

Middle East Respiratory Syndrome Coronavirus (MERS-CoV); Announcement of the Coronavirus Study Group

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During the summer of 2012, in Jeddah, Saudi Arabia a hitherto unknown coronavirus was
isolated from the sputum of a patient with acute pneumonia and renal failure (1, 2). The isolate
was provisionally called human coronavirus EMC (3). Shortly thereafter, September 2012, the
same type of virus, named human coronavirus England 1, was recovered from a patient with
severe respiratory illness, who had been transferred from the Gulf region of the Middle East to
London, United Kingdom (4, 5). The onset of the new disease was traced back to an even earlier
time point. Already in April 2012, a cluster of pneumonia cases in health care workers occurred in
an intensive care unit of a hospital in Zarqa, Jordan (6). Two persons died, both of which were
confirmed to have been infected with the novel coronavirus through retrospective analysis of
stored samples (7). These findings met with considerable concern. Although the number of cases
documented is limited (thirty as of 6 May 2013), the morbidity and mortality of the infection is
alarming, as is its uncanny resemblance -at least in its clinical features- to SARS. While a small
minority of the known cases developed mild disease, most patients presented with a severe acute
respiratory condition requiring hospitalization; the mortality rate is approximately 60% (8)

The infection appears to be geographically linked -at least for now- to the Middle East, in
particular the Arabian Peninsula, with patients originating from Jordan (n=2), Saudi Arabia
(n=17), Qatar (n=2) and the United Arab Emirates (n=1). The only two cases known to have
contracted the virus outside of the Middle East, became infected in the United Kingdom through
contact exposure to an index patient, shortly after the latter returned from a visit to Pakistan and
Saudi Arabia (9). Full length genome sequences determined for three independent virus isolates
from Saudi Arabia (3), Jordan (10) and the UK (5, 11) revealed more than 99% sequence identity
(~100 nucleotide variations in a 30,1 kb genome), indicating that these viruses diverged from a
common ancestor very recently.

Within the subfamily *Coronavirinae* (12), the novel virus is a representative of a new yet-
to-be established species in lineage C of the genus *Betacoronavirus*, which currently includes the
species *Tylonycteris bat coronavirus HKU4* and *Pipistrellus bat coronavirus HKU5* (Fig. 1) (3). The
novel coronavirus seems most closely related to as yet non-classified viruses from insectivorous
European and African bats in the *Vespertilionidae* and *Nycteridae* family, respectively (3, 11, 13-
15). Of note, for the latter viruses only partial genome sequences are available. The scarce
epidemiological data available suggest that the infection is primarily zoonotic in nature with limited

human-to-human transmission. From what we already know of coronavirus biology (16) and from the accumulating evidence for this particular virus (3, 11, 15), bats appear to be the natural host, and it would be tempting to assume that these animals are also the immediate source. However, this is difficult to reconcile with the fact that most patients were unlikely to have been exposed directly to bats, or with the close genetic relationship between the human isolates, indicative of a recent bottleneck. A more likely scenario is that a single variant from a spectrum of related betacoronaviruses in bats successfully crossed over to and rapidly established itself in (an) intermediate animal host species (at least in the Middle East), with subsequent incidental spill-over into the human population. Such spill over events would be facilitated through frequent intermediate host-human interactions and perhaps through viral adaptations acquired during the initial species jump. Although at present, there is no evidence for sustained community transmission, the obvious concern is that the virus may take the next step and adapt to efficient human-to-human transmission.

Since the initial discovery, isolates of the virus have been described in the scientific literature, databases, and popular press under various names (e.g. human betacoronavirus 2c EMC, human betacoronavirus 2c England-Qatar, human betacoronavirus 2C Jordan-N3, betacoronavirus England 1) with novel coronavirus (NCoV) as the one used most often. As this lack of uniformity in virus nomenclature complicates communication both in the research field and with health-care authorities, governments and the general public, the Coronavirus Study Group (CSG) of the International Committee on Taxonomy of Viruses (17) took the lead to address this issue. After careful consideration and broad consultation, the CSG has decided to call the new coronavirus "Middle East Respiratory Syndrome Coronavirus" (MERS-CoV). This name is endorsed by the discoverers of the virus and other researchers that pioneered MERS-CoV studies, by the World Health Organization and by the Saudi Ministry of Health. We strongly recommend the use of this name in scientific and other communications. New MERS-CoV isolates or variants detected by RT-PCR may be provided with an affix, analogous to convention in influenza virus nomenclature (host/country of origin + strain identification number/year; e.g. MERS-CoV Hu/Jordan-N3/2012). As our knowledge of the epidemiology and host preference of this virus is still incomplete, it seems prudent to refrain from labeling MERS-CoV as a "human coronavirus", at least for the time being.

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Legend to Fig. 1

Fig. 1. Phylogenetic relationships among members of the subfamily *Coronavirinae* and taxonomic position of MERS-CoV. A rooted Neighbor-Joining tree was generated from amino acid sequence alignments of Coronaviridae-wide conserved domains in replicase polyprotein 1ab (ADRP, nsp3; M^{pro}, nsp5; RdRP, nsp12; Hel, nsp13; ExoN, nsp14; NendoU, nsp15; O-MT, nsp16) for MERS-CoV strain Hu/Jordan-N3/2012 (10) and for twenty other coronaviruses, each a representative of a currently recognized coronavirus species (12); equine torovirus Berne served as outgroup. Virus names are given with strain specifications; species and genus names are in italics as per convention. The tree shows the four main monophyletic clusters, corresponding to genera *Alpha*-, *Beta*-, *Gamma*- and *Deltacoronavirus* (color-coded), and the position of MERS-CoV. Also indicated are betacoronavirus lineages A through D (corresponding to former CoV subgroups 2A through D).

