

Ebola-Reston virus in pigs



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Ebolavirus Reston was detected in samples taken from pigs on two farms in the northern Philippines in mid-2008. This was the first known case of any of the filoviruses being detected in pigs anywhere in the world. Previously, filoviruses have only been isolated from humans and non-human primates, although serological evidence indicates that bats may also be infected with these viruses. Serological evidence of infection was also detected in six of 147 in-contact people tested as part of the investigation into this outbreak.

Although there has been no evidence that this outbreak has caused clinical disease in either pigs or in-contact humans,



The hammer-headed bat may be a reservoir of Ebola in Africa, say researchers. *Credit: Wikimedia.*

some concern has been expressed that pigs could serve as an amplifying host in much the same way that they did for the initial outbreak of Nipah virus, with subsequent transmission of infection to humans. The origin of the infection in these pigs is unknown, but is likely due to ongoing exposure to an as yet unknown reservoir host. Previous research implicates bats as the most likely suspect ¹.

Sequencing of the Ebola-Reston virus genome, recovered from these pigs, found some genetic variability, with three variants being identified from the one herd of pigs. For a virus which is relatively stable genetically (unlike influenza viruses) this level of divergence may indicate that this virus is not a recent import into the northern Philippines. It is likely to be prevalent in a reservoir host, which has close contact with pigs in this area, allowing multiple introductions to these herds.

Background

Outbreaks of clinical disease which caused increased levels of production loss in piggeries located to the north of Manila, the Philippines, in early- to mid-2008, prompted veterinary investigation by the Bureau of Animal Industry (BAI), Department of Agriculture of the Philippines.

Atypical porcine reproductive and respiratory syndrome (PRRS) was suspected as the primary cause. This disease agent had been implicated in causing significant disease in pigs in other parts of the Philippines as well as in China and Vietnam.

Blood and tissue samples for analysis were obtained from 28 pigs originating from four piggeries, located in Santo Nino in Bulacan province, Pinagpanaan in Nueva Ecija province and Manaoag in Pangasinan province, all to the north of Manila.

These samples were sent to the United States Department of Agriculture – Foreign Animal Disease Laboratory – at Plum Island, New York for classical and molecular virological analysis.

Results provided by Plum Island on 30 October 2008 confirmed the presence of atypical PRRS virus (an arterivirus) with 98% homology to the Vietnamese strain, as well as porcine circovirus-2 (PCV-2). In addition, there was an incidental finding of Ebola-Reston virus (a filovirus) in six of the 28 samples, detected using a microarray. These results were confirmed by the Centers for Disease Control (CDC), which isolated the Ebola-Reston virus and sequenced it ².

In response to the current outbreak, the Philippines authorities quarantined the affected farms and instigated testing of pigs and in-contact workers and their families. Following evidence of ongoing viral replication in the pigs on one farm, the decision was taken to depopulate this farm, which resulted in the slaughter of

approximately 6000-6500 pigs. The Philippines authorities, in cooperation with the World Health Organization, the Food and Agriculture Organization and the World Organization for Animal Health, will continue to conduct surveillance of pigs and humans for further evidence of this virus, as well as to examine potential reservoir host species, specifically bats.

Current knowledge

Ebola haemorrhagic fever virus (Ebola) is a member of the family Filoviridae which it shares with Marburg virus. These are RNA viruses with a single negative genomic strand.

Ebola-Reston is one of five currently identified strains of Ebola virus and is often referred to as the Asian filovirus. Other members include Zaire, Sudan, Cote d'Ivoire and Bundibugyo strains, all of African origin.

The five currently identified Ebola strains have diverged from a common ancestor and show complete genomic (nucleotide) divergence of 32-45%. Similarly Marburg virus shows a 72% divergence of nucleotide sequences from any of the Ebola group³. This suggests that these viruses are diverging due to transcription errors of the RNA genome during replication. This level of mutation is approximately similar to that seen in adenoviruses but less than that observed with influenza viruses.

Significant points include

- No reservoir host is known for any of the strains. However, recent serological and polymerase chain reaction analysis suggests that three species of arboreal bats may be carriers of Ebola-Sudan and other work has implicated a cave dwelling fruit bat as a natural host for Marburg virus⁴
- The mode of transmission from the unknown reservoir host to hosts in which clinical disease occurs (primates) is unknown. It is unknown whether any vector (arthropod or other) is involved.

Ebola-Reston

This variant of Ebola was first identified in cynomolgus monkeys (crab-eating macaques) imported from the Philippines to the Hazelton Laboratories in Virginia, USA in late 1989. This virus was discovered during the investigation of an extensive mortality event involving these monkeys, which was probably primarily caused by a co-infection with simian haemorrhagic fever virus (SHFV).

Further investigation showed that this new variant of the Ebola filovirus family was unlike previously known Ebola strains in that, although it caused disease and mortality in monkeys, it only caused subclinical infections in humans exposed to the virus. Secondly, this virus was able to be transmitted via the respiratory route through the production of infectious aerosols by viraemic monkeys.

In 1990 and 1993, investigations lead by the CDC Special Pathogens Branch revealed a low level of seropositive monkeys being imported from the Philippines and Indonesia, but field trips to these locations failed to isolate the virus from animals tested^{3,5}.

Discussion

Of all of the significant pathogens of humans, the filoviruses are perhaps the most cryptic. Monath, 1999¹, has written a very interesting paper exploring alternative theories on the ecology of the filoviruses.

The most accepted theory is that the reservoir host is a cryptic species, which has little interaction with the spillover hosts or is rarely infectious, due to low disease prevalence in the metapopulation.

The leading contenders for the cryptic maintenance host are various species of bats. Although much of the evidence for this is circumstantial, bats have shown similar ecological patterns with henipaviruses, which as paramyxoviruses share similar genomic characteristics with filoviruses and rhabdoviruses^{3,4}. These animals often show low seroprevalence and unusual patterns of infection with these families of viruses, which is unlike any other mammalian hosts.

The story could be even more complicated if the maintenance host was not a vertebrate but rather an arthropod which transmitted the infection to an intermediate vertebrate host through either blood-feeding and transfer of the virus through saliva or through being eaten by the intermediate vertebrate host. Monath¹ draws parallels with African swine fever and ticks.

Further investigations are needed to elucidate the ecology of Ebolavirus Reston and the potential threat posed by this newly emergent transboundary infectious agent.

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Dr Lee is a veterinary pathologist and epidemiologist with an interest in emerging infectious diseases, especially zoonoses. He has extensive experience in field-based surveillance and diagnosis associated with these diseases.