

Zoonotic potential of astroviruses in Madagascar fruit bats

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Background

Astrovirusus (family: Astroviridae)

- two genera infect >80 hosts, including bats^{1,2}
- Fecal-oral transmission
- Non-enveloped; environmentally-stable
- Human astroviruses cause 2%-9% of all acute non-bacterial gastroenteritis cases in children³
- Evidence of frequent cross-species transmission events, including likely zoonotic spillover⁴
- Partial astrovirus sequences have been detected in Madagascar in two locations and two species of bat⁵
- 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



fecal, urine, and throat swabs from bats captured in Brook lab longitudinal sampling

Madagascar bat

Paraphyly among bat-hosted astroviruses

Moderate to low levels of similarity between bat and

human ORF2 region which contains spike protein

- 2. RNA extraction and mNGS sequencing
- 3. Data cleaning and phylogenetic analysis

For more detailed methods, see github.com/brooklabteam

Questions or comments? Send me an email or follow me on twitter! shorigan@uchciago.edu @sophiahorigan

Results NC 037655 | Sichuan takin astrovirus | Budorcas taxicolor tibetana | China | 2013 NC 023630 | Bovine astrovirus B76-2/HK | Bos taurus | Hong Kong | NA NC 023631 | Bovine astrovirus B18/HK | Bos taurus | Hong Kong | NA 100 NC_023632 | Bovine astrovirus B170/HK | Bos taurus | Hong Kong | NA madagascariensis NC 023674 | Porcine astrovirus 2 | Sus scrofa | USA | 2010 OC 023675 | Porcine astrovirus 4 | Sus scrofa | USA | 2010 NC 016896 | Astrovirus wild boar/WBAstV-1/2011/HUN | Sus scrofa | Hungary | 2011 10 indiv NC_030922 | Mamastrovirus 1 | Unknown | India:Kolkata | 2004 80 km NC_022249 | Feline astrovirus 2 | Felis catus | Hong Kong | 2012 NC_025379 | Mamastrovirus 3 | Sus scrofa | China: Guangxi | 2013 Fig 1: Spatial detection of astroviruses in fecal and urine bat samples from three species of Malagasy fruit bat. ● NC 025346 | Rabbit astrovirus TN/2208/2010 | Oryctolagus cuniculus | USA | 2010 NC 016155 | Astrovirus MLB2 | Homo sapiens | USA | 2008 NC 019028 | Astrovirus MLB3 | Homo sapiens | India | 2004 032423 | Bastrovirus/VietNam/Porcine/17489 85 | Sus scrofa | Viet Nam NC_019027 | Astrovirus VA4 | Homo sapiens | Nepal | 2008 NC 013443 | HMO Astrovirus A | Homo sapiens | Nigeria | 2007 NC 019026 | Astrovirus VA3 | Homo sapiens | India | 2005 Fig 2: Nucleotide NC 013060 | Mamastrovirus 9 | Homo sapiens | USA | 2008 similarity plot of bat NC 024472 | Burkina Faso astrovirus | Homo sapiens | Burkina Faso | 2010 astroviruses using most closely related human astrovirus genome as reference (NC_024472). F_MIZ141 NC 024498 | Bovine astrovirus CH13 | Bos taurus | Switzerland | 2012 F_MIZ141 -● NC 002469 | Mamastrovirus 13 | Ovis aries | Unknown | N F_MIZ141_RR034B_198_NODE_5_length_6456_cov_49.595532 | Bat astrovirus | Rousettus madagascariensis | Madagascar | 2018 2000 4000 5000 6000 F MIZ141 RR034B 198 NODE 4 length 6593 cov_808.543744 | Bat astrovirus | Rousettus madagascariensis | Madagascar | 2018 MT734809 | Bat astrovirus | Chiroptera | USA | 2020 MN832787 | Bat astrovirus | Myotis daubentonii | Denmark | 2014 NC 015935 | Mouse astrovirus M-52/USA/2008 | Mus musculus | USA | 2008 **Key Findings** 11/501 (2.2%) of sampled bats tested positive for Astrovirus NC 023636 | Porcine astrovirus 5 | Sus scrofa | USA | 2011 → NC_002470 | Turkey astrovirus | Meleagris gallopavo | Unknown | NA **Detection across all 3 species in all 3 sampled sites** Identification of the first whole genome astrovirus from

Fig 3: Maximum-likelihood phylogeny of full genome Mamastrovirus sequences (RAxML, GTR+R), 500 bootstraps. **Bootstrap support values computed using Felsentein'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

Bovidae

Camelidae

Canidae

Hominidae

Leproidae

Muridae

Phasianidae

Pteropidae

Sciuridae

Suidae

Unknown

△ bat host

Novel Madagascar

fruit bat full

astrovirus genomes

non-bat host

Vespertillionidae

- 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
- Animo acid similarity

Acknowledgements





References

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