

Supporting Information

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Table S1. SIVgor infection in wild gorillas

Collection sites*	Country	Subspecies	No. of fecal samples collected	No. of SIVgor antibody-positive samples	Estimated no. of gorillas [†]	No. of SIVgor antibody-positive gorillas [‡]	No. of vRNA-positive samples	No. of vRNA-positive gorillas [§]	SIVgor prevalence, % [¶]	95% confidence interval, % [¶]
AK	Cameroon	<i>G.g.g.</i>	12	0	7	0	0	0	0	na
AM	Cameroon	<i>G.g.g.</i>	104	0	58	0	0	0	0	0–6.2
BP	Cameroon	<i>G.g.g.</i>	161	48	55	10 (+2) [#]	36	7	22	12.9–34.8
BQ	Cameroon	<i>G.g.g.</i>	435	9	132	1	6	1	0.8	0–4.2
BY	Cameroon	<i>G.g.g.</i>	141	0	78	0	0	0	0	0–4.7
DJ	Cameroon	<i>G.g.g.</i>	237	12	99	4	4	3	4	1.6–9.9
DK	Cameroon	<i>G.g.g.</i>	11	0	6	0	0	0	0	na
EK	Cameroon	<i>G.g.g.</i>	101	0	43	0	0	0	0	0–8.2
HC	Cameroon	<i>G.g.g.</i>	11	0	6	0	0	0	0	na
LD	Cameroon	<i>G.g.g.</i>	146	1	50	1	0	0	2	0.3–10.5
MB	Cameroon	<i>G.g.g.</i>	118	0	49	0	0	0	0	0–7.3
MI	Cameroon	<i>G.g.g.</i>	22	0	12	0	0	0	0	na
NG	Cameroon	<i>G.g.g.</i>	167	0	93	0	0	0	0	0–4
NY	Cameroon	<i>G.g.g.</i>	30	0	12	0	0	0	0	na
LE	Gabon	<i>G.g.g.</i>	18	0	10	0	0	0	0	na
LO	Gabon	<i>G.g.g.</i>	35	0	19	0	0	0	0	0–16.8
MI	Gabon	<i>G.g.g.</i>	365	0	152	0	0	0	0	0–2.5
MK	Gabon	<i>G.g.g.</i>	21	0	12	0	0	0	0	na
LA	Gabon	<i>G.g.g.</i>	72	0	40	0	0	0	0	0–8.8
MA	Gabon	<i>G.g.g.</i>	67	0	20	0	0	0	0	0–16.1
MC	Gabon	<i>G.g.g.</i>	7	0	4	0	0	0	0	na
IV	Gabon	<i>G.g.g.</i>	3	0	1	0	0	0	0	na
DJ	Gabon	<i>G.g.g.</i>	34	0	19	0	0	0	0	0–16.8
ML	Gabon	<i>G.g.g.</i>	10	0	4	0	0	0	0	na
WA	Gabon	<i>G.g.g.</i>	31	0	17	0	0	0	0	0–18.4
LN	Gabon	<i>G.g.g.</i>	22	0	9	0	0	0	0	na
OY	Gabon	<i>G.g.g.</i>	77	0	32	0	0	0	0	0–10.7
IY	Gabon	<i>G.g.g.</i>	27	0	15	0	0	0	0	0–20.4
OD	Gabon	<i>G.g.g.</i>	1	0	1	0	0	0	0	na
LO	Gabon	<i>G.g.g.</i>	125	0	69	0	0	0	0	0–5.5
<i>n</i> = 33			2,611	70	1,134	16 (+2) [#]	46	11	1.6	1.0–2.5
VR	DRC	<i>G.b.b.</i>	97	0	51	0	0	0	0	0–7.0
BI	Uganda	<i>G.b.b.</i>	121	0	64	0	0	0	0	0–5.7
KB	DRC	<i>G.b.g.</i>	103	0	54	0	0	0	0	0–6.6
<i>n</i> = 3			321	0	169	0	0	0	0	0–2.2
Total			2,932	70	1,303	18	46	11		

G.b.b., *Gorilla berengei berengei*; *G.b.g.*, *Gorilla berengei graueri*; *G.g.g.*, *Gorilla gorilla gorilla*; na, not applicable.

*Collection sites are indicated with a two letter code, and their locations are shown in Fig. 1.

[†]Number of sampled gorillas was estimated as described in *Materials and Methods*.

[‡]Number of SIVgor-infected gorillas was determined by microsatellite analysis.

[§]Viral RNA (vRNA) was detected by RT-qPCR and/or nested PCR; the number of vRNA-positive individuals was determined by microsatellite analysis.

[¶]Prevalence of SIVgor infection was estimated based on the proportion of SIVgor-positive gorillas; confidence intervals were only calculated when the number of gorillas was greater than 15.

[#]At the BP site, two additional SIVgor-infected gorillas were identified by RT-qPCR (*Results*).

Table S3. Primer sets used to amplify partial SIVgor *gag*, *pol*, and *env* sequences

Fragment name	Gene	Round	Primer	Primer sequences (5'–3')*	Amplicon size, bp	Ref.
Polmini	<i>pol</i>	1	Polmini F1	CATGTRGCHAGTGGNTWCMTAGARGCAGARGT	518	(1)
			Polmini R1	ACBACYGCNCCTTCHCCTTTC		
		2	Polmini F2	AYAAYCCHCAAAGTCAAGGAGTRGT	285	
			Polmini R2	GTCCTTTCCAAATDGGRTCTCTGCTGTC		
PgorGAG [†]	<i>gag</i>	1	PgorGAGF1	AGGGRCCCTAAGGAACCATTYMGAG	513	
			PgorGAGR1	CTGYACATAGTTGCCTGGCCTCT		
		2	PgorGAGF2	ATTCTACAAAACYCTCAGAGC	408	
			PgorGAGR2	CTGATYTGCACTCTTTCATTTGRT		
GOR-GP41	<i>env</i>	1	GOR-GP41 F1	AGCARGAATTGCTGAGACTYTCTG	359	(2)
			GOR-GP41 R1	CCANTNTGTTATGTCAAGCCAAC		
		2	GOR-GP41 F2	GGCATAAGACARCTCMGAGCTCGC	315	
			GOR-GP41 R2	AAGCCAACCTCCAAGRTCTGC		
GP41	<i>env</i>	1	CPZ-gp41-F1	TCTTAGGAGCAGCAGGAAGCACTATGGG	595	(3)
			CPZ-gp41-R1	AACGACAAAGGTGAGTATCCCTGCCTAA		
		2	CPZ-gp41-F2	ACAATTATTGTCTGGTATAGTGCAACAGCA	454	
			CPZ-gp41-R2a	TCCTACTATCATTATGAATATTTTATATA		
GP41-Nef	<i>env</i>	1	GP41neff1b	AWTGGYTRWGGTAYATHARRAT	704	(4)
			GP41neff1b	CCCHTCCAGTCCYCCCTTTTC		
		2	GP41neff2c	TAGTAAVWAGAGTTAGGCAGGG	692	
			GP41neff2b	CAGTCCYCCCTTTTCTTTYAAAAA		
BQgorGP41 [†]	<i>env</i>	1	BQgorgp41F1	AGCTCGCCTGCTGGCCATWGARAC	289	
			BQgorgp41R1	CCAMARATCTGCCCACTTRTCYAA		
		2	BQgorgp41F2	AGCAACTCCTRGMCTGTGGGG	155	
			BQgorgp41R2	GTARTTGTCTACCARTTTGTCCATT		

*B = C/G/T, D = A/G/T, H = A/C/T, M = A/C, N = A/C/T/G, R = A/G, V = A/C/G, Y = C/T, W = A/T.

[†]Primers designed for this study.

1. Takehisa J, et al. (2009) Origin and biology of simian immunodeficiency virus in wild-living western gorillas. *J Virol* 83(4):1635–1648.
2. Neel C, et al. (2010) Molecular epidemiology of simian immunodeficiency virus infection in wild-living gorillas. *J Virol* 84(3):1464–1476.
3. Keele BF, et al. (2006) Chimpanzee reservoirs of pandemic and nonpandemic HIV-1. *Science* 313(5786):523–526.
4. Van Heuverswyn F, et al. (2006) Human immunodeficiency viruses: SIV infection in wild gorillas. *Nature* 444(7116):164.