The discovery of a new ebolavirus Bombali virus: Further support for bats as hosts of ebolaviruses

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2014-2016 Ebola Virus Disease Outbreak



Ebolaviruses

- Despite more than 40 years of research and continued outbreaks, reservoir(s) remain unknown
- Five species to date: Zaire (EBOV), Bundibugyo (BDBV), Sudan (SUDV), Taï Forest (TAFV), and Reston ebolavirus (RESTV)
- Past outbreaks linked to contact with infected non-human primates
- Evidence suggests they are maintained in bats

Bats as Hosts

- EBOV RNA and antibodies found in bats across Africa, in Bangladesh, China, Singapore
- Other filoviruses found in bats: Marburg (Egyptian fruit bat) Lloviu (Schreiber's long-fingered bat)
- Evolutionary relationship between NPC1 in bats and filoviruses
- Index case in 2014 outbreak in West Africa believed to have contact with Angolan free-tailed insectivorous bat

Survey in Sierra Leone to identify hosts of EBOV and additional filoviruses in wildlife

Non-destructive animals sampling No human biological sampling

- Goal: 20,000 animals
 - Geographic distribution
 - Urban vs rural vs forest
 - Host species distribution
 - Reservoirs: bats, rodents, primates
 - Spillover hosts: dogs, cats, pigs, goats/sheep
 - Seasonality
 - Multiple samplings over time, dry vs wet season



Viral Discovery

- March to September 2016 1278 oral, rectal, blood samples from 535 animals: 244 bats, 46 rodents, 240 dogs, and 5 cats
- Samples screened:
 1) a nested filovirus 'family level' cPCR
 2) an *Ebolavirus* 'genus level' cPCR
 3) a real-time PCR specific for the EBOV
 4) BOMV load, quantitative real-time PCR
- Genome sequencing

	Bat Species	Bat Family	No. Tested	No. Positive by Filovirus cPCR	No. Positive by Ebolavirus genus PCR	No. Positive l qRT- PCR f(BOMV
	Insectivorous Rats					
$\boldsymbol{<}$	Chaerephon pumilus	Molossidae	55	3	2	4
	Glauconycteris poensis	Vespertillionidae	1			
	Hipposideros abae	Hipposiderdae	7			
	Hipposideros jonesi	Hipposiderdae	4			
	Hipposideros ruber	Hipposiderdae	50			
<	Mops condylurus	Molossidae	52	1		
	Myotis bocagii	Vespertillionidae	3			
	Neoromicia rendalli	Vespertillionidae	2			
	Nycteris hispida	Nycteridae	1			
	Pipistrellus nanulus	Vespertillionidae	3			
	Rhinolophus fumigatus	Rhinolophidae	3			
	Rhinolophus landeri	Rhinolophidae	1			
	Rhinopoma microphyllum	Rhinopomatidae	1			
	Scotophilus viridis	Vespertillionidae	26			
	Unidentified Chaerephon bat	Molossidae	1			
	Unidentified Molossid bat	Molossidae	1			
	Unidentified Hipposiderod bat	Hipposiderdae	1			
	Unidentified Nycterid bat	Nycteridae	3			
	Fruit Bats					
	Eidolon helvum	Pteropodidae	2			
	Epomophorus gambianus	Pteropodidae	1			
	Epomops buettikoferi	Pteropodidae	2			
	Micropteropus pusillus	Pteropodidae	2			
	Myonycteris angolensis	Pteropodidae	14			
	Unidentified Myonycteris/Enomonhorous bat	Pteropodidae	3			
	Unidentified Epomophorous bat	Pteropodidae	5			
	Total	1 toropoulduo	244	4	2	5

Viral Detection

Positive sampling site
Sampling site







Comparison to other Ebolaviruses



Ability to Infect Human Cells



Significance

- First full ebolavirus genome from a bat
- Strong evidence that bats are a natural reservoir of ebolaviruses
- Insectivorous bats play a role in ebolavirus ecology
- BOMV GP able to mediate entry into human cells, first critical step for spillover
- Suggests BOMV has zoonotic potential
- Bats found roosting inside houses, potential for human transmission
- Further studies needed to investigate whether exposure has actually occurred or if BOMV is pathogenic in humans

Future Directions

- Virus isolation and viral rescue ongoing
- Surveys to examine exposure in people
- Prevalence and patterns of shedding in bats
- Comparison to other ebolaviruses



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