Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

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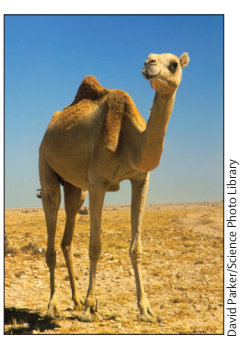
MERS-CoV: the intermediate host identified?

As of Aug 2, 2013, Middle East respiratory syndrome coronavirus (MERS-CoV) has caused 94 human cases—with most having severe respiratory disease—46 of these patients have died.[1] Cases have been reported in Jordan, Qatar, United Arab Emirates, Saudi Arabia, France, Germany, Italy, the UK, and Tunisia. All cases detected outside the Arabian peninsula were linked to one of the Middle Eastern countries, either as a result of travel to those countries or through transmission from a person thought to have acquired the infection there.

The high similarity of MERS-CoV to virus sequences detected in bats[2–5] suggests that it originates from bats. However, no one with the disease reported having direct contact with bats and bat-to-human transmission seems unlikely. The large geographical area of the MERS-CoV outbreak across the Arabian peninsula, the sequence variation between isolates, and the projected date of emergence some time before the first human cases were reported,[6,7] suggest multiple zoonotic introductions of MERS-CoV and could indicate the involvement of an intermediate host.

In *The Lancet Infectious Diseases*, Chantal Reusken and colleagues[8] provide some insight into one potential animal reservoir that might be involved in the emergence of MERS-CoV in people—for the first time since the discovery of the virus a year ago.[9] They detected neutralising antibodies in 100% of serum samples from 50 dromedary camels collected in Oman in March, 2013. Surprisingly, 15 (14%) of 105 of dromedary camels from the Canary Islands (Spain) also had such antibodies. Serum samples collected from various other livestock species did not contain MERS-CoV-specific antibodies, although they were not collected in the same area as the camels, thereby potentially indicating geographical rather than host restriction.

Whether the camels were infected with MERS-CoV itself or with a closely related virus is unclear. No human cases of infection have been reported in Oman so far, despite its proximity to countries with human cases and the high prevalence of neutralising antibodies against the virus in the local camel population. The detection of sequences similar to MERS-CoV in bats in Africa, the Americas, and Eurasia, and the presence of neutralising antibodies in camels from the Canary Islands suggest that MERS-CoV-like viruses have a wide geographical distribution. The absence of an association between the high prevalence of neutralising antibodies and morbidity or mortality in camels suggests that circulation of MERS-CoV-like viruses in camels might go undetected. This fact begs the question of whether the detection of MERS-CoV neutralising antibodies in camels from both Spain and Oman is a result of unrelated cross-species transmission events or whether the virus has been circulating in camels for a long time. Regardless, a change in the ecology of MERS-CoV must have occurred to enable emergence in people.



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This change could have been genetic, enabling the virus to efficiently replicate in the human respiratory tract, as happened with severe acute respiratory syndrome coronavirus, which acquired the ability to bind to human ACE2.[10] Alternatively, an environmental or agricultural change could have enabled the introduction of MERS-CoV into a new host species, similar to the establishment of pig farming in Malaysia that enabled cross-species transmission of Nipah virus into pigs and subsequent spillover to people.[11]

The report by Reusken and colleagues stresses the urgent need for an integrated, one health, approach by public and veterinary health stakeholders in all involved countries, combined with the rapid dissemination of data. Extensive serosurveys should be done across the Arabian peninsula, in people, livestock, and wild animal species, combined with virological testing where possible, to identify the potential reservoirs of MERS-CoV. In the absence of prophylactic or therapeutic treatment options for MERS-CoV,[12] blocking zoonotic and human-to-human transmission could be the most promising and cost-effective method to prevent further human fatalities. However, doing so requires knowledge of the virus' hosts. Although the study by Reusken and colleagues leaves many questions unanswered, it is an important step to a more comprehensive understanding of the emergence of MERS-CoV.

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Extensively resistant VIM-2-positive *Pseudomonas aeruginosa*

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The Article[1] by Mikhail V Edelstein and colleagues published in *The Lancet Infectious Diseases* serves as a warning of how bad antibiotic resistance has become. The researchers describe how a major hospital epidemic of the ST235 clone of *Pseudomonas aeruginosa* has spread within a few years throughout Belarus, Kazakhstan, and Russia. Although originally an environmental bacteria of little harm to healthy people, *P aeruginosa* has gained a frightening reputation as a cause of severe infections in people with impaired immune systems (eg, those with cystic fibrosis, burns, or leukaemia, or those undergoing invasive procedures), and it is now the third most common cause of nosocomial infections after *Escherichia coli* and *Staphylococcus aureus*.

P aeruginosa has propensity to acquire antibiotic-resistance mechanisms, and very few antibiotics are active against it. For a long time carbapenems were the last line of treatment. However, many *P aeruginosa* strains in Edelstein and colleagues' study were resistant to carbapenems as a result of production of VIM-2, an enzyme that hydrolyses carbapenems and other β-lactams, rendering all members of this antibiotic family