S+Sk+B]), North Nandi Forest, 4 km SW of Chomisia, 26 November 1979, leg. F. Spitzenberger;
1 ♂, 2 ♀♀ (NMW 32787, 32788 [S+B], 32786 [S+A]), North Nandi Forest, 4 km SW of Chomisia, 29 November 1979, leg. F. Spitzenberger;
1 ♀ (NMW 32791 [S+A]), North Nandi Forest, 4 km SW of Chomisia, 9 December 1979, leg. F. Spitzenberger;
1 ♂, 1 ♀ (NMW 32789, 32790 [S+B]), North Nandi Forest, 7 km NE of Chomisia, 4 December 1979, leg. F. Spitzenberger;
2 ♀♀ (NMW 32784, 32785 [S+B]), North Nandi Forest, 7 km NE of Chomisia, 9 December 1979, leg. F. Spitzenberger;
1 ♂, 2 ♀♀ (NMW 32794, 32795 [S+Sk+B], 32796 [S+A]), North Nandi Forest, 7 km NE of Chomisia, 11 December 1979, leg. F. Spitzenberger.

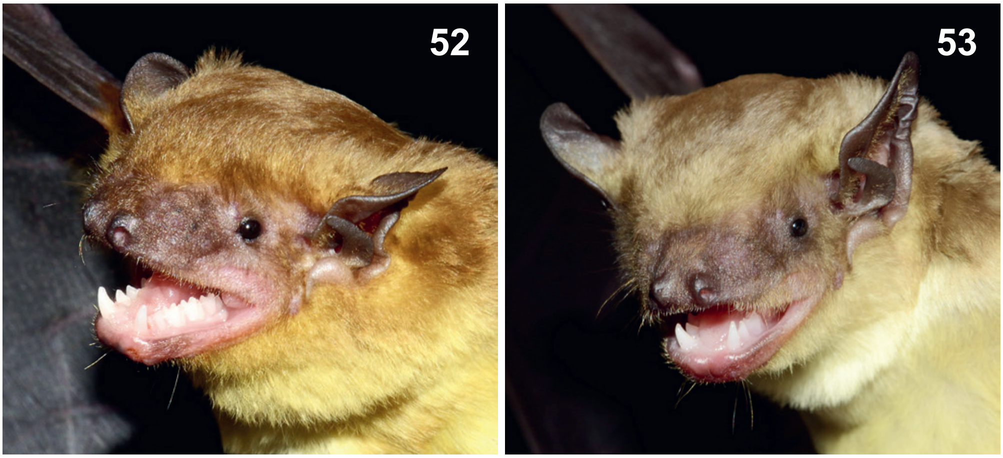
NMP Material (7). 1 ♂, 1 ♀ (NMP 97992, 97993 [S+A]), Voi, Tsavo East National Park, Sentrim Camp, 25 August 2022, leg. P. Benda & J. Červený;
4 ♂♂, 1 ♀ (NMP 98010–98013 [S+A], 98009 [A]; Fig. 52), Watamu, Mida Creek Camp, 2 July 2023, leg. P. Benda & J. Červený.

Scotophilus colias is a bat whose species rank has been suggested only recently by Vallo et al. (2011b), based on genetic differences from *S. dinganii* (Smith, 1833), a species formerly considered to be broadly distributed across the savanna zones of the whole Afrotropics (see Robbins et al. 1985, Moratelli 2019c). This former rank of the latter species, currently restricted in its distribution range to the southern half of the African continent (see Monadjem et al. 2024), covered *S. colias* as an East African subspecies (Kulzer 1959, Hayman & Hill 1971, Robbins et al. 1985, Aggundey & Schlitter 1984, Simmons 2005).

According to Vallo et al. (2011b), *S. colias* is distributed in Kenya, Ethiopia, and Yemen, and according to Moratelli (2019c) also in Eritrea. Considering the known occurrence of *S. colias* based on revised records, the species distribution range covers probably also parts of South Sudan, Uganda, Somalia, and northern Tanzania. The localities of the NMW and NMP specimens lie within the range of *S. dinganii* s.l. in Kenya (Aggundey & Schlitter 1984, Monadjem et al. 2024) and also, they do not shift margins of the range depicted by the revised occurrence of *S. colias* (Vallo 2011b, Demos et al. 2018).

However, the species status of *S. colias* has not been accepted universally. Additionally, Brooks & Bickham (2014) assigned the lineages affiliated with the latter name by Vallo et al. (2011b) to two other names described as two separate species, *S. andrewreborii* Brooks et Bickham, 2014 from Kenya and *S. ejetai* Brooks et Bickham, 2014 from Ethiopia. The prior name to the *dinganii* morphotype from eastern Africa, *S. nigrita colias* Thomas, 1904, described based on the specimen from Fort Hall, Kenya District, British East Africa [= Murang'a, central Kenya; 00°43'S, 37°09'E] (Thomas 1904: 208), was completely omitted by Brooks & Bickham (2014), concerning the comparisons of diagnostic characters and/or discussion of taxonomy and nomenclature of the newly delimited taxa (in fact, they did not discuss any of the names available in the synonymy of *Scotophilus* Leach, 1821 other than those affiliated with the full species by Simmons 2005). Moreover, the type locality of *S. andrewreborii* (Rift Valley Province [central Kenya], Nakuru District, 12 km S, 4 km E Nakuru; 00°24'S, 36°07'E; Brooks & Bickham 2014: 8) lies 120 km WNW of Murang'a, the type locality of *S. colias*.

However, according to the data published by Demos et al. (2018), the uncorrected genetic distance within the lineage containing *S. andrewreborii*, *S. ejetai*, *S.* cf. *ejetai*, and the clades 1 and 2 (naming of the clades sensu Demos et al. 2018: 6, Fig. 1) ranges up to 3.6%, including the haplotypes/specimens affiliated with *S. colias* by Vallo et al. (2011b). Given such a weak evidence and the lack of appropriate support for the distinction from the prior name available



Figs. 52, 53. Portraits of house bats from Kenya in the NMP collection; bats collected at the Mida Creek Camp, Watamu, on 2 July 2023. 52 – a male of *Scotophilus colias*. 53 – a female of *Scotophilus trujilloi* (NMP 98014).

Table 21. Biometric data on the NMW and NMP specimens of *Scotophilus colias*, *S. trujilloi*, and *S. nux* from Kenya. For abbreviations see Methods

dimension	*Scotophilus colias*					*Scotophilus trujilloi*					*Scotophilus nux*				
	n	**M**	min	max	SD	*n*	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*22*	**52.58**	49.2	55.9	1.707	*6*	**43.50**	40.2	48.6	2.898	*23*	**56.35**	53.8	59.4	1.288
LCr	*21*	**20.27**	19.28	21.64	0.645	*6*	**16.71**	15.38	17.52	0.749	*23*	**20.85**	20.24	21.61	0.423
LCb	*21*	**18.90**	18.03	19.75	0.548	*6*	**15.79**	14.88	16.58	0.647	*23*	**19.10**	18.61	19.82	0.372
LaZ	*21*	**14.11**	13.48	14.98	0.366	*6*	**12.29**	11.10	12.93	0.697	*23*	**14.78**	14.31	15.34	0.300
LaI	*21*	**4.81**	4.44	5.21	0.228	*6*	**4.45**	4.35	4.57	0.088	*23*	**5.02**	4.65	5.34	0.163
LaInf	*21*	**7.38**	6.96	7.68	0.200	*6*	**5.91**	5.46	6.21	0.314	*23*	**7.25**	6.86	7.56	0.192
LaN	*21*	**9.80**	9.45	10.45	0.266	*6*	**8.76**	8.48	9.06	0.211	*23*	**10.14**	9.69	10.88	0.299
LaM	*21*	**12.24**	11.43	12.89	0.419	*6*	**10.78**	10.16	11.28	0.373	*23*	**12.98**	12.22	13.78	0.425
ANc	*21*	**8.16**	7.74	8.69	0.298	*6*	**7.70**	6.75	8.56	0.659	*23*	**8.91**	8.34	10.35	0.472
LBT	*20*	**4.22**	3.90	4.61	0.191	*6*	**3.81**	3.51	4.04	0.185	*23*	**3.99**	3.82	4.32	0.116
CC	*21*	**7.26**	6.82	7.68	0.227	*6*	**5.77**	5.42	6.17	0.274	*23*	**6.93**	4.02	7.45	0.656
M^3M^3	*21*	**9.23**	8.56	9.64	0.302	*6*	**7.88**	7.47	8.24	0.283	*23*	**8.93**	8.01	9.72	0.320
CM^3	*21*	**7.10**	6.69	7.44	0.245	*6*	**5.78**	5.63	6.02	0.162	*23*	**7.08**	6.74	7.42	0.171
LMd	*21*	**14.77**	14.12	15.58	0.400	*6*	**12.26**	11.44	12.94	0.527	*23*	**15.03**	14.52	15.52	0.278
ACo	*21*	**6.38**	5.94	6.98	0.270	*6*	**4.76**	4.36	5.08	0.263	*23*	**6.29**	5.86	6.71	0.202
CM_3	*21*	**7.98**	7.45	8.42	0.225	*6*	**6.57**	6.37	6.93	0.219	*23*	**7.97**	7.64	8.23	0.185

for this lineage, *colias* Thomas, we stick to the use of this name for this lineage until further data provide adequate support for the (prematurely) introduced new names.

The dimensions of the NMW and NMP specimens from Kenya (Table 21) correspond to the data on *S. colias* from Ethiopia given by Vallo et al. (2011b), and are in concord with the dimensions of the holotype of *S. nigrita colias* Thomas, 1904 (BMNH 2.7.6.11.): LAt 54.7 mm, LCb 19.23 mm, LaZ 14.06 mm, LaInf 7.38 mm, CM^3 7.21 mm, LMd 15.03 mm (see also Vallo et al. 2011b). Both NMW and NMP series showed almost identical variation ranges of basic dimensions (despite the different sizes of the series, and different altitudes of their localities; NMW vs. NMP): LAt 49.4–55.9 mm vs. 49.2–53.6 mm, LCb 18.18–19.75 mm vs. 18.03–19.67 mm, CM^3 6.71–7.38 mm vs. 6.69–7.44 mm. On average, the NMW and NMP specimens are smaller than those of *S. dinganii* s.str. from southern Africa (Monadjem et al. 2020, own unpubl. data).

Sequences of the cytochrome *b* gene from the NMP specimens of *S. colias* from south-eastern Kenya were in high congruence with the haplotypes assigned to *S. andrewreborii* and to the closely positioned clades sensu Demos et al. (2018), for details see also Trujillo et al. (2009) and Brooks & Bickham (2014). The sequences from the specimens NMP 97992 and 97993 agreed in 100% with the haplotype EU750965 from three specimens (CM 98044, 98045, 98054) collected at Bushwackers near Kibwezi, south-eastern Kenya (Trujillo et al. 2009, Brooks & Bickham 2014); additionally, these sequences agreed in 100% with the haplotype MH299525 from the specimen FMNH 216151 collected at Komboyo in the Tsavo West NP (Demos et al. 2018). The haplotypes from NMP 98009 and NMP 98013 agreed in 99.8% and 100%, respectively, with the haplotype EU750963 from the specimen CM 98043 collected at Kwale, south-eastern Kenya (Trujillo et al. 2009).

Scotophilus trujilloi Brooks et Bickham, 2014

NMW Material (5). 2 ♂♂ (NMW 32399, 32400 [S+B]), Pangani, near the Lwandani Cave, 9 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
3 ♂♂ (NMW 32401–32403 [S+B]), Pangani, near the Lwandani Cave, 12 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

NMP Material (1). 1 ♀ (NMP 98014 [S+A]; Fig. 53), Watamu, Mida Creek Camp, 2 July 2023, leg. P. Benda & J. Červený.

Reference. Aggundey & Schlitter (1984).

Scotophilus trujilloi is a recently recognised species (Trujillo et al. 2009, Brooks & Bickham 2014), it was described based on a peculiar genetic lineage of the small-sized *Scotophilus* morphotype originally referred to *S. viridis* (Peters, 1852). The latter species was formerly considered to occur in a large part of the savanna zone of Africa (Robbins et al. 1985, Simmons 2005) and currently its distribution has been restricted to the south-eastern part of the continent (Monadjem et al. 2024). The new species was described based on a series of three specimens from the Moana Marine Station at Ukunda, on the sea coast of south-eastern Kenya (04°18'S, 39°35'E; Brooks & Bickham 2014).

Despite the lack of comparison with a relevant type material in the description by Brooks & Bickham (2014), similarly as in the case of the previous species (*S. colias*, see above), according to the currently available genetic comparisons with published museum materials of *S. viridis* s.str. and other species of the genus, *S. trujilloi* seems to be a sufficiently substantiated taxon. However, we consider the status of this species rather as tentative, since an additional study showed the mutual positions of various populations of the *S. viridis* morphotype as unresolved (Demos et al. 2018), and the final taxonomic arrangement will most probably concern also *S. trujilloi*. Anyway, here we adopt *S. trujilloi* as a valid name for the herein presented series of the NMW and NMP specimens.

The confirmed distribution range of *S. trujilloi* based on the localities of sequenced specimens covers southern Kenya and northern Tanzania, including Pemba Island (Demos et al. 2018, Monadjem et al. 2024). The localities of both the NMW and NMP specimens, situated in the sea coast regions of Kenya, fit to the known occurrence range of this bat.

The dimensions of the NMW and NMP specimens of *S. trujilloi* from Kenya are shown in Table 21. Sequence of the cytochrome *b* gene obtained from the specimen NMP 98014 showed 100% congruence with the haplotype MH299595 from the specimen FMNH 216156 collected at Jilore Quarters in the Arabuko-Sokoke Reserve situated some 12 km of the NMP specimen collection site.

Scotophilus nux Thomas, 1904

NMW Material (24). 1 ♂, 5 ♀♀ (NMW 32758–32762 [S+B], 32763 [S+Sk]), North Nandi Forest, 3 km W of Chomisia, 20 November 1979, leg. F. Spitzenberger;
3 ♂♂ (NMW 32764–32766 [S+B]), North Nandi Forest, 3 km W of Chomisia, 21 November 1979, leg. F. Spitzenberger;
1 ♀ (NMW 32767 [S+B]), North Nandi Forest, 3 km W of Chomisia, 24 November 1979, leg. F. Spitzenberger;
1 ♂ (NMW 32768 [S+B]), North Nandi Forest, 4 km SW of Chomisia, 26 November 1979, leg. F. Spitzenberger;

4 ♂♂, 5 ♀♀ (NMW 32769–32772, 32774 [S+B], 32773, 32775–32777 [S+A]), North Nandi Forest, 4 km SW of Chomisia, 29 November 1979, leg. F. Spitzenberger;
1 ♀ (NMW 32778 [S+B]), North Nandi Forest, 7 km NE of Chomisia, 4 December 1979, leg. F. Spitzenberger;
1 ♀ (NMW 32779 [S+B]), North Nandi Forest, 7 km NE of Chomisia, 9 December 1979, leg. F. Spitzenberger;
2 ♀♀ (NMW 32780, 32781 [S+A]), North Nandi Forest, 7 km NE of Chomisia, 11 December 1979, leg. F. Spitzenberger.

Scotophilus nux is a forest dwelling bat, its range stretches patchily across the high rainforest zone belt from Sierra Leone to Kenya (Robbins et al. 1985, Monadjem et al. 2024). In East Africa, it was recorded only in Uganda and Kenya, and in western Kenya, this species reaches the eastern margin of its distribution range. While most of the species range lies in the lowlands of the Guinean coastal areas and of the Congo Basin (altitude range of the records 0–870 m a. s. l., mean 361 m, n=29; Monadjem et al. 2024), in the eastern range margin *S. nux* inhabits upland forests (altitude range 795–2,510 m a. s. l., mean 1,609 m, n=12; Monadjem et al. 2024, our data). From Kenya, all records available till now come from the Kakamega and Kisere Forests, two spots of tropical rainforest at ca. 1600 m a. s. l., covering some 245 km^2 in total (Aggundey & Schlitter 1984, Robbins et al. 1985, Schlitter et al. 1986, Demos et al. 2018, Webala et al. 2019, Monadjem et al. 2024). The NMW series of *S. nux* originates from a neighbouring forest unit, the North Nandi Forest covering 105 km^2 and separated from the Kakamega Forest by the Nandi Escarpment. The three localities are situated at the altitudes between 1892 and 2005 m a. s. l. These records enlarge the Kenyan range area of *S. nux* by a third and represent a new eastern margin of the whole species distribution range (with a shift of ca. 20 km). The North Nandi Forest represents the second highest area of known occurrence of this bat after the Kigezi Highlands in south-western Uganda (~2510 m; Thorn & Kerbis Peterhans 2009). The dimensions of the NMW specimens of *S. nux* from Kenya are shown in Table 21.

Miniopteridae

***Miniopterus* aff. *inflatus* Thomas, 1903**

NMW Material (33). 1 ♀ (NMW 32454 [S+B]), Kiminini, Chepkelele Cave, 31 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
7 ♂♂, 1 ♀ (NMW 32445–32450, 32453 [S+B], 32452 [B]), Kiminini, Nabongo Cave, 30 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♀ (NMW 32421 [S+B]), Mount Elgon National Park, Chepnyalil Cave, 26 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♀ (NMW 32423 [A]), Mount Elgon National Park, Rongai Camp, 26 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂ (NMW 32429 [S+Sk]), Mount Elgon National Park, Rongai Camp, 27 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂, 2 ♀♀ (NMW 32431–32433 [S+B]), Mount Elgon National Park, Rongai Camp, 28 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂ (NMW 32797 [S+B]), North Nandi Forest, 3 km W of Chomisia, 20 November 1979, leg. F. Spitzenberger;
2 ♂♂, 3 ♀♀ (NMW 32799 [S+Sk+B], 32798, 32800–32802 [S+B]), North Nandi Forest, 4 km SW of Chomisia, 29 November 1979, leg. F. Spitzenberger;

1 ♀ (NMW 32805 [S+Sk+B]), North Nandi Forest, 4 km SW of Chomisia, 11 December 1979, leg. F. Spitzenberger;
1 ♂ (NMW 32803 [S+B]), North Nandi Forest, 7 km NE of Chomisia, 4 December 1979, leg. F. Spitzenberger;
1 ♂ (NMW 32804 [S+B]), North Nandi Forest, 7 km NE of Chomisia, 9 December 1979, leg. F. Spitzenberger;
1 ♂, 1 ♀ (NMW 32807 [S+Sk+B], 32806 [S+A]), North Nandi Forest, 7 km NE of Chomisia, 11 December 1979, leg. F. Spitzenberger;
1 ♂, 1 ♀ (NMW 32467, 32469 [S+B]), Pangani, near the Lwandani Cave, 9 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♀ (NMW 32473 [S+B]), Pangani, near the Lwandani Cave, 12 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♀ (NMW 32458 [S+B]), Saboti, Kapkulkul Caves, 2 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂, 1 ♀ (NMW 32476, 32477 [S+B]), Suswa, Suswa Cave, 16 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♀ (NMW 32478 [S+B]), Suswa, Suswa Cave, 17 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

NMP Material (1). 1 ♀ (NMP 98063 [S+A]), Mount Elgon National Park, Rongai Camp, 21 July 2010, leg. A. Konečný, J. S. Mbau & R. Šumbera.

Miniopterus aff. *inflatus* is a parataxon representing the large-sized African morphotype of the genus *Miniopterus* Bonaparte, 1837, that was traditionally assigned to *M. inflatus* [s.l.] (Hayman & Hill 1971, Kingdon 1974, Aggundey & Schlitter 1984, Koopman 1994, Patterson & Webala 2012). However, this morphotype is paraphyletic, it comprises several genetic lineages whose relevant taxonomic and biogeographic interpretations are still impossible (Demos et al. 2020, 2023). At least two of these lineages occur in East Africa (Demos et al. 2023, Monadjem et al. 2024); Monadjem et al. (2024) affiliated them with *M. africanus* Sanborn, 1936 and *M*. cf. *inflatus*. According to the latter authors, *M. africanus* is distributed in the northern part of eastern Africa, from northern Eritrea southwards via Ethiopia and southern Somalia to Kenya, where numerous records are concentrated in the southern part of the country. The records of the *inflatus* morphotype from the southern part of Africa, from south-western Kenya, Uganda, and north-eastern DR Congo to the Cape, were assigned by Monadjem et al. (2024) to the other named form, *M*. cf. *inflatus*. Both these lineages/species meet in south-western Kenya and in the coast region of Kenya and Tanzania; both forms are reported to occur in the Mount Elgon region of Kenya, and additionally *M. africanus* at Watamu in south-eastern Kenya, and *M*. cf. *inflatus* at Tanga in north-eastern Tanzania. The localities of the *Miniopterus* bats of the *inflatus* morphotype housed in the NMW and NMP collections are situated in the two latter regions (in their broader sense), these specimens thus could not be simply identified based on the geographic reasons (and the morphological distinctnesses of the lineages have not yet been tested). The only geographically exclusive record is available from the Suswa Cave, from where Demos et al. (2020, 2023) and Monadjem et al. (2024) reported *M. africanus* / clade 8 (originally the specimen FMNH 216800). The NMW specimen from the Suswa Cave thus could belong to the latter form / clade, rather than to *M*. cf. *inflatus*. However, this is just a theoretical surmise as both forms may live in sympatry in this part of southern Kenya. Thus, all specimens of the *inflatus* morphotype from both collections are here tentatively attributed to *M*. aff. *inflatus*, until a profound revision gives identification clues to distinguish the two

Table 22. Biometric data on the NMW and NMP specimens of *Miniopterus* aff. *inflatus* and *M.* aff. *arenarius* from Kenya. For abbreviations see Methods

dimension		*Miniopterus* aff. *inflatus*					*Miniopterus* aff. *arenarius*			
	n	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*34*	**48.19**	46.2	50.5	1.190	*44*	**44.96**	42.5	47.10	1.109
LCr	*32*	**16.73**	16.23	17.29	0.248	*38*	**14.89**	14.22	15.57	0.299
LCb	*32*	**16.12**	15.69	16.63	0.226	*38*	**14.42**	13.87	15.29	0.290
LaZ	*32*	**9.26**	8.94	9.63	0.169	*38*	**8.28**	8.05	8.81	0.160
LaI	*32*	**3.71**	3.43	4.03	0.167	*38*	**3.60**	3.37	3.82	0.128
LaInf	*32*	**4.34**	4.06	4.56	0.120	*38*	**3.78**	3.61	3.93	0.095
LaN	*32*	**8.23**	6.88	9.24	0.421	*38*	**7.74**	7.44	8.55	0.198
LaM	*32*	**9.14**	8.71	9.45	0.171	*38*	**8.41**	8.14	8.77	0.161
ANc	*32*	**6.41**	6.02	6.86	0.211	*38*	**6.08**	5.76	6.51	0.182
LBT	*32*	**3.15**	2.98	3.38	0.108	*32*	**2.87**	2.68	3.28	0.136
CC	*32*	**4.97**	4.04	5.25	0.261	*38*	**4.32**	4.12	4.56	0.110
M^3M^3	*32*	**7.00**	6.75	7.27	0.147	*38*	**6.06**	5.84	6.47	0.178
CM^3	*32*	**6.58**	6.23	6.81	0.120	*38*	**5.68**	5.42	6.06	0.132
LMd	*32*	**12.13**	11.18	12.54	0.256	*38*	**10.49**	10.23	11.06	0.175
ACo	*32*	**3.00**	2.74	3.20	0.122	*38*	**2.51**	2.37	2.72	0.082
CM_3	*32*	**7.00**	6.62	7.38	0.170	*38*	**6.05**	5.68	6.41	0.159

lineages based on morphological characters. The dimensions of the NMW and NMP specimens of *M.* aff. *inflatus* from Kenya are shown in Table 22.

Miniopterus aff. *arenarius* Heller, 1912

NMW Material (44). 1 ♂, 1 ♀ (NMW 32459, 32460 [S+B]), Kiminini, 2 km NE of Hanson's farm, 2 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

2 ♂♂, 1 ♀ (NMW 32439–32441 [S+B]), Kiminini, Bodeny Cave, 29 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

1 ♀ (NMW 32455 [S+B]), Kiminini, Chepkelele Cave, 31 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

1 ♂ (NMW 32437 [S+B]), Kiminini, Kipsiryori Cave, 29 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

3 ♂♂ (NMW 32443, 32444, 32451 [S+B]), Kiminini, Nabongo Cave, 30 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

1 ♂ (NMW 32438 [S+B]), Kiminini, Namino Cave, 30 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

1 ♂ (NMW 32442 [S+B]), Kiminini, Nyungu ya Mawe Cave, 30 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

4 ♂♂, 1 ♀ (NMW 32404–32406 [S+B], 32408 [S+Sk], 32407 [B]), Mount Elgon National Park, Chepnyalil Cave, 24 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

2 ♂♂, 1 ♀ (NMW 32409–32411 [S+B]), Mount Elgon National Park, Kitum Cave, 24 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

1 ♂ (NMW 32412 [S+B]), Mount Elgon National Park, Makingeny Cave, 24 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

4 ♂♂ (NMW 32413, 32416 [S+B], 32414, 32415 [B]), Mount Elgon National Park, Rongai Camp, 24 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
3 ♂♂, 1 ♀ (NMW 32417–32420 [S+B]), Mount Elgon National Park, Rongai Camp, 25 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♀♀ (NMW 32422, 32424 [A]), Mount Elgon National Park, Rongai Camp, 26 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♂♂, 2 ♀♀ (NMW 32425, 32427, 32428 [S+Sk], 32426 [Sk]), Mount Elgon National Park, Rongai Camp, 27 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
2 ♂♂, 2 ♀♀ (NMW 32434–32436 [S+B], 32430 [S+Sk]), Mount Elgon National Park, Rongai Camp, 28 December 1980, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;
1 ♂ (NMW 32808 [S+B]), North Nandi Forest, 2 km W of Chomisia, 10 December 1979, leg. F. Spitzenberger;
2 ♀♀ (NMW 32809, 32810 [S+A]), North Nandi Forest, 2 km W of Chomisia, 11 December 1979, leg. F. Spitzenberger;
2 ♂♂ (NMW 32456, 32457 [S+B]), Saboti, Kapkulkul Caves, 2 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

Miniopterus aff. *arenarius* is a parataxon representing the medium-sized morphotype of the genus *Miniopterus* occurring in north-eastern Africa that was traditionally affiliated with *M. schreibersii* (Kuhl, 1817) [s.l.] (Hayman & Hill 1971, Kingdon 1974, Aggundey & Schlitter 1984) and later with *M. natalensis* (Smith, 1833) [s.l.] (Koopman 1994, Simmons 2005, Patterson & Webala 2012). As the range of *M. schreibersii* is nowadays confined to the Mediterranean region (covering also parts of Central Europe), in Africa it occurs only in the northern parts of the Maghreb and Cyrenaica, and in Macaronesia (cf. Benda et al. 2014, Borloti et al. 2020). The occurrence of *M. natalensis* is currently reported from the southern part of Africa, up to the south of Zambia and Angola, inclusive (Demos et al. 2020, 2023, Monadjem et al. 2024). Similarly as in the previous parataxon, also *M.* aff. *arenarius* is a morphotype comprising several taxonomically undefined genetic lineages (Demos et al. 2020, 2023). At least two lineages of this morphotype occur in Kenya according to Monadjem et al. (2024), *M. arenarius* and *M. mossambicus*. The latter species is rather well defined by molecular genetic characters and in Kenya, it remains limited to the south-eastern corner of the country, see below for details. The rest of the Kenyan occurrence of the medium-sized *Miniopterus* bats – the majority of the specimens (26 localities in total) reported by Aggundey & Schlitter (1984) under *M. schreibersii* – was attributed to *M. arenarius* by Monadjem et al. (2024). The extensive NMW series of this *Miniopterus* morphotype originates from south-western Kenya, the Mount Elgon region and the adjacent North Nandi Forest, the area where only *M. arenarius* is reported by Monadjem et al. (2024), and the type locality of *M. natalensis arenarius* Heller, 1912 is situated nearby (Guaso Nyuki, Northern Guaso Nyiro River, British East Africa [= Engare Nanyuki, Laikipia County, west-central Kenya; 00°21'N, 36°55'E]; Heller 1912: 2). Most probably, the majority of the NMW series belongs to this taxon. Here, we attribute the series tentatively to *M.* aff. *arenarius*, since only rough morphologic and geographic characters could be used for identification, which therefore remains only approximate. The dimensions of the NMW specimens of *M.* aff. *arenarius* from Kenya are shown in Table 22.

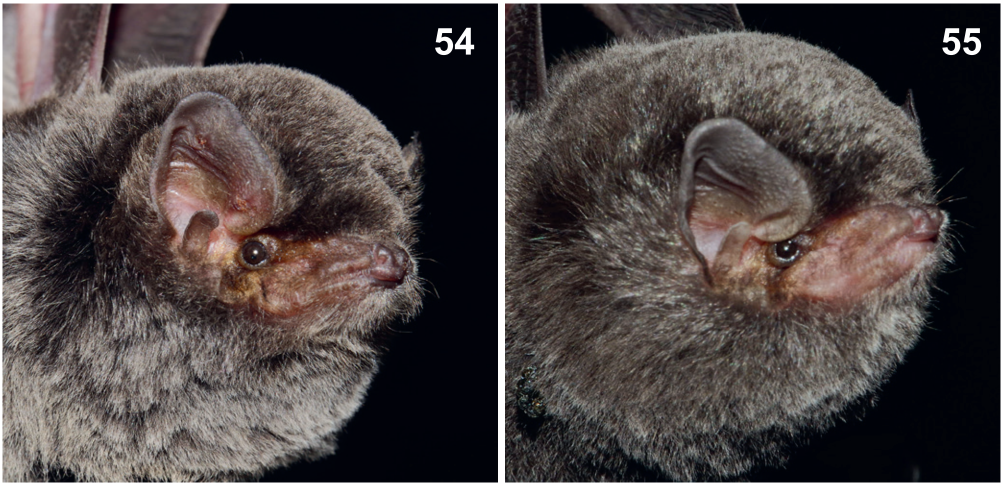
***Miniopterus mossambicus* Monadjem, Goodman, Stanley et Appleton, 2013**

NMP Material (7). 2 ♂♂, 4 ♀♀ (NMP 97956, 97957, 97959, 97960 [S+A], 97958, 97961 [A]; Fig. 54), Tsavo West National Park, Ngulia Lodge, 19 August 2022, leg. P. Benda & J. Červený;

1 ♂ (NMP 97963 [S+A]), Tsavo West National Park, Ngulia Lodge, 20 August 2022, leg. P. Benda & J. Červený.

The distribution range of the recently described *Miniopterus mossambicus* stretches across the savanna belt of eastern and south-eastern Africa, between southern Mozambique and eastern South Africa in the south, and central DR Congo and southern Kenya in the north (Demos et al. 2020, Monadjem et al. 2020, 2024). Only few records of *M. mossambicus* are known from East Africa, Monadjem et al. (2024) reported two sites from Tanzania and two from Kenya, and the Kenyan occurrence spot represents the north-easternmost extension of the species distribution range. For the first time, *M. mossambicus* was reported from Kenya by López-Baucells et al. (2017) from the Taita Hills, two additional localities from adjacent regions (Chyulu Hills NP, Tsavo West NP) were reported by Demos et al. (2020). The Guano Cave 1 in the Chyulu Hills NP is the northernmost known point of the species range (02°19'S, 37°42'E), and the Taita Hills (unspecified site) is the easternmost area (ca. 03°17'S, 38°26'E). The locality of the NMP specimens, the Ngulia Lodge, is the second easternmost site of *M. mossambicus* in East Africa, while the most eastern site of the whole range of this bat is its type locality, Nampula (15°06'S, 39°13'E) in Mozambique (Monadjem et al. 2013b, 2024).

The dimensions of the NMP specimens of *M. mossambicus* from Kenya are shown in Table 23. The values of the dimensions are very similar to those from Mozambique given by Monadjem et al. (2013b) and Zambia by Benda et al. (2022). However, they demonstrate slight differences in the skull shape of the Kenyan bats in comparison with the southern African samples (Mozambique and Zambia); the Kenyan specimens are smaller in body size (LAt Mozambique 41.0–44.9 mm [mean 43.9 mm], Zambia 43.5–45.5 [44.5], Kenya 42.1–43.8 [43.1]), similar in skull size (LCr 14.15–15.20 [14.68], 14.68–15.16 [14.99], 14.84–15.02 [14.94]), but have relatively longer



Figs. 54, 55. Portraits of long-fingered bats from Kenya in the NMP collection. 54 – a female of *Miniopterus mossambicus* netted in the Ngulia Lodge, Tsavo West National Park, on 19 August 2022. 55 – a female *Miniopterus minor* collected from the Kaboga Cave at Watamu on 3 July 2023.

Table 23. Biometric data on the NMW and NMP specimens of *Miniopterus mossambicus* and *M. minor* from Kenya. For abbreviations see Methods

dimension	*Miniopterus mossambicus*					*Miniopterus minor*				
	n	**M**	min	max	SD	*n*	**M**	min	max	SD
LAt	*7*	**43.07**	42.1	43.8	0.599	*15*	**39.66**	38.5	41.7	0.757
LCr	*5*	**14.94**	14.84	15.02	0.065	*13*	**14.08**	13.54	14.38	0.204
LCb	*5*	**14.40**	14.21	14.54	0.129	*13*	**13.41**	12.88	13.73	0.211
LaZ	*4*	**8.24**	8.16	8.36	0.093	*13*	**7.72**	7.57	7.89	0.098
LaI	*5*	**3.52**	3.45	3.64	0.076	*13*	**3.37**	3.17	3.58	0.096
LaInf	*5*	**3.81**	3.64	4.02	0.152	*13*	**3.51**	3.41	3.71	0.081
LaN	*5*	**7.56**	7.48	7.62	0.053	*13*	**7.22**	7.06	7.35	0.090
LaM	*4*	**8.18**	8.08	8.24	0.068	*13*	**7.77**	7.58	7.92	0.107
ANc	*5*	**5.89**	5.74	6.05	0.113	*13*	**5.53**	5.37	5.81	0.108
LBT	*5*	**3.07**	2.91	3.35	0.176	*13*	**2.77**	2.62	3.01	0.120
CC	*4*	**4.38**	4.23	4.58	0.148	*13*	**3.99**	3.82	4.21	0.113
M^3M^3	*5*	**6.17**	5.93	6.32	0.152	*13*	**5.69**	5.61	5.81	0.059
CM^3	*5*	**5.89**	5.84	5.97	0.051	*13*	**5.28**	5.11	5.42	0.087
LMd	*5*	**10.52**	10.45	10.61	0.069	*13*	**9.82**	9.61	10.07	0.148
ACo	*5*	**2.54**	2.44	2.61	0.067	*13*	**2.34**	2.18	2.48	0.086
CM_3	*5*	**6.26**	6.18	6.35	0.061	*13*	**5.62**	5.41	5.76	0.106

rostra (CM^3 5.20–5.73 [5.49], 5.67–5.93 [5.75], 5.84–5.97 [5.89]) and narrower braincases (LaM 7.47–8.50 [7.98], 8.26–8.52 [8.37], 8.08–8.24 [8.18]). Thus, the Kenyan populations of *M. mossambicus*, living at the northern margin of the species range, seem to represent a slightly different morphotype in skull shape than the populations living in the southern range parts. However, despite these morphometric differences, the sequences of the cytochrome *b* gene from five examined Kenyan specimens showed agreement of 99.0–100% (mean 99.22%) with the haplotype OQ224761 from Zambia (= NMP 97575, Bwarenunka Cave, Zambia; Benda et al. 2022), i.e. from a population occurring some 1800 km away. These results suggest that *M. mossambicus* is moderately plastic in its morphological characters despite its conservatism in genetic traits.

Miniopterus minor Peters, 1867

NMW Material (12). 4 ♂♂ (NMW 32463–32466 [S+B]), Pangani, Lwandani Cave, 9 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

1 ♂ (NMW 32468 [S+B]), Pangani, near the Lwandani Cave, 9 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

1 ♂ (NMW 32470 [S+B]), Pangani, near the Lwandani Cave, 10 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

1 ♂ (NMW 32471 [S+B]), Pangani, near the Lwandani Cave, 11 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

3 ♂♂ (NMW 32472, 32475 [S+B], 32474 [B]), Pangani, near the Lwandani Cave, 12 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss;

2 ♂♂ (NMW 32461 [S+B], 32462 [B]), Shimoni, Main Well Cave, 7 January 1981, leg. K. Bauer, A. Mayer, F. Spitzenberger & E. Weiss.

NMP Material (4). 1 ♂, 3 ♀♀ (NMP 98017–98019 [S+A], 98020 [A]; Fig. 55), Watamu, Kaboga Cave, 3 July 2023, leg. P. Benda & J. Červený.

Reference. Aggundey & Schlitter (1984).

Miniopterus minor s.str. is an endemic of East Africa (cf. Demos et al. 2023), although the populations of the western Congo Basin, from locations that are situated more than 2600 km west of the East African sites, are also attributed to this species by some authors (Hayman & Hill 1971, Juste & Ibáñez 1992, Koopman 1994, Simmons 2005, Juste et al. 2007, Bates et al. 2013, Monadjem et al. 2024). Additionally, the lineage of *M. minor* s.str. has been recently discovered also in south-western Kenya (Demos et al. 2020, 2023), although Monadjem et al. (2024) referred these populations to *M.* cf. *fraterculus* Thomas et Schwann, 1906 instead of *M. minor*. The traditional East African range of *M. minor* (= *M. m. minor* sensu Juste & Ibáñez 1992) covers only the coastal regions of south-eastern Kenya and eastern Tanzania, including Zanzibar* (Peters 1867a, Swynnerton & Hayman 1951, Aggundey & Schlitter 1984, Juste & Ibáñez 1992, Weyeneth et al. 2008, Monadjem et al. 2013b, 2024, Musila et al. 2020). The NMW series of *M. minor* was already published by Aggundey & Schlitter (1984). It originates partly from the Lwandani Cave and its surroundings at Pangani, north of Mombasa (mentioned as from 'Ribe' by Aggundey & Schlitter 1984), and partly from the Main Well Cave in Shimoni, from a previously known site of this bat (see Falcoz 1923, Harrison 1961, Aggundey & Schlitter 1984). The locality of the NMP series of *M. minor* documents again the recently discovered part of the species occurrence, the coral cave region around Watamu creating currently the northern limits of the distribution range of this bat (Musila et al. 2020, Monadjem et al. 2024).

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* Certain confusion is related to the type locality of *Miniopterus minor* Peters, 1867. Peters (1867a: 885) accompanied the species description by a note on the type specimen as follows: "Ein einziges ausgewachsenes Männchen von der Küste von Zanzibar." Later on, Peters (1869: 7) repeated this note almost verbatim as follows: "Ein einziges männliches Exemplar von der Küste von Sansibar befindet sich in der Sammlung des Barons von der Decken, […]." The description of the type locality, "Küste von Zanzibar" and "Küste von Sansibar", respectively, was interpreted by many subsequent authors as a part of the mainland of Africa situated opposite to the island of Zanzibar. Perhaps for the first time the type locality of *M. minor* was mentioned under this explicit meaning by Swynnerton & Hayman (1951: 295), see as follows: " 'Zanzibar Coast,' i.e. mainland of East Africa opposite Zanzibar Island." This understanding of the type locality followed the revision by Swynnerton (1945: 80), who described the delimitation of the above geographical term as follows: "Formerly, the Sultan of Zanzibar held a sort of suzerainty over a strip of country on the mainland of East Africa […]. This strip, which did not extend inland more than a few miles, was at one time referred to as the "Zanzibar Coast" by collectors and others. It will be seen that the […] species, said to have been obtained on the "Zanzibar Coast" can be given no definite type-locality; they might have been collected anywhere between Capo Delgado in the south and Lamu or beyond in the north, in Tanganyika or in Kenya."

The specification made by Swynnerton & Hayman (1951) was followed by other authors, see as follows: "[…] the Zanzibar coast (*i.e.*, the mainland of East Africa opposite Zanzibar Island) […]." (Harrison 1959: 191); "[…] type specimen came from the coast opposite to Zanzibar (Tanzania)." (Juste & Ibáñez 1992: 355); "Tanzania, coast opposite Zanzibar Isl." (Koopman 1993: 230; Simmons 2005: 521); "Tanzania, coast opposite Zanzibar Island." (Patterson & Webala 2012: 33; Van Cakenberghe & Seamark 2022: 679). On the other hand, some authors just repeated the simple expression given by Peters (1867a) to specify the type locality of *M. minor*, see as follows: "Sansibarküste" (Matschie 1895: 25); "Coast of Zanzibar." (Allen 1938: 103; Harrison 1961: 294); "Coast of Zanzibar, Tanzania." (Aggundey & Schlitter 1984: 140).

The dimensions of the NMW and NMP specimens of *M. minor* from Kenya are shown in Table 23. Sequences of the cytochrome *b* gene obtained from three NMP specimens (NMP 98017–98019) were in congruence of 99.8% with the haplotype FJ232806 from a specimen of *M. minor* collected at Tanga, north-eastern Tanzania (Weyeneth et al. 2008). The haplotype extracted from the specimen NMP 98020 agreed in 99.5% with the haplotype MN504273 from the specimen NMK 187235 from the Kakamega County, south-western Kenya (Demos et al. 2020), referred to as *M. minor* by Demos et al. (2023). At the same time, the sequence from the latter NMP specimen agreed in 98.2% with the haplotype FJ232806 (Tanga, Tanzania; Weyeneth et al. 2008). The latter NMP specimen from the Koboga Cave shows close similarity in its genetic traits to the south-western Kenyan populations instead of those from south-eastern Kenya, unlike the other specimens of the NMP series coming from the same cave colony. Thus, it creates a phylogenetic link between the eastern and western Kenyan populations. This suggests a much broader distribution range of *M. minor* s.str. in East Africa than just the coastal strip along the Indian Ocean shore (contra e.g. Juste & Ibáñez 1992, Van Cakenberghe et al. 2017, Monadjem et al. 2024).

Turni & Kock (2008: 52), who published a catalogue of type specimens of mammals of the ZMB collection, mentioned the type locality of *M. minor* as follows: " 'Sansibar Küste' = Tanzania mainland coast opposite Zanzibar;" However, it is not clear whether they quoted the record from the specimen label, the entry in the museum evidence concerning the items collected by the explorer Carl Claus von der Decken (1833–1865), or (inaccurately) the type locality delimitation by Peters (1867a). For instance, Turni & Kock (2008: 32) mentioned this specification also concerning the type locality of *Rhinolophus deckenii* Peters, 1867 (based on a specimen collected also by von der Decken), see as follows: " 'Sansibar Küste' = mainland opposite Zanzibar Id., Tanzania." However, in this case Peters (1867b: 706) reported "Zanzibarküste" as the site of origin of the (type) specimen of *R. deckenii*, and not "Küste von Zanzibar".

Generally, the conclusion by Swynnerton (1945) was certainly correct, the term "Zanzibar-Küste" was used in the sense he specified at the time when von der Decken collected materials and described his travellings over East Africa, see e.g. Anonymous (1862, 1863a, b). However, Peters (1867a: 885–891) describing the origin of the items included in von der Decken's collection, used five geographical terms containing the word Zanzibar, see as follows (under original names): Festland bei Zanzibar (for *Megaderma frons*, *Nyctinomus limbatus*), Zanzibarküste (*Nycteris fuliginosa*, *Rhinolophus fumigatus*, *Scotophilus borbonicus*, *Viverra genetta*, *Felis serval*, *Sciurus cepapi*, *Mus decumanus*, *M. alexandrinus*, *Meriones* sp., *Cephalopus Campbelliae*, *Choeropotamus africanus*, *Testudo radiata*, *Chamaeleo dilepis*, *Hemidactylus frenatus*, *Eremias lugubris*, *Euprepis punctatissimus*, *Eumeces afer*, *Philothamnus punctatus*, *Boodon capensis*, *Crotaphopeltis rufescens*, *Bitis arietans*, *Phrynobatrachus natalensis*, *Hyperolius citrinus*), Innern der Zanzibarküste (*Lepus saxatilis*), Zanzibar (*Otolemur agisymbanus*, *Nesotragus moschatus*, *Gerrhosaurus major*, *Rana nilotica*, *Hylambates maculatus*), and Küste von Zanzibar (*Miniopterus minor*, *Varanus saurus*).

The former three terms can be clearly co-identified with the mainland coastal regions of the present-days Tanzania, as suggested by Swynnerton (1945), while the latter two rather with the island of Zanzibar. The type specimen of *M. minor* is reported to originate not from the "Zanzibarküste", i.e. from the Zanzibar Coast, like majority (23) of the species of the collection, but from the "Küste von Zanzibar", coast of Zanzibar, like a single other species, the monitor lizard. This obvious difference in the naming of the original locality of just two of 33 species collected by von der Decken suggests that the type specimen of *M. minor* came from Zanzibar Island *per se*. A revision of the type specimen of *M. minor* (ZMB 3268 [S+A]) made by the senior author in 2023 showed the record on the specimen label as follows: "Sansibar, von der Decken". These findings indicate that the type locality of *M. minor* Peters, 1867 is probably somewhere in the coastal part of Zanzibar Island and not in the Tanzanian mainland. However, a detailed check of von der Decken's travel diary and field catalogue could help to confirm this conclusion.

CONCLUSIONS

The mammal collections of the Natural History Museum, Vienna (NMW) and National Museum, Prague (NMP) contain 711 specimens of bats from Kenya belonging to 55 species of all 11 families known to occur in the country (Table 1, 24). Of them, 494 specimens belonging to 39 species of nine families are housed in the NMW collection, and 217 specimens belonging to 34 species of nine families in the NMP collection. These bats originate from 64 localities that cover almost completely the territory of Kenya (33 NMW localities, 35 NMP localities; Figs. 1, 2). The frequency is 1–16 species per locality, on average 3.1 species (3.8 NMW, 2.3 NMP) and 11.1 specimens (14.9 NMW, 6.2 NMP) per locality. Particular species originate from 1–13 localities, altogether representing 188 records (species vs. locality), on average 3.4 records per species (2.9 NMW, 2.3 NMP), and the species are represented by 1–44 specimens, on average 12.9 specimens (12.8 NMW, 6.4 NMP) per species. Most of the specimens belong to common species of bats, which can be frequently found in other collections containing material from Kenya and East Africa in general (Harrison 1961, Aggundey & Schlitter 1984, Van Cakenberghe & Seamark 2022, Monadjem et al. 2024) and moreover, some faunistic records referring to the NMW specimens were already published (see Aggundey & Schlitter 1984, Claessen & De Vree 1991, Bergmans 1994, 1997, Van Cakenberghe & De Vree 1998, Fahr & Ebigbo 2003). On the other hand, some of the specimens or specimen series have an undoubted value for zoological research. Generally, the two collections contribute to the knowledge of the bat fauna of Kenya rather substantially.

According to the recent review by Monadjem et al. (2024), the bat fauna of Kenya is currently composed of 109 species (Table 1; or 108 species, when *Scotoecus hindei* is not accepted as a full species) belonging to eleven families; of these, 39 species are housed in the NMW collection, making up 36.1% of the fauna, and 34 species in the NMP collection, i.e. 31.5% of the bat fauna of the country (Table 24). The evaluation of the NMP collection brought confirmation of the occurrence of one bat species for the Kenyan fauna, *Neoromicia capensis*, based

Table 24. Composition of the NMW and NMP bat collections from Kenya; numbers of species, records, and specimens (record = species vs. locality; spcmns. = specimens)

family	NMW+NMP		NMW			NMP		
	species	records	species	records	spcmns.	species	records	spcmns.
Pteropodidae	7	30	7	15	57	4	15	47
Rhinopomatidae	1	1	–	–	–	1	1	2
Megadermatidae	2	13	–	–	–	2	13	30
Rhinolophidae	5	21	5	21	74	–	–	–
Rhinonycteridae	1	3	1	3	16	–	–	–
Hipposideridae	6	15	5	8	33	4	8	25
Emballonuridae	3	11	2	6	45	3	6	17
Nycteridae	2	7	2	4	9	1	3	4
Molossidae	6	9	2	2	31	5	8	29
Vespertilionidae	18	50	12	29	140	11	22	51
Miniopteridae	4	28	3	26	89	3	3	12
total	55	188	39	114	494	34	79	217

on molecular genetic evidence. This species was formerly considered a part of the Kenyan fauna but its occurrence in the country was doubted (see Monadjem et al. 2024), while now it seems to be sure. The bat fauna of Kenya now comprises 110 species in total (when two dark-winged species of *Scotoecus* are included, sensu Aggundey & Schlitter 1984 and Monadjem et al. 2024, see above).

In several bat species, localities of the NMW and NMP specimens represent significant occurrence records, making their distribution ranges in Kenya more precise. Besides *Neoromicia capensis* whose distribution limits have newly crossed the state borders, this is true mainly for the bat species documented rather rarely in Kenya, like *Platymops setiger*, *Vansonia rueppellii*, *Neoromicia zuluensis*, *Pseudoromicia nyanza*, *Afropipistrellus grandidieri*, *Scotophilus nux*, and *Miniopterus mossambicus*, but also for some of the common bats, namely *Cardioderma cor* and *Coleura afra*, with significant new records in the northern part of the country.

In some bat species of the NMP collection, sequences of the mitochondrial genome were examined and compared with the available data, namely in *Epomophorus wahlbergi*, *E. labiatus*, *E. minimus*, *Hipposideros tephrus*, *H. ruber*, *Macronycteris vittata*, *Coleura afra*, *Taphozous perforatus*, *T. hildegardeae*, *Nycteris thebaica*, *Chaerephon pumilus*, *Mops condylurus*, *Otomops harrisoni*, *Afronycteris nana*, *Neoromicia zuluensis*, *N. somalica*, *N. capensis*, *Pseudoromicia nyanza*, *Scotophilus colias*, *S. trujilloi*, *Miniopterus mossambicus*, and *M. minor*. In most of these species, the analyses confirmed their close relation with other Kenyan or East African samples, and confirmed them to be an integral part of the local populations. However, in some cases, the molecular genetic examination enabled us to report certain notes on phylogenetic relationships or even taxonomic positions of the Kenyan populations.

A discrepancy between the morphotype and genotype was observed in fruit-bats of the genus *Epomophorus* (Fig. 3). Three species of this genus were identified based on their morphological traits. However, their mtDNA sequences only partly agreed with this identification, while in most specimens the sequences pointed at other species, giving the following combinations of morphotype and genotype: *E. wahlbergi* × *E. wahlbergi* / *E. labiatus*, *E. labiatus* × *E. gambianus* / *E. wahlbergi*, *E. minimus* × *E. wahlbergi* / *E. gambianus* / *E. labiatus* / *E. pusillus* (see Fig. 3). Since the morphology-based identification of the *Epomophorus* species is not a problem and the misidentification in such degree is unlikely, these results rather suggest sharing of the mitochondrial genome among the fruit bat species (see also Nesi et al. 2011).

The evaluation of the new sequences by using the available haplotype data on bats of the *Hipposideros caffer* group suggested a revised species affiliation of the Kenyan populations of this complex, that was not clear previously. The bats of the *caffer* morphotype (the A2 lineage sensu Vallo et al. 2008) affiliate with *H. tephrus*, and those of the *caffer/ruber* morphotype from south-eastern Kenya (the B2 lineage sensu Vallo et al. 2008) with *H. ruber* s.str. (the populations of the *ruber* morphotype from south-western Kenya remain still unaffiliated and kept as *H*. aff. *ruber*).

The mitochondrial sequences of East African populations of *Coleura afra*, including those newly obtained from the Kenyan NMP samples, clustered with two rather deeply separated lineages, the genetic distances between these lineages were in the range of 3.39–3.81%. However, the newly demonstrated syntopic occurrence of these lineages in a Kenyan cave suggests rather a complex phylogenetic history of the species than a relevance of this lineage separation for the intraspecific taxonomic arrangement.

The sequence obtained from the NMP specimen of *Taphozous perforatus* from Kenya did not show any substantial distance from the haplotypes of this species available from other populations from Africa and the Middle East, all samples created a single lineage. This result supports the formerly suggested separate taxonomic position of *T. perforatus* populations from eastern Africa as unjustified. Thus, we suggest to consider the name of the eastern African subspecies, *haedinus* Thomas, as well as the name of the western African subspecies, *swirae* Harrison, as junior synonyms of *perforatus* Geoffroy. For the first time, sequences of *Taphozous hildegardeae* were analysed and the phylogenetic position of this bat was evaluated. Two haplotypes obtained from six NMP specimens from Kenya represented a single lineage that formed a separated branch within the genus *Taphozous*, in a sister position to the lineage comprising the Oriental species *T. melanopogon*, a species morphologically very similar to *T. hildegardeae*.

Our taxonomic assessment of the available data on populations of the *Scotophilus dinganii* morphotype occurring in eastern Africa, which were assigned by some authors to two separate species, *S. andrewreborii* from Kenya and *S. ejetai* from Ethiopia, does not corroborate this division and naming. It indicates that these lineages represent a single species (besides *S. livingstonii* Brooks et Bickham, 2014, occurring in East Africa only marginally). Thus, we suggest to use the prior available name *S. colias* for these populations/lineages instead of the two recently introduced names, and to consider the names *andrewreborii* Brooks et Bickham and *ejetai* Brooks et Bickham as junior synonyms of *colias* Thomas. On the other hand, we accepted the name *S. trujilloi* for the small-sized *Scotophilus* morphotype occurring in south-eastern Kenya.

The morphometric comparisons of some series of Kenyan bat specimens from the NMW and NMP collections with comparative sample sets from other collections and/or populations also led to several conclusions concerning the phylogenetic positions of the Kenyan populations (see under *Rhinolophus acrotis*, *Triaenops afer*, *Taphozous perforatus*, *T. hildegardeae*, *Nyctinomus aegypticus*, *Pipistrellus hesperidus*, and/or *Miniopterus mossambicus*). Perhaps the most considerable finding is the observation of an extraordinarily small-sized morphotype of the Mount Elgon populations of *Rhinolophus acrotis*. However, since the available genetic evidence shows the Mount Elgon populations as an integral part of the eastern African haplogroup of *R. acrotis*, and does not suggest a phylogenetic separation, the morphotype seems to represent just a local form, may be an ecomorph of the mountain conditions of the Great Rift region of East Africa.

In summary, the two collections of bats from Kenya, NMW and NMP, one created mostly in a short time at the end of the 1970s and the other in the period between 2004 and 2022, represent valuable series of specimens, providing an important addition to the knowledge of composition, distribution, morphometry, molecular genetics, and also taxonomy of the bat fauna of this country.

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APPENDIX 1

Gazetteer

Localities of the NMW specimens (NM = number in the map in Fig. 1)

site	coordinates	altitude	NM
2 km NE of Hanson's farm, Kiminini (Trans-Nzoia County)	00°52'N, 34°51'E	1768	4
2 km W of Chomisia, North Nandi Forest (Nandi County)	00°15'N, 35°00'E	2005	6
3 km W of Chomisia, North Nandi Forest (Nandi County)	00°15'N, 35°00'E	2005	6
4 km SW of Chomisia, North Nandi Forest (Nandi County)	00°13'N, 35°01'E	1892	6
7 km NE of Chomisia, North Nandi Forest (Nandi County)	00°17'N, 35°05'E	1910	6
Belfry Cave, Pangani (Kilifi County)	03°51'S, 39°40'E	110	12
Bodeny Cave, Kiminini (Trans-Nzoia County)	00°52'N, 34°50'E	1880	4
Chasimba (Kilifi County)	03°44'S, 39°41'E	210	11
Chepkelele Cave, Kiminini (Trans-Nzoia County)	00°51'N, 34°49'E	1816	4
Chepnyalil Cave, Mount Elgon National Park (Trans-Nzoia County)	01°03'N, 34°45'E	2500	2
Diani, Ukunda (Kwale County)	04°17'S, 39°36'E	5	14
Kapkulkul Caves, Saboti (Trans-Nzoia County)	00°58'N, 34°50'E	1900	3
Kauka Cave, Kiminini (Trans-Nzoia County)	00°52'N, 34°50'E	1880	4
Khybe Sawmill Cave, Mount Elgon Reserve North (Trans-Nzoia C.)	01°06'N, 34°44'E	2548	1
Kiminini, 2 km NE of Hanson's farm (Trans-Nzoia County)	00°52'N, 34°51'E	1768	4
Kiminini, Bodeny Cave (Trans-Nzoia County)	00°52'N, 34°50'E	1880	4
Kiminini, Chepkelele Cave (Trans-Nzoia County)	00°51'N, 34°49'E	1816	4
Kiminini, Kauka Cave (Trans-Nzoia County)	00°52'N, 34°50'E	1880	4
Kiminini, Kipsiryori Cave (Trans-Nzoia County)	00°52'N, 34°50'E	1880	4
Kiminini, Nabongo Cave (Trans-Nzoia County)	00°51'N, 34°49'E	1841	4
Kiminini, Namino Cave (Trans-Nzoia County)	00°52'N, 34°50'E	1865	4
Kiminini, Nyungu ya Mawe Cave (Trans-Nzoia County)	00°51'N, 34°50'E	1846	4
Kipsiryori Cave, Kiminini (Trans-Nzoia County)	00°52'N, 34°50'E	1880	4
Kitum Cave, Mount Elgon National Park (Trans-Nzoia County)	01°02'N, 34°45'E	2413	2
Kol Cave, Mount Elgon National Park (Trans-Nzoia County)	00°59'N, 34°46'E	2334	2
Lwandani Cave, Pangani (Kilifi County)	03°51'S, 39°40'E	106	12
Main Well Cave, Shimoni (Kwale County)	04°37'S, 39°21'E	20	16
Makingeny Cave, Mount Elgon National Park (Trans-Nzoia County)	01°02'N, 34°45'E	2436	2
Menengai Caves, Nakuru (Nakuru County)	00°15'S, 36°03'E	2109	7
Mombasa, Shimola Tewa (Mombasa County)	03°58'S, 39°44'E	21	13
Mount Elgon National Park, Chepnyalil Cave (Trans-Nzoia County)	01°03'N, 34°45'E	2500	2
Mount Elgon National Park, Kitum Cave (Trans-Nzoia County)	01°02'N, 34°45'E	2413	2
Mount Elgon National Park, Kol Cave (Trans-Nzoia County)	00°59'N, 34°46'E	2334	2
Mount Elgon National Park, Makingeny Cave (Trans-Nzoia County)	01°02'N, 34°45'E	2436	2
Mount Elgon National Park, Rongai Camp (Trans-Nzoia County)	01°02'N, 34°47'E	2213	2
Mount Elgon Reserve North, Khybe Sawmill Cave (Trans-Nzoia C.)	01°06'N, 34°44'E	2548	1
Msambweni, Msambweni Caves (Kwale County)	04°28'S, 39°28'E	17	15
Nabongo Cave, Kiminini (Trans-Nzoia County)	00°51'N, 34°49'E	1841	4
Nairobi (Nairobi County)	01°17'S, 36°49'E	1666	9
Nakuru, Menengai Caves (Nakuru County)	00°15'S, 36°03'E	2109	7
Namino Cave, Kiminini (Trans-Nzoia County)	00°52'N, 34°50'E	1865	4
North Nandi Forest, 2 km W of Chomisia (Nandi County)	00°15'N, 35°00'E	2005	6
North Nandi Forest, 3 km W of Chomisia (Nandi County)	00°15'N, 35°00'E	2005	6
North Nandi Forest, 4 km SW of Chomisia (Nandi County)	00°13'N, 35°01'E	1892	6

site	coordinates	altitude	NM
North Nandi Forest, 7 km NE of Chomisia (Nandi County)	00°17’N, 35°05’E	1910	6
Nyungu ya Mawe Cave, Kiminini (Trans-Nzoia County)	00°51’N, 34°50’E	1846	4
Pangani, Belfry Cave (Kilifi County)	03°51’S, 39°40’E	110	12
Pangani, Lwandani Cave (Kilifi County)	03°51’S, 39°40’E	106	12
Road Side Cave, Shimoni (Kwale County)	04°39’S, 39°23’E	1	17
Rongai Camp, Mount Elgon National Park (Trans-Nzoia County)	01°02’N, 34°47’E	2213	2
Saboti, Kapkulkul Caves (Trans-Nzoia County)	00°58’N, 34°50’E	1900	3
Sabatia (Kakamega County)	00°14’N, 34°31’E	1397	5
Shimola Tewa, Mombasa (Mombasa County)	03°58’S, 39°44’E	21	13
Shimoni, Main Well Cave (Kwale County)	04°37’S, 39°21’E	20	16
Shimoni, Road Side Cave (Kwale County)	04°39’S, 39°23’E	1	17
Suswa, Suswa Cave (Kajiado County)	01°08’S, 36°24’E	1830	8
Tsavo East National Park, Voi Gate (Taita-Taveta County)	03°22’S, 38°36’E	558	10
Ukunda, Diani (Kwale County)	04°17’S, 39°36’E	5	14
Voi Gate, Tsavo East National Park (Taita-Taveta County)	03°22’S, 38°36’E	558	10

Localities of the NMP specimens (NM = number in the map in Fig. 2)

site	coordinates	altitude	NM
Archers Post, Buffalo Springs Reserve, Simba Lodge (Isiolo County)	00°36’N, 37°37’E	853	10
Archers Post, Samburu Reserve, King Lion Camp (Samburu County)	00°34’N, 37°32’E	879	11
Aruba Ashnil Lodge, Voi, Tsavo East National Park (Taita-Taveta C.)	03°21’S, 38°49’E	431	26
Buffalo Springs Reserve, Archers Post, Simba Lodge (Isiolo County)	00°36’N, 37°37’E	853	10
Diani Marine, Ukunda, Diani (Kwale County)	04°19’S, 39°35’E	5	30
Diani, Ukunda, Leisure Lodge (Kwale County)	04°17’S, 39°36’E	5	30
Diani, Ukunda, Diani Marine (Kwale County)	04°19’S, 39°35’E	5	30
Engilae (Samburu County)	01°10’N, 37°16’E	1239	6
Ewangan, Oldarpoi Camp (Narok County)	01°31’S, 35°21’E	1739	20
Fikirini, Mbenyenye Cave (Kwale County)	04°37’S, 39°21’E	20	31
former Lake Bogoria Reserve headquarter, Loboi (Baringo County)	00°21’N, 36°04’E	1005	16
Forolle (Marsabit County)	03°43’N, 37°58’E	909	1
Gilgil, Oasis Camp (Nakuru County)	00°29’S, 36°16’E	1730	17
Gof Bongolle, Karare (Marsabit County)	02°13’N, 37°55’E	1120	4
Gof Sokorete Gudha, Marsabit National Park (Marsabit County)	02°16’N, 37°56’E	1332	3
Gotu Falls, Sempire Camp (Isiolo County)	00°47’N, 38°05’E	644	9
Hells Gate National Park, Kwa Muhia, Naiburta Camp (Nakuru C.)	00°52’S, 36°21’E	1967	18
Kaboga Cave, Watamu (Kilifi County)	03°20’S, 40°02’E	12	28
Kalacha (Marsabit County)	03°08’N, 37°26’E	383	2
Kampi Ya Samaki, Soi Safari Lodge (Baringo County)	00°37’N, 36°02’E	991	14
Karare, Gof Bongolle (Marsabit County)	02°13’N, 37°55’E	1120	4
Kimana (Kajiado County)	02°50’S, 37°31’E	1396	23
King Lion Camp, Archers Post, Samburu Reserve (Samburu County)	00°34’N, 37°32’E	879	11
Kwa Muhia, Hells Gate National Park, Naiburta Camp (Nakuru C.)	00°52’S, 36°21’E	1967	18
Kwale, Shimba Hills National Park, Shimba Hills Lodge (Kwale C.)	04°12’S, 39°26’E	290	29
Lake Baringo, Lesukut Island (Baringo County)	00°35’N, 36°05’E	932	13
Lake Bogoria Reserve, Loboi, former headquarter (Baringo County)	00°21’N, 36°04’E	1005	16
Leisure Lodge, Ukunda, Diani (Kwale County)	04°17’S, 39°36’E	5	30
Lesukut Island, Lake Baringo (Baringo County)	00°35’N, 36°05’E	932	13

site	coordinates	altitude	NM
Loboi, former Lake Bogoria Reserve headquarter (Baringo County)	00°21’N, 36°04’E	1005	16
Loboi, Zakayos Camp (Baringo County)	00°21’N, 36°04’E	1005	16
Marsabit National Park, Gof Sokorete Gudha (Marsabit County)	02°16’N, 37°56’E	1332	3
Mbenyenye Cave, Fikirini (Kwale County)	04°37’S, 39°21’E	20	31
Mida Creek Camp, Watamu (Kilifi County)	03°19’S, 39°58’E	6	27
Mount Elgon National Park, Rongai Camp (Trans-Nzoia County)	01°02’N, 34°47’E	2213	15
Naiburta Camp, Hells Gate National Park, Kwa Muhia (Nakuru C.)	00°52’S, 36°21’E	1967	18
Namanga (Kajiado County)	02°32’S, 36°47’E	1314	22
Nanyuki, Ol Pejeta, Stable (Laikipia County)	00°02’N, 36°54’E	1793	12
Ngulia Lodge, Tsavo West National Park (Taita-Taveta County)	03°01’S, 38°13’E	954	24
Nyiro River Camp, Ol Kirimatian (Kajiado County)	01°53’S, 36°07’E	643	21
Oasis Camp, Gilgil (Nakuru County)	00°29’S, 36°16’E	1730	17
Ol Kirimatian, Nyiro River Camp (Kajiado County)	01°53’S, 36°07’E	643	21
Ol Kirimatian, Shompole Conservancy (Kajiado County)	01°51’S, 36°06’E	666	21
Ol Pejeta, Nanyuki, Stable (Laikipia County)	00°02’N, 36°54’E	1793	12
Oldarpoi Camp, Ewangan (Narok County)	01°31’S, 35°21’E	1739	20
Ololokwe, Sabache Camp (Samburu County)	00°51’N, 37°33’E	1095	8
Rongai Camp, Mount Elgon National Park (Trans-Nzoia County)	01°02’N, 34°47’E	2213	15
Sabache Camp, Ololokwe (Samburu County)	00°51’N, 37°33’E	1095	8
Samburu Reserve, Archers Post, King Lion Camp (Samburu County)	00°34’N, 37°32’E	879	11
Sempire Camp, Gotu Falls (Isiolo County)	00°47’N, 38°05’E	644	9
Sentrim Camp, Voi, Tsavo East National Park (Taita-Taveta County)	03°22’S, 38°41’E	436	25
Shimba Hills Lodge, Shimba Hills National Park, Kwale (Kwale C.)	04°12’S, 39°26’E	290	29
Shimba Hills National Park, Kwale, Shimba Hills Lodge (Kwale C.)	04°12’S, 39°26’E	290	29
Shimoni, Slave Cave (Kwale County)	04°39’S, 39°23’E	1	32
Shompole Conservancy, Ol Kirimatian (Kajiado County)	01°51’S, 36°06’E	666	21
Simba Lodge, Archers Post, Buffalo Springs Reserve (Isiolo County)	00°36’N, 37°37’E	853	10
Slave Cave, Shimoni (Kwale County)	04°39’S, 39°23’E	1	32
Soi Safari Lodge, Kampi Ya Samaki (Baringo County)	00°37’N, 36°02’E	991	14
South Horr (Marsabit County)	02°06’N, 36°55’E	1067	5
Stable, Ol Pejeta, Nanyuki (Laikipia County)	00°02’N, 36°54’E	1793	12
Suswa, Suswa Cave (Kajiado County)	01°08’S, 36°24’E	1830	19
Tsavo East National Park, Voi, Aruba Ashnil Lodge (Taita-Taveta C.)	03°21’S, 38°49’E	431	26
Tsavo East National Park, Voi, Sentrim Camp (Taita-Taveta County)	03°22’S, 38°41’E	436	25
Tsavo West National Park, Ngulia Lodge (Taita-Taveta County)	03°01’S, 38°13’E	954	24
Ukunda, Diani, Diani Marine (Kwale County)	04°19’S, 39°35’E	5	30
Ukunda, Diani, Leisure Lodge (Kwale County)	04°17’S, 39°36’E	5	30
Voi, Tsavo East National Park, Aruba Ashnil Lodge (Taita-Taveta C.)	03°21’S, 38°49’E	431	26
Voi, Tsavo East National Park, Sentrim Camp (Taita-Taveta County)	03°22’S, 38°41’E	436	25
Wamba (Samburu County)	00°59’N, 37°20’E	1294	7
Watamu, Kaboga Cave (Kilifi County)	03°20’S, 40°02’E	12	28
Watamu, Mida Creek Camp (Kilifi County)	03°19’S, 39°58’E	6	27
Zakayos Camp, Loboi (Baringo County)	00°21’N, 36°04’E	1005	16

APPENDIX 2

GenBank Accession Numbers of the examined NMP bats from Kenya and Ethiopia

species	NMP voucher	haplotype (GenBank No.)
Afronycteris nana	NMP 97874	PV460768
Afronycteris nana	NMP 97875	PV460769
Chaerephon pumilus	NMP 97877	PV460771
Chaerephon pumilus	NMP 97878	PV460772
Chaerephon pumilus	NMP 97879	PV460773
Chaerephon pumilus	NMP 97880	PV460774
Chaerephon pumilus	NMP 97950	PV460800
Chaerephon pumilus	NMP 97951	PV460801
Chaerephon pumilus	NMP 98045	PV460760
Coleura afra	NMP 97986, 97987	PV460813
Coleura afra	NMP 97988	PV460814
Coleura afra	NMP 97989	PV460815
Coleura afra	NMP 97991	PV460817
Coleura afra	NMP 98038	JQ956454
Epomophorus labiatus	NMP 97937, 97939	PV460793
Epomophorus labiatus	NMP 97938	PV460794
Epomophorus minimus	NMP 97853, 97920	PV460765
Epomophorus minimus	NMP 97854	PV460766
Epomophorus minimus	NMP 97885	PV460778
Epomophorus minimus	NMP 97886	PV460779
Epomophorus minimus	NMP 97887, 97888	PV460780
Epomophorus minimus	NMP 97921	PV460784
Epomophorus minimus	NMP 97922	PV460785
Epomophorus wahlbergi	NMP 97940, 97942	PV460795
Epomophorus wahlbergi	NMP 97941	PV460796
Epomophorus wahlbergi	NMP 97946	PV460798
Epomophorus wahlbergi	NMP 97952	PV460802
Epomophorus wahlbergi	NMP 97953	PV460803
Epomophorus wahlbergi	NMP 97954	PV460804
Epomophorus wahlbergi	NMP 97955	PV460805
Epomophorus wahlbergi	NMP 97968, 98026, 98070	PV460810
Epomophorus wahlbergi	NMP 97990	PV460816
Epomophorus wahlbergi	NMP 98006, 98007	PV460821
Epomophorus wahlbergi	NMP 98023, 98034, 98035	PV460824
Hipposideros ruber	NMP 98028	PV460825
Hipposideros ruber	NMP 98029	PV460826
Hipposideros ruber	NMP 98030, 98031	PV460827
Hipposideros ruber	NMP 98032	PV460828
Hipposideros tephrus	NMP 97872	PV567369
Hipposideros tephrus	NMP 97873	PV567370
Hipposideros tephrus	NMP 97896, 97897, 97899, 97928–97930	PV567371
Macronycteris vittata	NMP 97973, 97985, 98016	PV567372
Macronycteris vittata	NMP 97982	PV567373
Macronycteris vittata	NMP 97984	PV567374
Macronycteris vittata	NMP 98015	PV567375
Miniopterus minor	NMP 98017, 98018, 98019	PV460822
Miniopterus minor	NMP 98020	PV460823

species	NMP voucher	haplotype (GenBank No.)
Miniopterus mossambicus	NMP 97956	OQ224761
Miniopterus mossambicus	NMP 97958	PV460806
Miniopterus mossambicus	NMP 97959	PV460807
Miniopterus mossambicus	NMP 97960	PV460808
Miniopterus mossambicus	NMP 97961	PV460809
Mops condylurus	NMP 97924, 97927	PV460786
Mops condylurus	NMP 97925	PV460787
Mops condylurus	NMP 97926	PV460788
Neoromicia capensis	NMP 97944	PV460797
Neoromicia somalica	NMP 97884	PV460777
Neoromicia somalica	NMP 97949	PV460799
Neoromicia zuluensis	NMP 97869	PV460767
Neoromicia zuluensis	NMP 97881	PV460775
Neoromicia zuluensis	NMP 97882	PV460776
Neoromicia zuluensis	NMP 97996	PV460818
Neoromicia zuluensis	NMP 97997	PV460819
Neoromicia zuluensis	NMP 97998	PV460820
Nycteris thebaica	NMP 97866	PV567376
Nycteris thebaica	NMP 98027	PV567377
Nycteris thebaica	NMP 98033	PV567378
Otomops harrisoni	NMP 97933	PV460789
Otomops harrisoni	NMP 97934	PV460790
Otomops harrisoni	NMP 97935	PV460791
Otomops harrisoni	NMP 97936	PV460792
Pipistrellus hesperidus	NMP 97876	PV460770
Pseudoromicia nyanza	NMP 97902	PV460781
Pseudoromicia nyanza	NMP 97903	PV460782
Scotophilus colias	NMP 97992	PV467365
Scotophilus colias	NMP 98009	PV467366
Scotophilus colias	NMP 98010	PV467367
Scotophilus trujilloi	NMP 98014	PV467368
Taphozous hildegardeae	NMP 97976–97978, 97980	PV460811
Taphozous hildegardeae	NMP 97979, 97981	PV460812
Taphozous perforatus	NMP 97911	PV460783
Taphozous perforatus	NMP 96901	PV460761
Taphozous perforatus	NMP 96904	PV460762
Taphozous perforatus	NMP 96907	PV460763
Taphozous perforatus	NMP 96908	PV460764