

# Zoonotic potential of astroviruses in Madagascar fruit bats

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## Background

Astrovirus (family: Astroviridae)

- two genera infect >80 hosts, including bats<sup>1,2</sup>
- Fecal-oral transmission
- Non-enveloped; environmentally-stable
- Human astroviruses cause 2%-9% of all acute non-bacterial gastroenteritis cases in children<sup>3</sup>
- Evidence of frequent cross-species transmission events, including likely zoonotic spillover<sup>4</sup>
- Partial astrovirus sequences have been detected in Madagascar in two locations and two species of bat<sup>5</sup>
- Hunting, handling, and consumption of Madagascar fruit bats increases spillover risk

## Research Questions

1. Are astroviruses detected in Malagasy fruit bats?
  2. What is the evolutionary history of these astroviruses, and how do they relate to astroviruses known to infect humans?
1. What can we say about zoonotic risk of these astroviruses?

## Methods

1. fecal, urine, and throat swabs from bats captured in Brook lab longitudinal sampling
2. RNA extraction and mNGS sequencing
3. Data cleaning and phylogenetic analysis

For more detailed methods, see [github.com/brooklabteam](https://github.com/brooklabteam)

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## Results

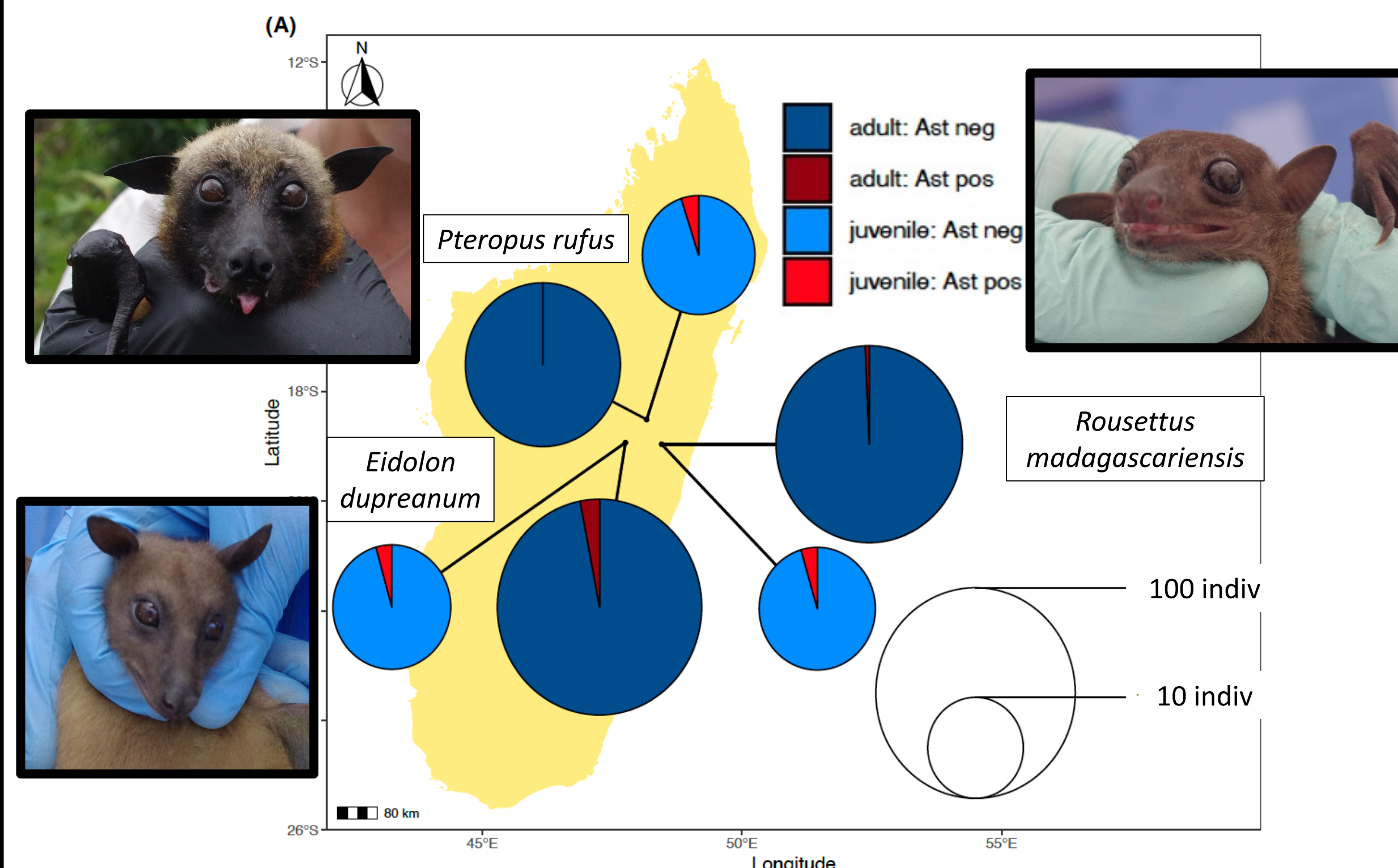


Fig 1: Spatial detection of astroviruses in fecal and urine bat samples from three species of Malagasy fruit bat.

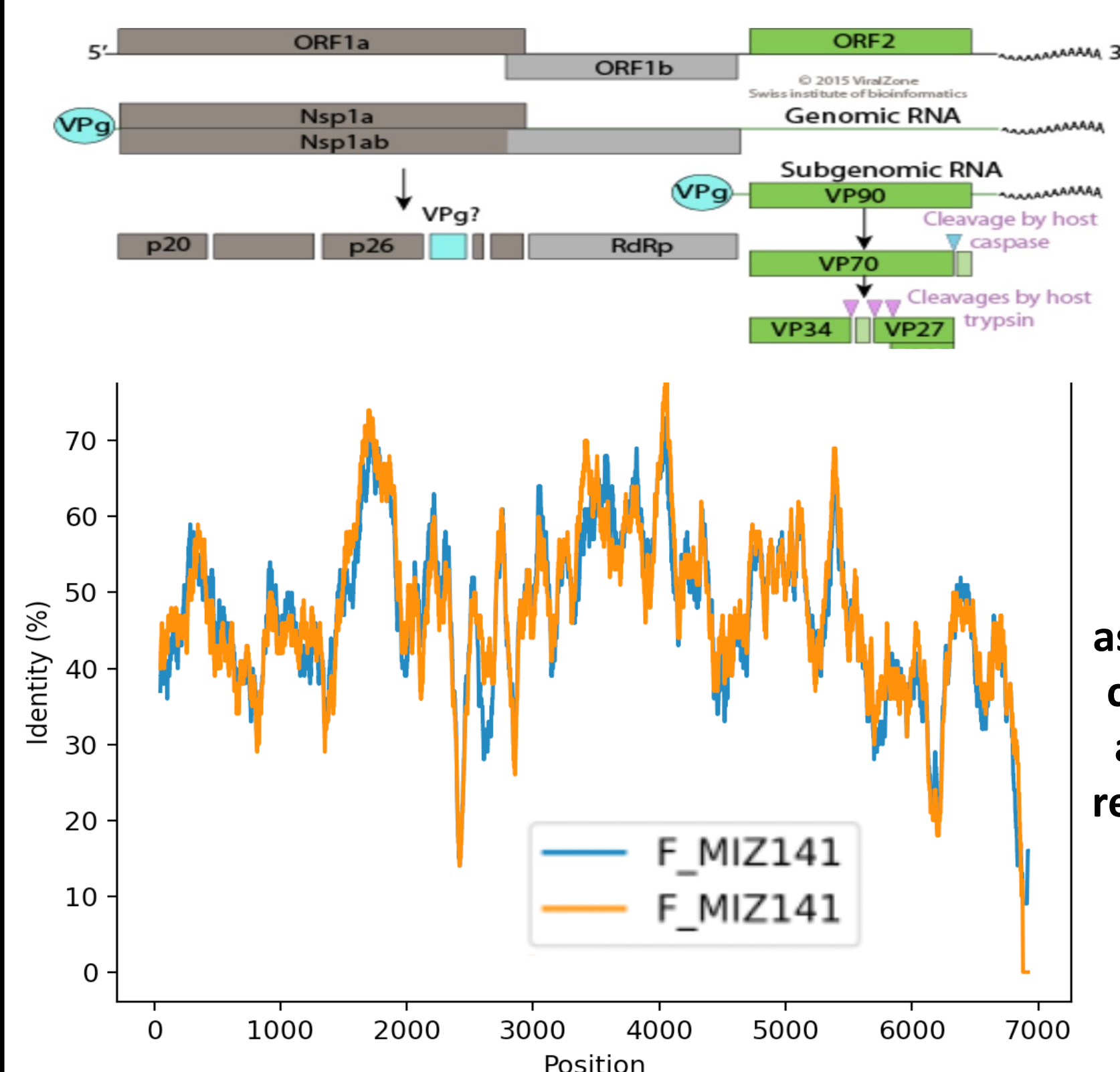


Fig 2: Nucleotide similarity plot of bat astroviruses using most closely related human astrovirus genome as reference (NC\_024472).

### Key Findings

- 11/501 (2.2%) of sampled bats tested positive for Astrovirus
- Detection across all 3 species in all 3 sampled sites
- Identification of the first whole genome astrovirus from Madagascar bat
- Paraphyly among bat-hosted astroviruses
- Moderate to low levels of similarity between bat and human ORF2 region which contains spike protein

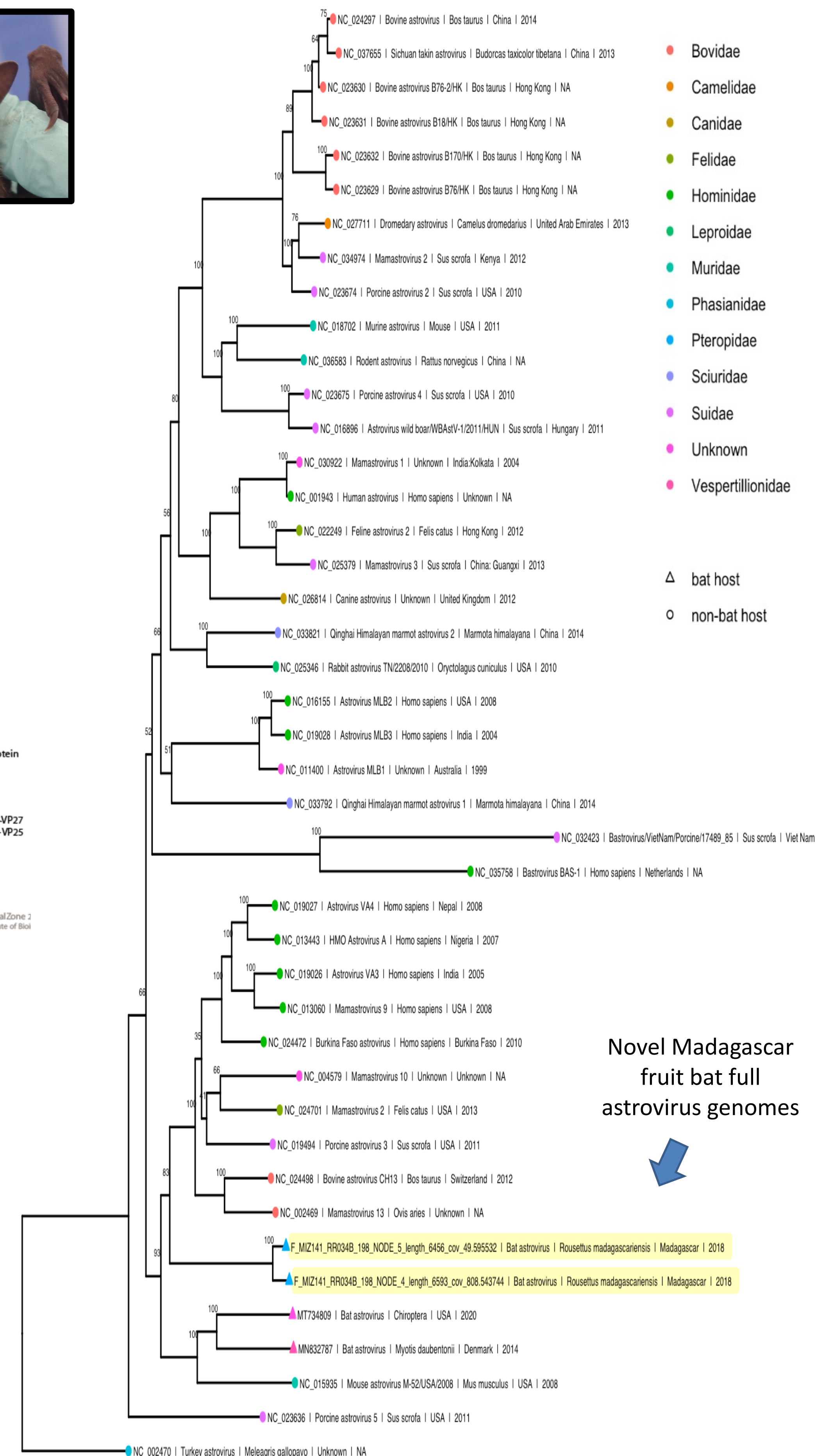


Fig 3: Maximum-likelihood phylogeny of full genome Mamastrovirus sequences (RAxML, GTR+R), 500 bootstraps. Bootstrap support values computed using Felsenstein's method are visualized on tree branches. Branch lengths are scaled by nucleotide substitutions per site.

## Discussion

### Detection

- We detected low levels of astrovirus infection across all sampled species and locations
- In combination with previously published work, astroviruses have now been detected in 5 species of bats across 5 locations in Madagascar
- This suggests that astroviruses may be ubiquitous, if at somewhat low infection levels, in bats across the island

### Evolutionary history and similarity

- Although very similar in nucleotide sequence, bat-hosted astroviruses are paraphyletic, with our novel Madagascar sequences more closely related to a clade containing human astroviruses
- This supports the narrative of frequent cross-species transmission likely due to recombination

### Zoonotic Risk

- Zoonotic risk is increased by frequent human contact/consumption, moderate similarity to a human astrovirus in the first region of ORF2, close phylogenetic placement to human astroviruses
- Zoonotic risk is decreased by low infection levels, low similarity to a human astrovirus in some regions of ORF2

### Next Steps

- ORF2 phylogeny
- Amino acid similarity

## Acknowledgements

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## References

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