

The first report of a spiny mouse related to *Acomys ignitus* (Rodentia: Muridae) in Somaliland: Phylogenetic affinities of a new distinct mitochondrial lineage

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Abstract. We report here the first record of a spiny mouse of the genus *Acomys* Geoffroy, 1838 belonging to the “*ignitus*” clade from Somaliland. This clade is distributed in southern Kenya, northernmost Tanzania, and southernmost Ethiopia. Our finding extends the distribution of this clade considerably further east. The locality is situated in dry savannah with red sand semi-desert elements, which is quite different from the typical rocky habitats of the other *Acomys* species in the Horn of Africa. Molecular phylogenetic analyses place our specimen in the *A. cahirinus* species group. It is a well-supported new lineage within the “*ignitus*” clade that we call *Ign5*. Although the inner relationships have remained resolved only partially, it is clearly more related to *A. ignitus* Dollman, 1910 than to *A. kempfi* Dollman, 1911. In addition to phylogenetic affinities, we briefly discuss its basic morphology and habitat requirements.

Key words. Phylogeny, distribution, *Acomys*, Somalia-Masai bushland, Somaliland, Horn of Africa.

INTRODUCTION

During the last century many contradictory revisions of the taxonomy of spiny mice (*Acomys* Geoffroy, 1838) within the *A. ignitus* species group were published (Dollman 1914, Hollister 1919, Ellerman 1941, Matthey 1965). Fiery spiny mouse (*A. ignitus* Dollman, 1910) was originally described as a new species at the beginning of the 20th century. Latter it was recognized as a valid species by Hollister (1919) and confirmed by Ellerman (1941). Chromosomal (Matthey 1965), electrophoretic (Janecek et al. 1991) and cytochrome *c* (Barome et al. 2000) studies revealed similar results. Janecek et al. (1991) regard *A. ignitus* as closely related to *A. cahirinus*. Kemp’s spiny mouse (*A. kempfi* Dollman, 1911) was traditionally considered to be a subspecies of *A. ignitus* (Dollman 1914, Hollister 1919, Ellerman 1941) but was later shown to be a valid species based on analyses of electrophoretic data (Janecek et al., 1991). Later on, Lavrenchenko et al. (2010) described a genetically and cytogenetically divergent lineage of *Acomys* sp. C in the Babile Elephant Sanctuary in eastern Ethiopia. This possibly distinct species was later treated as a molecular operational taxonomic unit (MOTU) *Ign1* (Aghová et al. 2019) and placed as a sister taxon of *A. kempfi* (*Ign4* in Aghová et al. 2019). Moreover, a new lineage called *Ign2* first described from south-eastern Ethiopia, clusters with *A. ignitus* (*Ign3* in Aghová et al. 2019). In conclusion, the most recent multi-locus phylogeny of spiny mice based on three genetic markers delimit the “*ignitus*” clade to four MOTUs (*Ign1*, *Ign2*, *Ign3*, and *Ign4*), which potentially cor-

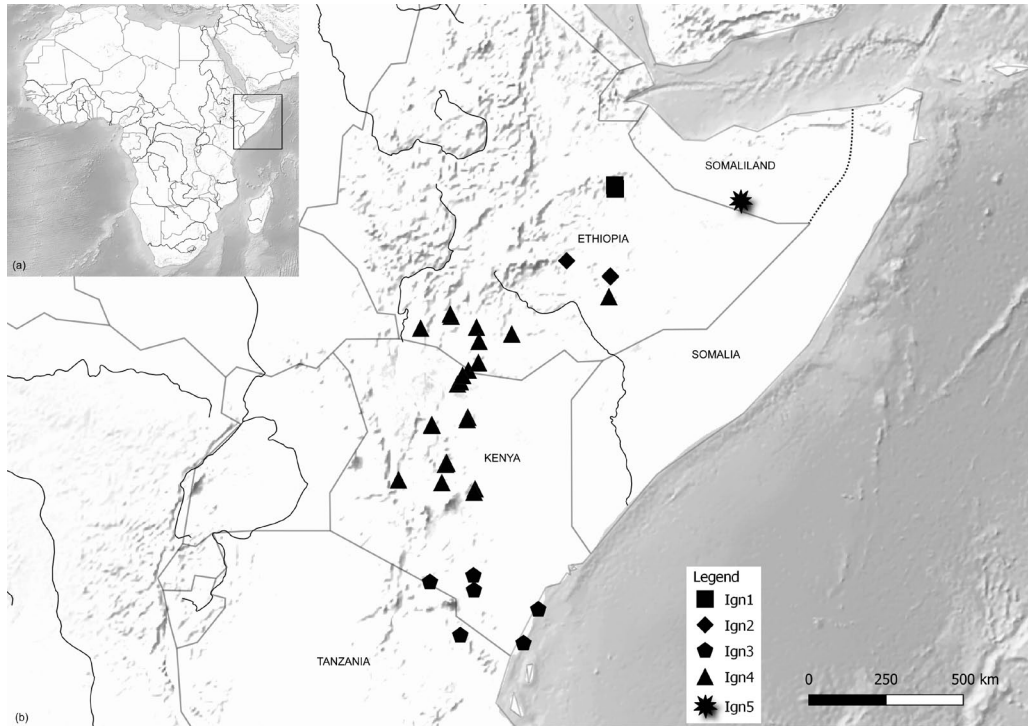


Fig. 1. Map of Somaliland and adjoining parts of Ethiopia and Somalia forming the Horn of Africa with the locality of *Ign5* (star) extending the border of the “*ignitus*” clade considerably further east. This specimen was caught in a close proximity of Shanshacade village. Remaining symbols are for previously published localities of spiny mice belonging to the “*ignitus*” clade.

respond to separate species and support the inclusion of this clade inside the *A. cahirinus* species group (sensu Aghová et al. 2019).

Acomys ignitus occurs in southern Kenya and northernmost Tanzania and *A. kempfi* in Kenya and southernmost Ethiopia. The published molecular samples of *A. ignitus* are only for Ethiopia and Kenya (Aghová et al. 2019), but are completely missing from the rest of the Horn of Africa (HOA). *Ign1* with the northernmost known locality of *A. ignitus* indicates the northern boundary of its distribution. Lavrenchenko et al. (2010) mention that this spiny mouse was very common and abundant in Babile. *Acomys kempfi* and *A. ignitus* are reported in southern Somalia (Petter 1983, Happold 2013), but the actual localities are unknown. These findings indicate that the distribution of the “*ignitus*” clade might be larger than previously suggested. Nevertheless, the region of HOA (especially Ogaden (Ethiopia) and Somalia including Somaliland) due to political instability is not well studied. The new samples from this biodiversity hotspot (Brook et al. 2001, Burges et al. 2004) are worthy of interest.

In this study, we report the first record of *Acomys* belonging to the “*ignitus*” clade from the south of Somaliland, an independent state internationally recognized as an autonomous region of Somalia. We describe the morphology and ecology of this specimen and its phylogenetic affinity with the rest of the “*ignitus*” clade.

MATERIAL AND METHODS

Sampling

The survey was carried out in Somaliland. The reported specimen was caught near the watering-place close to Shanshacade village (8.658°N, 45.956°E; Fig. 1). The habitat there is dry savannah with red sand semi-desert elements (Fig. 2a). The mouse was trapped in snap trap baited with peanut butter and identified to genus based on external characters, measured with a digital calliper to the nearest 0.01 mm, weighed on a digital balance to the nearest 0.01 g, photographed and a small

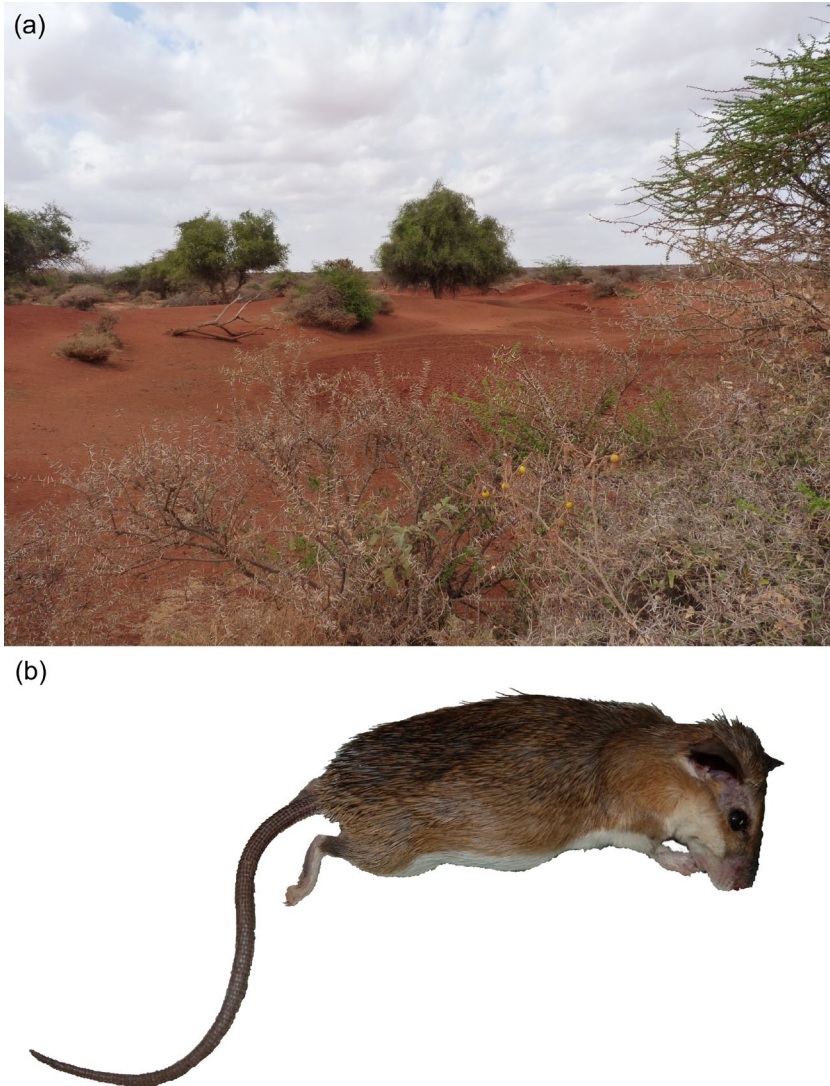


Fig. 2. Semi-desert habitat at Shanshacade (Somaliland), where specimen *Ign5* was caught (a); general body habitus (b). Photo by Daniel Frynta, September 2018

piece of its spleen was collected and stored in 96% ethanol until required for DNA extraction. This specimen is deposited in the zoological collection of Charles University (CUP/MAMM/SOMALILAND/170). GPS coordinates of the locality were recorded. We measured five standard characters including head and body length (HB), tail length (T), hind foot from 'ankle bone' to tip of the longest digit not including the claw (HF), length of external (outer) ear measured from tip of ear to the posterior point of the ear conch (E) and body weight (W). Skulls were cleaned and magnified under an Olympus SZX 12 stereomicroscope and detailed photographs of the skull, lower jaw, upper and lower molars were taken using an Olympus DP70 camera. Moreover, we visualised the lower jaw using μ CT (Bruker SkyScan 1275 micro-CT) and processed the videos using CT Vox software (version 3.1.1 r1191 Bruker). We employed QGIS to prepare a map of the localities (QGIS Development Team 2019).

All fieldwork in this study complied with legal Somaliland regulations and sampling was in accordance with local legislation (export permit Ref. MOERD/M/I/251/2017).

DNA extraction, amplification and sequencing

Genomic DNA was extracted from ethanol-preserved tissue samples using a DNeasy Blood and Tissue kit (Qiagen, Hilden, Germany) following the manufacturer's instructions. We amplified and sequenced two mitochondrial fragments, cytochrome b (CYTB) and control region (D-loop) and one nuclear exon Interphotoreceptor Binding Protein (IRBP). For amplification and sequencing see Methods in Aghová et al. (2019). New sequences were deposited in GenBank under accession numbers MN547495 (CYTB), MN547497 (D-loop), and MN547496 (IRBP).

Phylogenetic analysis

Sequences were aligned and manually checked using Chromas Lite 2.01 (http://www.technelysium.com.au/chromas_lite.html), BioEdit (Hall 1999) and Clustal X 1.81 (Thompson et al. 1997). The final dataset for phylogenetic analyses contains sequences of CYTB, D-loop and IRBP with a total length 2665 bp (for the list of specimens see Table 1). As outgroups we used clades (KE734, K4_210, SIN1, IRA2, ABC-006, CAIR, CHAD, E12-S37, VV1998-087, ETH0548, ETH0610, ET168, ETH0033, 601476, 602643, LAV2211, LAV2229, ABC-008, RUS2, ETH0323, KE697, KE030, KE042, ETH1057, KE628) from Aghová et al. (2019). Bayesian inference analysis was performed using MrBayes v3.2.6 (Ronquist et al. 2012) and the multiple alignment was selected into seven particular partitions (see Aghová et al. 2019). There were two independent runs with four MCMCs. It ran for 40 million generations, with trees sampled every 1000 generations. A conservative 25% burn-in was used after checking for stability on the log-likelihood curves and split-frequencies of the runs. Support of nodes for MrBayes analysis was provided in terms of clade posterior probabilities as directly estimated from the majority-rule consensus topology.

Maximum likelihood (ML) analysis was performed using RAxML v8.2.8 (Stamatakis 2014) with the GTR + G model substitution model. The ML tree was obtained using heuristic searches with 100 random additional replicates and clade support was then assessed using a non-parametric bootstrap procedure with 1000 replicates.

Maximum parsimony (MP) analysis was performed using Mega X (Kumar et al. 2018). We conducted heuristic search analyses with 1000 random replicates of taxa additions using tree-bisection and reconnection (TBR) branch swapping. The branch support was evaluated using 1000 bootstrap pseudo replicates (Felsenstein 1985). All characters were equally weighted and unordered.

RESULTS

The spiny-mouse examined is the easternmost specimen belonging to the "ignitus" clade (see below) ever reported. Thus, this finding extends the distribution of the "ignitus" clade further east.

The specimen was an adult female with HB=99.3 mm, T=97.4 mm, HF=15.7 mm, E=15.7 mm, W=25.9 g. The dorsal fur was spiny from shoulders to base of the tail and a greyish brown colour with darker spines towards the tail. Ventral fur was pure white and soft (Fig. 2b). Uterus duplex contained one placental scar on the left and one embryo in the right horn of the uterus. We cannot conclude anything about species-specific morphological characters due to low sample size. Nevertheless, we include detailed photographs of lower jaw and molars for further study (Fig. 3, SI 1, 2).

Both Bayesian inference (BI) and Maximum Likelihood (ML) analyses of concatenated multi-locus data provided similar phylogenetic relationships and supports (see Fig. 4 for BA tree). The molecular characterization of the specimen from Shanshacade revealed that it is a member of the "ignitus" clade ($BA_{pp}=1$, $ML_{bootstrap}=100$) belonging to the *cahirinus* species group in the genus

Table 1. List of specimens included in the molecular analysis

ID	species	lineage	country	locality	latitude	longitude	publication
ETH0054	sp. C	Ign1	Ethiopia	Babile Elephant Sanctuary	9.120	42.257	Aghová et al. (2019)
ETH0055	sp. C	Ign1	Ethiopia	Babile Elephant Sanctuary	9.120	42.257	Aghová et al. (2019)
ETH1020	sp. Ign2	Ign2	Ethiopia	Sof Omar Caves	6.906	40.849	Aghová et al. (2019)
ETH1058	sp. Ign2	Ign2	Ethiopia	Imi	6.431	42.132	Aghová et al. (2019)
KE519	<i>ignitus</i>	Ign3	Kenya	Tsavo West NP	-2.747	38.133	Aghová et al. (2019)
KE625	<i>ignitus</i>	Ign3	Kenya	Gede	-3.309	40.018	Aghová et al. (2019)
ETH0332	<i>kempi</i>	Ign4	Ethiopia	Turmi	4.933	36.569	Aghová et al. (2019)
KE824	<i>kempi</i>	Ign4	Kenya	Marigat, Egerton University Field Station	0.489	35.921	Aghová et al. (2019)
170		Ign5	Somaliland	Shanshacade	8.658	45.956	this study

Acomys. The specimen is a new lineage within the “*ignitus*” clade that we hereafter call *Ign5*. Thus, the “*ignitus*” clade is currently composed of five deep branches. It further splits into two well-supported sister clades ($BA_{pp}=1$, $ML_{bootstrap}=100$). There is a distinct clade consisting of *Ign5*, *Ign2*, and *Ign3* (= *A. ignitus* s. str.) with unresolved inner relationships. The second clade includes both the remaining MOTU’s, *Ign1* and *Ign4* (= *A. kempi*). There are marked divergences among MOTU’s in the “*ignitus*” clade, with p-distances ranging from 6.1 to 7.8% (Table 2) from multiple alignments and 8.1 to 12.6% (Table 3) from CYTB.

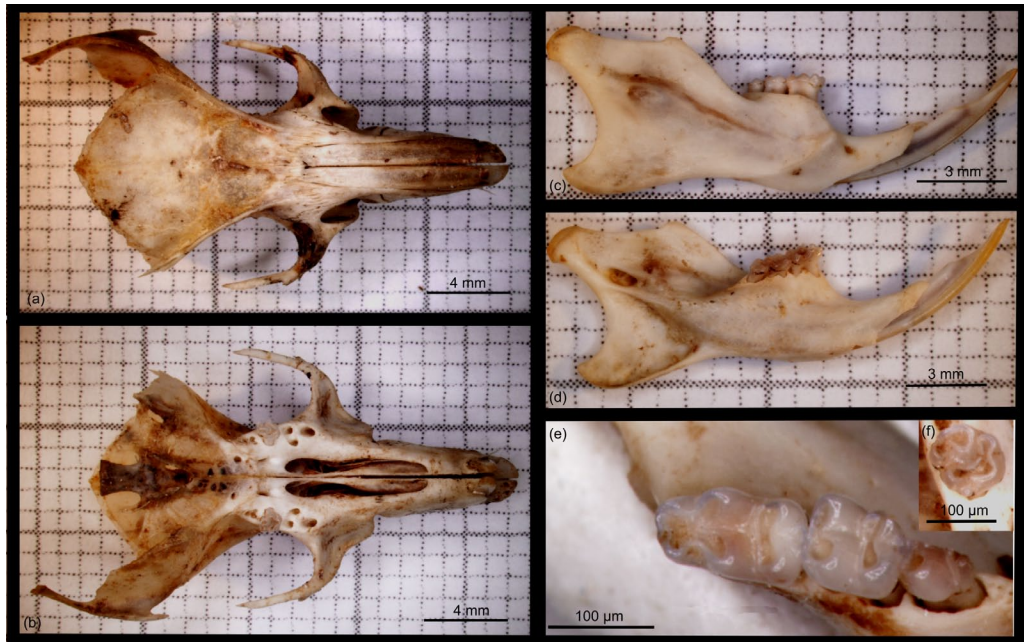


Fig. 3. Skull morphology with details of the dorsal (a) and ventral (b) part of the skull; lower jaw from the lateral (c) and medial (d) view; detail of lower molars (e) and upper M² (f).

DISCUSSION

Spiny mice of the genus *Acomys* belonging to the “*ignitus*” clade of the *A. cahirinus* species group are rodents that occur in the Somalia-Masai Bushland biotic zone in east Africa (Happold & Lock 2013). Nevertheless, the area of Somalia located on the Horn of Africa is not well studied. In basic monographs devoted to the systematics of rodents in Africa (Happold 2013, Monadjem et al. 2015), there is little information (lacking specific coordinates) about the distribution of *A. ignitus* and *A. kempi* in Somalia. In this paper, we report the first record of a spiny mouse belonging to the “*ignitus*” clade in Somaliland with an accurate GPS locality, and morphological and molecular characterization. Our finding extends the boundary of the “*ignitus*” clade further to the east than previously reported.

That is, the “*ignitus*” clade occurs not only in the eastern part of Ethiopia, northernmost Tanzania and southern Kenya, but also in Somaliland (Fig. 1). It is possible that the “*ignitus*” clade is more specious and occurs in the whole of the HOA, which is famous for its high level of endemism (cf. e.g., Agnelli et al. 1990, Gippoliti 2006, Varshavsky et al. 2007, or Lewin et al. 2016).

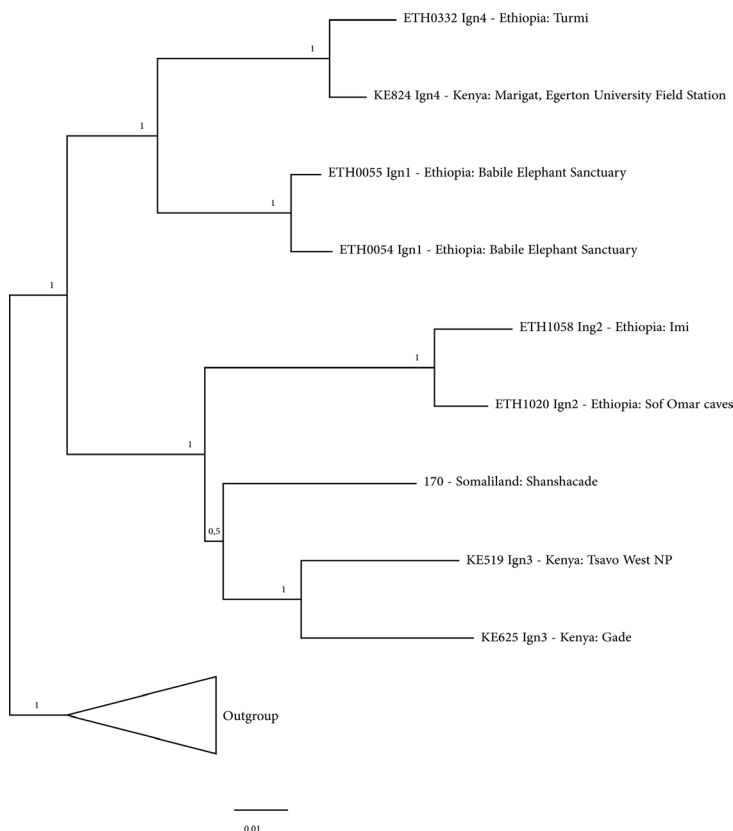


Fig. 4. Multi-locus phylogeny of the “*ignitus*” clade. Bayesian phylogeny of concatenated multi-locus matrix calculated using MrBayes with posterior probabilities.

Table 2. Genetic distances calculated from multiple alignments in Geneious. Interspecific distances from the nearest lineage in percentages (%)

lineage	nearest lineage	inter dist
170	Ign3	6.1
170	Ign2	6.9
170	Ign4	7.4
170	Ign1	7.8

The phylogenetic analysis revealed clear evidence for the existence of a new lineage (*Ign5*), which belongs close to *A. ignitus* (*Ign3*) and MOTU *Ign2*. The cluster of these three lineages (*Ign2*, *Ign3* and *Ign5*) is well supported, nevertheless, the inner relationships remain unresolved. Our analysis supports *A. kempi* (*Ign4*) and *Ign1* as sister taxa representing a sister clade to the group of *Ign2*, *Ign3* and *Ign5*. Genetic distances derived from the BI phylogenetic tree using the species delimitation algorithm is rather high, which suggest that our five MOTU's are potentially separate species. Nevertheless, more samples are needed for a further consideration of these lineages as distinct species.

Generalized morphology of the genus *Acomys* encourages the use of molecular methods for taxonomic identification (Barome et al. 1998, 2000, 2001a, b, Nicolas et al. 2009, Verheyen et al. 2011, Alhajeri et al. 2015, Petruželka et al. 2018), even though morphological characters (Ellerman 1941, Chevret et al. 1993) and chromosomes (Matthey 1968, Setzer 1975) are also employed. Morphological characters can be used to distinguish groups of spiny mice (Petter & Roche 1981, Petter 1983, Denys et al. 1994), nevertheless, discrimination inside lineages is much less reliable. First morphological characters delimitating *A. ignitus* from other spiny mice are from Petter (1983), who studied the morphology of their teeth and skull. The teeth of this species are characterized by: “the existence of a crest between t4 and t8, by very longitudinal t1 and t4, as well as by differentiated t3 and t6. The t8 is well separated from t9 and is more anterior.” (Denys et al. 1994). Later Janeczek et al. (1994) confirmed that this species has a long and narrow skull with rounded rather than a V-shaped fronto-parietal suture. Unfortunately, the skull of our specimen was slightly damaged during trapping and several upper molars are missing. We can confirm the rounded shaped fronto-parietal suture (Fig. 3a). Nevertheless, it is not possible to compare molars due to low sample size and the absence of detailed descriptions of the molars of specimens belonging the other MOTUs of the “*ignitus*” clade. The tail of our specimen is slightly shorter than the head and body length, which is consistent with Denys et al. (1994). More specimens of *Ign5* are needed for proper morphological characterization. Thus, we only report the size of its body and present photographs of whole body and elements of its skull.

The habitat of the *Acomys cahirinus* species group is reported to be rocky dry savannah and semi-desert. Our specimen was caught near the watering-place close to Shanshacade. The habitat

Table 3. Uncorrected P-distances calculated from cytochrome b. Interspecific distances from the nearest lineage in percentages (%)

lineage	nearest lineage	inter dist
170	Ign3	8.1
170	Ign2	10.6
170	Ign4	11.5
170	Ign1	12.6

was more desert-like with mainly red sand and shrubs (Fig. 2a). This type of habitat is completely different from other Somaliland localities where spiny mice (*Acomys louisae* Thomas, 1896 and *A. mullah* Thomas, 1904) were common (Frynta et al. 2020).

CONCLUSIONS

In conclusion, we report the first record of *Acomys* belonging to the “*ignitus*” clade for Somaliland. This extends its distribution considerably further east. We designate this specimen as MOTU *Ign5*. The multi-locus phylogeny classifies this new lineage in a group including *Ign2* and *Ign3*. Thus, it is more related to *A. ignitus* (= *Ign3*) than *A. kempi* (= *Ign4*) and *Ign1*.

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SUPPLEMENTARY INFORMATION

Supplementary Information is available at Figshare: <https://doi.org/10.6084/m9.figshare.13140368.v1>

Supplementary Information 1. Video file. The visualization of the lower jaw of spiny mouse *Ign5* from a medial and lateral view using μ CT.

Supplementary Information 2. Video file. The visualization of the lower jaw and detailed view of molars of spiny mouse *Ign5* using μ CT.