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Highly diversified coronaviruses in neotropical bats

Victor Max Corman,[1] Andrea Rasche,[1,2] Thierno Diawo Diallo,[1] Veronika M. Cottontail,[3] Andreas Stöcker,[4] Breno Frederico de Carvalho Dominguez Souza,[4] Jefferson Ivan Corrêa,[4] Aroldo José Borges Carneiro,[5] Carlos Roberto Franke,[5] Martina Nagy,[6] Markus Metz,[7] Mirjam Knörnschild,[3] Elisabeth K. V. Kalko,[3,8]† Simon J. Ghanem,[9] Karen D. Sibaja Morales,[10] Egoitz Salsamendi,[3,11] Manuel Spínola,[10] Georg Herrler,[2] Christian C. Voigt,[9] Marco Tschapka,[3,8] Christian Drosten[1] and Jan Felix Drexler[1]

Correspondence
Christian Drosten
drosten@virology-bonn.de
Jan Felix Drexler
drexler@virology-bonn.de

[1]Institute of Virology, University of Bonn Medical Centre, Bonn, Germany

[2]University of Veterinary Medicine Hannover, Foundation, Hannover, Germany

[3]Institute of Experimental Ecology, University of Ulm, Ulm, Germany

[4]Infectious Diseases Research Laboratory, University Hospital Professor Edgard Santos, Federal University of Bahia, Salvador, Brazil

[5]School of Veterinary Medicine, Federal University of Bahia, Salvador, Brazil

[6]Museum für Naturkunde, Leibniz Institute for Research on Evolution and Biodiversity, Berlin, Germany

[7]Fondazione Edmund Mach, Research and Innovation Centre, Department of Biodiversity and Molecular Ecology, S. Michele all'Adige, Italy

[8]Smithsonian Tropical Research Institute, Balboa, Panama

[9]Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany

[10]Instituto Internacional en Conservación y Manejo de Vida Silvestre, Universidad Nacional, Heredia, Costa Rica

[11]Department of Zoology and Animal Cell Biology, University of the Basque Country, Bilbao, The Basque Country

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Bats host a broad diversity of coronaviruses (CoVs), including close relatives of human pathogens. There is only limited data on neotropical bat CoVs. We analysed faecal, blood and intestine specimens from 1562 bats sampled in Costa Rica, Panama, Ecuador and Brazil for CoVs by broad-range PCR. CoV RNA was detected in 50 bats representing nine different species, both frugivorous and insectivorous. These bat CoVs were unrelated to known human or animal pathogens, indicating an absence of recent zoonotic spill-over events. Based on *RNA-dependent RNA polymerase* (*RdRp*)-based grouping units (RGUs) as a surrogate for CoV species identification, the 50 viruses represented five different alphacoronavirus RGUs and two betacoronavirus RGUs. Closely related alphacoronaviruses were detected in *Carollia perspicillata* and *C. brevicauda* across a geographical distance exceeding 5600 km. Our study expands the knowledge on CoV diversity in neotropical bats and emphasizes the association of distinct CoVs and bat host genera.

INTRODUCTION

Coronaviruses (CoVs) belong to the order *Nidovirales*, family *Coronaviridae*, subfamily *Coronavirinae* and are enveloped viruses with a positive-sense single-stranded RNA genome. They are classified into four genera: *Alphacoronavirus*, *Betacoronavirus*, *Gammacoronavirus* and *Deltacoronavirus* (Adams & Carstens, 2012).

†Deceased.

The GenBank/EMBL/DDBJ accession numbers for the coronavirus sequences reported in this paper are JQ731775–JQ731800 and KC633193–KC633197.

Two supplementary tables are available with the online version of this paper.

In the aftermath of the severe acute respiratory syndrome (SARS)-epidemic in 2002/2003 caused by CoV of likely bat origin (Lau *et al.*, 2005), a large number of novel bat CoVs were described (Calisher *et al.*, 2006). The majority of these CoVs originated from African, Asian and European bats (Chu *et al.*, 2006; Drexler *et al.*, 2010, 2011; Gloza-Rausch *et al.*, 2008; Pfefferle *et al.*, 2009; Poon *et al.*, 2005; Quan *et al.*, 2010; Tang *et al.*, 2006; Tong *et al.*, 2009). In addition to SARS-CoV, four human coronaviruses (HCoVs), termed HCoV-OC43, -229E, -NL63 and -HKU1 are known (Drosten *et al.*, 2003; Fouchier *et al.*, 2004; Gaunt *et al.*, 2010; Hamre & Procknow, 1966; McIntosh *et al.*, 1967; van der Hoek *et al.*, 2004; Weiss & Navas-Martin, 2005; Woo *et al.*, 2005). Recently, a sixth HCoV was described, causing illness in at least 49 confirmed cases by 29 May 2013 (WHO, 29 May 2013; Zaki *et al.*, 2012). Close relatives of this betacoronavirus termed MERS-CoV and of HCoV-229E exist in Old World bats and HCoV-NL63 could be grown in immortalized bat cells (Annan *et al.*, 2013; de Groot *et al.*, 2013; Drexler *et al.*, 2010; Huynh *et al.*, 2012; Lau *et al.*, 2005; Pfefferle *et al.*, 2009), demonstrating the zoonotic potential of previously reservoir-bound bat CoVs. The recent description of a bat CoV related to MERS-CoV in Mexican bats (Anthony *et al.*, 2013) emphasized the relevance of investigating neotropical bats for CoVs.

Bats constitute up to 60 % of the local mammalian fauna in pristine neotropical ecosystems and neotropical bats represent nearly 30 % of the worldwide bat species (351 out of 1152) (IUCN, 2012; Rex *et al.*, 2008; Schipper *et al.*, 2008). Six of the 18 extant bat families are endemic to the Neotropics and only three occur both in the New and Old World. Neotropical bats occupy a broad range of ecological niches including insectivorous, nectarivorous, carnivorous, sanguivorous and frugivorous feeding habits (Masters, 2006; Rex *et al.*, 2008; Simmons, 2005a; Teeling *et al.*, 2005). This species richness contrasts with the scarce information on neotropical bat CoVs. There are only two studies on bat CoVs from the Neotropics, one from Trinidad and Tobago yielding two highly diversified alphacoronaviruses (Carrington *et al.*, 2008) and a recently published second one from Mexico yielding alpha and betacoronaviruses summarized in 13 different clades (Anthony *et al.*, 2013). From the neighbouring temperate northern American areas, additional bat alphacoronavirus clades have been described (Dominguez *et al.*, 2007; Donaldson *et al.*, 2010; Huynh *et al.*, 2012; Misra *et al.*, 2009; Osborne *et al.*, 2011).

To increase our knowledge on neotropical CoVs, we analysed 1866 faecal, blood and intestine specimens from 1560 individual bats sampled in four neotropical countries. Seven novel alpha- and betacoronavirus clades were detected.

RESULT AND DISCUSSION

The samples comprised 1868 specimens from 1562 individual bats collected between 2008 and 2012 in Costa Rica, Panama, Ecuador and Brazil. Table 1 provides details of the number of specimens per bat species and Fig. 1(a) shows sampled countries. Table S1 (available in JGV Online) provides the GPS coordinates of specific sampling sites and individual permit numbers. As shown in Fig. 1(b), these specimens represented 54 different bat species from seven of the nine families within the phylogeny of neotropical bats. Table 1 shows that CoV RNA was detected by nested reverse-transcription polymerase chain reaction (RT-PCR) targeting the *RNA-dependent RNA polymerase* (*RdRp*) in 50 specimens from nine different bat species (2.7 % of the total samples). In three out of four countries, bat CoVs were detected, while all samples from Ecuador were negative. This was likely due to the smaller sample size from this country. All but one of the detections were made in faecal or intestinal tissue specimens (2.8 % of the total faecal/intestinal specimens). Additionally, one blood specimen from an *Artibeus jamaicensis* bat tested positive (0.9 % of all blood specimens). No faecal specimen was available from this individual. For all PCR screening amplicons, extension of the partial *RdRp* fragment to 816 nt was attempted as described previously (Drexler *et al.*, 2010). All CoV sequences were submitted to GenBank under accession numbers JQ731775–JQ731800 and KC633193–KC633197. Table S2 provides details on accession numbers of individual CoVs.

Results of a Bayesian phylogenetic analysis based on the 816 nt *RdRp* fragment are given in Fig. 2(a). Because this larger fragment was not available for most previously described CoVs and could not be obtained for two alphacoronaviruses from this study, the 404 nt *RdRp* fragment generated by our and most other published CoV screening assays was also analysed. Fig. 2(b) shows the phylogeny of this shorter fragment for the genus *Alphacoronavirus*. The novel bat CoVs clustered as eight independent branches in the *Alpha-* and *Betacoronavirus* genera and were unrelated to any known Old World bat CoV. Table 2 shows the high diversification within the neotropical bat CoVs which ranged from 6.6 to 37.5 % amino acid sequence distance in the 816 nt *RdRp* fragments. As shown in Table 3, the novel CoVs were also unrelated to any known CoV from humans or other animals, with amino acid sequence distances ranging from 12.1 to 39.0 % in comparison with all defined CoV species. This contrasted with Old World bat CoVs for which zoonotic transmission to humans likely occurred, exemplified by SARS-related viruses in rhinolophid bats in Asia (Drexler *et al.*, 2010; Lau *et al.*, 2005) or HCoV-229E-related viruses in hipposiderid bats in Africa (Pfefferle *et al.*, 2009).

We previously proposed a simplified CoV classification into *RdRp*-based grouping units (RGU) separated by >4.8 % amino acid (aa) distance for alphacoronaviruses and >6.3 % for betacoronaviruses in the translated 816 nt *RdRp* fragment (Drexler *et al.*, 2010). Based on these criteria, the novel CoVs could be classified as five *Alphacoronavirus* RGUs and two *Betacoronavirus* RGUs.

Table 1. Bat species tested for coronaviruses

Family	Species	No. of samples			Total PCR positive (%) per specimen	Sampling site (year)†
		Faeces	Blood	Intestine		
Emballonuridae	*Peropteryx kappleri*	5				CRC(2010)
	Rhynchonycteris naso	1				ECU(2010)
	Saccopteryx bilineata	114				PAN(2010/2011); CRC(2010)
	Saccopteryx leptura	1				PAN(2011)
Phyllostomidae	*Anoura geoffroyi*	101			4 (3.96) faeces	CRC(2010*)
	Artibeus jamaicensis‡	295	68		3 (1.02) faeces	PAN(2010*/2011); ECU(2010)
	Artibeus lituratus	41	13		1 (2.44) faeces, 1 (7.69) blood	PAN(2010*/2011*); ECU(2010)
	Artibeus obscurus	2				ECU(2010)
	Artibeus phaeotis	4	1			PAN(2011)
	Artibeus watsoni	2	2			PAN(2011)
	Carollia brevicauda	3		104	6 (5.77) intestine	BRA(2009*); ECU(2010)
	Carollia castanea	34	11			PAN(2010/2011); CRC(2010); ECU(2010)
	Carollia perspicillata	283	1	175	14 (8.00) intestine, 7 (2.47) faeces	BRA(2009*); CRC(2010*/2011*/2012*); PAN(2010/2011); ECU(2010)
	Carollia spec.			15		BRA(2009)
	Chrotopterus auritus	1				ECU(2010)
	Desmodus rotundus		1	29		BRA(2008/2009); PAN(2011)
	Enchisthenes hartii	3				CRC(2010)
	Glossophaga commissarisi	3				CRC(2010)
	Glossophaga soricina	47		2		BRA(2009); PAN(2010/2011); CRC(2010/2012)
	Lampronycteris brachyotis	2				CRC(2012)
	Lonchorhina aurita			1		BRA(2009)
	Lonchophylla robusta	1				CRC(2012)
	Lophostoma brasiliense	2				PAN(2011)
	Lophostoma silvicolum	25	2			PAN(2010/2011); ECU(2010)
	Mesophylla macconnellii	1				ECU(2010)
	Micronycteris hirsuta	3				PAN(2010/2011)
	Micronycteris microtis	6				PAN(2010/2011)
	Micronycteris minuta	1	1			PAN(2011)
	Mimon crenulatum	10	1			PAN(2010/2011); ECU(2010)
	Phylloderma stenops	1	2			PAN(2011)
	Phyllostomus discolour	10			2 (20.00) faeces	PAN(2011*)
	Phyllostomus hastatus	5				PAN(2010/2011); ECU(2010)
	Phyllostomus elongatus	4				ECU(2010)
	Platyrrhinus brachycephalus	1				ECU(2010)
	Platyrrhinus helleri	1				PAN(2010)
	Platyrrhinus infuscus	2				ECU(2010)
	Rhinophylla pumilio	4				ECU(2010)
	Sturnira lilium	3				ECU(2010)
	Sturnira magna	3				ECU(2010)
	Tonatia saurophila	7				PAN(2010/2011); ECU(2010)
	Trachops cirrhosus	12	1	1		BRA(2009); PAN(2010/2011); ECU(2010)
	Uroderma bilobatum	32				PAN(2010/2011)/ ECU(2010)
	Vampyressa bidens	1				ECU(2010)
	Vampyressa thyone		1			PAN(2011)
	Vampyrodes caraccioli	5	4			PAN(2011)

Table 1. cont.

Family	Species	No. of samples			Total PCR positive (%) per specimen	Sampling site (year)†
		Faeces	Blood	Intestine		
Mormoopidae	*Pteronotus parnellii*	290	6	4	10 (3.45) faeces	PAN(2010/2011); CRC(2010*/2011*/2012*)
Noctilionidae	*Noctilio leporinus*	1				PAN(2011)
Vespertilionidae	*Myotis albescens*	2				ECU(2010)
	Myotis nigricans	7				PAN(2010/2011); ECU(2010)
	Rhogeessa tumida	3				PAN(2010); CRC(2012)
Molossoidea	*Eumops maurus*	1				ECU(2010)
	Molossus currentium			10	1 (10.00) intestine	BRA(2009*)
	Molossus molossus	1		1		BRA(2009); PAN(2010)
	Molossus rufus	2		17	1 (5.88) intestine	BRA(2009*); ECU(2010)
Natalidae	*Natalus lanatus*	5				CRC(2010/2012)
Total	**54 species, 1562 individual bats**	**1394**	**115**	**359**	**50 (2.68)**	

†CRC=Costa Rica, ECU=Ecuador, PAN=Panama, BRA=Brazil. A positive location is indicated by an asterisk; the year is given in parentheses.
‡Including three negative samples from *A. planirostris* summarized under *A. jamaicensis* according to (Simmons, 2005b).

Four of these five *Alphacoronavirus* RGUs were previously undefined and originated from bat species belonging to the genera *Phyllostomus*, *Artibeus* and *Anoura* in the Phyllostomidae family (shown according to the countries of origin in green and orange in Fig. 2a). In addition, the RGU defined by a previously described CoV from *Carollia perspicillata* from Trinidad and Tobago (Carrington *et al.*, 2008) was extended by novel *C. brevicauda* and *C. perspicillata* CoVs from Costa Rica and Brazil (shown in orange and pale blue in Fig. 2a). As shown in Table 2, the amino acid sequence distance within all known alphacoronaviruses from *Carollia* bats was only 1.1 %. Another novel *Alphacoronavirus* clade could be detected in *Molossus rufus* and *M. currentium* from Brazil (shown in pale blue in Fig. 2b). An RGU could not be defined because only the 404 nt *RdRp* fragment was available. Still, these two viruses differed by 6.8 % aa distance within this smaller sequence fragment, indicating they might constitute two separate RGUs. The novel *Betacoronavirus* RGUs differed from each other by 14.0–14.3 % aa sequence distance and were defined by CoVs detected in samples from *Pteronotus parnellii* and *C. perspicillata* (shown in orange in Fig. 2a).

A recent study on bat CoVs from Mexico (Anthony *et al.*, 2013) yielded alpha and betacoronaviruses summarized in 13 different clades whose phylogenetic position indicated relatedness to some of the bat CoVs described in this study. Because only short sequence fragments of 243 to 297 nt were available for these bat CoVs and because these sequences did not overlap with our *RdRp* fragments, these CoVs could not be included in our phylogenetic analyses. Still, consideration of the phylogeny and the bat hosts of these Mexican CoVs could indicate that some of these viruses were related to three of the nine RGUs we describe in this study, including the *Carollia* and *Artibeus* alphacoronavirus RGUs and the *Pteronotus* betacoronavirus RGU.

Some bat species are widely distributed across the Neotropics. As illustrated in Fig. 3, closely related alphacoronaviruses were detected in *C. perspicillata* from Brazil and Costa Rica, 5600 km apart. Since *C. perspicillata* does not migrate over long distances (Fleming & Heithaus, 1986; Kunz & Fenton, 2003), recent transmission events are unlikely to explain these findings. Interestingly, the same virus was also detected in other *Carollia* species including *C. brevicauda* and possibly related CoV sequences from *C. sowelli* and *C. perspicillata* from Mexico (Anthony *et al.*, 2013). This was compatible with SARS-related CoVs in different rhinolophid bat species from Europe and China and with alphacoronaviruses detected in vespertilionid bats of one genus across geographical distances exceeding 2000 km (Drexler *et al.*, 2010; Tang *et al.*, 2006). The host genus, rather than the host species, may therefore define the habitat of CoV species (Drexler *et al.*, 2010).

In addition to local species richness, ecological host factors such as feeding and roosting habits (Drexler *et al.*, 2011),

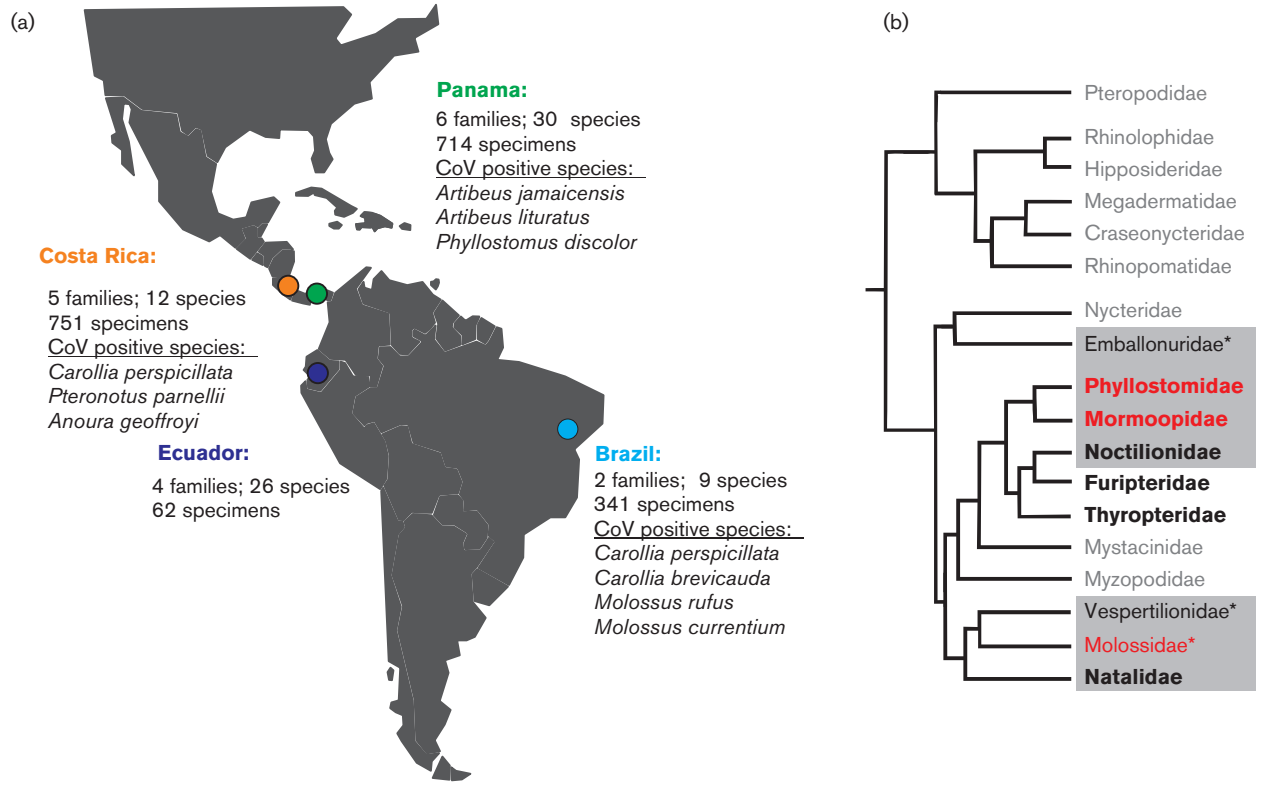

Fig. 1. Sampling sites and bat phylogeny. (a)The bat samples used in this study and their countries of origin are listed according to their species and families, with coronavirus-positive bat species additionally named. (b) Chiropteran phylogeny adapted from (Simmons, 2005a). Bat families only distributed in the Old World are shown in grey, those endemic to the Neotropics are printed boldface and those distributed in both the New and the Old World are marked with an asterisk. Families included in the analyses are framed with grey boxes and families testing positive for CoV in this study are given in red.

and contacts with other animals in the ecosystem likely influence the diversification and occurrence of bat CoVs (Parrish *et al.*, 2008). For example, closely related viruses were detected in nectarivorous *Glossophaga soricina* described previously (Carrington *et al.*, 2008) and omnivorous *Phyllostomus discolour* from our study (3.8 % aa distance in the 404 nt *RdRp* fragment). *P. discolour* is mainly nectarivorous and visits some of the same flowers as *G. soricina* (Kwiecinski, 2006), which may facilitate hypothetical exchange of viruses between the two bat genera. Sporadic observations of closely related CoVs in different bat species and even families were shown previously by us (Drexler *et al.*, 2010) and other groups (Anthony *et al.*, 2013; Lau *et al.*, 2010). It remains unclear whether ecological factors such as population density and feeding habits influence the exchange of viruses between different bat species and the co-segregation of hosts and viruses.

No bat CoVs closely related to HCoV-OC43, -HKU1 and -NL63 have so far been found. Huynh *et al.* (2012) recently described alphacoronaviruses from northern American bats that showed 12.9–17.6 % aa distance to HCoV-NL63 in a translated 675 nt fragment partially overlapping with the *RdRp* sequences generated in our study. Previous detections of alphacoronaviruses in Old World bats showed even lower sequence distances to HCoV-NL63 in the same 675 nt *RdRp* fragment, exemplified by 11.5 % aa distances of *Miniopterus* and *Nyctalus* bat CoVs (Drexler *et al.*, 2010). Furthermore, bat CoVs closely related to the other human alphacoronavirus, HCoV-229E, exist in African *Hipposideros* bats (Pfefferle *et al.*, 2009). These data jointly highlight the possibility that bat CoVs closely related to HCoV-NL63 may exist, but are yet to be described.

The nearly complete absence of neotropical bat CoVs more closely related to human pathogens could be due to lower chances of transmission, such as rare consumption of bats as bushmeat in the New World in contrast to the Old World tropics (Mickleburgh *et al.*, 2009; Setz & Sazima, 1987). However, the growing invasion and destruction of neotropical habitats (Dale *et al.*, 1994; Kolb & Galicia, 2012) may provide further exposure of humans to bats and their viruses, as exemplified by the emergence of Nipah virus in 1998 (Daszak *et al.*, 2001; Keesing *et al.*, 2010). The recent identifications of betacoronaviruses related to MERS-CoV in Mexican *Nyctinomops* (Anthony *et al.*,

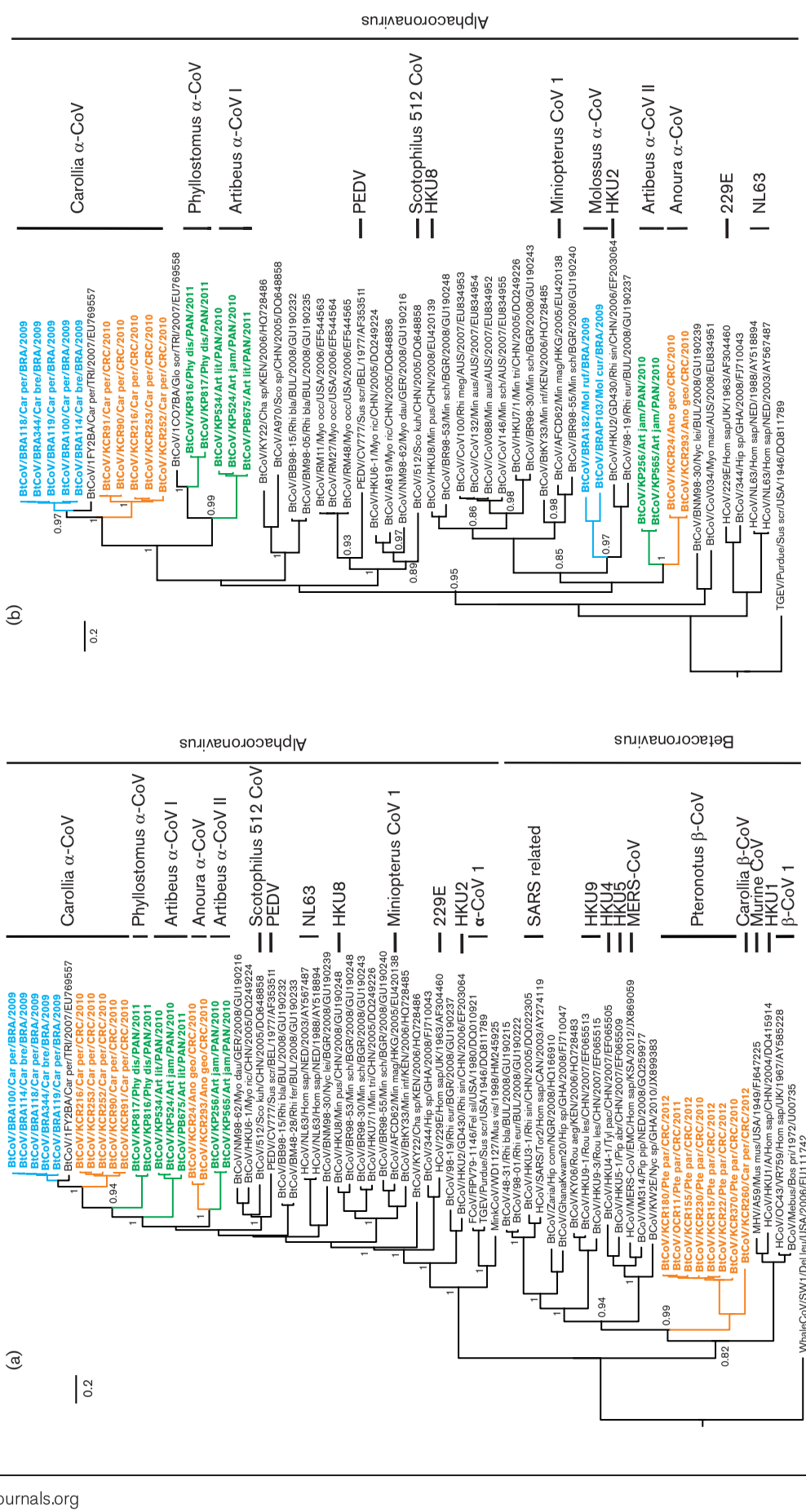

Fig. 2. Legend on following page.

Fig. 2. *RdRp*-based phylogeny including novel bat coronaviruses. Bayesian phylogenies of translated 816 nt (a) and 404 nt (b) gap-free *RNA-dependent RNA-polymerase (RdRp)* gene sequence fragments. For (a), a whale gammacoronavirus and for (b), transmissible gastroenteritis virus of swine (TGEV) were used as outgroups. For clarity of presentation, only posterior probability values above 0.7 are shown and values at crown positions were removed. Novel bat coronaviruses from this study are coloured according to their country of origin (pale blue=Brazil; orange=Costa Rica; green=Panama). New World bat coronaviruses described previously are shown in boldface. Taxa are named according to the following pattern: identification code/strain or isolate/typical host/country/collection year/accession number. The right-hand columns show novel Bat-CoV RGUs and designated CoV species used for further analysis. Car bre, *Carollia brevicauda*; Car per, *Carollia perspicillata*; Phy dis, *Phyllostomus discolour*; Art jam, *Artibeus jamaicensis*; Art lit, *Artibeus lituratus*; Min sch, *Miniopterus schreibersii*; Min pus, *Miniopterus pusillus*; Min tri, *Miniopterus tristis*; Min mag, *Miniopterus magnater*; Min inf, *Miniopterus inflatus*; Nyc lei, *Nyctalus leisleri*; Ano geo, *Anoura geoffroyi*; Rhi bla, *Rhinolophus blasii*; Rhi fer, *Rhinolophus ferrumequinum*; Myo dau, *Myotis daubentonii*; Myo ric, *Myotis ricketti*; Sco kuh, *Scotophilus kuhlii*; Sus scr, *Sus scrofa*; Cha sp., *Chaerephon* sp.; Hip sp, *Hipposideros* sp.; Hom sap, *Homo sapiens*; Rhi sin, *Rhinolophus sinicus*; Rhi eur, *Rhinolophus euryale*; Mus vis, *Mustela vison*; Hip com, *Hipposideros commersoni*; Fel sil, *Felis silvestris*; Rou les, *Rousettus leschenaulti*; Rou aeg, *Rousettus aegyptiacus*; Pte par, *Pteronotus parnellii*; Pip abr, *Pipistrellus abramus*; Tyl pac, *Tylonycteris pachypus*; Bos pri, *Bos primigenius*; Mus mus, *Mus musculus*; Del leu, *Delphinapterus leucas*; Glo sor, *Glossophaga soricina*; Myo occ, *Myotis occultus*; Rhi meg, *Rhinolophus megaphyllus*; Min aus, *Miniopterus australis*; Mol ruf, *Molossus rufus*.

2013), European *Pipistrellus* and African *Nycteris* (Annan *et al.*, 2013) bats highlight the relevance of studying the diversity of CoVs in bat reservoirs. It is important to note that actions aiming at eradication of bats as potential virus hosts may disrupt important ecological functions, e.g. pollination and natural pest reduction (Cleveland *et al.*, 2006; Kalka *et al.*, 2008).

The diversified ecology, a high number of co-existing bat species and their local abundance in relation to other mammalian species (Rex *et al.*, 2008), could make neotropical bats a leading receiver and spreader of viruses in neotropical ecosystems. For example, sanguivorous bats only exist in the Neotropics and could hypothetically facilitate viral host switches between bats and other mammals. This is exemplified by the detection of a small sequence fragment of bovine CoV in vampire bat faeces (Brandão *et al.*, 2008), which could hypothetically result from feeding on cattle. Further studies on bat CoV could therefore focus on animals with close bat contact, such as prey of vampire bats or feline, canine and non-human primate bat predators (Delpietro *et al.*, 1994; Rodriguez-Duran *et al.*, 2010; Souza *et al.*, 1997; Taylor & Lehman, 1997).

METHODS

We declare that all sampling and capture of wild animals as well as sample transfers were done with the proper wildlife permits and ethics clearances and complied with the current laws of host countries. Sampling was performed between 2008 and 2012 at 44 different sites in four countries (Fig. 1). The complete geographical coordinates of all sampling sites and corresponding sampling permits are given in Table S1. In Brazil and Costa Rica, bats were mainly caught in front of caves, while bat catching in Ecuador and Panama focused mainly in neotropical forests. No bat species were specifically targeted. In Costa Rica and Ecuador, bats were caught using mist nets and kept in individual cotton bags for a few minutes until examination. Faecal pellets produced in the meantime were taken directly from individual bags and stored in 500 µl of RNAlater RNA stabilization solution (Qiagen) until further processing. Fifty microlitres of the supernatants were suspended in 560 µl of buffer AVL from the Viral RNA mini kit (Qiagen) and processed according to the manufacturer's instructions. Blood samples were taken from Panamanian bats for an ecological study on blood parasites (Cottontail *et al.*, 2009). Depending on the available quantity, up to 50 µl of blood was

Table 2. Amino acid identities within neotropical bat coronaviruses

	Percentage amino acid identity across 272 amino acids within the translated 816 nt fragment*						
CoV RGU/clade	**Carollia α-CoV†**	**Phyllostomus α-CoV**	**Artibeus α-CoV I**	**Anoura α-CoV**	**Artibeus α-CoV II**	**Pteronotus β-CoV**	**Carollia β-CoV**
Carollia α-CoV†	98.9–100	92.3–93.4	86.4–86.8	85.7–86.4	83.5–83.8	66.9–67.6	65.1
Phyllostomus α-CoV		98.9–100	88.2–89.0	84.9–85.7	82.7–83.5	65.1–65.8	62.5–62.9
Artibeus α-CoV I			99.6–100	83.8	83.8–84.2	64.7–65.1	63.2
Anoura α-CoV				100	90.1	66.9	63.2
Artibeus α-CoV II					100	67.3–67.6	66.2
Pteronotus β-CoV						99.3–100	85.7–86
Carollia β-CoV							100

*Analyses were conducted in MEGA5 (Tamura *et al.*, 2011) using the pairwise deletion option.
†Including EU769557 described by Carrington *et al.* (2008).

Table 3. Amino acid identities of neotropical bat coronaviruses with designated CoV species

	Percentage amino acid identity across 272 amino acids within the translated 816 nt fragment*							
	Alpha CoV1‡	**PEDV§**	**Scotophilus 512 BtCoV‖**	**HKU2#**	**229E****	**NL63††**	**HKU8‡‡**	**Miniopterus BtCoV 1§§**
Carollia α-CoV†	77.6–78.3	85.3–85.7	82.7–83.5	79–79.4	80.1–80.9	83.5–84.2	84.6–85.3	83.8–84.2
Phyllostomus αCoV	76.8–77.9	83.5–84.2	81.6–82	78.7–78.7	81.6–82.4	82.0–82.7	85.3–86	84.9–85.7
Artibeus α-CoV I	78.3–78.7	84.2–84.6	82.7–83.1	79.8	80.5–80.9	82.7–83.1	84.2	84.2
Anoura αCoV	87.9–79.4	83.8	82	80.9	80.9	83.8	87.1	87.9
Artibeus α-CoV II	80.1–80.5	86	83.8	79.8	79.8	82	84.2	84.6
Pteronotus β-CoV	70.2–71	68.4–68.7	66.9–67.3	68.4–68.7	64.7–65.1	65.1–65.4	66.5–66.9	64–64.3
Carollia β-CoV	68.4–68.7	66.5	65.8	66.5	62.9	61	63.2	64
	BetaCoV 1‖‖‖	**HKU1##**	**Murine CoV*****	**HKU4†††**	**HKU5‡‡‡**	**HKU9§§§**	**SARS related‖‖‖‖**	**MERS-CoV###**
Carollia α-CoV	62.1–62.5	61.8	61.8–62.1	64.3–64.7	64.0–64.7	63.6–64.7	63.6–64.3	65.1–65.4
Phyllostomus α-CoV	62.1–62.9	61.8–61.4	62.1–62.5	62.5–62.9	62.5–62.9	63.6–65.1	62.9–63.6	63.2–63.6
Artibeus α-CoV I	62.5	61	61	61.8	61.8	62.5–63.6	61.8–62.1	61.8
Anoura α-CoV	64–64.3	63.6	62.9	63.6	64.7	62.5–63.2	63.6	63.6
Artibeus α-CoV II	64.7–65.1	64	63.2	64.3	65.1	63.2–64.0	66.2–66.5	64.3
Pteronotus β-CoV	75–75.7	74.3–74.6	73.2–73.5	77.2–77.6	77.2–77.6	79.4–80.1	77.6–77.9	76.8–77.2
Carollia β-CoV	73.5–73.9	73.5	73.2	76.5	77.2	76.8–77.2	77.2–77.9	77.2

*Analyses were conducted in MEGA5 (Tamura *et al.*, 2011) using the pairwise deletion option.
†Including EU769557 described by Carrington *et al.* (2008).
GenBank accession numbers:
‡DQ010921, DQ811789 Alpha CoV1.
§AF353511 PEDV.
‖DQ648858 Scotophilus 512 BtCoV.
#EF203064 HKU2.
**AF304460 229E.
††AY567487, AY518894 NL63.
‡‡GU190248 HKU8.
§§EU420138 Miniopterus BtCoV 1.
‖‖‖AY585228, U00735 BetaCoV 1.
##DQ415914 HKU1.
***FJ647225 Murine CoV.
†††EF065505 HKU4.
‡‡‡EF065509 HKU5.
§§§EF065513, EF065515 HKU9.
‖‖‖‖DQ022305, AY274119 SARS related.
###JX869059 MERS-CoV.

similarly extracted. For some of the Panamanian bats sampled in 2011, faecal samples were additionally available and processed as described above. The Brazilian specimens were sampled during activities on prevention of rabies (Carneiro *et al.*, 2010). Bats were caught at roosts using mist nets, killed with ether and transported on ice to the laboratory where bats were typed and dissected. Approximately 30 mg of intestinal tissue was homogenized in a bead mill, followed by extraction of RNA using the RNeasy kit (Qiagen). Elution volumes were 50 µl for faecal and blood specimens and 100 µl for tissue specimens.

RT-PCR covering the subfamily *Coronavirinae* was done as described previously (de Souza Luna *et al.*, 2007). The 455 bp amplicons from the *RNA-dependent RNA polymerase* (*RdRp*) generated by the screening RT-PCR (404 nt after exclusion of PCR primers) were extended towards the 5′-end of the genome using virus-specific reverse primers and upstream consensus forward primers, as described previously (Drexler *et al.*, 2010). Translated nucleic acid alignments containing the novel viruses and CoV reference strains were done using the BLOSUM algorithm in the MEGA5 software package (Tamura *et al.*, 2011). The final datasets used for phylogenetic analyses consisted of 816 and 404 nt gap-free coding *RdRp* alignments. Bayesian phylogenies were conducted with MrBayes v3.1 using the translated nucleotide sequences and a WAG amino acid substitution model over 4 000 000 generations sampled every 100 steps. The resulting 40 000 final trees were annotated using a burn-in of 10 000 in TreeAnnotator V1.5 and visualized with FigTree v1.4 from the BEAST package (Drummond & Rambaut, 2007; Ronquist & Huelsenbeck, 2003).

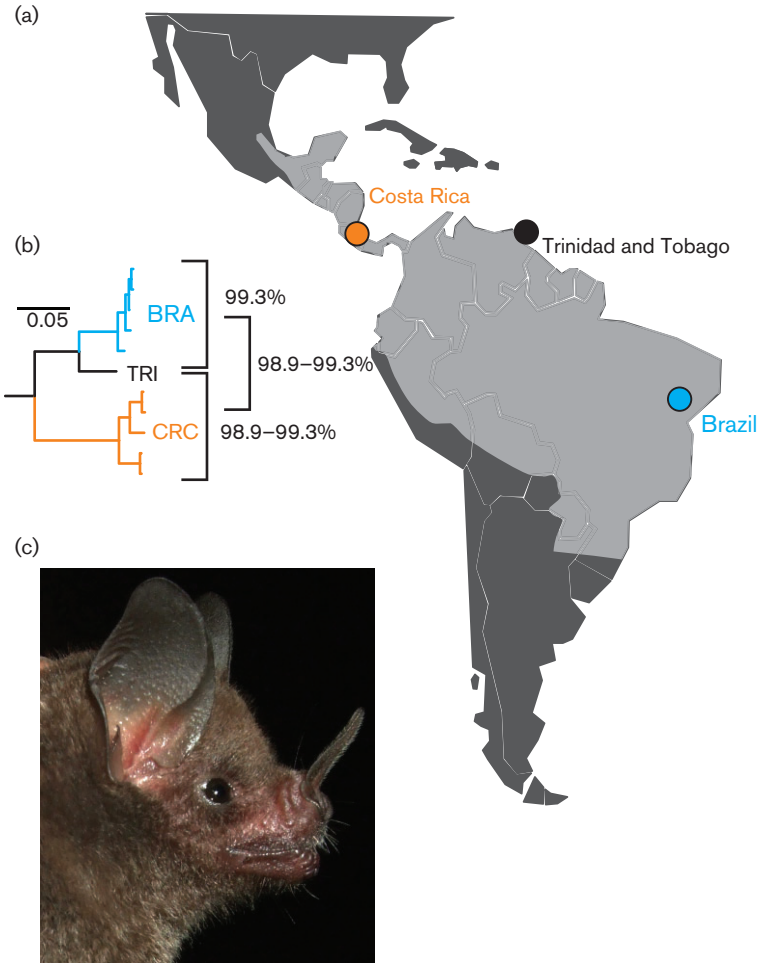

Fig. 3. *Carollia perspicillata* distribution and detection of related alphacoronaviruses. (a) Distribution of *Carollia perspicillata* adapted from the *IUCN Red List* (IUCN, 2012) is shown in grey. Sampling sites with detection of *Carollia* alphacoronaviruses are marked with dots. (b) Extract of the coronavirus phylogeny shown in Fig. 2 representing the *Carollia* alphacoronavirus clade, including two viruses from Brazilian *C. brevicauda*. CoV amino acid identities between Trinidad and Tobago, Panama and Brazil are shown next to the brackets. (c) *C. perspicillata* caught in Costa Rica (photo by A. R.).

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REFERENCES

Adams, M. J. & Carstens, E. B. (2012). Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2012). *Arch Virol* **157**, 1411–1422.

Annan, A., Baldwin, H. J., Corman, V. M., Klose, S. M., Owusu, M., Nkrumah, E. E., Badu, E. K., Anti, P., Agbenyega, O. & other authors (2013). Human betacoronavirus 2c EMC/2012–related viruses in bats, Ghana and Europe. *Emerg Infect Dis* **19**, 456–459.

Anthony, S. J., Ojeda-Flores, R., Rico-Chávez, O., Navarrete-Macias, I., Zambrana-Torrelio, C. M., Rostal, M. K., Epstein, J. H., Tipps, T., Liang, E. & other authors (2013). Coronaviruses in bats from Mexico. *J Gen Virol* **94**, 1028–1038.

Brandão, P. E., Scheffer, K., Villarreal, L. Y., Achkar, S., Oliveira, R. N., Fahl, W. O., Castilho, J. G., Kotait, I. & Richtzenhain, L. J. (2008). A coronavirus detected in the vampire bat *Desmodus rotundus*. *Braz J Infect Dis* **12**, 466–468.

Calisher, C. H., Childs, J. E., Field, H. E., Holmes, K. V. & Schountz, T. (2006). Bats: important reservoir hosts of emerging viruses. *Clin Microbiol Rev* **19**, 531–545.

Carneiro, A. J. B., Franke, C. R., Stocker, A., Dos Santos, F., Ungar de Sa, J. E., Moraes-Silva, E., Alves, J. N., Brunink, S., Corman, V. M. & other authors (2010). Rabies virus RNA in naturally infected vampire bats, northeastern Brazil. *Emerg Infect Dis* **16**, 2004–2006.

Carrington, C. V., Foster, J. E., Zhu, H. C., Zhang, J. X., Smith, G. J., Thompson, N., Auguste, A. J., Ramkissoon, V., Adesiyun, A. A. & Guan, Y. (2008). Detection and phylogenetic analysis of group 1 coronaviruses in South American bats. *Emerg Infect Dis* **14**, 1890–1893.

Chu, D. K., Poon, L. L., Chan, K. H., Chen, H., Guan, Y., Yuen, K. Y. & Peiris, J. S. (2006). Coronaviruses in bent-winged bats (Miniopterus spp.). *J Gen Virol* **87**, 2461–2466.

Cleveland, C. J., Betke, M., Federico, P., Frank, J. D., Hallam, T. G., Horn, J., López, J. D., Jr, McCracken, G. F., Medellin, R. A. & other authors (2006). Economic value of the pest control service provided by Brazilian free-tailed bats in south-central Texas. *Front Ecol Environ* **4**, 238–243.

Cottontail, V. M., Wellinghausen, N. & Kalko, E. K. (2009). Habitat fragmentation and haemoparasites in the common fruit bat, *Artibeus jamaicensis* (Phyllostomidae) in a tropical lowland forest in Panamá. *Parasitology* **136**, 1133–1145.

Dale, V. H., Pearson, S. M., Offerman, H. L. & O'Neill, R. V. (1994). Relating patterns of land-use change to faunal biodiversity in the Central Amazon. *Conserv Biol* **8**, 1027–1036.

Daszak, P., Cunningham, A. A. & Hyatt, A. D. (2001). Anthropogenic environmental change and the emergence of infectious diseases in wildlife. *Acta Trop* **78**, 103–116.

de Groot, R. J., Baker, S. C., Baric, R. S., Brown, C. S., Drosten, C., Enjuanes, L., Fouchier, R. A., Galiano, M., Gorbalenya, A. E. & other authors (In press). Middle East Respiratory Syndrome Coronavirus (MERS-CoV); Announcement of the Coronavirus Study Group. *J Virol.*

de Souza Luna, L. K., Heiser, V., Regamey, N., Panning, M., Drexler, J. F., Mulangu, S., Poon, L., Baumgarte, S., Haijema, B. J. & other authors (2007). Generic detection of coronaviruses and differentiation at the prototype strain level by reverse transcription-PCR and nonfluorescent low-density microarray. *J Clin Microbiol* **45**, 1049–1052.

Delpietro, H., Konolsaisen, F., Marchevsky, N. & Russo, G. (1994). Domestic cat predation on vampire bats (*Desmodus rotundus*) while foraging on goats, pigs, cows and human beings. *Appl Anim Behav Sci* **39**, 141–150.

Dominguez, S. R., O'Shea, T. J., Oko, L. M. & Holmes, K. V. (2007). Detection of group 1 coronaviruses in bats in North America. *Emerg Infect Dis* **13**, 1295–1300.

Donaldson, E. F., Haskew, A. N., Gates, J. E., Huynh, J., Moore, C. J. & Frieman, M. B. (2010). Metagenomic analysis of the viromes of three North American bat species: viral diversity among different bat species that share a common habitat. *J Virol* **84**, 13004–13018.

Drexler, J. F., Gloza-Rausch, F., Glende, J., Corman, V. M., Muth, D., Goettsche, M., Seebens, A., Niedrig, M., Pfefferle, S. & other authors (2010). Genomic characterization of severe acute respiratory syndrome-related coronavirus in European bats and classification of coronaviruses based on partial RNA-dependent RNA polymerase gene sequences. *J Virol* **84**, 11336–11349.

Drexler, J. F., Corman, V. M., Wegner, T., Tateno, A. F., Zerbinati, R. M., Gloza-Rausch, F., Seebens, A., Müller, M. A. & Drosten, C. (2011). Amplification of emerging viruses in a bat colony. *Emerg Infect Dis* **17**, 449–456.

Drosten, C., Günther, S., Preiser, W., van der Werf, S., Brodt, H. R., Becker, S., Rabenau, H., Panning, M., Kolesnikova, L. & other authors (2003). Identification of a novel coronavirus in patients with severe acute respiratory syndrome. *N Engl J Med* **348**, 1967–1976.

Drummond, A. J. & Rambaut, A. (2007). BEAST: Bayesian evolutionary analysis by sampling trees. *BMC Evol Biol* **7**, 214.

Fleming, T. H. & Heithaus, E. R. (1986). Seasonal foraging behavior of the frugivorous bat *Carollia perspicillata*. *J Mammal* **67**, 660–671.

Fouchier, R. A., Hartwig, N. G., Bestebroer, T. M., Niemeyer, B., de Jong, J. C., Simon, J. H. & Osterhaus, A. D. (2004). A previously undescribed coronavirus associated with respiratory disease in humans. *Proc Natl Acad Sci U S A* **101**, 6212–6216.

Gaunt, E. R., Hardie, A., Claas, E. C., Simmonds, P. & Templeton, K. E. (2010). Epidemiology and clinical presentations of the four human coronaviruses 229E, HKU1, NL63, and OC43 detected over 3 years using a novel multiplex real-time PCR method. *J Clin Microbiol* **48**, 2940–2947.

Gloza-Rausch, F., Ipsen, A., Seebens, A., Göttsche, M., Panning, M., Drexler, J. F., Petersen, N., Annan, A., Grywna, K. & other authors (2008). Detection and prevalence patterns of group I coronaviruses in bats, northern Germany. *Emerg Infect Dis* **14**, 626–631.

Hamre, D. & Procknow, J. J. (1966). A new virus isolated from the human respiratory tract. *Proc Soc Exp Biol Med* **121**, 190–193.

Huynh, J., Li, S., Yount, B., Smith, A., Sturges, L., Olsen, J. C., Nagel, J., Johnson, J. B., Agnihothram, S. & other authors (2012). Evidence supporting a zoonotic origin of human coronavirus strain NL63. *J Virol* **86**, 12816–12825.

IUCN (2012). IUCN red list of threatened species. Version 2012.1. www.iucnredlist.org

Kalka, M. B., Smith, A. R. & Kalko, E. K. (2008). Bats limit arthropods and herbivory in a tropical forest. *Science* **320**, 71.

Keesing, F., Belden, L. K., Daszak, P., Dobson, A., Harvell, C. D., Holt, R. D., Hudson, P., Jolles, A., Jones, K. E. & other authors (2010). Impacts of biodiversity on the emergence and transmission of infectious diseases. *Nature* **468**, 647–652.

Kolb, M. & Galicia, L. (2012). Challenging the linear forestation narrative in the Neo-tropic: regional patterns and processes of deforestation and regeneration in southern Mexico. *Geogr J* **178**, 147–161.

Kunz, T. H. & Fenton, M. B. (2003). *Bat Ecology*. Chicago, IL: University of Chicago Press.

Kwiecinski, G. G. (2006). *Phyllostomus discolor*. *Mamm Species* **801**, 1–11.

Lau, S. K., Woo, P. C., Li, K. S., Huang, Y., Tsoi, H. W., Wong, B. H., Wong, S. S., Leung, S. Y., Chan, K. H. & Yuen, K. Y. (2005). Severe acute respiratory syndrome coronavirus-like virus in Chinese horseshoe bats. *Proc Natl Acad Sci U S A* **102**, 14040–14045.

Lau, S. K., Poon, R. W., Wong, B. H., Wang, M., Huang, Y., Xu, H., Guo, R., Li, K. S., Gao, K. & other authors (2010). Coexistence of different genotypes in the same bat and serological characterization of Rousettus bat coronavirus HKU9 belonging to a novel Betacoronavirus subgroup. *J Virol* **84**, 11385–11394.

Masters, P. S. (2006). The molecular biology of coronaviruses. *Adv Virus Res* **66**, 193–292.

McIntosh, K., Dees, J. H., Becker, W. B., Kapikian, A. Z. & Chanock, R. M. (1967). Recovery in tracheal organ cultures of novel viruses from patients with respiratory disease. *Proc Natl Acad Sci U S A* **57**, 933–940.

Mickleburgh, S., Waylen, K. & Racey, P. (2009). Bats as bushmeat: a global review. *Oryx* **43**, 217–234.

Misra, V., Dumonceaux, T., Dubois, J., Willis, C., Nadin-Davis, S., Severini, A., Wandeler, A., Lindsay, R. & Artsob, H. (2009). Detection

of polyoma and corona viruses in bats of Canada. *J Gen Virol* **90**, 2015–2022.

Osborne, C., Cryan, P. M., O'Shea, T. J., Oko, L. M., Ndaluka, C., Calisher, C. H., Berglund, A. D., Klavetter, M. L., Bowen, R. A. & other authors (2011). Alphacoronaviruses in New World bats: prevalence, persistence, phylogeny, and potential for interaction with humans. *PLoS ONE* **6**, e19156.

Parrish, C. R., Holmes, E. C., Morens, D. M., Park, E. C., Burke, D. S., Calisher, C. H., Laughlin, C. A., Saif, L. J. & Daszak, P. (2008). Cross-species virus transmission and the emergence of new epidemic diseases. *Microbiol Mol Biol Rev* **72**, 457–470.

Pfefferle, S., Oppong, S., Drexler, J. F., Gloza-Rausch, F., Ipsen, A., Seebens, A., Müller, M. A., Annan, A., Vallo, P. & other authors (2009). Distant relatives of severe acute respiratory syndrome coronavirus and close relatives of human coronavirus 229E in bats, Ghana. *Emerg Infect Dis* **15**, 1377–1384.

Poon, L. L., Chu, D. K., Chan, K. H., Wong, O. K., Ellis, T. M., Leung, Y. H., Lau, S. K., Woo, P. C., Suen, K. Y. & other authors (2005). Identification of a novel coronavirus in bats. *J Virol* **79**, 2001–2009.

Quan, P. L., Firth, C., Street, C., Henriquez, J. A., Petrosov, A., Tashmukhamedova, A., Hutchison, S. K., Egholm, M., Osinubi, M. O. & other authors (2010). Identification of a severe acute respiratory syndrome coronavirus-like virus in a leaf-nosed bat in Nigeria. *MBio* **1**, e00208–e00210.

Rex, K., Kelm, D. H., Wiesner, K., Kunz, T. H. & Voigt, C. C. (2008). Species richness and structure of three Neotropical bat assemblages. *Biol J Linn Soc Lond* **94**, 617–629.

Rodriguez-Durán, A., Perez, J., Montalban, M. A. & Sandoval, J. M. (2010). Predation by free-roaming cats on an insular population of bats. *Acta Chiropt* **12**, 359–362.

Ronquist, F. & Huelsenbeck, J. P. (2003). MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* **19**, 1572–1574.

Schipper, J., Chanson, J. S., Chiozza, F., Cox, N. A., Hoffmann, M., Katariya, V., Lamoreux, J., Rodrigues, A. S., Stuart, S. N. & other authors (2008). The status of the world's land and marine mammals: diversity, threat, and knowledge. *Science* **322**, 225–230.

Setz, E. Z. F. & Sazima, I. (1987). Bats eaten by Nambiquara Indians in western Brazil. *Biotropica* **19**, 190.

Simmons, N. B. (2005a). Evolution. An Eocene big bang for bats. *Science* **307**, 527–528.

Simmons, N. B. (2005b). Order Chiroptera. In *Mammal species of the World: a taxonomic and geographic reference*, pp. 312–529. Edited by D. E. Wilson & D. M. Reeder. Baltimore, MD: Johns Hopkins University Press.

Souza, L. L., Ferrari, S. F. & Pina, A. L. C. B. (1997). Feeding behaviour and predation of a bat by *Saimiri sciureus* in a semi-natural Amazonian environment. *Folia Primatol (Basel)* **68**, 194–198.

Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M. & Kumar, S. (2011). MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Mol Biol Evol* **28**, 2731–2739.

Tang, X. C., Zhang, J. X., Zhang, S. Y., Wang, P., Fan, X. H., Li, L. F., Li, G., Dong, B. Q., Liu, W. & other authors (2006). Prevalence and genetic diversity of coronaviruses in bats from China. *J Virol* **80**, 7481–7490.

Taylor, L. L. & Lehman, S. M. (1997). Predation on an evening bat (*Nycticeius* sp.) by squirrel monkeys (*Saimiri sciureus*) in southern Florida. *Florida Sci* **60**, 112–114.

Teeling, E. C., Springer, M. S., Madsen, O., Bates, P., O'Brien, S. J. & Murphy, W. J. (2005). A molecular phylogeny for bats illuminates biogeography and the fossil record. *Science* **307**, 580–584.

Tong, S., Conrardy, C., Ruone, S., Kuzmin, I. V., Guo, X., Tao, Y., Niezgoda, M., Haynes, L., Agwanda, B. & other authors (2009). Detection of novel SARS-like and other coronaviruses in bats from Kenya. *Emerg Infect Dis* **15**, 482–485.

van der Hoek, L., Pyrc, K., Jebbink, M. F., Vermeulen-Oost, W., Berkhout, R. J., Wolthers, K. C., Wertheim-van Dillen, P. M., Kaandorp, J., Spaargaren, J. & Berkhout, B. (2004). Identification of a new human coronavirus. *Nat Med* **10**, 368–373.

Weiss, S. R. & Navas-Martin, S. (2005). Coronavirus pathogenesis and the emerging pathogen severe acute respiratory syndrome coronavirus. *Microbiol Mol Biol Rev* **69**, 635–664.

WHO (29 May 2013). Middle East respiratory syndrome- coronavirus – update.

Woo, P. C., Lau, S. K., Chu, C. M., Chan, K. H., Tsoi, H. W., Huang, Y., Wong, B. H., Poon, R. W., Cai, J. J. & other authors (2005). Characterization and complete genome sequence of a novel coronavirus, coronavirus HKU1, from patients with pneumonia. *J Virol* **79**, 884–895.

Zaki, A. M., van Boheemen, S., Bestebroer, T. M., Osterhaus, A. D. & Fouchier, R. A. (2012). Isolation of a novel coronavirus from a man with pneumonia in Saudi Arabia. *N Engl J Med* **367**, 1814–1820.