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Origins of MERS-CoV, and lessons for 2019-nCoV

In *The Lancet Planetary Health*, Sherif El-Kafrawy and colleagues did an enzootic genomic study in camels to analyse the genetic diversity, geographical origin, and infection prevalence of Middle East respiratory syndrome coronavirus (MERS-CoV).¹ Not long after the Article's publication in December, 2019, the 2019 novel coronavirus (2019-nCoV) was found in China, with patient zero suspected to have originated in Wuhan. Incidence of new cases and corresponding mortalities have been escalating daily.

The current 2019-nCoV public health emergency can take lessons from El-Kafrawy and colleagues' timely study. First, coronaviruses originated in animals before transferring to humans. El-Kafrawy and colleagues found that MERS-CoV was present in 22.8% of the camels sampled, indicating a high prevalence and even an occupational hazard for people who work with them. For example, camel shepherds are more likely to be infected. The authors further found that MERS-CoV presence was higher among local camels in Saudi Arabia than imported camels from African trade ports.¹ For 2019-nCoV, bats are the likely origin, based on sequencing evidence of samples in early patients who developed pneumonia, where researchers found an 85% identity with a previously

published genome of bat SARS-like coronavirus (bat-SL-CoVZC45, MG772933.1). The clade of 2019-nCoV is within the subgenus *Sarbecovirus*, *Orthocoronavirinae* subfamily.² How 2019-nCoV arrived in Wuhan is currently undetermined, but recent evidence shows 27 (66%) of 41 initial infected patients had direct exposure to Huanan seafood market.³ Public health officials should investigate whether other coronaviruses exist where 2019-nCoV is likely to have originated so as to prevent future epidemics, especially if infection is an occupational hazard.

Second, Saudi Arabian scientists confirmed that MERS-CoV is capable of human-to-human transmission. 2019-nCoV is also capable of human-to-human transmission, based on evidence of a Shenzhen-based family who visited infected family members in Wuhan and subsequently developed symptoms of acute respiratory disease syndrome, including shortness of breath, fever, weakness, and diarrhoea.⁴ This is most troubling given the time of year—the Spring Festival celebration, which sees a lot of movement to and around China, with people rushing home to celebrate and subsequently returning to their usual place or country of residence. Compared with containment of the SARS-CoV outbreak in 2003, China now has a far greater transportation capacity. The basic reproduction number of 2019-nCoV is evolving quickly, with estimates in mid-January of each case infecting 2.6 other people (uncertainty range 1.5–3.5).⁵

Stopping the disease will be best achieved by prevention at the source. Like John Snow, who removed the handle of the water pump on Broad Street following the cholera outbreak in London, public health officials need to find the key lever at the sources of disease through a greater understanding of the enzootic patterns.

I served as the Asia Editor of *The Lancet* in 2017.

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