

# New coronavirus related to viruses from bats

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The virus that is causing alarm among global public health authorities after it killed a man in Jeddah, Saudi Arabia earlier this year and is now linked to two other cases of disease is a novel type of coronavirus most closely related to viruses found in bats, according to a genetic analysis to be published in *mBio* on November 20. Researchers studied the genome of the HCoV-EMC/2012 virus in detail to learn about its relatedness to other viruses and about possible sources. The results of the sequencing and analysis could be used to develop diagnostic methods and possibly in creating therapies and vaccines if they are eventually needed for this emerging disease.

"The [virus](#) is most closely related to [viruses](#) in bats found in Asia, and there are no human viruses closely related to it," says Ron Fouchier of the Erasmus Medical Center in the Netherlands, who headed up the study. "Therefore, we speculate that it comes from an animal source."

The case in Saudi Arabia earlier this year, in which a 60-year-old man suffered from acute [pneumonia](#) and [renal failure](#) before his death, reminded public health authorities around the world of the threat posed by coronaviruses, a group that includes the the [SARS virus](#), a pathogen that emerged in 2002 and eventually lead to the deaths of more than 900 people.

The HCoV-EMC/2012 virus is under increasing scrutiny today as two other patients suffering from infections with similar viruses have been identified. Since the patient in Saudi Arabia died in June, an individual from Qatar has been diagnosed with a very similar condition and is

currently being cared for at a hospital in London. The full [genomic sequence](#) of the virus from that patient was made available on November 13, and Fouchier says it is a very close match with the HCoV-EMC/2012 virus sequence he analyzed in the *mBio* paper, showing only 99 single [nucleotide](#) differences (in an unpublished analysis).

"That makes it clear they are the same species. Ninety-nine nucleotides on the full genome amounts to only 0.3 – 0.4% difference," says Fouchier. "That, of course raises new questions."

Now a third case of illness from this new virus has been identified, this time in Saudi Arabia again, but the [genome sequence](#) of that virus is not yet available.

The genome of the HCoV-EMC/2012 virus that is the focus of the *mBio*® study was fully sequenced within a few days by combining an optimized random amplification deep sequencing approach, which covered about 90% of the genome, with conventional Sanger sequencing to confirm these draft findings.

Phylogenetic analyses place the virus within the *Betacoronavirus* genus, where its closest fully sequenced relatives are viruses called BtCoV-HKU4 and BtCoV-HKU5, both of which were originally isolated in Asia from Lesser bamboo bats (*Tylonycteris pachypus*) and Japanese house bats (*Pipistrellus abramus*), respectively. HCoV-EMC/2012 bears only 77% sequence similarity with the BtCoV-HKU5 virus, however, making it distinct enough to be called a novel species of virus, says Fouchier. A partial sequence from a virus that was isolated from a species of bat in the Netherlands appears to be a closer match with HCoV-EMC/2012, but without a full genome sequence the exact degree of relatedness is impossible to tell.

Based on the similarities the HCoV-EMC/2012 virus shares with viruses

from bats, and taking into account a separate serological study carried out in Saudi Arabia that showed 2,400 hospital visitors had no antibodies to the virus, Fouchier feels confident saying the virus is new to humans. That source may well be bats, he says, since *Pipistrellus* bats are present in Saudi Arabia and neighboring countries.

The relatedness between the HCoV-EMC/2012 virus and the virus that infected the patient in the unnamed London hospital is interesting, says Fouchier, since they are similar enough to be the same species but different enough that they are probably not directly linked. "It is unlikely they would be infected from the same source. We really need to understand whether these viruses are coming from a single source or multiple sources" before more cases come to light, he says.

In addition to the insights it provides for identifying the source of the virus and linking cases of illness together, the genome sequence of the HCoV-EMC/2012 virus will also enable scientists to study the virus in more detail. By making synthetic copies of the virus genome, Fouchier says scientists can reconstruct the virus in the lab and study its properties to identify the sources of its virulence.

The genome sequence could also be pivotal to protecting public health. "A well-annotated [genome](#) sequence is crucial to further the development of diagnostic methods and antivirals and vaccines that might be needed," says Fouchier. Considering that three cases of disease from the virus have already been identified, he says, "we certainly need the diagnostics already."

"Whether we would need antivirals and vaccines? Well, I certainly hope not," says Fouchier.

Provided by American Society for Microbiology

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