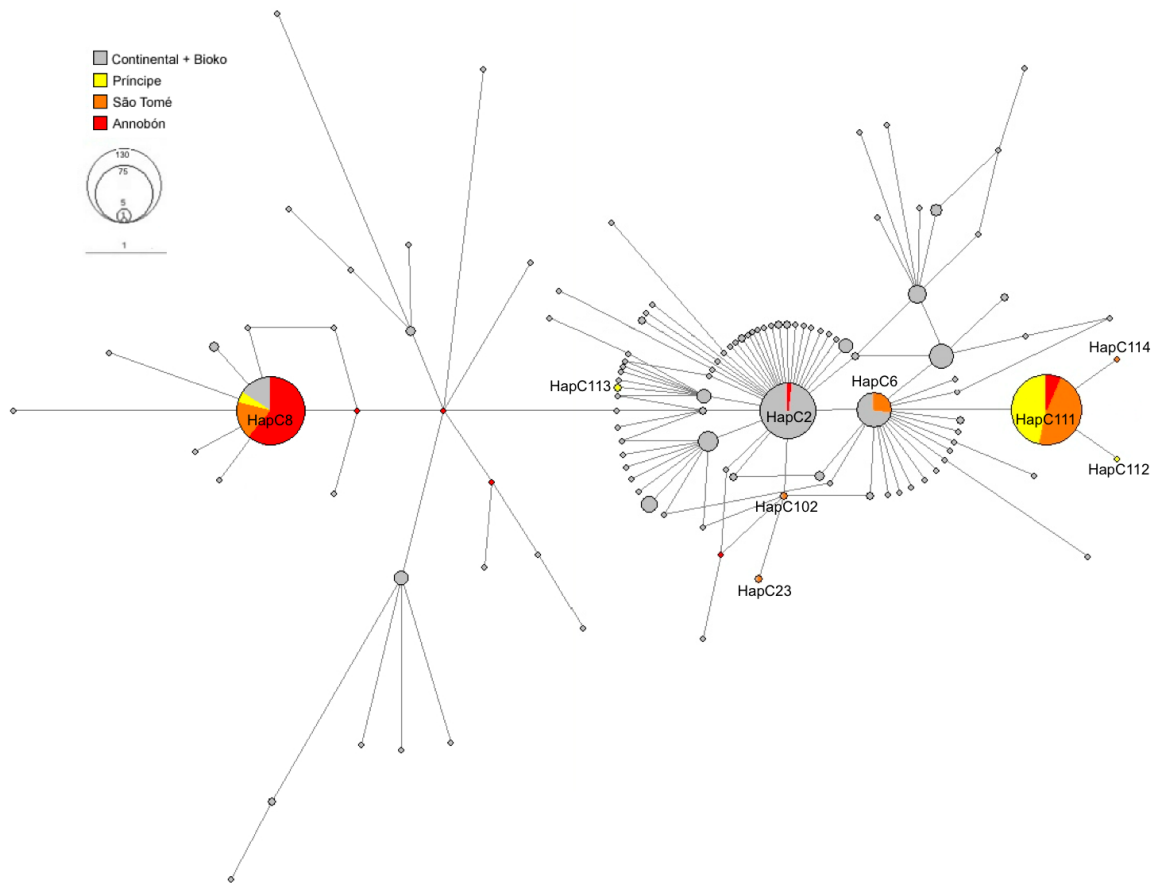
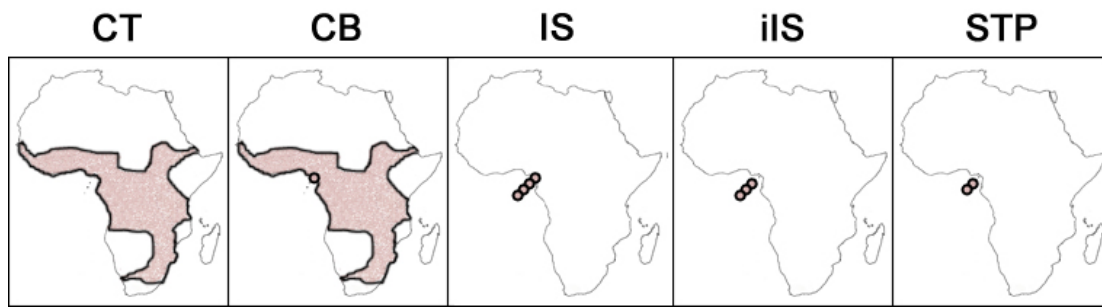


Supplementary Fig. S1: *E. helvum* cytochrome *b* haplotype Bayesian phylogeny with *E. dupreanum* used as an outgroup. Three main ‘clades’ are identified: A, B and C. Posterior probabilities are shown on the main branch nodes. * refers to a haplotype which was represented in continental Africa and Bioko (CB) and on isolated island (iIS), † refers to haplotypes represented only on Príncipe, ‡ refers to haplotypes represented only on São Tomé and § refers to haplotypes present in multiple iIS, but not in CB populations.



Supplementary Fig. S2: *Eidolon helvum* cytochrome *b* median joining haplotype network. Each circle represents a unique haplotype, and its size is proportional to its frequency. Lines represent base pair changes between two haplotypes, with the length proportional to the number of base pair changes. Main haplotypes and those containing island samples are labeled by name. This is the same figure as Fig 2 in the manuscript, but with continental and Bioko samples colored as a single panmictic population, and demonstrating that isolated Gulf of Guinea islands (Príncipe, São Tomé and Annobón) are clustered into two main (and other secondary) haplotypes.



Supplementary Fig. S3: Demonstration of regional population groupings used in genetic analyses, including all continental populations (CT), all continental populations plus Bioko (CB), all four island populations (IS), three isolated island populations (São Tomé, Príncipe and Annobón) (iIS), and São Tomé and Príncipe (STP)

Supplementary Table S1. Estimates of population pairwise Φ_{ST} values from mtDNA (below the diagonal) and F_{ST} values from microsatellites (above the diagonal) among twelve *E. helvum* populations. Bold values represent significance at $p < 0.05$, bold and italicised values represent significance at $p < 0.01$.

		Microsatellites											
		GH	DR	KE	ZA	MA	TZ	UG	RM	BI	PR	ST	AN
mtDNA	GH		0.00	-0.00	-0.01	-0.01	-0.00	-0.03	-0.01	-0.00	0.05	0.04	0.12
	DR	-0.01		0.00	-0.00	-0.01	-0.00	-0.03	0.01	-0.00	0.05	0.03	0.11
	KE	-0.00	-0.02		0.00	-0.01	-0.01	-0.03	0.00	-0.00	0.05	0.03	0.12
	ZA	0.02	-0.00	-0.02		-0.01	-0.01	-0.04	-0.00	-0.00	0.05	0.03	0.12
	MA	0.04	0.02	-0.01	-0.02		-0.01	-0.04	0.00	-0.01	0.03	0.02	0.10
	TZ	0.05	0.02	-0.00	-0.00	-0.03		-0.03	0.00	-0.00	0.03	0.02	0.12
	UG	-0.02	-0.01	-0.05	-0.05	-0.03	-0.03		-0.02	-0.03	0.02	0.02	0.11
	RM	0.03	-0.01	-0.03	-0.03	-0.04	-0.04	-0.05		0.01	0.05	0.04	0.15
	BI	-0.00	-0.01	-0.01	0.00	0.02	0.03	-0.04	0.00		0.04	0.03	0.11
	PR	0.50	0.54	0.51	0.53	0.57	0.49	0.61	0.59	0.46		0.01	0.07
	ST	0.31	0.27	0.27	0.30	0.32	0.28	0.33	0.28	0.29	0.07		0.07
	AN	0.57	0.59	0.54	0.53	0.49	0.39	0.60	0.46	0.50	0.77	0.58	

Supplementary Table S2. Assignment probabilities of admixed individuals from STRUCTURE analyses. The majority of individuals in the analyses (n=483/502) had assignment probabilities of >80% to the cluster they were sampled from, and are not shown in this table. No recent (first generation) immigrants (>80% assignment probability to a cluster other than the cluster they were sampled from) were identified. The table therefore contains data from individuals classified as 'admixed' (20-80% assignment probability to a cluster other than the cluster they were sampled from). The proportional assignment of individual, and its previous two generations of ancestors to each of three Bayesian population clusters, is shown (I = Individual, P = Parent, G = Grandparent). Four bats (#411, 430, 734, 792) had assignment probabilities of <50% to the cluster from which they were sampled (highlighted in bold), indicating the possibility of immigration within the previous two generations.

Sample ID	Sampling location		Assignment % to cluster CB			Assignment % to cluster STP			Assignment % to cluster AN		
	Population	Cluster	I	P	G	I	P	G	I	P	G
252	ZA	CB	77%			7%	7%	7%	0%	0%	0%
472	TZ	CB	78%			0%	1%	4%	0%	0%	0%
980	TZ	CB	75%			0%	2%	5%	0%	1%	1%
608	UG	CB	76%			2%	11%	8%	0%	0%	0%
411	RM	CB	32%			0%	30%	12%	0%	13%	13%
398	BI	CB	69%			3%	6%	9%	0%	1%	1%
864	BI	CB	57%			0%	9%	9%	0%	0%	0%
931	BI	CB	64%			1%	17%	12%	0%	0%	0%
430	PR	STP	29%	9%	12%	49%			0%	0%	0%
431	PR	STP	14%	5%	6%	74%			0%	0%	0%
734	PR	STP	22%	17%	19%	42%			0%	0%	0%
769	ST	STP	0%	0%	0%	68%			0%	13%	13%
973	ST	STP	0%	0%	1%	74%			3%	13%	13%
612	ST	STP	0%	6%	12%	80%			0%	0%	0%
673	ST	STP	1%	14%	15%	69%			0%	0%	0%
690	ST	STP	0%	0%	1%	75%			0%	1%	1%
792	AN	AN	0%	0%	13%	1%	18%	18%	36%		
795	AN	AN	0%	1%	22%	0%	0%	0%	76%		
819	AN	AN	0%	0%	4%	0%	4%	4%	74%		

Supplementary Table S3: GenBank Acquisition numbers for sequences used in phylogenetic analyses of known henipaviruses and henipavirus-like viruses globally and other known Paramyxovirinae.

GenBank Accession	Description
NC_005339	Mossman virus
FJ362497	Nariva virus
NC_007454	J virus
NC_007803	Beilong virus
HQ660129	Bat Paramyxovirus ¹³
FJ609191	Bat Paramyxovirus ¹³
HQ660151	Bat Paramyxovirus ¹³
HQ660123	Bat Paramyxovirus ¹³
HQ660149	Bat Paramyxovirus ¹³
HQ660146	Bat Paramyxovirus ¹³
HQ660143	Bat Paramyxovirus ¹³
HQ660125	Bat Paramyxovirus ¹³
HQ660124	Bat Paramyxovirus ¹³
HQ660126	Bat Paramyxovirus ¹³
HQ660148	Bat Paramyxovirus ¹³
AY988601	Nipah virus Bangladesh
AF212302	Nipah virus Malaysia
NC_001906	Hendra virus
HM044317	Hendra virus strain HeV/Australia/Horse/2008/Redlands
HQ660144	Bat Paramyxovirus ¹³
HQ660141	Bat Paramyxovirus ¹³
JQ001776	Cedar virus
HQ660139	Bat Paramyxovirus ¹³
HQ660145	Bat Paramyxovirus ¹³
HQ660132	Bat Paramyxovirus ¹³
HQ660131	Bat Paramyxovirus ¹³
HQ660133	Bat Paramyxovirus ¹³
FJ971936	Bat Paramyxovirus ¹³
HQ660142	Bat Paramyxovirus ¹³
HQ660127	Bat Paramyxovirus ¹³
HQ660135	Bat Paramyxovirus ¹³
HQ660134	Bat Paramyxovirus ¹³
FJ971938	Bat Paramyxovirus ¹³
FJ609194	Bat Paramyxovirus ¹³
HQ660150	Bat Paramyxovirus ¹³
FJ971937	Bat Paramyxovirus ¹³
HQ660140	Bat Paramyxovirus ¹³
FJ971940	Bat Paramyxovirus ¹³
HQ660147	Bat Paramyxovirus ¹³
HQ660120	Bat Paramyxovirus ¹³
HQ660121	Bat Paramyxovirus ¹³
HQ660122	Bat Paramyxovirus ¹³
HQ660128	Bat Paramyxovirus ¹³
HQ660118	Bat Paramyxovirus ¹³
HQ660137	Bat Paramyxovirus ¹³
HQ660119	Bat Paramyxovirus ¹³
HQ660152	Bat Paramyxovirus ¹³
HQ660138	Bat Paramyxovirus ¹³
HQ660136	Bat Paramyxovirus ¹³
FJ971935	Bat Paramyxovirus ¹³
FJ971939	Bat Paramyxovirus ¹³
JF828297	Bat Paramyxovirus ¹³
Z11575	Human parainfluenza virus 3
NC_002161	Bovine parainfluenzavirus 3
PAFZSTR	Sendai virus
NC_005084	Fer de Lance virus
NC_009640	Porcine rubulavirus
NC_009489	Mapuera virus
NC_002200	Mumps virus
HQ660095	Bat Paramyxovirus 3

X64275	Simian parainfluenza virus 41
NC_003443	Human parainfluenza virus 2
AF052755	Simian virus 5
GU128082	Tuhoko virus 3
GU128081	Tuhoko virus 2
AF326114	Menangle virus
AF298895	Tioman virus
GU128080	Tuhoko virus 1
EU627591	Human parainfluenza virus 4
AF077761	Newcastle Disease virus
NC_001781	Human respiratory syncytial virus
M74568	Human respiratory syncytial virus
AF092942	Bovine resp syncytial virus
AY743910	Pneumonia virus of mice
AY525843	Human metapneumovirus
DQ009484	Avian metapneumovirus
AB016162	Measles virus
Z30697	Rinderpest
NC_006383	Peste des petits ruminants
NC_005283	Dolphin morbillivirus
AF014953	Canine distemper
Y09630	Phocine distemper
AF079780	Tupaia paramyxovirus