**Full genome *Astrovirus* sequences from Madagascar bats support divergence of Madagascan viruses**

**Divergent chiropteran *Astrovirus* from Madagascar shed lght**

**Target Journal:**

Viruses (https://www.mdpi.com/journal/viruses , IF 5.8)

Emerging Microbes & Infections (<https://www.emi2012.org/>, IF 19.5, they did it as a letter to the editor)

**Frontiers in Public Health (IF 6.4)**

**Frontiers in virology (viruses)**

**Virus Evolution (IF 5.6)**

Virology (IF3.5) (<https://www.sciencedirect.com/journal/virology/about/aims-and-scope>),

Virology Journal (https://virologyj.biomedcentral.com/about?gclid=CjwKCAjwqauVBhBGEiwAXOepkcqA5fEsYx3vKc0m7PXwDBljXfmSGstp-9Pn0luWOmBgDlWHPvZ3vBoC0K4QAvD\_BwE)

**Our draw:** broadens detection in bats in mada, two new full genomes improve understanding of host diversity, a look at rdrp in SWIO bats sheds light on trends in spp-crossover

**Abstract**

**Introduction**

Astros are important, are they in this system?

* What are astroviruses
* Astroviruses are understudied, despite their symptoms
* Hosted in a wide variety of organisms
  + Including bats, detected
* Bats host many things, also bats are eaten in Mada
  + Increases zoonotic risk
* Characterize potential for zoonotic risk, look for astroviruses

**Methods**

**Results**

1. Expansion of known species/locations to host astroviruses

Fig1: map

Diagram

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* Three new species
* Three new locations
* Low levels, but across all spp and locations, suggesting ubiquity
* \*\*juveniles

1. Identification of first near complete full astrovirus genome from Madagascar bat. What does it say about astroviruses and their diversity of hosts?

Fig2A: full genome Mamastrovirus phylogeny

* Our seqs fall out within Chiroptera group
* Closest to Cameroon bat
* Looks like closest to fruit bat but probs geography (Africa bat seqs)
* But paraphyletic, and basal to human clade. (zoonotic?)

Fig2B: Simplot of: seq1&seq2 X bat full1, bat full2, a human one?, a zoonotic one?

* Two distinct genomes, meaning coinfection
  + What does this mean?
* Both seqs fairly divergent from other bat full Astros
  + What does this mean?
* In fact, as or more similar to closets human astrovirus

Conclusion: of the bat Astro genomes, these new mada seqs have highest zoonotic risk

1. How do these seqs compare to other bats/other Madagascar bats in particular

Fig3: Bat RdRp phylogeny (basically same as previous paper, but with our new two seqs?) (colored by family, shape by Mada, non Mada)

\*get insight into mixing of bat populations (insect & fruit)

Diagram, schematic

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Diagram, schematic

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* Relationships follow phylogeny more than location
* Interestingly, our seqs fall out in a fairly basal position, within yang and within reunion island
* But other yangs are doing similar things. Within phylogeny, yin more likely to be intermixed within yan, than other way around (more blue in the green area)’
* Cite freaky one – fell out within Avastrovirus

**Discussion**

* Ubiquity
  + Our seqs with known seqs
* Divergence
* Not strong zoonotic potential
* Yin vs yang
* Coinfection

**Conclusion**

* Astroviruses are prevalent in Madagascar bats that are consumed, and their risk of zoonotic potential is high
  + They warrant watching out for
* Full genomes are divergent from other bat Astros, reflecting mada’s long isolated evolutionary history (timing of divergence)
* Rdrp tree suggests that yang is more likely to get infections from yin (\*\*in this region\*\*)

**Supplement**

* BLAST hits
* Zoonotic ?
* Table of bats that hit astrovirus positive

Shape

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Figure X: Nucleotide similarity plot comparing the two novel bat Madagascar full-genome astroviruses (F\_MIZ141\_1, F\_MIZ141\_2) to the most closely related human full-genome astrovirus sequence (NC\_024472) as indicated by phylogenetic analysis (see Figure X). Line color indicates sequence identity. Genome position of known ORF’s indicated by the colored bar at the bottom of the plot. Computed in pySimplot (CITE) using a window size of 200bp and a step size of 20bp.