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Surveillance for Paramyxoviruses in West African Bats.

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Introduction

Emerging paramyxoviruses from the family *Paramyxoviridae* pose a significant public health concern.[1,5] Paramyxoviruses are found in a variety of hosts including humans, birds, rodents, and bats, and many of these viruses cause diseases deadly to both humans and animals.[1,3,4] In this study, we focused on bats because they are established reservoirs for many viruses, including paramyxoviruses, and because there are increasing rates of spillover from bats to humans.[3,6] Our understanding of the diversity of these viruses in nature is still very poor. Describing the pre-emergent diversity of viruses in wildlife can help with pandemic preparedness efforts by targeting behavioral, ecological, and medical interventions towards viruses with the highest risk of emergence. In this project, samples were collected from different species of bats in Liberia have been screened for the presence of paramyxoviruses to better understand the diversity of viruses circulating in this region.

Hypothesis

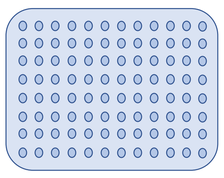
We hypothesize that bats in Liberia will host diverse paramyxoviruses, and of the sample types, the urine samples will have a greater paramyxovirus detection rate compared to other sample types.

Aims

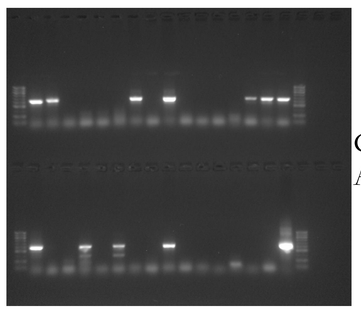
Aim 1 – Discovery Phase
Detect paramyxoviruses from samples collected from bats in Liberia.

Aim 2 – Analysis Phase
Compare the diversity of viruses using phylogenetic analysis, and a regression analysis will be performed to determine the factors associated with the presence of paramyxoviruses in different sample types and species.

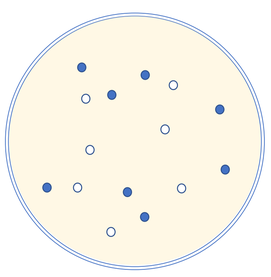
Methods



Hemi-nested Consensus PCR on cDNA
Target: RNA-dependent RNA Polymerase
Protocol: Tong, S et al. (2008)



Gel Electrophoresis
Amplicon: ~561 bp



PCR Product Cloning
Strataclone Cloning Kit
Agar Plate with
Ampicillin and X-gal

Sanger Sequencing

After Sanger sequencing, Geneious Prime was used to trim and align sequences. NCBI Nucleotide BLAST was used to confirm sequences are paramyxoviruses. Mega X was used to determine the Maximum Likelihood substitution model and to create a Maximum Likelihood phylogenetic tree.

Results

Figure 1A.

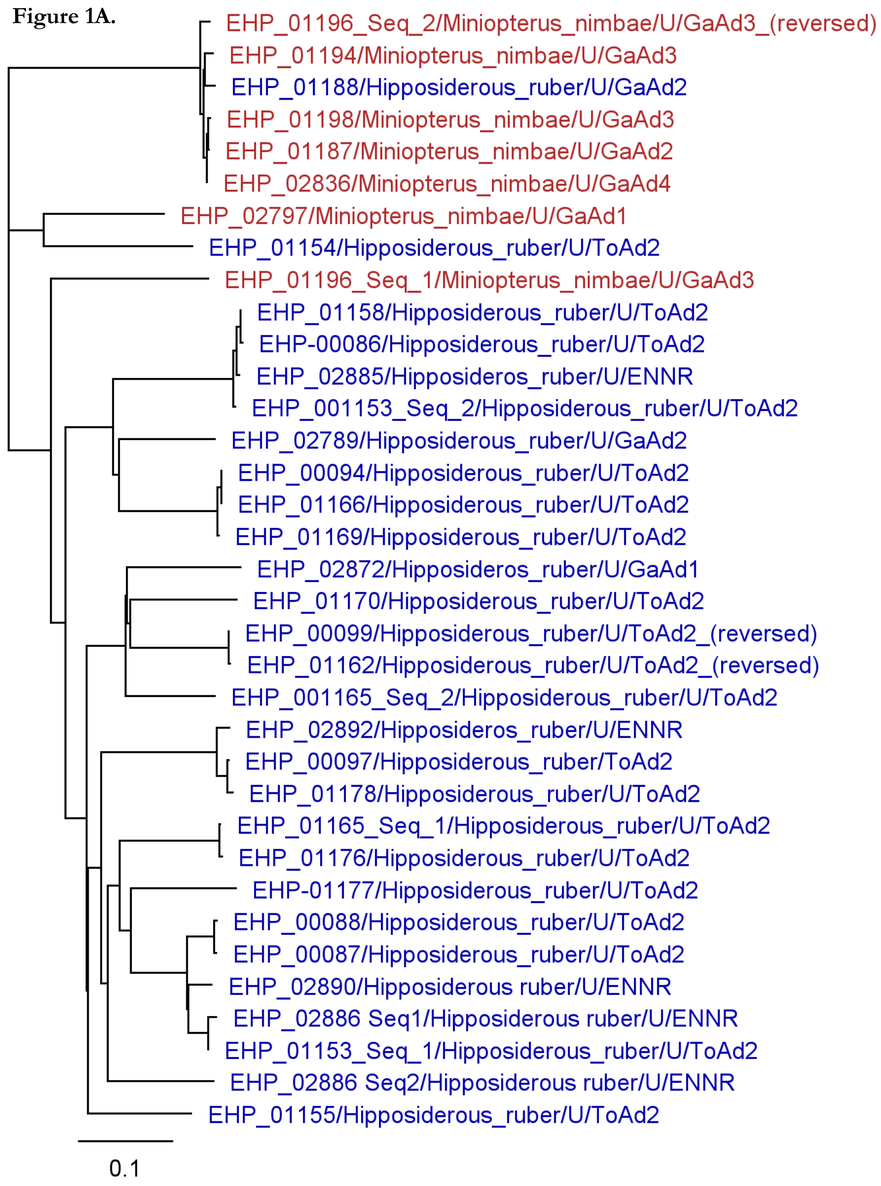


Figure 1B.

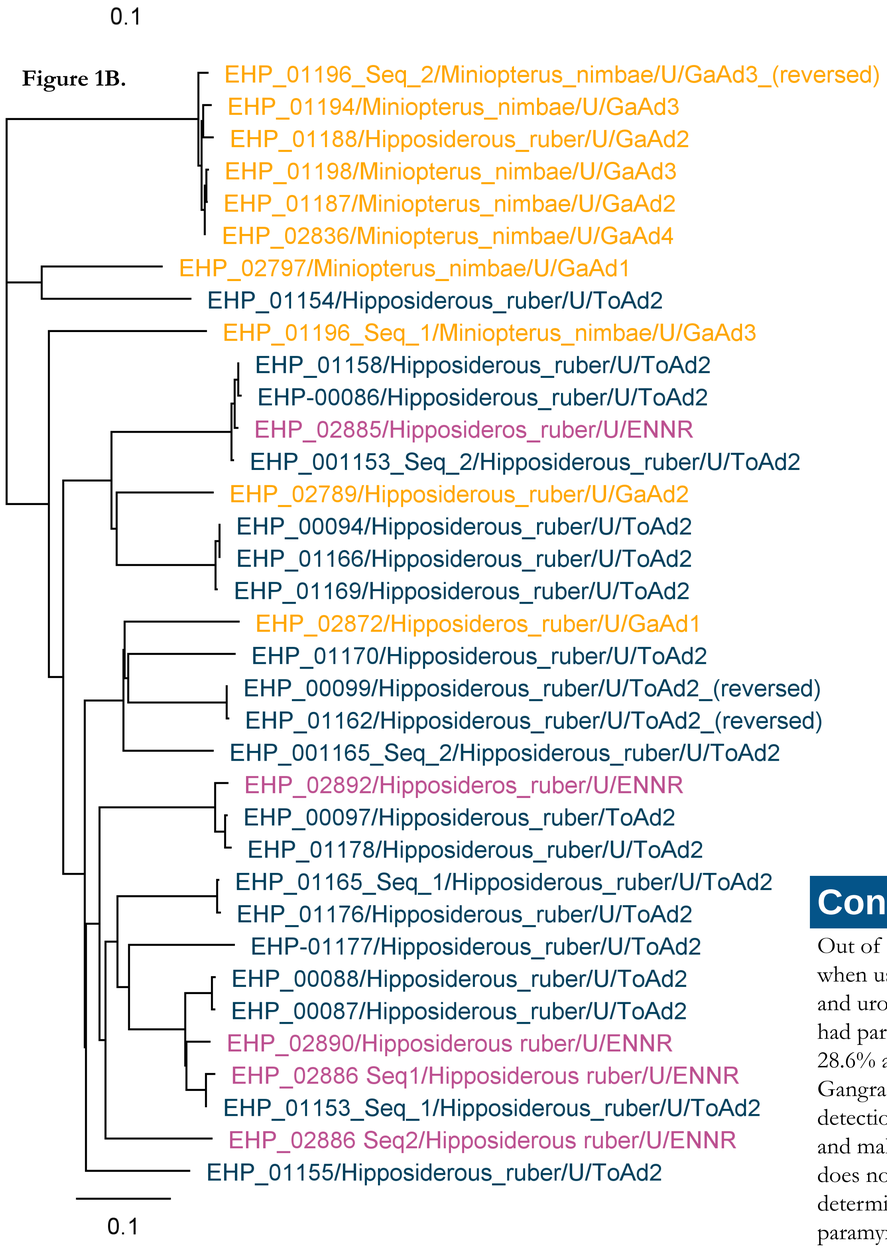


Figure 1. Neighbor-Joining phylogenetic trees of 35 paramyxovirus sequences that were detected in the samples, and they are being used to display cluster of sequences. 1A displays the two species that were represented and a multispecies cluster. 1B displays the different collection sites to illustrate some clustering. 1C displays the co-infections that have been found.

Figure 1C.

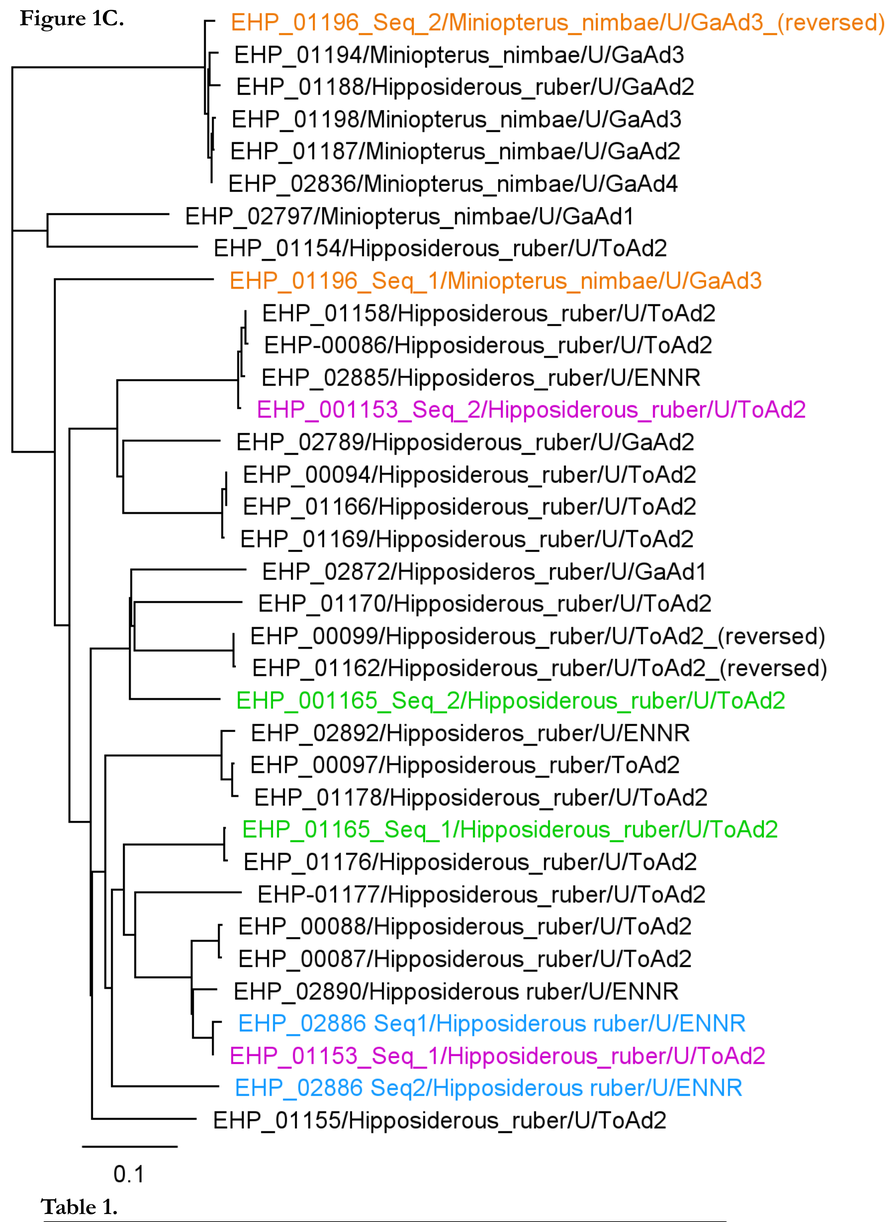


Table 1.

	Total # of Samples	# of PmVs	% of Samples	% of PmVs
Oral Sawb	542	0	30%	0
Rectal Swab	86	0	5%	0
Urine/Urogenital Swab	206	35	11%	100%
Blood	602	0	33%	0
Feces	393	0	21%	0
Hipposideros ruber	968	28	53%	80%
Miniopterus nimbae	775	7	42%	20%
Lissonycteris angolensis	87	0	5%	0
Tokadeh Adit	509	20	27%	57%
Gangra Adit	1230	10	67%	29%
East Nimba Nature Reserve	86	5	6%	14%
Yuelliton Adit	5	0	0.3%	0

Table 1 includes the sample type, species, and collection sites that were represented, with the number and percentage of samples out of 1,830 samples, and paramyxoviruses number and percentage.

Conclusion & Future Research

Out of 1,830 samples, 35 paramyxoviruses and 4 co-infections were detected. 17 of the paramyxoviruses were novel when using <85% nucleotide identity match for NCBI GenBank. All of the paramyxoviruses were detected in urine and urogenital swab samples. The collection sites Gangra Adit, Tokadeh Adit, and East Nimba Nature Reserve all had paramyxoviruses with Tokadeh Adit having the most at 57.1% of paramyxoviruses while Gangra Adit had 28.6% and East Nimba Nature Reserve had 14.3%.Tokadeh Adit samples represented 37.2% of all samples, while Gangra Adit and East Nimba Nature Reserve were 56.4% and 6.3%, respectively. *Hipposideros ruber* had the highest detection with 80% of the sequences while *Miniopterus nimbae* was 20%. *H. ruber* is more common than *M. nimbae* and makes up 66% samples while *M. nimbae* only makes up 32% of the samples. Due to being common, *H. ruber* does not necessarily have a higher virus prevalence than *M. nimbae*. A regression analysis will be performed to determine whether the difference is significant. Around 8,000 more samples need to be screened for paramyxoviruses for the project to finish. Once complete, whole genome sequencing will be performed on the sequences.

References & Acknowledgements

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