Adam W. Ferguson*, Houssein R. Roble and Molly M. McDonough

Noteworthy record of the Ethiopian genet, *Genetta abyssinica*, (Carnivora, Viverridae) from Djibouti informs its phylogenetic position within *Genetta*

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Abstract: The molecular phylogeny of extant genets (Carnivora, Viverridae, *Genetta*) was generated using all species with the exception of the Ethiopian genet *Genetta abyssinica*. Herein, we provide the first molecular phylogenetic assessment of *G. abyssinica* using molecular sequence data from multiple mitochondrial genes generated from a recent record of this species from the Forêt du Day (the Day Forest) in Djibouti. This record represents the first verified museum specimen of *G. abyssinica* collected in over 60 years and the first specimen with a specific locality for the country of Djibouti. Multiple phylogenetic analyses revealed conflicting results as to the exact relationship of *G. abyssinica* to other *Genetta* species, providing statistical support for a sister relationship to all other extant genets for only a subset of mitochondrial analyses. Despite the inclusion of this species for the first time, phylogenetic relationships among *Genetta* species remain unclear, with limited nodal support for many species. In addition to providing an alternative hypothesis of the phylogenetic relationships among extant genets, this recent record provides the first complete skeleton of this species to our knowledge and helps to shed light on the distribution and habitat use of this understudied African small carnivore.

Keywords: distribution; Djibouti; *Genetta abyssinica*; habitat; phylogeny.

Introduction

The Ethiopian or Abyssinian genet (*Genetta abyssinica*, Rüppell 1836) is a diminutive species of genet (Carnivora, Viverridae) restricted to the Horn of Africa (Gaubert 2013). Originally thought to occur only in arid habitats, subsequent investigations indicated that *G. abyssinica* actually inhabits a broad altitudinal and ecological range (Yalden et al. 1996). Based solely upon 18 museum specimens and a single ecological study from the highlands of Ethiopia (Diaz Behrens and Van Rompaey 2002), *G. abyssinica* is thought to occur from coastal plains and dry lowlands to high plateaus in Eritrea, Djibouti, Ethiopia, Somalia and Sudan (Gaubert 2013). Predictions based on ecological niche models generated using 12 georeferenceable museum vouchers indicated that open/sparse grasslands in Eritrea and surrounding countries and deciduous-shrubland and montane forest in western Ethiopia composed the most suitable range for *G. abyssinica* (Papeş and Gaubert 2007). Papeş and Gaubert (2007) also found that such suitable areas for *G. abyssinica* were often isolated by unsuitable areas dominated by croplands, where a majority of historical records are now located. Even with this understanding of its broad niche, newly gathered information continues to shed light on the ecology of this poorly studied species, e.g. the first discovery of *G. abyssinica* in forested habitats of the Abune Yosef Massif, Ethiopia (Diaz Behrens and Van Rompaey 2002). Thus, continued studies of *G. abyssinica* across its range are important for elucidating its ecological requirements, conservation status and distributional limits.

Beyond the limited understanding of the ecology of *Genetta abyssinica*, its phylogenetic relationship to other genets also remains obscure. Traditionally included in the subgenus *Pseudogenetta* Dekeyser, 1949 together with the similar-sized Haussa genet *Genetta thierryi* Matschie, 1902 (Crawford-Cabral 1981), *G. abyssinica* is considered a primitive genet based on shared characteristics (e.g. hairless central depression of the forefoot) with African linsangs or oyans of the genus *Poiana* Gray, 1864 (Crawford-Cabral 1981). Although the validity of *Pseudogenetta* has been brought into question, morphological analyses have

***Corresponding author: Adam W. Ferguson**, Field Museum of Natural History, 1400 South Lake Shore Drive, Chicago, IL 60605, USA, e-mail: aferguson@fieldmuseum.org

Houssein R. Roble: Environment and Sustainable Development Ministry of Housing, Urban Planning and Environment, BP 2091, Republic of Djibouti

Molly M. McDonough: National Museum of Natural History, Smithsonian Institution, 10th St. and Constitution Ave. NW, Washington, DC 20560, USA; and Center for Conservation Genomics, Smithsonian Conservation Biology Institute, National Zoological Park, 3001 Connecticut Ave NW, Washington, DC 20008, USA

confirmed the monophyletic sister-relationship between *G. abyssinica* and *G. thierryi* (Gaubert et al. 2002). Molecular studies aimed at addressing the debated systematics and phylogenetics of the genus *Genetta* Cuvier, 1816 have included all living species of morphologically recognized genets with the exception of *G. abyssinica* (Gaubert et al. 2004, Gaubert and Begg 2007). Thus, although Gaubert et al. (2004) predict a sister relationship between *G. abyssinica* and *G. thierryi*, no molecular data, neither DNA sequence nor karyological, exist for evaluating this relationship (Gaubert et al. 2004, Gaubert and Begg 2007). Given the potential sister relationship of *G. thierryi* and *G. abyssinica* and their hypothesized primitive status in relation to extant genets, including the basal rain forest lineage, elucidating the phylogenetic position of *G. abyssinica* is crucial for understanding evolutionary transitions from forest dependent to savanna adapted *Genetta* species or vice versa (Gaubert et al. 2004). Although historical museum specimens can provide alternatives to modern tissue samples, work on genets indicates that obtaining fresh samples from morphologically recognizable/vouchered specimens is critical for accurately assessing phylogenies of these closely related species (Gaubert and Begg 2007).

Herein, we report the first record of an Ethiopian genet, *Genetta abyssinica* from Djibouti with verifiable locality data in over 60 years together with a first assessment of its position within the *Genetta* molecular phylogeny based on mitochondrial DNA sequences. Based on previous assessments using morphological cladistics, we hypothesize that *G. abyssinica* will form a monophyletic clade with *Genetta thierryi* which will be sister to all other extant *Genetta*. This recently collected specimen of *G. abyssinica* provides important information regarding the species habitat requirements, confirms its modern presence in the country of Djibouti, and facilitates the first molecular sequence data for assessing its phylogenetic relationship to other living genets.

Materials and methods

Sampling

In February 2016, a joint expedition between the Global Genome Initiative (GGI) at the Smithsonian Institution's National Museum of Natural History (NMNH) and the US Navy's Natural Resources Program was undertaken to characterize biodiversity of the US military base at Camp Lemonnier, Djibouti, Africa. During this time, a brief visit to the Forêt du Day (the Day Forest) was arranged through the Environment and Sustainable Development Ministry

of Housing, Urban Planning and Environment. On 18 February 2016, a single adult male (testes = 12 × 8 mm, scrotal) specimen of *Genetta abyssinica* was captured in a Tomahawk live trap [Model 205, (Hazelhurst, WI, USA) 66 × 23 × 23 cm] baited with raw chicken and raw beef. The trap was set in the Forêt du Day along a dry, rocky drainage flowing southwest from the Garab Plateau into the Ourano Wadi (11° 46' 6.35"N, 42° 39' 6.15"E, 1420 m a.s.l., Figures 1 and 2). Additional mammals observed in the vicinity of the trap included: Hamadryas baboon *Papio hamadryas* (Linnaeus, 1758), rock hyrax *Procavia capensis* (Pallas, 1766), white-tailed mongoose *Ichneumia albicauda* (G. [Baron] Cuvier, 1829), domestic cat (*Felis catus* Linnaeus, 1758), striped hyaena *Hyaena hyaena* (Linnaeus, 1758), pygmy gerbil (*Gerbillus* Desmarest, 1804), and Cairo spiny mouse *Acomys* cf. *cahirinus* (Desmarest, 1819). The Forêt du Day, Republic of Djibouti, or Day National Forest, consists of dry tropical Afromontane mixed woodland dominated by the African pencil juniper *Juniperus procera* and is best known for maintaining the world's largest population of the critically endangered Djiboutian Francolin, *Francolinus ochropectus* (Fisher et al. 2009). Other dominant plants in the Forêt du Day include *Buxus hildebrandtii*, *Olea africana* and *Tarchonanthus camphoratus*. Once captured, the animal was euthanized following ethical guidelines provided by the American Society of Mammalogists (Sikes and Animal Care and Use Committee of the American Society of Mammalogists 2016) and the NMNH Institutional Animal Care and Use Committee (IACUC Permit #2014-11). The skin, skull and post-cranial skeleton were prepared and deposited in the Smithsonian Institution's National Museum of Natural History [The U.S. National Museum (USNM) 602624] together with a whole blood sample in an RNA stabilization buffer and ectoparasites (fleas and ticks in 95% ethanol). Tissue samples, including muscle in lysis buffer (USNM Biorepository numbers AE7VV87, AE7VV88, AE7VV89) and liver in 95% ethanol (AD5JH94) were collected in the field and transferred to long-term liquid nitrogen storage facilities at the NMNH Biorepository (<http://naturalhistory.si.edu/rc/biorepository/>).

DNA sequencing

A single tissue sample stored in buffer was extracted using DNeasy blood and tissue kit (Qiagen, Valencia, CA, USA) following manufacturer's protocols. The entire mitochondrial genome was amplified using two sets of universal primers: 1) tRNA Leuc1 and 16S rRNA1, and 2) tRNA Leuc2 and 16S rRNA2 (Sasaki et al. 2005). The amplification reactions included 50 ng of genomic DNA, 12.5 µl of KAPA HiFi

Figure 1: Distribution of *Genetta abyssinica* based on IUCN with new (USNM 602624) and historical records referenced in this study. All geographic coordinates for specimens depicted in this map with the exception of the new record were taken verbatim from Papeş and Gaubert (2007).

Figure 2: Specimen and habitat photographs of the Ethiopian genet (*Genetta abyssinica*) collected in Djibouti that was used to test its molecular phylogenetic position for the first time.

Adult male *Genetta abyssinica* (USNM 602624) collected in the Forêt du Day, Tadjourah Province, Djibouti on 18 February 2016 (A). Photograph of the left front foot of *Genetta abyssinica* (USNM 602624) depicting the hairless central depression (black arrow) that is characteristic of this species (B). Habitat immediately surrounding trap location (black arrow) where USNM 602624 was captured (C). Photograph from the top of the plateau where USNM 602624 was collected (D).

Hotstart ReadyMix (KAPA Biosystems, Boston, MA, USA), 0.3 μM of each primer, and polymerase chain reaction (PCR)-grade water for a final volume of 25 μl . Reactions were denatured at 98°C for 5 min followed by 35 cycles of: 95°C for 20 s and 68°C for 10 min; followed by a final extension at 72°C for 5 min. PCR products were visualized for correct size fragments using 3 μl of product in a 1.5% agarose gel with GelRed (Biotium, Hayward, CA, USA) and NEB 1 kb ladder (New England Biolabs, Beverly, MA, USA). The remaining PCR products were cleaned with 1.8X SeraPure magnetic beads (Rohland and Reich 2012). The PCR fragments were quantified using Qubit 2.0 (Life Technologies, Thermo Fisher Scientific, Waltham, MA, USA) fluorometric assay and were pooled at an equimolar ratio. The library construction was performed using a Nextera XT DNA Library Kit (Illumina, San Diego, CA, USA) following manufacturer's protocols. The final products were cleaned using 1.8X SeraPure magnetic beads and resuspended in 52.5 μl of the Nextera resuspension buffer. The fragment sizes were validated using an Agilent High Sensitivity DNA Kit (Agilent Technologies, Santa Clara, CA, USA). The final library was quantified using Qubit and the concentration in nanomole was calculated following the Illumina protocol. The library was diluted to 4 nM using 10 mM Tris pH 8.5 and sequences were generated on a single MiSeq run using a 300 cycle v2 PE Kit (Illumina).

Phylogenetic analysis

Paired-end reads were trimmed of adapter sequences using Cutadapt v.1.4.2 (Martin 2011) and poor quality sequences (scores below 20) and exact PCR replicates were removed using prinseq-lite v.0.20.4 (Schmieder and Edwards 2011). Reads were mapped to the mitochondrial genome of *Genetta servalina* Pucheran, 1855 (KJ624980) with Burrows-Wheeler algorithm (BWA) v.7.10 (Li and Durbin 2009) using the “bwa mem” algorithm.

The cytochrome-b (*Cytb*), 12S rRNA (*12S*), 16S rRNA (*16S*), control region (*Dloop*) and cytochrome oxidase-I (*COI*) genes were extracted from the whole mitochondrial genome read alignment and saved as FASTA files. A single representative for each genet species and outgroups included in the most recent phylogenetic analysis (Gaubert and Begg 2007) were downloaded from GenBank and aligned to the novel sequence using the Geneious alignment algorithm (Table 1). Phylogenies were inferred for the following datasets: 1) 5-gene dataset (*Cytb*, *Dloop*, *12S*, *16S*, and *COI*), 2) 2-gene dataset (*Cytb* and *Dloop*), and 3) 1-gene dataset (*Cytb*) (Table 1). The most appropriate models of sequence evolution were

selected using PartitionFinder v.2.1 (Lanfear et al. 2017) using the corrected Akaike information criterion (AIC), greedy search algorithm, and only using models available in MrBayes (Table 2).

Phylogenetic trees were inferred using Bayesian inference (BI) and maximum likelihood (ML). BI was performed using MrBayes v.3.2.6 (Ronquist and Huelsenbeck 2003) using four Markov-chain Monte Carlo (MCMC) runs with three heated and one cold chain. Two independent runs were conducted with 10 million generations, sampling trees and parameters every 1000 generations, and a burn-in of 25% of the sampled trees. ML analysis was performed with RAxML v. 8 (Stamatakis 2014) using GTRCAT and 1000 rapid bootstrap inferences. Both BI and ML estimates were implemented on the CIPRES science gateway (<http://www.phylo.org/index.php/portal/about/>). The final trees were visualized using FigTree v.1.4.3 (<http://tree.bio.ed.ac.uk/software/figtree/>).

Results

Specimen information

The single specimen of an adult male *Genetta abyssinica* (USNM 602624) was collected by A.W. Ferguson (AWF 1220) from the following locality: Djibouti: Tadjourah Province; Forêt du Day, 0.07 mi N, 0.16 mi E of Airolaf, 11.7684°N, 42.65171°E elevation = 1420 a.s.l. (Garmin 62stc GPS unit, WGS84, accuracy = 3 m) on 18 February 2016. This specimen represents the 19th museum voucher in the world, the first collected in over 60 years, and the first record with a precise locality for the country of Djibouti. Of the 18 other museum specimens, only 13 have detailed enough localities for obtaining unambiguous latitude and longitude coordinates, making mapping the distribution of this species challenging (Figure 1; Diaz Behrens and Van Rompaey 2002, Papeş and Gaubert 2007). The single adult male specimen's (USNM 602624) measurements including total length, tail length, hind foot length, ear length and weight were as follows: 798 mm, 374 mm, 68 mm, 47 mm and 720 g (798-374-68-47 $\equiv$ 720 g). Its testes were scrotal with internal maximum length by maximum width measurements of 12 mm $\times$ 8 mm. These measurements fall within those provided for the other two specimens with physical measurements, i.e. 811-403-75-46 $\equiv$ X g (USNM 342066, adult male) and 684-361-66-43 $\equiv$ X g (FMNH 80818, juvenile female). As the only specimen with field weights available it is hard to compare to others, although USNM 602624 weighed less than the 1.3–2.0 kg reported in Haltenorth and Diller

Table 1: GenBank accession numbers for individuals used to generate phylogenetic analyses for assessing the relationship of *Genetta abyssinica* to all other *Genetta* species.

Species	1-gene		2-gene		5-gene		12S	16S	COI
	Cytb	Dloop	Cytb	Dloop	Cytb	Dloop			
<i>Genetta abyssinica</i>	MG489822	MG489822	MG489822	MG489822	MG489822	MG489822	MG489822	MG489822	MG489822
<i>Genetta angolensis</i>	DQ395207	DQ395221	DQ395207	DQ395221	DQ395207	DQ395221	M	M	M
<i>Genetta boursini</i>	AY241898	M	AY241898	M	AY241898	M	M	M	M
<i>Genetta cristata</i>	AY241887	M	AY241887	M	AY241887	M	M	M	M
<i>Genetta felina</i> ^a	AY241901	M	AY241901	M	AY241901	M	M	M	M
<i>Genetta genetta</i>	AY241922	EF371687	AY241906	EF371687	AY241906	EF371687	M	M	M
<i>Genetta johnstoni</i>	AY241892	DQ395230	AY241892	DQ395230	AY241892	DQ395230	M	M	M
<i>Genetta maculata</i>	AY241914	DQ395227	AY397719	DQ395227	HQ450796	DQ395227	KI192516	KI193079	KI192811
<i>Genetta pardina</i>	AY241896	DQ395223	AY397706	DQ395223	KI193373	DQ395223	KI192538	KI193101	KI192829
<i>Genetta piscivora</i>	AF511050	M	AF511050	M	AF511050	M	M	M	M
<i>Genetta poensis</i>	AY241897	M	AY241897	M	AY241897	M	M	M	M
<i>Genetta schoutedeni</i>	AY241899	M	AY241899	M	AY241899	M	M	M	M
<i>Genetta servalina</i>	KI624980	KI624980	KI624980	KI624980	KI624980	KI624980	KI624980	KI624980	KI624980
<i>Genetta thierryi</i>	DQ395206	DQ395233	DQ395206	DQ395233	KI193372	DQ395233	KI192537	KI193100	M
<i>Genetta tigrina</i>	AY241889	M	AY241889	M	AY241889	M	M	M	M
<i>Genetta "tigrina"</i>	AY397705	M	AY397705	M	AY397705	M	M	M	M
<i>Genetta victorinae</i>	AY241894	M	AY241894	M	AY241894	M	M	M	M
<i>Civettictis civetta</i>	AF511043	KX891743	KX891743	KX891743	KX891743	KX891743	KX891743	KX891743	KX891743
<i>Paguma larvata</i>	KT191130	KT191130	KT191130	KT191130	KT191130	KT191130	KT191130	KT191130	KT191130
<i>Poiana richardsonii</i>	AF511049	M	AF511049	M	AF511049	M	M	M	M
<i>Prionodon linsang</i>	AF125141	M	AF125141	M	AF125141	M	M	M	M
<i>Prionodon pardicolor</i>	AF511048	KX447638	KX447638	KX447638	KX447638	KX447638	KX447638	KX447638	KX447638
<i>Viverra zibethica</i>	AF511045	M	AF511045	M	AF511045	M	M	M	M
<i>Viverricula indica</i>	AF511044	KM276554	KM276554	KM276554	KM276554	KM276554	KM276554	KM276554	KM276554

Letter "M" indicates genes that were scored as missing data for individual taxa in the nucleotide matrix. ^aCurrently identified as *Genetta maculata* on GenBank.

Table 2: Models of nucleotide evolution estimated from PartitionFinder version 2.1.1 (Lanfear et al. 2017) used for phylogenetic analyses of the position of *Genetta abyssinica* in relation to all other viverrid species.

Subset	Best model	# Sites	Partition name
<i>Cytb</i> (1-gene)			
1	K80+I+G	380	CYTB_pos1
2	HKY+I	380	CYTB_pos2
3	GTR+I+G	380	CYTB_pos3
<i>Cytb</i> , <i>Dloop</i> (2-gene)			
1	K80+I	380	CYTB_pos1
2	HKY+I	380	CYTB_pos2
3	HKY+G	380	CYTB_pos3
4	GTR+G	390	Dloop_pos1, Dloop_pos2
5	HKY+G	194	Dloop_pos3
<i>Cytb</i> , <i>Dloop</i> , <i>12S</i> , <i>16S</i> , <i>COI</i> (5-gene)			
1	HKY	308	12S_pos2, 16S_pos1
2	SYM+G	394	COI_pos2, 16S_pos2
3	GTR	820	12S_pos3, 16S_pos3, CYTB_pos1, 12S_pos1
4	HKY	220	COI_pos1
5	F81	219	COI_pos3
6	GTR	380	CYTB_pos2
7	GTR+G	380	CYTB_pos3
8	GTR+G	380	Dloop_pos1, Dloop_pos2
9	HKY+G	194	Dloop_pos3

(1980). External morphological characteristics including short, straight and soft pelage; dorsal spots merged in two or three dark lines (Figure 2A); central depression of the forefoot hairless (Figure 2B); the neck spots coalesced with shoulder spots forming stripes; narrow tail with 7–9 pail rings ($n=8$ for USNM 602624) indicated that morphologically the genet we collected could be identified as only *G. abyssinica* (Gaubert et al. 2008).

Phylogenetic analysis

The final mitochondrial genome alignment consisted of 1302 reads that successfully mapped to 97.4% of the *Genetta servalina* mitochondrial genome. We compared our mitochondrial genome alignment to three previously published viverrids and one prionodontid available on GenBank: *G. servalina* (KJ624980), *Civettictis civetta* (Schreber, 1776) (KX891743), *Paguma larvata* (C.E.H. Smith, 1827) (KT191130), and *Prionodon pardicolor* Hodgson, 1842 (KX447638). The *Genetta abyssinica* mitochondrial genome was similar in size structure and gene arrangement to other mammalian genomes; however, we were unable to determine the exact size because of several regions with low sequencing depth or poor alignment due to repetitive regions within the control region.

The *G. abyssinica* mitochondrial genome was 16,849 base pairs (bps) long, with ~300 bps of missing data in the following regions: 44 bps in *16S* rRNA (pos. 1489–1532), 9 bps in NADH dehydrogenase subunit 2 (*ND2*) (pos. 4130–4139), 41 bps at the origin of replication (pos. 5182–5222), 45 bps in *COX1* (pos. 6756–6800), 41 bps at the end of *COX2* and beginning of the tRNA (pos. 7713–7753), 49 bps in *Cytb* (pos. 14,933–14,981), and ~137 bps in the control region (pos. ~16,395–16,532). The control region for *G. servalina* contains two kinds of repetitive sequences, RS2 and RS3 (Hoelzel et al. 1994, Hassanin 2016), the first containing a 74 bps motif for which *G. abyssinica* shares 39 bps, and two 81 bps motifs that are shared among both species. We did not compare RS3 motifs between the species due to poor alignment in this region for *G. abyssinica*.

The final nucleotide alignment for the 5-gene dataset consisted of 3305 bps for each of the 24 taxa; however, 15 taxa were missing three or four of the genes resulting

Figure 3: Phylogenetic tree for extant *Genetta* species and other viverrids using 3305 nucleotides of five mitochondrial genes (*Cytb*+*Dloop*+*12S*+*16S*+*COI*).

Black dots indicate well-supported nodes (BPP ≥ 0.95 , BS ≥ 70), nodal support values provided for nodes include Bayesian posterior probability and likelihood bootstrap. The position of the newly acquired sample of *Genetta abyssinica* (USNM 602624) is highlighted in dark gray. Outgroup taxa are presented in light gray text. Illustration of *G. abyssinica* adapted from figure 11 by artist Friedrich Carl Vogel as published in Rüppell (1835–1840).

in a final matrix with 41% missing data. Both BI and ML recovered support for the monophyly of *Genetta* [Bayesian posterior probabilities (BPP) = 1.0, bootstrap (BS) = 100; Figure 3]. Interspecific relationships within the genus were poorly resolved, including the relationship of *Genetta abyssinica* to the other species of *Genetta* (BPP = 0.98, BS = 64; Figure 3).

Phylogenetic analyses of the 1-gene (1140 bps of *Cytb*, 24 taxa) and 2-gene (1140 bps of *Cytb* and 584 bps of *Dloop*, 24 taxa) datasets also recovered support for the monophyly of *Genetta* (BPP = 1.0, BS = 100 and BPP = 1.0, BS = 99, respectively; Figure 4A and B). However, the relationship of *Genetta abyssinica* to other *Genetta* taxa was only supported with ML bootstrap analysis and not BPP (BPP = 0.57, BS = 70 and BPP = 0.91, BS = 81, respectively).

Our phylogenetic tree appeared to match the topology reported in Gaubert et al. (2004) and Gaubert and Begg (2007) with the exception of the placement of *Genetta felina* (Thunberg, 1811) [AY241901, currently identified as *Genetta maculata* (Gray, 1830) in GenBank], which was sister to *Genetta tigrina* (Schreber, 1776) (AY397705) in Gaubert and Begg (2007) but sister to *G. maculata* AY241913 (*G. maculata* AY241914, *G. tigrina* AY241889) in our analysis (Figure 3, light gray shading). In addition, the positions of *G. maculata*

(AY241913) and *G. maculata* (AY241914) were reversed in our phylogeny, with *G. maculata* AY241913 sister to (*G. maculata* AY241914, *G. tigrina* AY241889).

Discussion

Distribution of *Genetta abyssinica*

Our record provides the first verifiable documentation of *Genetta abyssinica* for the country of Djibouti in over 60 years. The single previous specimen for Djibouti is represented by a skin collected in 1954 by E. Chèdeville deposited in the Muséum National d'Histoire Naturelle, Paris, France (MNHN 1954-323). The only additional information provided beyond collector and year collected was a locality of "Somalie Française", or French Somalia, which until 1977 was the name used for the currently recognized country of The Republic of Djibouti (Clarke 1977). However, Laurent and Laurent (2002) stated, based on Chèdeville (in litt, 12 May 1992), that the specimen was most likely captured in the northern highlands, either in the Goda or in the Mabila Mountains. Laurent and Laurent

Figure 4: Phylogenetic tree for all extant *Genetta* species and seven outgroup taxa (not shown) generated using 1140 nucleotides of the cytochrome-b gene (A). Phylogenetic tree for *Genetta* species and seven outgroup taxa (not shown) using 1140 nucleotides of the cytochrome-b gene and 584 nucleotides of the *Dloop* gene (B). Black dots indicate well-supported nodes (BPP ≥ 0.95, BS ≥ 70), nodal support values provided for nodes include Bayesian posterior probability and likelihood bootstrap. The position of the newly acquired sample of *Genetta abyssinica* (USNM 602624) is highlighted in dark gray. The conflicting placement of *G. felina* (AY241901) is highlighted in light gray.

(2002) go on to state that *G. abyssinica* is present in the country, although probably rare to very rare. Despite this assertion, *G. abyssinica* does not have any special protection and is currently recognized by the International Union for Conservation of Nature (IUCN) as Data Deficient (Gaubert et al. 2016), limiting our ability to draw any meaningful conclusions about its conservation status in Djibouti. Künzel et al. (2000) questioned the presence of this genet in Djibouti. Interestingly, it appears that despite being considered a non-forest species of genet, current records of *G. abyssinica* from Djibouti are restricted to the high elevation montane juniper forests of the Goda and the Mabla Mountains, including the Forêt du Day. Of course, additional sampling of lowland habitats contiguous with those that have existing records of *G. abyssinica* such as the Ethiopian xeric grasslands and shrublands (Olson et al. 2001) along coastal Somalia (BMNH 34.9.14.20; Figure 1) are vital to understanding the distribution of this species in Djibouti. Although not exhaustive, 24 live-trap nights spent in this habitat in and around Camp Lemmonier (11°32'30"N, 43°10'00"E; 5 m a.s.l.) resulted in the capture of a single white-tailed mongoose but no genets, although animal control agents reported capturing unknown genet species on the base. Additional carnivores observed in this area at the time of trapping included Ruppell's fox *Vulpes rueppelli* (Schinz, 1825) and domestic cats.

The 20 records of *Genetta abyssinica* with localities precise enough to allow for coordinate assignment (see Papeş and Gaubert 2007 and Diaz Behrens and Van Rompaey 2002 for tables of records) are distributed across six major ecoregions: East Sudanian savanna (n=1); Ethiopian montane grasslands and woodlands (5); Ethiopian montane moorlands (9); Ethiopian xeric grasslands and shrublands (2, including our specimen); Sahelian Acacia Savanna (2); Somali *Acacia-Commiphora* Bushlands and thickets (1). Although identifying suitable ecoregions based on these records are confounded by imprecise locality information and the coarse resolution of the ecoregions themselves (Olson et al. 2001), such information provides a starting point for continued surveys of this species. Only through additional, verifiable records in the form of vouchers, with precise locality data will we be able to truly delimit the ecologic and geographic limits of *G. abyssinica* across the Horn of Africa.

Phylogenetic position of *Genetta abyssinica*

Our phylogenetic results provided the first exhaustive molecular phylogeny for all 14 currently recognized species of *Genetta* (Gaubert et al. 2004, Gaubert 2013) and indicate that *Genetta abyssinica* may be the sister taxa

to all other genets (Figures 3 and 4). Although statistical support for this relationship between *G. abyssinica* and all other *Genetta* varied across the different analyses, if this relationship holds true it would differ from that proposed by Gaubert et al. (2002) based on morphological characters alone. Using these morphological characters, Gaubert et al. (2004) hypothesized that *G. abyssinica* would be sister to *Genetta thierryi*, and a clade sister to all other *Genetta* (see Figure 3 in Gaubert et al. 2004). The potential lack of phylogenetic support for a sister relationship between *G. abyssinica* and *G. thierryi* would be surprising given the fact that they share several morphological synapomorphies (Gaubert et al. 2002). However, the proximity of *G. abyssinica* to the oyans (*Poiana*) and *G. thierryi* is not surprising given the shared plesiomorphic characters between these species (Gaubert et al. 2002). The overall lack of consistent statistical support for the placement of *G. abyssinica* in the *Genetta* phylogeny as well as limited support for additional internal nodes indicates that additional data, taxa and molecular markers are still necessary to resolve the evolutionary relationships among extant genets. Our results, although not consistently supported statistically, provide a potential alternative hypothesis for future testing, specifically that *G. abyssinica* is sister to all other species of genets, including *G. thierryi*.

The phylogenetic placement of *Genetta abyssinica* has consequences for interpreting the biogeographic history of this complex and diverse group of African small carnivores. In particular, a lack of phylogenetic support for the sister relationship to *Genetta thierryi* implies that there would be two independent "exits" of genets into African open habitats from the rain-forest adapted ancestor (Gaubert et al. 2004). However, in light of recent records of *G. abyssinica* in forested habitats (Diaz Behrens and Van Rompaey 2002, this article), perhaps assuming it is truly an "open habitat" species is a bit premature; without additional records with good locality information, we are left with weak inference into this species ecology and habitat requirements. Nevertheless, *G. abyssinica* is clearly not a rain forest species and therefore does represent a divergence from the estimated ancestral state of *Genetta* (Gaubert et al. 2004). Although a number of studies address the phylogenetic relationships of *Genetta*, there still appears to be a need for additional systematic studies of this group using nuclear markers or next-generation approaches.

Ecology of *Genetta abyssinica* and implications for conservation

This article highlights the need for continued surveys and collecting of vouchered specimens of small carnivores

such as *Genetta abyssinica* in order to better understand both their evolutionary history and ecological requirements. The need for vouchers for these morphologically complex species is further highlighted by the recent report of a road-killed *G. abyssinica* from Ethiopia (Balakrishnan and Afework 2008), which subsequent inspections confirmed was actually *Genetta genetia* (Linnaeus, 1758) (Gaubert et al. 2009). Without the availability of a voucher for subsequent re-identification, this record could have been perpetuated as a new occurrence for *G. abyssinica* in Ethiopia, potentially confounding the ability to determine the species range and habitat requirements. Collection of a single individual allowed us to increase our understanding of this species from an evolutionary, ecological and biological standpoint, providing materials for use in future studies including pathogen exploration and ecomorphological analysis of postcranial materials. This record provides information on a misunderstood and little studied species of mammal from an area ecologically important to the critically endangered Djibouti Francolin, bolstering the need to protect this fragile yet important wooded ecosystem. Additional surveys of both montane forested regions (e.g. the Mabila Mountains) and lowland desert scrub (e.g. south-east Djibouti) should provide further information on the geographic distribution of this species in Djibouti, facilitating appropriate management and conservation of *G. abyssinica*.

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