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Applying lessons from SARS to a newly identified coronavirus

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Human infection with a newly identified novel coronavirus has rapidly focused global attention on risk assessment^{1–6} because its epidemic potential is not known. First detected in September, 2012, in a patient who had died of an acute respiratory illness in Saudi Arabia,⁴ it was soon confirmed in a Qatari patient with a similar illness in London, UK. These cases triggered collaborations between the Kingdom of Saudi Arabia Ministry of Health (KSA-MoH), Qatar, and other global partners. The immediate need was to ensure the safety of the 3 million pilgrims attending the Hajj pilgrimage in October, 2012. Testing of pilgrims before and after Hajj 2012, and case based surveillance for the novel coronavirus during Hajj, suggested that the virus was not in circulation at the time.⁷

Continued risk assessment of the global threat of the novel coronavirus involves close collaborations between KSA-MoH, WHO, the UK Health Protection Agency (HPA), and other global partners. As of March 12, 2013, 15 patients—eight from Saudi Arabia, four from UK, one from Germany, and two from Jordan—were reported with confirmed infections, and nine of these have died. Ascertainment of the country of initial infection remains unclear and at least three cases had a history of travel to another country (including Pakistan and Egypt). Eight cases occurred in three clusters, and 13 required intensive care. In the UK cluster, three members of the same family were infected: one individual had recently travelled to Pakistan and Saudi Arabia, whereas the other two had no recent travel history,⁸ suggesting person to person transmission. Although two of the cases had severe respiratory symptoms, one had mild symptoms suggesting a range of clinical expression. Contacts of the UK cases have been identified by the HPA and KSA-MoH, and follow-up tests have so far been negative for the molecular targets of the novel coronavirus.⁸

Coronaviruses are very common, and widely dispersed in animals and in human beings. They can infect the

respiratory tract, gut, liver, and CNS, causing a range of illnesses. Sequence data have classified the virus as a β coronavirus similar to bat coronaviruses.⁹ Not much is known about the novel coronavirus with respect to the source, mode of transmission, epidemiology, geographic distribution, predisposing factors for infection and disease, incubation period, immunopathogenesis, range of clinical manifestations, and epidemic potential.

Previous WHO guidelines for screening of the novel coronavirus were determined by travel to, or residence in, the Arabian Peninsula.^{2,10,11} Although by definition these might indicate the pattern of diagnosed infections, the focus on the Middle East would have led to individuals with this viral infection in other geographical regions being missed. Latest WHO guidelines now recommend universal screening to define the epidemiology of this novel coronavirus.¹²

Available molecular tests for detection of active cases of infection and screening of contacts are experimental and their sensitivity and specificity require definition. Serological tests for the novel coronavirus are urgently needed for accurate assessment of infection in asymptomatic contacts and for large-scale serosurveys to improve understanding of the epidemiology and global geographical distribution of this virus. Validated standard treatment protocols and case investigation forms are also needed. Findings of controlled studies of cases and contacts could provide information that leads to the source of infection.

Lessons from the severe acute respiratory syndrome (SARS) epidemic showed the importance of rapid genetic sequencing, and these have been applied for study of the novel coronavirus,^{4,9} enabling effective sharing of clinical, epidemiological, and microbiological information.^{2,7–13} Another lesson was that although laboratory testing is important to confirm infection, it does not replace accurate case definitions, regular updates as information

evolves for identifying and managing cases,¹⁴ isolation of suspect cases, follow-up of contacts, and prevention of hospital-acquired infection—all essential for interruption of transmission.¹⁵

Although the novel coronavirus does not seem to be as readily transmissible between people as that which caused the SARS epidemic in 2003, vigilance and continued risk assessment are needed. One of the main goals of the Centre for Mass Gatherings Medicine¹⁶ are collaborative risk assessment and surveillance for new and emerging infections. Because of the global nature of religious and sporting events, active surveillance of the participants is of paramount global importance. A unique opportunity now exists for global collaboration, with transparent sharing of information as was done during the SARS outbreak, to improve elucidation of the risks associated with the novel coronavirus so that another SARS-like epidemic does not begin to spread undetected. Collaborations with other consortia such as the International Severe Acute Respiratory and Emerging Infection Consortium will ensure that the lessons from the SARS epidemic are applied to provide a valuable resource for risk assessment, surveillance, and response in accordance with the international health regulations.

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Taxonomy of medically important fungi in the molecular era

Traditionally, fungi have been allowed to carry multiple names that describe different asexual and sexual morphological stages. This duplicated name system is because these phases can propagate independently and thus their shared identity is not always obvious. At the molecular genetic level the two stages are identical, and therefore this system is becoming increasingly impractical. For this reason Article 59 regulating dual naming in fungi in the Code of Botanical Nomenclature was recently abolished.¹

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This amendment has a potentially profound effect on clinical mycology, because with this fundamental change all established fungal names and many disease names are jeopardised. Additionally, many well known, clinically important species, such as *Aspergillus fumigatus*, *Coccidioides immitis*, *Exophiala jeanselmei*, and *Sporothrix schenckii*, have been found to consist of several molecular siblings. The molecular diversity leads to an enormous increase in the number of clinically relevant fungi and to changes of