Key topics: Madagascar bats, astroviruses in bats, astroviruses in Madagascar, astroviruses, bats as reservoirs

Astroviruses

* general astrovirus facts
  + De Benedictis P, Schultz-Cherry S, Burnham A et al. Astrovirus infections in humans and animals – molecular biology, genetic diversity, and interspecies transmissions. Infect Genet Evol 2011; 11: 1529–1544.
* Infection in children 2%-9%
  + Bosch A, Pinto RM, Guix S. Human astroviruses. Clin Microbiol Rev 2014; 27: 1048–1074.
* Infection in Malagasy children
  + Papaventsis DC, Dove W, Cunliffe NA et al. Human astrovirus gastroenteritis in children, Madagascar, 2004-2005. Emerg Infect Dis 2008; 14: 844–846.
* Frequent cross spp transmission & host diversity
  + Mendenhall IH, Smith GJD, Vijaykrishna D. Ecological drivers of virus evolution: astrovirus as a case study. J Virol 2015; 89: 6978–6981.
  + Karlsson EA, Small CT, Freiden P et al. Non-human primates harbor diverse mammalian and avian astroviruses including those associated with human infections. PLoS Pathog 2015; 11: 1–17.
* Zoonotic potential
  + Bosch A, Pinto RM, Guix S. Human astroviruses. Clin Microbiol Rev 2014; 27: 1048–1074
  + Finkbeiner SR, Kirkwood CD, Wang D (2008): Complete Genome Sequence of a Highly Divergent Astrovirus Isolated from a Child with Acute Diarrhea. Virol. J. 5, 117.
  + Finkbeiner SR, Le BM, Holtz LR, Storch GA, Wang D (2009): Detection of Newly Described Astrovirus MLB1 in Stool Samples from Children. Emerg. Infect. Dis. 15, 441–444.
  + Chu, D.K.W.; Chin, A.W.H.; Smith, G.J.; Chan, K.H.; Guan, Y.; Peiris, J.S.M.; Poon, L.L.M. Detection of novel astroviruses in urban brown rats and previously known astroviruses in humans. J. Gen. Virol. 2010, 91, 2457–2462.
  + Kapoor, A.; Li, L.; Victoria, J.; Oderinde, B.; Mason, C.; Pandey, P.; Zaidi, S.Z.; Delwart, E. Multiple novel astrovirus species in human stool. J. Gen. Virol. 2009, 90, 2965–2972.
* Evidence for recombination events in other mammals
  + Karlsson, E.A.; Small, C.T.; Freiden, P.; Feeroz, M.M.; Matsen, F.A.T.; San, S.; Hasan, M.K.; Wang, D.; Jones-Engel, L.; Schultz-Cherry, S. Non-Human Primates Harbor Diverse Mammalian and Avian Astroviruses Including Those Associated with Human Infections. PLoS Pathog. 2015, 11, e1005225.
  + Nagai, M.; Omatsu, T.; Aoki, H.; Otomaru, K.; Uto, T.; Koizumi, M.; Minami-Fukuda, F.; Takai, H.; Murakami, T.; Masuda, T.; et al. Full genome analysis of bovine astrovirus from fecal samples of cattle in Japan: Identification of possible interspecies transmission of bovine astrovirus. Arch. Virol. 2015, 160, 2491–2501.s
  + Ulloa, J.C.; Gutierrez, M.F. Genomic analysis of two ORF2 segments of new porcine astrovirus isolates and their close relationship with human astroviruses. Can. J. Microbiol. 2010, 56, 569–577.
  + Wolfaardt, M.; Kiulia, N.M.; Mwenda, J.M.; Taylor, M.B. Evidence of a recombinant wild-type human astrovirus strain from a Kenyan child with gastroenteritis. J. Clin. Microbiol. 2011, 49, 728–731.
* Genetic diversity of bat astroviruses seems to be remarkable
* Co-occurrence of different strains within bat colonies might favor the potential of co-infection of individuals with multiple strains at the same time
  + fischer
* Therefore, recombination events between different bat strains seem possible
  + Lead to novel virus strains to which the affected hosts have lower immunity, or enable viruses to cross species barriers
  + fischer
* close genetic relationship
* High genetic diversity
  + Fischer K, dos Reis VP, Balkema-buschmann A. Bat Astroviruses: towards understanding the transmission dynamics of a neglected virus family. Viruses. 2017;9:34.
  + Chu DKW, Poon LLM, Guan Y et al. Novel astroviruses in insectivorous bats. J Virol 2008; 82: 9107–9114.
  + Kemenesi G, Dallos B, Gördöl T et al. Molecular survey of RNA viruses in Hungarian bats: discovering novel astroviruses, coronaviruses, and caliciviruses. Vector Borne Zoonotic Dis 2014; 14: 846–855.
  + Rougeron V, Suquet E, Maganda GD et al. Characterization and phylogenetic analysis of new bat astroviruses detected in Gabon, Central Africa, 2016. Acta Virol 60: 386–392.
* \* high genetic diversity associated with the wide variety of host species suggest and confirm 1. Efficiency in cross-species transmission, 2. Great adaptability to new environments, 3. Potential zoonotic capability
* Low levels of host restriction and limited phylogenetic clustering between distant locations
  + Fischer K, dos Reis VP, Balkema-Buschmann A et al. Towards understanding the transmission dynamics of a neglected virus family. Viruses 2017; 9: 34.
* Ecological drivers of AstV epidemiology and evolution remain to be determined
  + Mendenhall IH, Smith GJD, Vijaykrishna D. Ecological drivers of virus evolution: astrovirus as a case study. J Virol 2015; 89: 6978–6981.
* Limited genetic information
  + Mendenhall IH, Smith GJD, Vijaykrishna D. Ecological drivers of virus evolution: astrovirus as a case study. J Virol 2015; 89: 6978–6981.
* High saturation of genome makes phylogenetic resolution more difficult
  + Lukashov VV, Goudsmit J. Evolutionary relationships among Astroviridae. J. Gen. Virol. 2002;83:1397–405.

Bats as reservoirs

* Bats are second most abundant, diverse, and geographically dispersed vertebrate species after rodents
  + Calisher CH, Childs JE, Field HE, Holmes VK, Schountz T (2006): Bats: Important Reservoir Hosts of Emerging Viruses. Clin. Microbiol. Rev. 19, 531–545.
  + Kasso M, Balakrishnan M (2013): Ecological and Economic Importance of Bats (Order Chiroptera), Ecological and Economic Importance of Bats (Order Chiroptera). International Scholarly Research Notices (November): e187415.
  + Koopman, K. F. A synopsis of the families of bats, part VII. Bat Research News 25, 25–27 (1984).
* Harbor more than 80 virus species and are considered the reservoirs of many emerging viruses
  + Rupprecht, C. E. et al. (1995) ‘The Ascension of Wildlife Rabies: A Cause for Public Health Concern or Intervention?’, Emerging Infectious Diseases, 1: 107–14.
  + Chua, K. B. et al. (2002) ‘Isolation of Nipah Virus from Malaysian Island Flying-Foxes’, Microbes and Infection, 4: 145–51.
  + Lau, S. K. P. et al. (2005) ‘Severe Acute Respiratory Syndrome Coronavirus-like Virus in Chinese Horseshoe Bats’, Proceedings of the National Academy of Sciences of the United States of America, 102: 14040–5.
  + Leroy, E. M. et al. (2005) ‘Fruit Bats as Reservoirs of Ebola Virus’, Nature, 438: 575–6.
  + Towner, J. S. et al. (2007) ‘Marburg Virus Infection Detected in a Common African Bat’, PLoS One, 2: e764.
  + Memish, Z. A. et al. (2013) ‘Middle East Respiratory Syndrome Coronavirus in Bats, Saudi Arabia’, Emerging Infectious Diseases, 19: 1819–23.
* Bats are frequently considered the reservoir host for a broad variety of newly emerging viruses, especially in the tropics, although their general role in the epidemiology and spillover of zoonotic viral diseases is not fully understood
  + Moratelli, R.; Calisher, C.H. Bats and zoonotic viruses: Can we confidently link bats with emerging deadly viruses? Mem. Inst. Oswaldo Cruz 2015, 110, 1–22.
  + Han, H.J.; Wen, H.L.; Zhou, C.M.; Chen, F.F.; Luo, L.M.; Liu, J.W.; Yu, X.J. Bats as reservoirs of severe emerging infectious diseases. Virus Res. 2015, 205, 1–6.
* The roosting of certain bat species in gatherings of thousands if not millions of individuals is thought to facilitate high intra- and interspecies contact rates that might allow efficient virus transmission
  + Calisher, C.H.; Childs, J.E.; Field, H.E.; Holmes, K.V.; Schountz, T. Bats: Important reservoir hosts of emerging viruses. Clin. Microbiol. Rev. 2006, 19, 531
  + Luis, A.D.; Hayman, D.T.S.; O’Shea, T.J.; Cryan, P.M.; Gilbert, A.T.; Pulliam, J.R.C.; Mills, J.N.; Timonin, M.E.; Willis, C.K.R.; Cunningham, A.A.; et al. A comparison of bats and rodents as reservoirs of zoonotic viruses: Are bats special? Proc. R. Soc. Lond. B Biol. Sci. 2013, 280, 20122753.
* Have features that enhance their ability to facilitate virus evolution and transmission (longevity, migratory activity, large and dense roosting communities, close social interactions)
  + Prendergast, B. J. et al. (2002) ‘Periodic Arousal from Hibernation Is Necessary for Initiation of Immune Responses in Ground Squirrels’, American Journal of Physiology. Regulatory, Integrative and Comparative Physiology, 282: R1054–62.
  + Luis, A. D. et al. (2013) ‘A Comparison of Bats and Rodents as Reservoirs of Zoonotic Viruses: Are Bats Special?’, Proceedings: Biological Sciences, 280: 20122753.
* Direct contact with bats through hunting, selling, and/or eating might provide a great opportunity for zoonotic transmission
  + Morse, S. S. (2001) ‘Factors in the Emergence of Infectious Diseases BT - Plagues and Politics: Infectious Disease and International Policy’, in Price-Smith A. T. (ed.), pp. 8–26. Palgrave Macmillan UK: London.
* Bats provide considerable ecosystem services, such as arthropod suppression, seed dispersal and pollination across a vast range of habitats and regions

Madagascar bats

* 46 bat species, of which nearly 80% are endemic
  + Goodman, S.M.; Schoeman, M.C.; Rakotoarivelo, A.; Willows-Munro, S. How many species of Hipposideros have occurred on Madagascar since the Late Pleistocene? Zool. J. Linn. Soc. 2016, 177, 428–449.
  + Foley, N.M.; Goodman, S.M.; Whelan, C.V.; Puechmaille, S.J.; Teeling, E. Towards navigating the Minotaur’s labyrinth: Cryptic diversity and taxonomic revision within the speciose genus Hipposideros (Hipposideridae). Acta Chiropterologica 2017, 19, 1–18.
* Basal split of placental mammals from ancestors approx. 80mya and diversification of bat families at approximately 62mya
  + Teeling, E. C. et al. A molecular phylogeny for bats illuminates biogeography and the fossil record. Science 307, 580–584, doi: 10.1126/science.1105113 (2005).
* It is assumed that most originated from Africa
* In certain cases, phylogenetic analyses provide evidence for recent periods of diversification
* For example, Malagasy miniopterus colonized the island from an African source population approx. 4.5 and 2.5 mya, followed by a second phase between 2.5 and 1 mya
  + Christidis, L., Goodman, S. M., Naughton, K. & Appleton, B. Insights into the evolution of a cryptic radiation of bats: dispersal and ecological radiation of Malagasy Miniopterus (Chiroptera: Miniopteridae). PLoS One 9, e92440, doi: 10.1371/journal.pone.0092440 (2014)

Astros & Metagenomics

* Novel astroviruses have been identified by metagenomics approaches wherever diseases of unknown etiology have occurred
  + Quan, P.L.; Wagner, T.A.; Briese, T.; Torgerson, T.R.; Hornig, M.; Tashmukhamedova, A.; Firth, C.; Palacios, G.; Baisre-De-Leon, A.; Paddock, C.D.; et al. Astrovirus encephalitis in boy with X-linked agammaglobulinemia. Emerg. Infect. Dis. 2010, 16, 918–925.
  + Bouzalas, I.G.; Wuthrich, D.; Walland, J.; Drogemuller, C.; Zurbriggen, A.; Vandevelde, M.; Oevermann, A.; Bruggmann, R.; Seuberlich, T. Neurotropic astrovirus in cattle with nonsuppurative encephalitis in Europe. J. Clin. Microbiol. 2014, 52, 3318–3324.
  + Li, L.; Diab, S.; McGraw, S.; Barr, B.; Traslavina, R.; Higgins, R.; Talbot, T.; Blanchard, P.; Rimoldi, G.; Fahsbender, E.; et al. Divergent astrovirus associated with neurologic disease in cattle. Emerg. Infect. Dis. 2013, 19, 1385–1392.
  + Pfaff, F.; Schlottau, K.; Scholes, S.; Courtenay, A.; Hoffmann, B.; Höper, D.; Beer, M. A novel astrovirus associated with enephalitis and ganlionitis in domestic sheep. Transbound. Emerg. Dis. 2017, 1–6.
* Full lengths are super important!
* RdRp not included in ICTV definition for new sequences
* Most bat Astros show great diversity that would technically qualify them as different species
  + But they cluster monophyletically
* Some bat derived Astros were publishd and used for phylo were not made public
  + Karlsson, E.A.; Small, C.T.; Freiden, P.; Feeroz, M.M.; Matsen, F.A.T.; San, S.; Hasan, M.K.; Wang, D.; Jones-Engel, L.; Schultz-Cherry, S. Non-Human Primates Harbor Diverse Mammalian and Avian Astroviruses Including Those Associated with Human Infections. PLoS Pathog. 2015, 11, e1005225.
  + Zhu, H.C.; Chu, D.K.W.; Liu, W.; Dong, B.O.; Zhang, S.Y.; Zhang, J.X.; Li, L.F.; Vijaykrishna, D.; Smith, G.J.D.; Chen, H.L.; et al. Detection of diverse astroviruses from bats in China. J. Gen. Virol. 2009, 90, 883–887.

Surveillance

* Control and prevention of emerging infections requires rapid identification, determine origin and control further spread
* Continuous surveillance to unravel the viral communities present in bats is important
  + Gerald K. T. et al. (Eds). (2009) ‘National Research Council (US) Committee on Achieving Sustainable Global Capacity for Surveillance and Response to Emerging Diseases of Zoonotic Origin’. Sustaining Global Surveillance and Response to Emerging Zoonotic Diseases. Washington, DC: National Academies Press (US).
* Emerging infectious diseases threaten animal and human health
  + Daszak P, Cunningham AA, Hyatt AD. 2000 Emerging infectious diseases of wildlife: threats to biodiversity and human health. Science 287, 443449. (doi:10.1126/science.287.5452.443)
  + Smith KF, Sax DF, Lafferty KD. 2006 Evidence for the role of infectious disease in species extinction and endangerment. Conserv. Biol. 20, 1349–1357. (doi:10.1111/j.1523-1739.2006.00524.x)
  + Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, Daszak P. 2008 Global trends in emerging infectious diseases. Nature 451, 990–993. (doi:10.1038/nature06536)
* Most originate in wildlife and are increasing over time
  + Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, Daszak P. 2008 Global trends in emerging infectious diseases. Nature 451, 990–993. (doi:10.1038/nature06536)
  + Taylor LH, Latham SM, Woolhouse MEJ. 2001 Risk factors for human disease emergence. Phil. Trans. R. Soc. Lond. B 356, 983– 989. (doi:10.1098/ rstb.2001.0888)
  + Woolhouse MEJ, Gowtage-Sequeria S. 2005 Host range and emerging and reemerging pathogens. Emerg. Infect. Dis. 11, 1842–1847. (doi:10.3201/ eid1112.050997)

Astroviruses in Bats

* Detection in….
  + China
    - Zhu HC, Chu DKW, Liu W, Dong BQ, Zhang SY, Zhang JX, Li LF et al. (2009): Detection of Diverse Astroviruses from Bats in China. J. Gen. Virol. 90, 883–88
    - Chu DKW, Poon LLM, Guan Y, Peiris JSM (2008): Novel Astroviruses in Insectivorous Bats. J. Virol. 82, 9107–9114.
    - Xiao J, Li J, Hu G, Chen Z, Wu Y, Chen Y, Chen Z et al. (2011): Isolation and Phylogenetic Characterization of Bat Astroviruses in Southern China. Arch. Virol. 156, 1415–1423.
    - Hu B, Chmura AA, Li J, Zhu G, Desmond JS, Zhang Y, Zhang W, Epstein JH, Daszak P, Shi Z (2014): Detection of Diverse Novel Astroviruses from Small Mammals in China. J. Gen. Virol. 95, 2442–2449.
  + Germany/Hungary
    - Drexler JF, Corman VM, Müller MA, Maganga GD, Vallo P, Binger T, Gloza-Rausch F, et al. (2012): Bats Host Major Mammalian Paramyxoviruses. Nat. Commun. 3, 796.
    - Fischer, K.; Zeus, V.; Kwasnitschka, L.; Kerth, G.; Haase, M.; Groschup, M.H.; Balkema-Buschmann, A. Insectivorous bats carry host specific astroviruses and coronaviruses across different regions in Germany. Infect. Genet. Evol. 2016, 37, 108–116. [CrossRef] [PubMed]
    - Kemenesi, G.; Dallos, B.; Gorfol, T.; Boldogh, S.; Estok, P.; Kurucz, K.; Kutas, A.; Foldes, F.; Oldal, M.; Nemeth, V.; et al. Molecular survey of RNA viruses in Hungarian bats: Discovering novel astroviruses, coronaviruses, and caliciviruses. Vector Borne Zoonotic Dis 2014, 14, 846–855. [CrossRef] [PubMed]
    - Kemenesi, G.; Dallos, B.; Gorfol, T.; Boldogh, S.; Estok, P.; Kurucz, K.; Oldal, M.; Nemeth, V.; Madai, M.; Banyai, K.; et al. Novel European lineages of bat astroviruses identified in Hungary. Acta Virol. 2014, 58, 95–98. [CrossRef] [PubMed]
  + Czech republic
    - Dufkova, L.; Strakova, P.; Sirmarova, J.; Salat, J.; Moutelikova, R.; Chrudimsky, T.; Bartonicka, T.; Nowotny, N.; Ruzek, D. Detection of Diverse Novel Bat Astrovirus Sequences in the Czech Republic. Vector Borne Zoonotic Dis. 2015, 15, 518–521.
  + Cambodia
    - Lacroix, A.; Duong, V.; Hul, V.; San, S.; Davun, H.; Omaliss, K.; Chea, S.; Hassanin, A.; Theppangna, W.; Silithammavong, S.; et al. Diversity of bat astroviruses in Lao PDR and Cambodia. Infect. Genet. Evol. 2016, 47, 41–50.
  + Gabon
    - Rougeron, V.; Suquet, E.; Maganga, G.D.; Jiolle, D.; Mombo, I.M.; Bourgarel, M.; Motsch, P.; Arnathau, C.; Durand, P.; Drexler, F.; et al. Characterization and phylogenetic analysis of new bat astroviruses detected in Gabon, Central Africa. Acta Virol. 2016, 60, 386–392.
  + Pteropodidae
    - Table

      Description automatically generated
* Astros detected in a large variety of bats
  + Fischer K, dos Reis VP, Balkema-Buschmann A et al. Towards understanding the transmission dynamics of a neglected virus family. Viruses 2017; 9: 34.
* Detection varies widely depending on study design and tested species
  + Fischer K, dos Reis VP, Balkema-Buschmann A et al. Towards understanding the transmission dynamics of a neglected virus family. Viruses 2017; 9: 34.
* Compositions of Malagasy bat spp assemblages are correlated with factors associated with the diversity and transmission of infectious agents
  + Mélade J, Wieseke N, Ramasindrazana B et al. An eco-epidemiological study of Morbilli-related paramyxovirus infection in Madagascar bats reveals host-switching as the dominant macro-evolutionary mechanism. Sci Rep 2016; 6: 23752.
  + Gomard Y, Dietrich M, Wieseke N et al. Malagasy bats shelter a considerable genetic diversity of pathogenic Leptospira suggesting notable host-specificity patterns. FEMS Microbiol Ecol 2016; 92: 1–12.
* General?
  + Fischer K, dos Reis VP, Balkema-buschmann A. Bat Astroviruses: towards understanding the transmission dynamics of a neglected virus family. Viruses. 2017;9:34.
* African6–13 bat astrovirus epidemiology isn’t well known
  + Rougeron V, Suquet E, Maganda GD, Jiolle D, Mombo IM, Bourgarel M, et al. Characterization and phylogenetic analysis of new bat astroviruses detected in Gabon, Central Africa. Acta Virol. 2016;60:386–92.
  + Waruhiu C, Ommeh S, Obanda V, Agwanda B, Gakuya F, Ge XY, et al. Molecular detection of viruses in Kenyan bats and discovery of novel astroviruses, caliciviruses and rotaviruses. Virol Sin. 2017;32:101–14
* AstV’s reported in African insectivorous bats, in particular app of Miniopteridae and Rhinonycteridae
  + Hoarau, F.; Le Minter, G.; Joffrin, L.; Schoeman, M.C.; Lagadec, E.; Ramasindrazana, B.; Lebarbenchon, C. Bat astrovirus in Mozambique. Virol. J. 2018, 15, 1–5
  + Rougeron, V.; Suquet, E.; Maganda, G.D.; Jiolle, D.; Mombo, I.M.; Bourgarel, M.; Leroy, E.M. Characterization and phylogenetic analysis of new bat astroviruses detected in Gabon, Central Africa. Acta Virol. 2016, 60, 386–392.
  + Waruhiu, C.; Ommeh, S.; Obanda, V.; Agwanda, B.; Gakuya, F.; Ge, X.Y.; Shi, Z.L. Molecular detection of viruses in Kenyan bats and discovery of novel astroviruses, caliciviruses and rotaviruses. Virol. Sin. 2017, 32, 101–114.
  + Yinda, C.K.; Ghogomu, S.M.; Conceição-Neto, N.; Beller, L.; Deboutte, W.; Vanhulle, E.; Matthijnssens, J. Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. Virus Evol. 2018, 4, 1–15.
* Temporal variation in shedding
  + Drexler JF, Corman VM, Wegner T, Tateno AF, Zerbinati RM, Gloza-Rausch F, et al. Amplification of emerging viruses in a bat colony. Emerg Infect Dis. 2011;17:449–56.
* Risk of spillover demonstrated to coincide with changes in bat behavior and population structure
  + Plowright RK, Foley P, Field HE, Dobson AP, Foley JE, Eby P, et al. Urban habituation, ecological connectivity and epidemic dampening: the emergence of Hendra virus from flying foxes (Pteropus spp.). Proc Biol Sci. 2011;278:3703–12.
* Body condition and coinfection have been shown to be positively correlated with AstV infection in bats
  + Mendenhall, I.H.; Skiles, M.M.; Neves, E.S.; Borthwick, S.A.; Low, D.H.W.; Liang, B.; Smith, G.J.D. Influence of age and body condition on astrovirus infection of bats in Singapore: An evolutionary and epidemiological analysis. One Health 2017, 4, 27–33.
  + Seltmann, A.; Corman, V.; Rasche, A.; Drosten, C.; Czirjak, G.; Bernard, H.; Voigt, C. Seasonal fluctuations of astrovirus, but not coronavirus shedding in bats inhabiting human-modified tropical forests. Ecohealth 2017, 14, 272–284.
* Detection rates in insectivorous bats
  + Chu DKW, Poon LLM, Guan Y et al. Novel astroviruses in insectivorous bats. J Virol 2008; 82: 9107–9114.
  + Fischer K, Zeus V, Kwasnitschka L et al. Insectivorous bats carry host specific astroviruses and coronaviruses across different regions in Germany. Infect Genet Evol 2016; 37: 108–116.
  + Lebarchenon
* Mainly fecal samples but also urine, albeit cross-contamination of fecal and urine samples cannot be ruled out
* Some cluster with humans, but with weak support
  + Chu, D.K.W.; Poon, L.L.M.; Guan, Y.; Peiris, J.S.M. Novel astroviruses in insectivorous bats. J. Virol. 2008, 82, 9107–9114.
* Sequences with a close relationship to ungulate and porcupine hosts as well as to murines!!
  + Lacroix, A.; Duong, V.; Hul, V.; San, S.; Davun, H.; Omaliss, K.; Chea, S.; Hassanin, A.; Theppangna, W.; Silithammavong, S.; et al. Diversity of bat astroviruses in Lao PDR and Cambodia. Infect. Genet. Evol. 2016, 47, 41–50
* Also just clustering in other ways -- more similar to other things than to other bats
  + Fischer, K.; Zeus, V.; Kwasnitschka, L.; Kerth, G.; Haase, M.; Groschup, M.H.; Balkema-Buschmann, A. Insectivorous bats carry host specific astroviruses and coronaviruses across different regions in Germany. Infect. Genet. Evol. 2016, 37, 108–116.
  + Zhu, H.C.; Chu, D.K.W.; Liu, W.; Dong, B.O.; Zhang, S.Y.; Zhang, J.X.; Li, L.F.; Vijaykrishna, D.; Smith, G.J.D.; Chen, H.L.; et al. Detection of diverse astroviruses from bats in China. J. Gen. Virol. 2009, 90, 883–887.
  + Xiao, J.; Li, J.; Hu, G.; Chen, Z.; Wu, Y.; Chen, Y.; Chen, Z.; Liao, Y.; Zhou, J.; Ke, X.; et al. Isolation and phylogenetic characterization of bat astroviruses in southern China. Arch. Virol. 2011, 156, 1415–1423.

Astroviruses in Madagascar Bats

Astroviruses in SWIO Bats

**Specific papers**

Astroviruses in SWIO Bats

* Hoarau
  + Mayotte
    - 0% detection!
  + Mozambique
    - 52/259 (20.1% +-4.9%)
  + **Hipposiderae**, **minopteridae**, **molossidae**, **nycteridae**, rhinolophidae, **rhinocyteridae**, vespertillionidae
    - Significant differences between species
    - Significant differences between two sampling periods
    - Not between males and females
  + High genetic diversity (pairwise distance up to 45%)
  + Fair enough of phylogenetic clustering, some not
* Joffrin
  + Free tailed bat guano sampling
    - 7.1% positive guano samples
    - No differences between sampling location along transect
    - No variation between season
    - Significant variation between sampling dates
      * Suggests potential effect of pop age structure instead of changes in size and density
  + Samples collected before cave was occupied by bats tested positive for AstV
    - Environmental persistence – favor bat infection during cave colonization, create opportunity for virus to spillover to other species
  + High genetic diversity
  + Did not cluster in a single bat astrovirus clade
    - Couldn’t say for sure that samples came from bats

Astros in Madagascar bats

* Lebarchenon
  + Locations
    - Ambohitantely
      * Myotis guodoti in cave
      * Mormopterus jugularis in public school
    - Anjohibe
      * Multiple spp?
  + 40 of 178 tested positive for RdRp (mean 22.5% +- 6.13%)
    - Variation between sites (1.96%+-3.81%) and (30.7%+-8.02%)
      * Sampling bias or spp/site variation in infection
  + Phylogeny
    - High genetic sequence diversity
      * Viruses from same spp more related to other spp than each other
    - Close proximity of roosting sites may favor virus transmission between species
    - Astv’s may spread easily between bat populations
  + \*\*Malagasy bats may act as reservoirs of a large diversity of AstV’s
  + Further epidemiological work is necessary
  + Assess risk of zoonotic transmission of bat-origin AstVs
    - Source-attributed case-control studies

Astroviruses in African Bats

\*Rougheron – Gabon

* 45/193 – 4.57%
* Varied but present among all 5 species
  + Insectivorous and frugivorous
* Varied among location
* Pteropodidae! 4.57%
* All bat astrovirus sequences were genetically divergent from the sequences of astroviruses infecting humans and other mammals
* No clustering by location
* 43/44 sequences clustered within four bat AstV groups characterized by host
  + Suggests low degree of host species restriction within bat species and high capacity of adaptation to different bat species
  + In line with occurrence of multiple cross-species transmission events among different bat species, and probably other mammal species, that is facilitated by the bat lifestyle (co roosting, migration intermingling), the astrovirus tropism and the oral-fecal transmission of these viruses

Astros in Bats

\*Fischer et al 2017 – Bat astroviruses: towards understanding the transmission dynamics of a neglected virus family

* 19 species of mamastroviruses have been identified in wide geographic range of domestic animals, in wildlife including bats, and in humans
* In bats, astroviruses were found mostly in apparently healthy animals
* Since 2008, a growing number of bat species have been found to carry astroviruses with notable prevalence and diversity
* Most PCR-based screenings, isolates and/or **full-length genomes are still lacking**
* ? whether astroviruses might persistently infect bats without causing any clinical symptoms
  + Also observed for many highly pathogenic viruses such as henipas and filos
* Due to lack of virus isolates and experimental data, pathogenicity and shedding pattern of astros is not well understood
* Detection rates varied greatly depending on study designs and tested species
  + Highest in myotis – often around 40% or higher
* High degree of sequence variation among bat astroviruses
* Some showed little host restriction, others clustered to certain bat species
* some from same spp collected at different locations clustered together
  + Zhu, H.C.; Chu, D.K.W.; Liu, W.; Dong, B.O.; Zhang, S.Y.; Zhang, J.X.; Li, L.F.; Vijaykrishna, D.; Smith, G.J.D.; Chen, H.L.; et al. Detection of diverse astroviruses from bats in China. J. Gen. Virol. 2009, 90, 883–887.
  + Fischer, K.; Zeus, V.; Kwasnitschka, L.; Kerth, G.; Haase, M.; Groschup, M.H.; Balkema-Buschmann, A. Insectivorous bats carry host specific astroviruses and coronaviruses across different regions in Germany. Infect. Genet. Evol. 2016, 37, 108–116.
* High genetic diversity of astroviruses observed in bats of the same species of the same habitat at one time point, suggesting the circulation of multiple strains within a population – in accordance with other studies
* Current data indicate that bats may carry both host restricted astroviruses as well as more diverse strains that may cluster together with other important members of the Mamastrovirus genus and even with members of the Avastrovirus genus.
* More detailed sequence data will be necessary for further analyses and to predict the potential for recombination or cross-species transmission
* \* bats have been investigated and phylogenetically characterized since 2008, resulting in the detection of a wide geographic distribution, a great genetic diversity, and a varying degree of host restriction
* The ICTV defined an amino acid sequence diversity in the capsid gene of <0.312 and >0.378 within and between astrovirus species, respectively.
  + But since most Astros are PCR RdRp, full lengths are super important
* Genetic diversity of bat astroviruses seems to be remarkable
* Co-occurrence of different strains within bat colonies might favor the potential of co-infection of individuals with multiple strains at the same time
* Therefore, recombination events between different bat strains seem possible
  + Lead to novel virus strains to which the affected hosts have lower immunity, or enable viruses to cross species barriers
* Although Astros have been considered relatively species-specific in the past, the incidence of recombination events combined with widespread infections across many animal species and the high genetic diversity may generally permit the emergence of novel astroviruses from certain hosts with zoonotic potential
* The overall risk for astrovirus transmission from bats to humans is assumed to be relatively low and does not, to our current understanding, exceed the risk of an astrovirus transmission from other mammals such as minks, pigs, or cattles, to humans

Yinda – Cameroonian fruit bats harbor diverse viruses

* Fruit bats – Eidolon helvum and Epomophorus gambianus
* South-west region of Cameroon
* Fecal samples

Luis – A comparison of bats and rodents as reservoirs of zoonotic viruses: are bats special?

* Traits that make bats suited to hosting more viruses in general include
  + Relatively long lifespans for their body size, which may facilitate viral persistence for chronic infections
    - Munshi-South J, Wilkinson GS. 2010 Bats and birds: exceptional longevity despite high metabolic rates. Ageing Res. Rev. 9, 12 –19. (doi:10.1016/j.arr.2009. 07.006)
  + Reliance of some on prolonged torpor, which can decrease viral replication and immune function
    - Dempster G, Grodums EI, Spencer WA. 1966 Experimental Coxsackie B-3 virus infection in Citellus lateralis. J. Cell. Physiol. 67, 443–454. (doi:10.1002/ jcp.1040670309)
    - Prendergast BJ, Freeman DA, Zucker I, Nelson RJ. 2002 Periodic arousal from hibernation is necessary for initiation of immune responses in ground squirrels. Am. J. Physiol. Regul. Integr. Comp. Physiol. 282, R1054–R1062
  + Fight, allowing movement and dispersal over long distances
  + Gregarious, living in dense aggregations
  + Roosting sites can host a diverse assemblage of multiple bat species
    - Kuzmin IV, Mayer AE, Niezgoda M, Markotter W, Agwanda B, Breiman RF, Rupprecht CE. 2010 Shimoni bat virus, a new representative of the lyssavirus genus. Virus Res. 149, 197 –210. (doi:10. 1016/j.virusres.2010.01.018)
    - Kunz TH. 1982 Ecology of bats. New York, NY: Plenum Press.
  + High intra and interspecific contact rates can facilitate rapid transmission of pathogens and large population sizes could sustain acute-immunizing infections
* Traits that make bats more likely to host zoonoses in particular and/or transmit them to humans
  + Bats are ancient mammals and it has been hypothesized that viruses which evolved in bats may use highly conserved cellular receptors, thus enhancing their ability to transmit viruses to other mammals
    - Calisher CH, Childs JE, Field HE, Holmes KV, Schountz T. 2006 Bats: important reservoir hosts of emerging viruses. Clin. Microbiol. Rev. 19, 531–545. (doi:10.1128/CMR.00017-06)
  + Human contact – bushmeat
    - Mickleburgh S, Waylen K, Racey P. 2009 Bats as bushmeat: a global review. Oryx 43, 217–234. (doi:10.1017/S0030605308000938)
  + \*bats, on average, host more significantly zoonotic viruses than rodents
  + \*higher mass and longevity and more litters per year

Jenkins – Bats as bushmeat in Madagascar

Mickleburgh – Bats as Bushmeat: a global review

* Bats are eaten by people throughout Madagascar
* Larger species like p rufus, e dup, and r mada are preferred
* National hunting season is widely ignored and both unsuitable hunting practices and high takeoff represent a serious threat to bat populations in some areas

Drexler – Amplification of emerging viruses in a bat colony

* Astv’s showed 65-86% amino acid identities with related bat-associated AstVs from China
* Paraphyly of bats
* No amplification associated with parturition in the same samples
  + Detection rate 51.2% before birth and 40.5% after
* Viral host switching is probably determined by the chances of interspecies contact as well as by the concentration and prevalence of virus in the donor species
* Initial peak in annual AstV prevalence observed in study probably due to formation of a contiguous population of sufficient size and density, bringing together enough bats to establish a critical basic reproductive rate of infection
  + Edmunds WJ, Gay NJ, Kretzschmar M, Pebody RG, Wachmann H. The pre-vaccination epidemiology of measles, mumps and rubella in Europe: implications for modelling studies. Epidemiol Infect. 2000;125:635–50. DOI: 10.1017/S0950268800004672
  + Farrington CP, Whitaker HJ. Estimation of effective reproduction numbers for infectious diseases using serological survey data. Biostatistics. 2003;4:621–32. DOI: 10.1093/biostatistics/4.4.621
* Second amplification peak most probably associated with establishment of a susceptible population of newborn bats who had not yet mounted their own adaptive immunity
* AstVs underwent postparturition amplification when a new virus lineage gained predominance in the population
  + Strongly indicates antigen specific immune control of virus circulation

Melade – an eco-epidemiological study of morbilli-related paramyxovirus infection in Madagascar bats reveals host-switching as the dominant macro-evolutionary mechanism

* Host-switching: new host-parasite combination that results from the shift of the parasite to a new host and its subsequent specialization
* Colonization by a parasite of a phylogenetically closely related host species, often of the same genus or family, has been proven to be the typical macro-evolutionary mechanism for RNA viruses
  + Kitchen, A., Shackelton, L. A. & Holmes, E. C. Family level phylogenies reveal modes of macroevolution in RNA viruses. Proc. Natl. Acad. Sci. USA 108, 238–243, doi: 10.1073/pnas.1011090108 (2011).
* Gregarious roosting behavior of bats and as assortment of different ecological parameters (climate, season, migration) are important factors that can help shape viral transmission dynamics, which subsequently act upon evolutionary processes
  + Luis, A. D. et al. A comparison of bats and rodents as reservoirs of zoonotic viruses: are bats special? Proc. Biol. Sci. 280, 20122753, doi: 10.1098/rspb.2012.2753 (2013).
  + Luis, A. D. et al. Network analysis of host-virus communities in bats and rodents reveals determinants of cross-species transmission. Ecol. Lett, doi: 10.1111/ele.12491 (2015).
  + Streicker, D. G., Lemey, P., Velasco-Villa, A. & Rupprecht, C. E. Rates of viral evolution are linked to host geography in bat rabies. PLoS Pathog. 8, e1002720, doi: 10.1371/journal.ppat.1002720 (2012)
* \*Species co-occupy roost sites in caves, buildings, or tree cavities in different species combinations and varying numbers
* \*Considering notable species diversity and high levels of endemism in Malagasy bats, as well as varying community structure and ecological conditions in which they occur, Madagascar provides an excellent context to study the transmission of viruses in these animals
* \*31 sites contained at least two species, 21 sites were monospecific
* \*infection rates of PV highest in caves, as compared to buildings and forests (12.9%, 7.9%, 7.9%)
* \*fraction of sites hosting PV positive bats among 31 multispecies sites and 21 monospecific sites were 70.9% and 61.9%, respectively
* \*infection rates for PV were 11.4% in multispecies sites and 8.1% in monospecific sites
* \*infection rates varied from 0% - 38.1%
* \*”although UMRVs showed weak exclusivity to their bat host species”
* \*closely related UMRV sequences were hosted by bat species and families that are phylogenetically closely related, particularly those occupying day roost sites in the same caves
  + \*this feature suggests that host-switching events might be favored by physical proximity between phylogenetically closely related bat taxa
* \*some degree of host specificity was found, with indls of one host species having closely related umrvs, independent of other individuals occurring at the same site
* \*increasing geographical distance favors genetic differentiation and/or low levels of virus migration between bat roosting sites
* \*host-switching events appear to be the predominant aspect in the evolutionary history in UMRVs identified from Malagasy bats, as compared to co-speciation
* \*environments supporting more species are positively associated to viral transmission, with a marginal effect of natural habitats (caves) being more prone to PV infection, whereas habitat type alone was not a significant predictor of infection
* Other studies on bat rabies transmission dynamics demonstrated the importance of sympatric occurrence for viral infection
  + Streicker, D. G. et al. Host phylogeny constrains cross-species emergence and establishment of rabies virus in bats. Science 329, 676–679, doi: 10.1126/science.1188836 (2010).
* The high detection rate in multispecies sites likely results from greater species diversity in caves, inducing a proximity effect between individuals(cite), which has been previously shown to promote virus transmission
  + Goodman, S. M. Les chauves-souris de Madagascar. Association Vahatra, Antananarivo, Madagascar (2011).
* \*further work correlating cave infection and multispecies host switching
* \*UMRVs much more active among insectivorous bats than frugivorous bats, with only 3.8% of the latter testing positive
* This follows trends of other SWIO islands
  + Wilkinson, D. A. et al. Highly diverse Morbillivirus-related paramyxoviruses in wild fauna of the southwestern indian ocean islands: evidence of exchange between introduced and endemic small mammals. J. Virol. 88, 8268–8277, doi: 10.1128/JVI.01211-14 (2014).
  + Wilkinson, D. A. et al. Identification of novel paramyxoviruses in insectivorous bats of the southwest indian ocean. Virus Res 170, 159–163, doi: 10.1016/j.virusres.2012.08.022 (2012).
* \*host-switching, as opposed to co-speciation, is the predominant macroevolutionary process
  + \*lack of congruence between bat and UMRV phylogenies
* \*BUT some urmvs infect different bat species or families, leading to observed phylogenetic ingcongruence
  + \*explained by rapid evolution of some RNA viruses which as a consequence of their higher mutation rate generate large quasi-species virus populations, allowing for greater chances after a host-jump to adapt to a new host, or in other words, to promote a better adapted variant that can be sustained in the new host
    - Domingo, E. et al. Viruses as quasispecies: biological implications. Curr. Top. Microbiol. Immunol. 299, 51–82 (2006).
    - More citations in paper for specific bat species/viruses
* \*viral allopatric process, in which a virus speciates within a host species living in different geographical areas, and giving rise to independent evolution
  + de Vienne, D. M. et al. Cospeciation vs host-shift speciation: methods for testing, evidence from natural associations and relation to coevolution. New Phytologist. 198, 347–385 (2013).
  + Kitchen, A., Shackelton, L. A. & Holmes, E. C. Family level phylogenies reveal modes of macroevolution in RNA viruses. Proc. Natl. Acad. Sci. USA 108, 238–243, doi: 10.1073/pnas.1011090108 (2011).
  + \*occurred for their three spp which have relatively broad distributions on Madagascar
* \*circulation of 7 major strains infecting a large host range
* \*significant linkage associations between species and their virus lineages
* \*genetic difference between different groups of bats does not seem to be a major constraint for host switching
* Genetic distances between bat species are a key factor for host-switching events
  + Kitchen, A., Shackelton, L. A. & Holmes, E. C. Family level phylogenies reveal modes of macroevolution in RNA viruses. Proc. Natl. Acad. Sci. USA 108, 238–243, doi: 10.1073/pnas.1011090108 (2011).
  + Streicker, D. G. et al. Host phylogeny constrains cross-species emergence and establishment of rabies virus in bats. Science 329, 676–679, doi: 10.1126/science.1188836 (2010).
  + Faria, N. R., Suchard, M. A., Rambaut, A., Streicker, D. G. & Lemey, P. Simultaneously reconstructing viral cross-species transmission history and identifying the underlying constraints. Philos. Trans. R. Soc. Lond. B. Biol. Sci. 368, 20120196, doi: 10.1098/ rstb.2012.0196 (2013).
* \*our data indicate that genetically closely related UMRVs infecting different bat species, sometimes occurring in geographically distinct areas, may suggest the intervention of a probably vector, capable to connect these different populations!!
  + Woolhouse, M. E., Haydon, D. T. & Antia, R. Emerging pathogens: the epidemiology and evolution of species jumps. Trends Ecol. Evol. 20, 238–244, doi: 10.1016/j.tree.2005.02.009 (2005)

Joffrin – Bat coronavirus phylogeography in the Western Indian Ocean

* SWIO have diverse geographical origins that have influenced the process of bat colonization and species distributions
  + O’Brien, J. Bats of the Western Indian Ocean islands. Animals 1, 259–290 (2011).
* \*conserved groups of CoVs mostly clustering by bat family
* \*Molossidae bats formed a highly supported monophyletic clade including CoV from continental Africa
* \*co-phylogeny results support co-evolution between WIO bats and their CoVs
* \*high diversity of CoVs in bats in western Indian ocean islands
* \*significant variation in the prevalence of infected bats according to their family, species, sampling location, and season
* \*affected by strong heterogeneity of bat communities in the island of the WIO, in particular in terms of species richness
* High CoV genetic diversity from Mozambique and Mada likely to be associated with the higher bat species diversity
  + O’Brien, J. Bats of the Western Indian Ocean islands. Animals 1, 259–290 (2011).
* \*CoV prevalence may significantly vary across species, temporally, with bat parturition
* \*a strong geographical influence on CoVs diversity, with independent evolution of CoVs on each island, was expected in our study because of spatial isolation and endemism of the tested bat species
* Dominant evolutionary mechanism for African cov’s was host switching
  + Anthony, S. J. et al. Global patterns in coronavirus diversity. Virus Evol. 3, vex012 (2017).
* \*congruence between host and viral phyogenies however suggests a strong signal for co-evolution between WIO bats and their associated CoVs
* \*geographical influence seems to occur within bat families, as for Molossidae
* \*endemism resulting from geographic isolation may thus have played a role in viral diversification within bat families
* \*they found potential miniopteridae a-cov in a rhinolophidae bat co-roosting with miniopteridae in the same cave
  + Also in Australia where miniopteridae a cov was detected in rhinolophidae bats
    - Smith, C. S. et al. Coronavirus infection and diversity in bats in the Australasian region. Ecohealth 13, 72–82 (2016).
* \*host switching events could be favored when several bat species roost in syntopy
  + Luis are bats special
* \*infrequent host-switching events indicate that spillvoers happen but suggest that viral transmission is not maintained in the receiver host species
* \*nucleotide similarity to human sequences 85-93%

O’Brien - Bats of the western Indian ocean islands

* Madagascar is a continental fragment, reunion and Mauritius are isolated volcanic mounts have a range from 2.1 to 15 million years ago, mayotte is a coral atoll that is relatively young
* Evolutionary history of bats on each island depends on whether the islands in question can be considered isolated ‘oceanic’ islands requiring long-distance aerial or marine dispersal, or have at some stage been attached to a larger continental landmass, facilitatring terrestrial dispersal of a vicariant fauna
* Typically, the vertebrate fauna of the western Indian ocean islands is African derived
  + Peake, J.F. The evolution of terrestrial faunas in the western Indian Ocean. Phil. Trans. Roy. Soc. Lond. B Biol. Sci. 1971, 260, 581-610.
* *Rousettus* considered to have colonized Africa via India or the Middle East rhough forested corridors and arrival on the islands is likely to have occurred secondarily to arrival on the African continent
  + Álvarez, Y.; Juste, J.B.; Tabares, E.; Garrido-Pertierra, A.; Ibáñez C.; Bautista, J.M. Molecular phylogeny and morphological homoplasy in fruit bats. Mol. Biol. Evol. 1999, 16, 1061-1067.
  + Giannini, N.P.; Simmons, N.B. A phylogeny of megachiropteran bats (Mammalia: Chiroptera: Pteropodidae) based on direct optimization analysis of one nuclear and four mitochondrial genes. Cladistics 2003, 19, 496-511.
  + Giannini, N.P.; Simmons, N.B. Conflict and congruence in a combined DNA-morphology analysis of megachiropteran bat relationships (Mammalia: Chiroptera: Pteropodidae). Cladistics 2005, 21, 411-437.
* Eidolon is solely African, although genus not appear to be closely related to any other African bat
  + Citation
* Sub-fossils of Rousettus and eidolon from a cave in northwestern madagasar have been dated to approx. 80000 years ago but certainly this can only be considered a minimum time span for the presence of these genera on the island
* Eidolon helvum roosts in emergent trees but has also been reported in caves (cite)
* Rousettus bats tend to maintain close body contact when roosting in caves to reduce the energetic costs of homeotherapy
* Trianops furculus and T. menamena primarily roost in caves and do frequent co-habit
* Plant germination was significantly higher from seeds taken from the faeces of either p rufus or e dup in 80% of the plants tested
* Four species of scotophilus spp (vespers) from mada are not monophyletic, indicative of multiple colonization events
* Various cave roosting species may often be found in close association such as miniopterus spp, myotis guodoti, emballonura, triaenops auritius