Unexpected higher convergence of human-great ape enteric viromes in central African forest than in a European zoo: A One Health analysis

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INTRODUCTION

Human-animal pathogenic transmissions threaten both human and animal health, and the processes catalyzing zoonotic spillover and spillback are complex. Prior field studies offer partial insight into these processes but overlook animal ecologies and human perceptions and practices facilitating human-animal contact. **Conducted in Cameroon and a European zoo, this holistic study elucidates these processes, integrating metagenomic, historical, anthropological and great ape ecological analyses, and real-time evaluation of human-great ape contact types and frequencies**.
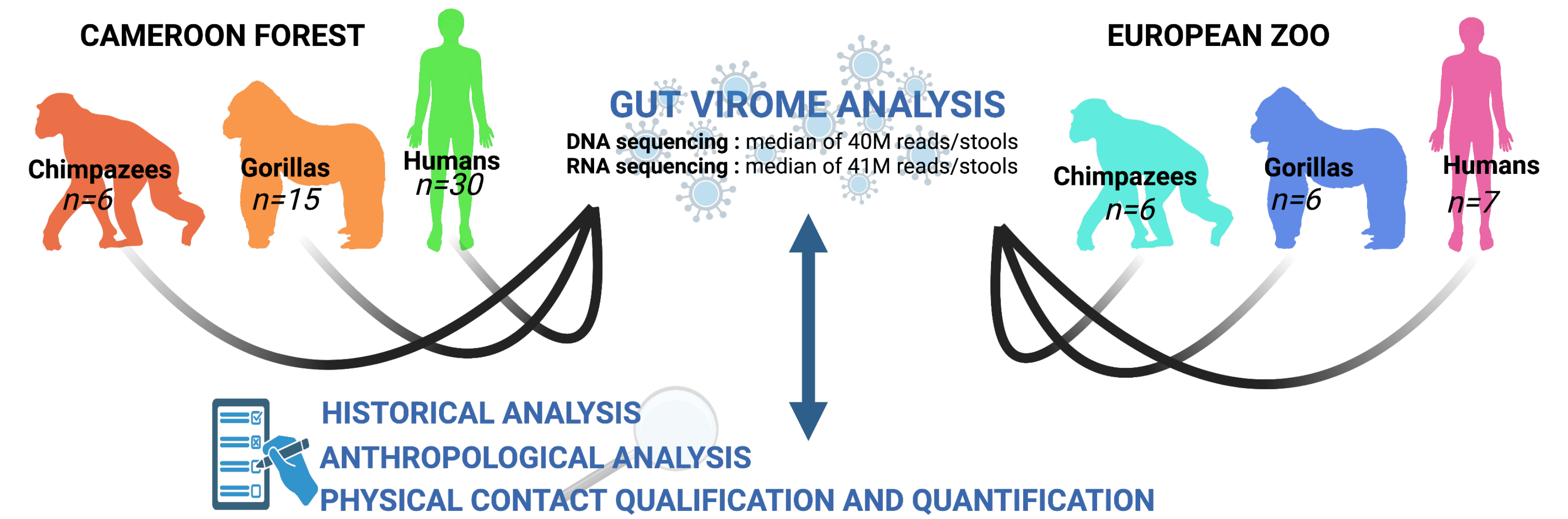
RESULTS

Our anthropological research shows that southeastern Cameroonians distinguish chimpanzees from gorillas, their perceptions shaping their practices around these great apes (not show). Quantitative data on human physical and environmental contacts, collected in real time, illuminates different human interactions with gorillas and chimpanzees. The mean frequency of human physical and environmental contact with gorillas was higher, but not significantly, than with chimpanzees; direct contact (seen alive, heard) did not differ between these great apes Based on questionnaires, physical contacts were more frequent (except for hunting) with gorillas than chimpanzees.

Contact category	Type of contact	Longitudinal survey N=18, data self-collected daily, 10 months		Questionnaire N=449	
		Pan t. troglodytes	Gorilla g. gorilla	Pan t. troglodytes	Gorilla g. gorilla
Environmental contact	Seen feces	2.3 (5.3)	3.5 (5.3)	Not addressed in questionnaires	
	Seen food remains	2.5 (5.3)	4.0 (5.6)		
	Seen nest	1.9 (3.5)	1.5 (3.5)		
	Seen footprints	2.2 (5.2)	3.8 (5.3)		
Direct contact	Seen alive	1.8 (5.1)	1.8 (4.1)	14.2 (31.4)	9.1 (22.3)
	Heard	3.2 (5.3)	2.6 (4.2)		
Physical contact	Hunt	0 (0, 0-0)	0 (0, 0-0)	0.08 (0.7)	0.07 (0.3)
	Butcher	0.1 (0.3)	0.2 (0.3)	0.7 (2.2)***	1.6 (7.3)***
	Cook	0.1 (0.4)	0.2 (0.6)	0.6 (2.1)***	1.0 (2.7)***
	Consume	0.2 (0.5)	1.1 (2.5)	0.7 (2.2)***	1.7 (7.3)***
	Buy/Sell	0.5 (1.2)	1.1 (2.6)	0.4 (1.6)***	1.3 (7.1)***

Mean (%) contact frequencies (SD) according to great ape species and type of contact in Cameroon. * indicates a p-value <0.001 from the Mann-Whitney statistical tests.**

Network and dissimilarity analyses (Figure 1) revealed that human enteric viromes from Cameroon forest and the zoo were more similar despite habitation in different biotopes, whereas virome composition for great apes appeared to be shaped more significantly by ecology than by species. Additionally, the zoo environment seems to have exercised a greater influence on great ape virome than the forest did for Cameroon great apes. Hence, our findings on human and great ape gut viromes reveal similar patterns to comparative gut microbiomes. Although phylogeny seems to exercise a greater impact on human gut virome and microbiome, environment apparently has a stronger influence on great ape viromes.
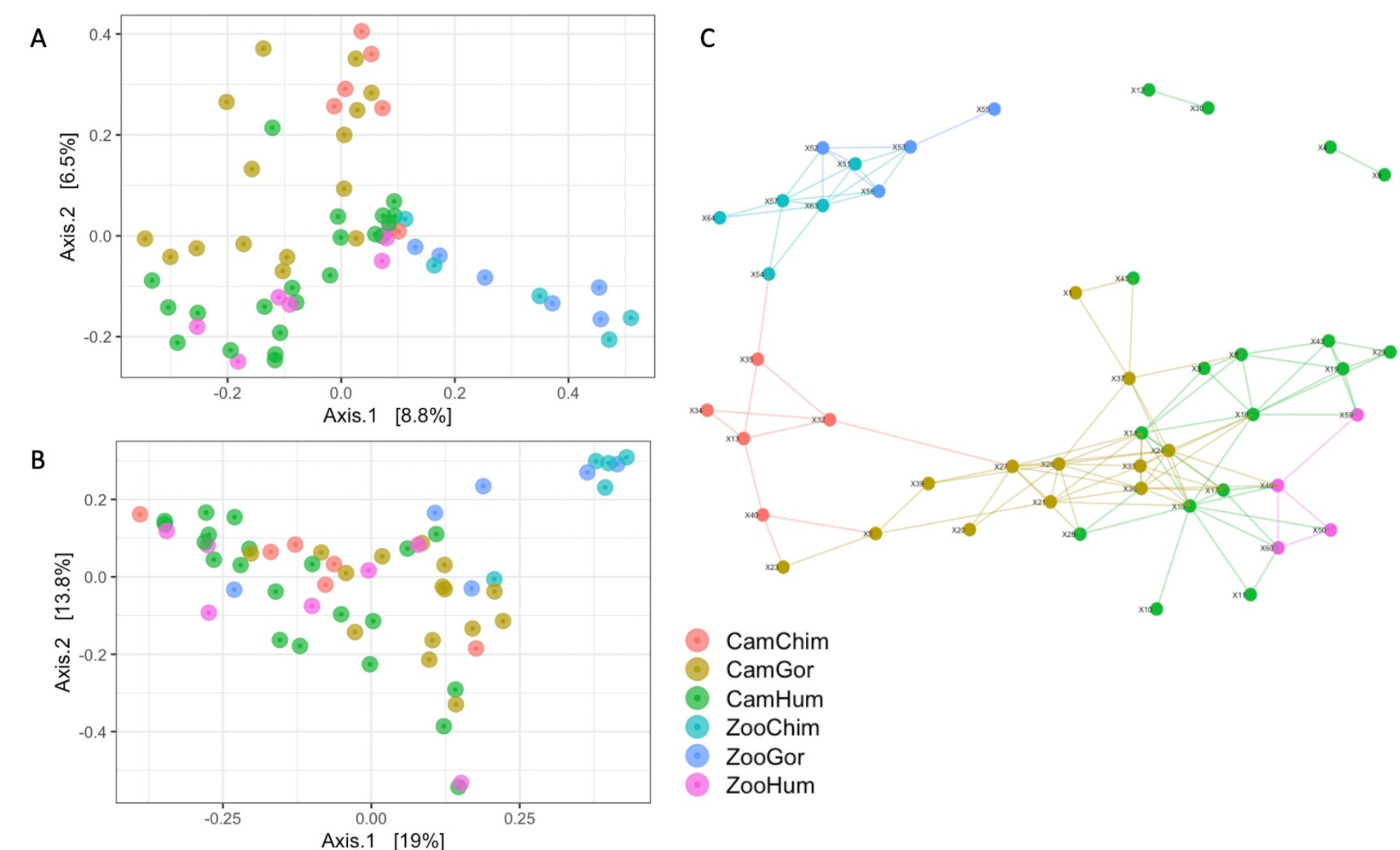

Figure 1 : PcoA analysis based on Bray-Curtis distances (A) and on weighted Unifrac distances (B). (C) Network plot based on Bray-Curtis distances showing similarities among all sample virome profiles. Only edges connecting individuals (i.e., nodes) with > 90% similarity in their virome are shown. Each group is defined by its habitation site (Cam=Cameroon, Zoo=European Zoo) and animal species (Chimp=Chimpanzee, Gor=Gorilla, Hum=Human)

Contrary to our prediction, viromes of Cameroon forest inhabitants and Cameroon gorillas more closely resembled one another than those of zookeepers and zoo gorillas and chimpanzees. The proportion of viral taxa shared between gorillas and humans was four times higher in Cameroon than in the European zoo, and among Cameroon humans and great apes, human-gorilla viral sharing was higher than for human-chimpanzee sharing (Figure 2).

Among vertebrate viruses known to cause disease in human beings, we identified Mastadenoviruses and Enteroviruses as the major viral genera that humans and great apes share in Cameroon (Figure 3). Both genera can be transmitted through physical contact and can remain infectious in the environment for several days.
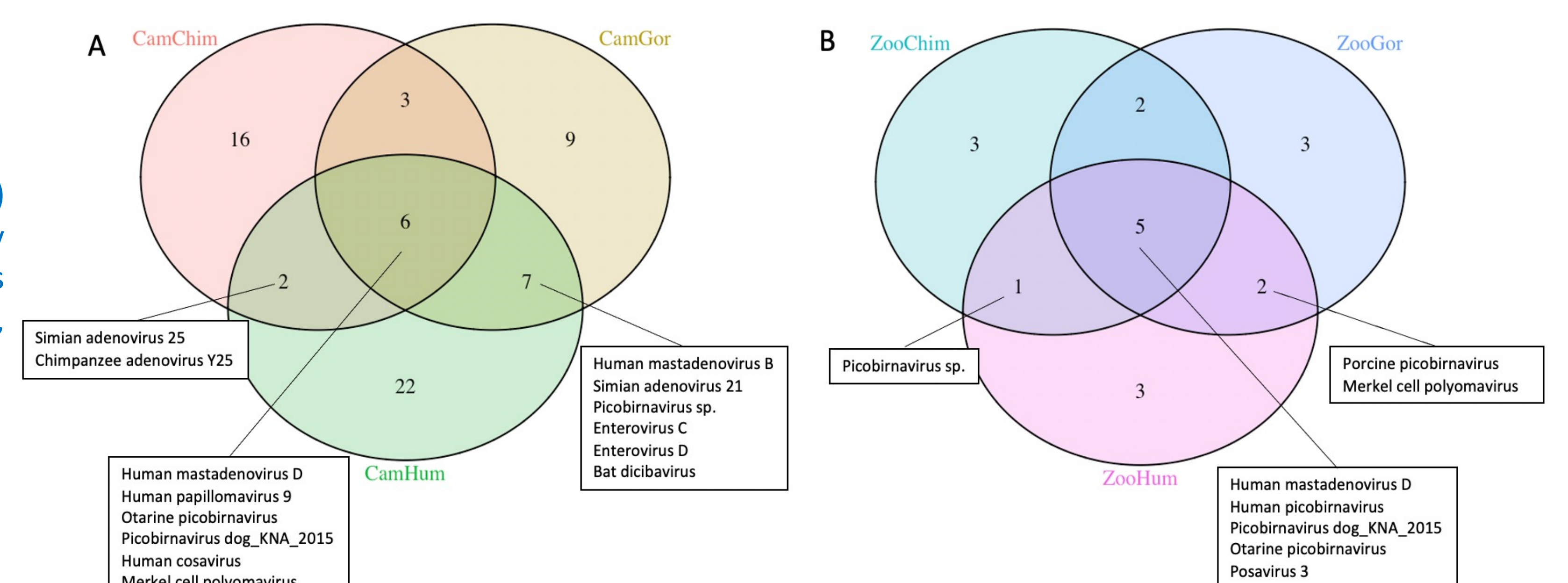

Figure 2 : Venn Diagrams of vertebrates viral lowest-common-ancestor (LCA) taxa identified in human and great ape stools in Cameroon (A) and European zoo (B). Each group is defined by its habitation site (Cam=Cameroon, Zoo=European Zoo) and animal species (Chimp=Chimpanzee, Gor=Gorilla, Hum=Human)

Figure 3 : Sequence similarity network representation of Mastadenovirus (a) and Picornavirus (b) contigs. Each node represents an individual contig or whole genome reference sequences. Edges are defined based on the Blast Bit-score across individual samples. Each contigs is colored according to the group to which it belongs. Grey nodes represent reference sequences.
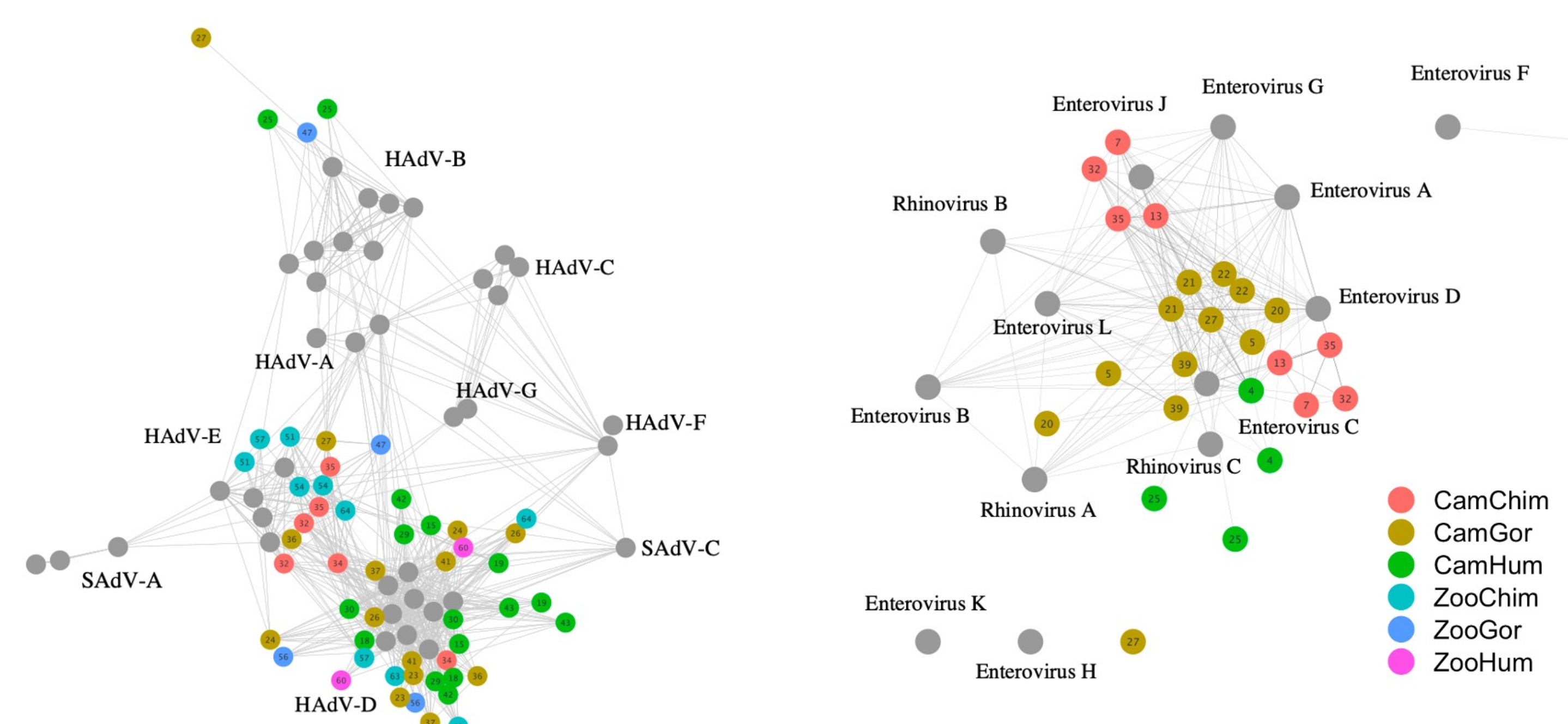
CONCLUSION

Surprisingly, we find more enteric virome sharing between Cameroonian humans and great apes than in the zoo, a virome convergence between Cameroonian humans and gorillas, and adenovirus and enterovirus taxa as most frequently shared between Cameroonian humans and great apes. In addition to physical contact from hunting, meat handling and fecal exposure, overlapping human cultivation and gorilla pillaging in forest gardens explain these unexpected findings. **Our multidisciplinary study identifies environmental co-use as a complementary mechanism for viral sharing.**

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