

Does the dangerous new Middle East coronavirus have an African origin?

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In this animal the scientists from the University Bonn (Germany) and from South Africa found a virus that ist genetically more closely related to MERS-CoV than any other known virus. Credit: M Corrie Schoeman/University of KwaZulu-Natal

The MERS-coronavirus is regarded as a dangerous novel pathogen: Almost 50 people have died from infection with the virus since it was first discovered in 2012. To date all cases are connected with the Arabian peninsula. Scientists from the University Bonn (Germany) and



South Africa have now detected a virus in the faeces of a South African bat that is genetically more closely related to MERS-CoV than any other known virus. The scientists therefore believe that African bats may play a role in the evolution of MERS-CoV predecessor viruses. Their results have just been published online in the journal "*Emerging Infectious Diseases*".

Infection with the novel "Middle East Respiratory Syndrome Coronavirus" or MERS-CoV has been diagnosed in 90 patients so far, half of whom have died. In severe cases, patients develop pneumonia and <u>acute kidney failure</u>. All cases so far are – sometimes indirectly through infected family members or close contacts – connected with the Arabian peninsula.

A collaboration of researchers from the Institute of Virology at the University Bonn, Germany, the University of Stellenbosch and several other South African institutions have recently found evidence that MERS-CoV could possibly originate from <u>bats</u> occurring in southern Africa. The South African scientists, headed by Prof. Wolfgang Preiser, tested faecal material from a total of 62 bats from 13 different species for coronaviruses. In collaboration with their colleagues in Bonn, headed by Dr. Jan Felix Drexler, they investigated the <u>genetic material</u> of the viruses that they found.

In a faecal sample from a bat of the species Neoromicia cf. zuluensis they found a virus that is genetically more closely related to MERS-CoV than any other known virus. They believe that MERS-CoV may originally come from bats and may have reached the human population via other animals acting as intermediate hosts.

Search for MERS-CoV progenitor should include Africa



This finding was made in one individual bat only, but nevertheless serves as an important pointer. When searching for the origin of MERS-CoV, Africa should be taken into account, in addition to the Arabian peninsula. This work is as important as searching for treatment, because once the origin and modes of spread are known, the risk for human beings can be minimised. An example for the spread of MERS-CoV could be Rift Valley fever that, coming from East Africa, caused outbreaks in Saudi Arabia and Yemen in 2000.

Further studies of bats and potential interim hosts are urgently needed to elucidate the origin of MERS-CoV. Finding a closely related virus in a bat does not mean that human beings can become infected directly through exposure to the bats. It should not be misunderstood as indicating a health risk from bats and does by no means justify their persecution; on the contrary, bats provide value to ecosystems in several respects and should enjoy strict protection. It is however likely that bats are the natural hosts for the virus, and that human infections are the result of contact with other animals such as camels acting as intermediate hosts. At this stage there is probably also direct human-tohuman transmission.

More information: *Emerging Infectious Diseases* <u>DOI:</u> <u>10.3201/eid1910.130946</u>

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