State of Knowledge and Data Gaps of Middle East Respiratory Syndrome Coronavirus (MERS-CoV) in Humans

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The WHO MERS-CoV Research Group

Abstract

BACKGROUND: Between September 2012 and 22 October 2013, 144 laboratory-confirmed and 17 probable MERS-CoV cases from nine countries were notified to WHO.

METHODS: We summarize what is known about the epidemiology, virology, phylogeny and emergence of MERS-CoV to inform public health policies.

RESULTS: The median age of patients (n=161) was 50 years (range 14 months to 94 years), 64.5% were male and 63.4% experienced severe respiratory disease. 76.0% of patients were reported to have 1 underlying medical condition and fatal cases, compared to recovered or asymptomatic cases were more likely to have an underlying condition (86.8% vs. 42.4%, p<0.001). Analysis of genetic sequence data suggests multiple independent introductions into human populations and modelled estimates using epidemiologic and genetic data suggest R<sub>0</sub> is <1, though the upper range of estimates may exceed 1. Index/sporadic cases (cases with no epidemiologic-link to other cases) were more likely to be older (median 59.0 years vs. 43.0 years, p<0.001) compared to secondary cases, although these proportions have declined over time. 80.9% vs. 67.2% of index/sporadic and secondary cases, respectively, reported 1 underlying condition. Clinical presentation ranges from asymptomatic to severe pneumonia with acute respiratory distress syndrome and multi-organ failure. Nearly all symptomatic patients presented with respiratory symptoms and 1/3 of patients also had gastrointestinal symptoms.

CONCLUSIONS: Sustained human-to-human transmission of MERS-CoV has not been observed. Outbreaks have been extinguished without overly aggressive isolation and quarantine suggesting that transmission of virus may be stopped with implementation of appropriate infection control measures.

Background

The first case of a novel coronavirus, now called Middle East respiratory syndrome coronavirus (MERS-CoV), was identified in a patient with acute pneumonia and renal failure in Jeddah, Kingdom of Saudi Arabia (KSA) in June 2012.1 Following identification of the virus a subsequent case from Qatar who was being treated in the UK was identified2 and a hospital cluster of pneumonia among health care workers in Zarqa, Jordan in March/April of 2012 was retrospectively determined to have been caused by the same virus.3 Since then, as of 22 October 2013, 144 laboratory-confirmed and 17 probable MERS-CoV cases from nine countries (Figure 1a) have been notified to the World Health Organization (WHO)3-4,5,6 in accordance with the provisions of the International Health Regulations (2005).

WHO, in coordination and cooperation with its affected member states, and an informal network of academic and public health researchers, has compiled available information on MERS-CoV. Here we summarize what is currently known about the epidemiology of MERS-CoV, including the geographic spread and timeline of cases, characteristics and severity of cases, clinical features and treatment strategies, description of clusters, and the epidemic potential of MERS-CoV; and the virology, phylogeny and emergence of the MERS-CoV virus. In addition to summarizing the published literature, we also present summary data on the known laboratory-confirmed and probable cases of MERS-CoV infection that have been reported to WHO. This compilation represents our current state of knowledge of MERS-CoV and the disease it causes and summarizes information needed to inform public health policies for surveillance, preparedness, and response.
Epidemiology of MERS-CoV infection in humans

Our understanding of the epidemiology and clinical presentation of MERS-CoV infection is heavily influenced by the recommended surveillance strategies for case detection, which largely focus on severe illness and virologic testing\(^4\), and published detailed investigations of cases. Contact tracing activities allow for the detection of confirmed cases with a broader spectrum of illness. Confirmed cases include only those with a positive polymerase chain reaction (PCR) in accordance with the laboratory guidelines for virus genetic material\(^7\). Probable cases are those that have a link with a confirmed case and a clinically compatible illness but without definitive laboratory confirmation. Antibody testing is not currently being used for confirmatory testing. In addition to summarizing data related to both confirmed and probable cases, we also examined the differences between secondary cases discovered around sporadic cases as a result of contact tracing. While the majority of cases now reported have likely acquired infection through human-to-human transmission the primary sporadic cases in clusters are more likely to have been acquired through contact with non-human sources of the virus. The differences between them may provide clues as to relevant exposures that result in infection.

Characteristics of MERS-CoV Cases

Between April 2012 and 22 October 2013, 144 laboratory-confirmed MERS-CoV cases have been identified in nine countries: France, Germany, Italy, Jordan, KSA, Qatar, Tunisia, United Arab Emirates (UAE), and the United Kingdom (UK) (Figure 1a). All cases have had a direct or indirect link with the Middle East. In KSA (Figure 1b), from which more than 80% of laboratory-confirmed cases have been reported, cases have been reported from six of its 13 provinces (Al Qasim, Al Madinah, Ar Riyad, Asir, Ash Sharqiyah and Makkah)\(^5\)\(^6\)\(^8\)\(^9\). In addition, 17 probable cases have been identified in Jordan (n=11), KSA (n=4) and Italy (n=2)\(^3\)\(^5\)\(^6\)\(^10\) and are included in our analyses. The number of cases reported rose markedly starting in April 2013 compared with the previous six months since virus discovery, with 21 laboratory-confirmed cases reported to have symptom onset in April, 22 in May, 22 cases in June, 14 cases in July, 20 cases in August, 28 cases in September, and 4 cases in October 2013 (Figure 2)
Overall, the median age of MERS-CoV patients is 50 years (range 14 months to 94 years) and 64.5% of patients were male (Table 1). As of 22 October 2013, WHO has confirmation that 65 patients (40.4%), of whom 62 were confirmed and 3 probable, have died, of these 4 deaths could not be matched up to specific cases due to a lack of identifying information. Outcome is unknown for 45 patients, either because they are still in hospital at the time of writing, their outcome has not been reported, or we are unable to match a fatal case to our line list (n=4). Age and sex varied by outcome, with a higher median age and proportion of male sex among patients who died (58 years old and 80.0%, respectively) versus those who recovered or were asymptomatic (34 years old and 60.0%, respectively).

The majority (63.4%) of patients experienced severe respiratory disease while 29.8% were reported to have non-severe disease, including 18 cases reported as asymptomatic. Severe disease was defined as admission to an intensive care unit [ICU]; use of extracorporeal membrane oxygenation (ECMO), mechanical ventilation, or vasopressors; or reported by the member state as "critical" or "severe"; or who died. Severity is unknown for 6.8% of patients. Fifty-three of the 114 hospitalized patients, for whom we had data, died.

Seventy-six per cent of patients are reported to have at least one underlying medical condition and fatal cases were more likely to have an underlying condition (86.8% among fatal cases vs. 42.4% among recovered or asymptomatic cases, p<0.001, Table 1). Of those who were reported to have at least one comorbid condition, specific comorbid diagnoses were not reported for 47.8% of patients. However, of those with data, the most commonly reported conditions include chronic renal failure (13.3%), diabetes (10.0%), and heart disease (7.5%). Of five patients who were immunocompromised, two reported use of immunosuppressive medication, two reported multiple myeloma, and solid tissue cancer was reported in one patient. A published analysis of 47 confirmed patients from KSA, most of whom were part of the Al Hasa cluster, found that almost all (45/47) had at least one underlying condition, including diabetes, hypertension, chronic cardiac disease and chronic renal disease 9.

We classified 51 patients as likely being sporadic (n=29) or “index” cases (n=22) based on the following criteria: 1) a report of having no exposure to other known cases, 2) occurring in an area with no previous cases or no cases within the last 2 months, or 3) reported as the index case in a cluster or being the first case reported with symptoms in a cluster. Ninety-five cases were classified as secondary cases with epidemiologic links to other confirmed MERS-CoV cases (Table 1). For 17 cases, epidemiological classifications remain unclear as no information about contact with other cases is available.

Seventy-three per cent of index/sporadic cases were male, as compared with 60.0% of secondary cases, though this difference was not significant. Notably, this proportion has declined over time; more than 90% of the earliest cases reported were male. Index/sporadic cases were older (median age 59 years vs. 43 years, p<0.001), and more likely to experience severe disease requiring hospitalization or advanced care (90.2% vs. 49.5%, p<0.001) (Table 1). A similar proportion of index/sporadic cases and secondary cases reported at least one underlying condition (80.9% and 67.2%, respectively), and diabetes, heart disease and immunosuppression were most often reported among index/sporadic cases.

The majority (90.2%) of index/sporadic cases had severe or fatal disease (Table 1). However, the proportion with reported chronic renal failure was higher among secondary cases, which is related to the large outbreak related to haemodialysis units in hospitals in Al Hasa 10. Only one of the secondary cases (n=95) that occurred outside of the Al Hasa outbreak reported chronic renal failure.

Among secondary cases, 13 MERS-CoV cases are believed to have been infected in household settings, 60 in health care settings (HCS), and one in a workplace other than a HCS. For twenty-one cases, the place of transmission was not reported. Cases associated with HCS in Jordan, France, KSA, UK, UAE, and Qatar3,10,11,12 included HCW (30 cases) treating MERS-CoV patients, patients seeking treatment in hospitals for conditions unrelated to MERS-CoV (19 cases) and visitors (6 cases). The type of exposure of five additional secondary cases associated with HCS is unknown. In households and the non-HCS workplace, secondary cases occurred among family contacts or co-workers. The specific types of exposure resulting in transmission are currently unknown.

Only 49 cases have information on exposure to animals, including owning or visiting a farm with camels, goats, sheep, chickens, ducks or other animals. Of these, exposure to animals has been reported for only a few cases (n=7; Table 1).
Clinical Features of MERS-CoV Infections in Humans

Data suggest that the clinical presentation of MERS-CoV infection ranges from asymptomatic to very severe pneumonia with the acute respiratory distress syndrome (ARDS), septic shock and multi-organ failure resulting in death. At least two cases had a consumptive coagulopathy during the course of their illness. The clinical course is more severe in patients with immunocompromising conditions and more likely to be mild in individuals without underlying medical conditions (Table 1). Only three cases have been reported in children under 5 years of age.

Typically, the disease starts with fever and cough, followed by dyspnea, and rapidly progresses to pneumonia, often requiring ventilatory and other organ support. Nearly all symptomatic patients presented with respiratory symptoms; however, one immunocompromised patient was initially admitted to hospital with fever, chills and diarrhoea and later found to have pneumonia [11]. At least one-third of patients also had gastrointestinal symptoms, such as vomiting and diarrhoea. Almost half of the patients developed pneumonia (44.1%), and 20 (12.4%) developed ARDS (Table 1).

Chest radiograph findings vary but are consistent with viral pneumonitis and ARDS: bilateral hilar infiltration, uni- or bilateral lower lobe infiltrates, ground glass appearance, and small pleural effusions have been described. Lower lobes tend to be affected more than upper lobes early in the course of illness; radiographic appearance progresses. Computed tomographic scans have shown interstitial infiltrates and consolidation compatible with ARDS in severe cases. In some severe cases, renal failure developed concurrently with respiratory failure.

Common laboratory findings include leucopenia, particularly lymphopaenia, and a consumptive coagulopathy during the course of their illness. The clinical course is more severe in patients with immunocompromising conditions and more likely to be mild in individuals without underlying medical conditions (Table 1). Only three cases have been reported in children under 5 years of age.

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Clinical Features of MERS-CoV Infections

<table>
<thead>
<tr>
<th>Clinical Features</th>
<th>Details</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fever and cough</td>
<td>Followed by dyspnea, rapid progression to pneumonia</td>
</tr>
<tr>
<td>Radiographic findings</td>
<td>Bilateral hilar infiltration, uni- or bilateral lower lobe infiltrates, ground glass appearance, small pleural effusions</td>
</tr>
<tr>
<td>Laboratory findings</td>
<td>Leucopenia, particularly lymphopaenia, consumptive coagulopathy</td>
</tr>
</tbody>
</table>

### Table 1. Characteristics of Confirmed and Probable MERS-CoV Patients by Outcome and By Epidemiologic Link

<table>
<thead>
<tr>
<th>Variable</th>
<th>Confirmed and Probable Cases</th>
<th>Fatal</th>
<th>Outcome</th>
<th>Case-Type</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n=161</td>
<td>n=61</td>
<td>Recovered or Asymptomatic n=55</td>
<td>Unknown Outcome n=45</td>
</tr>
<tr>
<td><strong>Demographic Data</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Median Age (years)</td>
<td>60.0 (157)</td>
<td>18.0</td>
<td>34.4 (51)</td>
<td>51.0</td>
</tr>
<tr>
<td>Age Range (years)</td>
<td>1-94 (157)</td>
<td>0.94</td>
<td>1.76 (51)</td>
<td>11.5</td>
</tr>
<tr>
<td>≤50 Years (n, %)</td>
<td>49.7 (157)</td>
<td>71.7%</td>
<td>71.6 (51)</td>
<td>51.1%</td>
</tr>
<tr>
<td>Male (%)</td>
<td>64.5% (155)</td>
<td>80.0%</td>
<td>60.6% (50)</td>
<td>48.9%</td>
</tr>
<tr>
<td><strong>Reported Underlying Conditions</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≥1 underlying condition (%)</td>
<td>75.8% (120)</td>
<td>86.4% (53)</td>
<td>42.4% (33)</td>
<td>91.2% (34)</td>
</tr>
<tr>
<td>Any immunocompromised (%)</td>
<td>5.0% (120)</td>
<td>7.6% (33)</td>
<td>3.0% (33)</td>
<td>2.9% (34)</td>
</tr>
<tr>
<td>Chronic Renal Failure (%)</td>
<td>13.3% (120)</td>
<td>20.8% (53)</td>
<td>6.1% (33)</td>
<td>8.8% (34)</td>
</tr>
<tr>
<td>Diabetes (%)</td>
<td>10.0% (120)</td>
<td>11.3% (53)</td>
<td>9.1% (33)</td>
<td>8.8% (34)</td>
</tr>
<tr>
<td>Heart Disease (%)</td>
<td>7.5% (120)</td>
<td>3.8% (53)</td>
<td>3.0% (33)</td>
<td>17.7% (34)</td>
</tr>
<tr>
<td><strong>Severity and Outcome Measures</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Severe Disease (%)</td>
<td>63.4%</td>
<td>100%</td>
<td>23.6%</td>
<td>62.2%</td>
</tr>
<tr>
<td>Non-Severe Disease (%)</td>
<td>25.8%</td>
<td>0</td>
<td>65.5%</td>
<td>26.7%</td>
</tr>
<tr>
<td>Unknown Severity (%)</td>
<td>6.8%</td>
<td>0</td>
<td>10.9%</td>
<td>11.1%</td>
</tr>
<tr>
<td>% Pneumonia</td>
<td>44.1%</td>
<td>63.9%</td>
<td>43.6%</td>
<td>17.8%</td>
</tr>
<tr>
<td>% ARDS</td>
<td>12.4%</td>
<td>27.9%</td>
<td>3.6%</td>
<td>2.2%</td>
</tr>
<tr>
<td>Required Hospitalization (%)</td>
<td>70.8%</td>
<td>86.9%</td>
<td>52.7%</td>
<td>71.1%</td>
</tr>
<tr>
<td>Required ICU (%)</td>
<td>51.6%</td>
<td>50.5%</td>
<td>23.6%</td>
<td>60.0%</td>
</tr>
<tr>
<td>Treated with ECMO (%)</td>
<td>3.7%</td>
<td>8.2%</td>
<td>0</td>
<td>2.2%</td>
</tr>
<tr>
<td><strong>Animal Exposure</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Contact with Animals (%)</td>
<td>14.3% (49)</td>
<td>20.0% (15)</td>
<td>14.3% (21)</td>
<td>7.7% (13)</td>
</tr>
<tr>
<td>Contact with Camels (%)</td>
<td>71.4% (77)</td>
<td>100% (33)</td>
<td>33.3% (11)</td>
<td>100% (11)</td>
</tr>
<tr>
<td>Contact with Sheep (%)</td>
<td>28.6% (37)</td>
<td>33.3% (33)</td>
<td>3.3% (11)</td>
<td>0% (11)</td>
</tr>
</tbody>
</table>

Notes: Outcome is reported as fatal if death occurred or as fatal if death occurred; outcome is confirmed or probable if death occurred or if death occurred. Data suggest that the clinical presentation of MERS-CoV infection ranges from asymptomatic to very severe pneumonia with the acute respiratory distress syndrome (ARDS), septic shock and multi-organ failure resulting in death. Data suggest that the clinical presentation of MERS-CoV infection ranges from asymptomatic to very severe pneumonia with the acute respiratory distress syndrome (ARDS), septic shock and multi-organ failure resulting in death. Clinical Features of MERS-CoV Infections in Humans

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vigilance for and prevention of complications. In specific circumstances, additional interventions have included empiric use of broad-spectrum antimicrobial agents, antivirals (oseltamivir and/or acyclovir), and the addition of anti-fungal agents to minimize risk of co-infections with opportunistic pathogens.

Lung-protective ventilatory strategies for ARDS, cardiovascular support, antimicrobial therapy for co-infections, and renal replacement therapy for acute renal failure have been used.1-2,11-13 Case reports of patients supported with ECMO are available for six patients, five of whom have died.1,2,11-12 No case-control data exist to evaluate the effectiveness of such interventions.

Many patients with severe disease have been treated with systemic high-dose corticosteroids, which was intended to reverse the progression of respiratory distress and to prevent lung fibrosis. This appears to have been unsuccessful.

None of the antimicrobial agents used so far, including the antivirals, appear to be successful in improving severe progressive disease. A large number of pharmacological agents have been screened against MERS-CoV and several agents have shown inhibitory effects against MERS-CoV in cell cultures. Among the agents tested in vitro are interferons, cyclosporin A, ribavirin, nitazoxanide, immunoglobulins, lopinavir and SARS CoV convalescent plasma.4,15-16,17,18 Currently, no clinical data support use of these agents. However, a recent study has found favorable outcomes in MERS-CoV infected rhesus macaques treated with ribavirin and interferon-alpha.2b,55

**Transmission of MERS-CoV**

**Clusters[1]**

[1] WHO defines a “cluster” as two or more persons with onset of symptoms within the same 14 day period, and who are associated with a specific setting, such as a classroom, workplace, household, extended family, hospital, other residential institution, military barracks or recreational camp (WHO Interim Surveillance Recommendations, 2013).

A number of the cases in France, Italy, Jordan, KSA, Tunisia, UAE, UK and Qatar have been reported in clusters, providing evidence that human-to-human transmission has occurred in HCS, households, and the workplace (Table 2).3-5,10,11,12,64 In France, Italy, Jordan, KSA, Qatar, Tunisia, UAE and UK, secondary cases were identified through intense case-finding and follow-up of contacts. Intensity of follow-up of close contacts of patients varies between countries and has included screening contacts for respiratory symptoms and evidence of infection either using reverse-transcriptase PCR (RT-PCR) or, in some situations, serologic assays (Table 2).

As the exposure that results in sporadic infection is unknown, it is impossible to estimate the incubation period in these cases. However, data for human-to-human transmission in the clusters are available from France,11-19 UK12, Italy20, Tunisia21, KSA10 and Jordan. The incubation period has been estimated to be just over five days, but could be as long as two weeks (median 5.2 days (95% CI: 1.9 to 14.7); 5.5 (95% CI: 3.6-10.2)). The incubation period for the primary cases who acquired infection from environmental or animal sources is unknown.

Transmission in all reported clusters has been observed to be limited, and current evidence from contact tracing suggests that transmission did not extend beyond close contacts into the community. Among clusters around exported cases travelling to France, UK, Italy, Germany and Tunisia from the Middle East, transmission to close contacts has been limited6,11-12,20-23, and secondary attack rates among family members of patients in other clusters appear to be low.8,5-6,10,12,24-25 Systematic implementation of infection prevention and control measures in reported clusters involving HCS has appeared to limit onward transmission to HCW and hospitalized patients.10-11,12

In HCWs infected by exposure to patients, fewer underlying conditions and milder presentations have been described; however, 37.5% experienced severe disease and at least three died. None of the HCW secondary cases had reported underlying immunosuppression; however, two had hypertension and one had an unspecified underlying comorbid condition. Among secondary cases in HCS who were patients admitted to hospital for other conditions at the time of MERS-CoV infection (n=19), all had underlying conditions, 5.3% reported immunosuppressing conditions, all experienced severe disease, and 89.5% died.
Two groups have evaluated the transmission potential of the MERS-CoV virus by estimating the basic reproduction number (the number of secondary cases that one case would produce in a completely susceptible population, $R_0$)\textsuperscript{22,26}.

Breban and colleagues\textsuperscript{26} used the first 55 laboratory-confirmed cases of MERS-CoV reported to WHO to assess the inter-

### Table 2 MERS-CoV follow-up investigations

<table>
<thead>
<tr>
<th>Location and Date</th>
<th>Setting and Cluster Size Description</th>
<th>Follow-up Investigations</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Zarqa, Jordan, March/April 2013</td>
<td>HCS; 2 confirmed; 11 probable cases</td>
<td>10 confirmed/probable cases were among HCW; Retrospective serologic investigation is on-going.</td>
<td>1</td>
</tr>
<tr>
<td>Riyadh KSA, November 2012</td>
<td>HH; 3 confirmed, 1 probable</td>
<td>24 HH and 124 HCW contacts followed for respiratory symptoms</td>
<td>5</td>
</tr>
<tr>
<td>UK ex Qatar, 2012</td>
<td>HCS; 1 case</td>
<td>64 contacts followed; no contacts with PCR or serologic evidence of infection</td>
<td>24</td>
</tr>
<tr>
<td>Riyadh KSA, February 2013</td>
<td>HH/HCS; 3 brothers</td>
<td>1 probable index case; 2 confirmed secondary cases in brothers of index case, at least 1 likely infected during hospital visit</td>
<td>25,64</td>
</tr>
<tr>
<td>Al-Hasa KSA, April 2013</td>
<td>4 HCS; 25 cases (23 confirmed/2 probable) among patients, HCW, family contacts</td>
<td>The April 2013 nosocomial outbreak spread between patients who were undergoing haemodialysis, in intensive care units and in in-patient units, and between patients and visiting family members and HCW before infection-control measures were implemented. Thirteen of 25 patients in this cluster were undergoing haemodialysis for end-stage renal disease. &gt;1000 followed; &gt;800 contacts tested from Al Hasa cluster; No new cases reported from the Al Hasa region since 18 July</td>
<td>6,10</td>
</tr>
<tr>
<td>UK ex KSA/Pakistan, February 2013</td>
<td>HCS/HH; 3 cases</td>
<td>107 airline, familial, HCW contacts of cases traced; No PCR evidence of infection; serologic results pending</td>
<td>12</td>
</tr>
<tr>
<td>France, May 2013</td>
<td>HCS; 2 cases</td>
<td>Second French case identified through contact tracing. No further secondary cases identified among 123 contacts of first patient, or 39 contacts of 2nd case during 10-day follow-up period</td>
<td>11,19</td>
</tr>
<tr>
<td>Germany ex Qatar and UAE, 2012/2013</td>
<td>HCS, 1 case in Nov 2012; 1 case in March 2013 not epidemiologically linked</td>
<td>207 contacts followed; 84 (13 symptomatic) contacts of 1st case, 123 contacts of 2nd case; No PCR or serologic evidence of infection</td>
<td>€</td>
</tr>
<tr>
<td>Abu Dhabi, UAE 2013</td>
<td>HCS; 5 cases</td>
<td>4 HCW identified through contact tracing of first laboratory-confirmed case</td>
<td>€</td>
</tr>
<tr>
<td>Italy ex Jordan, 2013</td>
<td>HH and occupational cluster; 1 confirmed, 2 probable</td>
<td>115 contacts followed, including family members, HCW, patients in emergency room at time index patient sought treatment, passengers on airplane with index patient; 2 close contacts probable (14-month-old and 42-year-old co-worker).</td>
<td>6,20</td>
</tr>
<tr>
<td>Tunisia ex Qatar, 2013</td>
<td>HH; 3 cases</td>
<td>Index case travelled to Qatar and KSA; Close family contacts followed; no PCR evidence of infection, serologic results pending</td>
<td>€</td>
</tr>
<tr>
<td>Eastern Region KSA, 2013</td>
<td>HCS; ≥5 cases</td>
<td>At least 2 cases shared a hospital room; follow-up investigations ongoing</td>
<td>€</td>
</tr>
<tr>
<td>Asir KSA, 2013</td>
<td>HH/HCS; 3 cases</td>
<td>Family contact investigation ongoing; 1 family member infected</td>
<td>€</td>
</tr>
<tr>
<td>Qatar, 2013</td>
<td>HCS; 2 cases</td>
<td>138 HCW, family and community contacts screened; all PCR negative</td>
<td>€</td>
</tr>
<tr>
<td>Hafar al-Batin KSA, 2013</td>
<td>HH; 9 cases</td>
<td>4 asymptomatic cases identified via contact tracing</td>
<td>€</td>
</tr>
</tbody>
</table>

Notes: Contact investigations ongoing as of 22 October 2013; Key: HCS = Health Care Setting; HCW = Health Care Worker Contact; HH= Household Contact; KSA = Kingdom of Saudi Arabia; UAE = United Arab Emirates; UK = United Kingdom

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**Epidemic Potential of MERS-CoV**

Two groups have evaluated the transmission potential of the MERS-CoV virus by estimating the basic reproduction number ($R_0$)\textsuperscript{22,26}.
human transmissibility of MERS-CoV. The authors estimated $R_0$ from the distribution of sizes of case transmission trees seen so far and compared their estimate with that of early data from the SARS-CoV epidemic in 2003. Two scenarios were considered. With the most pessimistic scenario, the authors estimated MERS-CoV $R_0$ to be 0.69 (95% CI 0.50–0.92); by contrast, the $R_0$ for SARS-CoV was 0.80 (0.54–1.13). The optimistic scenario resulted in a $R_0$ of 0.60 (0.42–0.80). The authors suggest that, based on their analyses using PCR-confirmed cases, MERS-CoV does not yet have pandemic potential.

Cauchemez and colleagues undertook independent analyses to assess the transmissibility and extent of spread of MERS-CoV to date. Using publicly available epidemiological data on 111 confirmed and probable MERS-CoV patients and genetic sequence data from 10 cases, the study found central estimates of $R_0$ between 0.8 and 1.3. This work suggests that current data are consistent with two scenarios: (a) a sustained epidemic in an animal reservoir with sporadic spillover into humans, or (b) sustained human-to-human transmission causing a slowly growing human epidemic. They also used epidemiological and genetic data to evaluate the underlying scale of the epidemic so far. Analyses using numbers of exported cases of returning travellers from countries in the Middle East (n=4) and average length of visitor stays to Jordan, Qatar, KSA and UAE suggest that by now at least 900 symptomatic cases of MERS-CoV have occurred, implying substantial under-ascertainment of cases in the region. Genetic analyses suggest that approximately 17490 (IQR 3900–95000) infections in humans and in the reservoir(s) may have occurred between June 2012 and August 2013.

An analysis of 21 genetic sequences from cases in KSA was compared to those already available in public databases and concluded that the genetic diversity of available sequences supported multiple introductions from a presumed zoonotic source, with subsequent human-to-human transmission. The authors could not exclude the possibility of unrecognized sustained transmission in humans associated with frequent movement of infected individuals to explain the observed genetic patterns.

Animal Reservoir

Several lines of evidence support the hypothesis that the virus originates in animals. Limited phylogenetic analyses using genetic material collected from MERS-CoV patients’ specimens shows that MERS-CoV has a close genetic relationship with coronaviruses found in hedgehogs (Corman et al. unpublished) and in bats in Southern China, Europe, Thailand, Mexico, Ghana, and South Africa. A 190-nucleotide fragment of the RNA-dependent RNA polymerase gene was recovered from a faecal sample from a *Taphozous perforatesbat* collected in Bisha, KSA, near the home of the first MERS-CoV patient. The fragment had 100% nucleotide identity with a MERS-CoV recovered from the human case that occurred in that area.

Neutralizing antibodies against MERS-CoV or a similar virus have been described in camels from the Spanish Canary Islands, Oman, and from Egypt. Approximately 15% of sera from camels from the Spanish Canary Islands, 100% of sera from unrelated retired racing camels from Oman and more than 90% of dromedary camels from Egypt were found to have antibody titres reactive with MERS-CoV using a variety of methods, including neutralization. No viral genetic material was detected in a limited number of tested camel sera and faecal samples.

Virological Characteristics of MERS-CoV

MERS-CoV is an enveloped, single-stranded, positive-sense RNA virus that is a newly recognized species in lineage C of the genus Betacoronavirus within the subfamily Coronavirus. The genome is approximately 30.1kb long and contains at least 10 predicted open reading frames (ORF) common to betacoronaviruses, which are expressed from seven subgenomic mRNAs. These ORFs mainly include ORF 1a/1ab, which encode for large replicate polyproteins containing conserved functional domains and several non-structural (NS) proteins of CoV, the spike-surface glycoprotein (S), the small-envelope (E) protein, the matrix (M) protein, and the nucleocapsid (N) protein.

Laboratory Testing of MERS-CoV

Initial detection of viral genome in human clinical samples was made using pancorona primers targeting highly conserved regions of the coronavirus genome. Specific assays for the detection of acute infection with MERS-CoV by real-time RT-PCR (rRT-PCR) have subsequently been developed. Several assays are now in widespread use, including those targeting a region upstream of the E gene (upE) or regions within ORF 1b (nsp14 protein), ORF 1a (nsp6 protein), and the nucleocapsid protein gene. The assays for the upE and the ORF 1a targets are considered equally sensitive, while the ORF 1b assay is considered less sensitive than the ORF 1a assay. The upE assay has been recommended for screening specimens with the ORF 1a assay or other specific gene targets being used for confirmation.

Currently, laboratory confirmation of a case is considered as a positive PCR result for at least two different specific targets on the MERS-CoV genome or one positive PCR result for a specific target on the MERS-CoV genome and an additional different PCR product sequenced, confirming identity to known sequences of MERS-CoV. Two suitable targets for sequencing are an RNA-dependent RNA polymerase (RdRp) and nucleocapsid (N) protein genes. Serologic assays for MERS-CoV are under development by several laboratories.
Genetics and Emergence of MERS-CoV

Twenty-two whole sequences, and partial genome sequences from 9 additional cases, have been published in GenBank, from thirty different MERS-CoV infected patients (Table 3)\textsuperscript{2-3,10-12,13-22,23,27,28,29}. Phylogenetic trees have been published by several groups\textsuperscript{10-13,22-29} and are not shown here.

Several estimates of the time frame of the emergence of MERS-CoV in humans have been developed using a variety of analytical tools with different statistical assumptions, and using both whole-genome sequences and individual genes derived from infections at different time points\textsuperscript{10-13,22-29}. All suggest the emergence of MERS-CoV in mid-2011, with the range of possible dates ranging broadly from November 2009–April 2012. One study of 10 full genome sequences, including one from a French patient\textsuperscript{22}, suggests the emergence in June 2011 with a narrower timeframe, from Sept 2010–Nov 2011 (Table 3). The study using most available sequences, estimates emergence in July 2011 with a broad credible interval, from July 2007 to June 2012\textsuperscript{27} (Table 3). Future studies providing more genome sequences from humans and animals should add to our understanding of transmission patterns and increase the accuracy of the estimated genomic evolutionary rate.

### Table 3 Available MERS-CoV Sequences

<table>
<thead>
<tr>
<th>GenBank Accession No</th>
<th>Subject</th>
<th>Country of presumed exposure</th>
<th>Source of viral RNA</th>
<th>Method</th>
<th>Genome Sequence &amp; Coverage</th>
<th>Sequences for tMRCA</th>
<th>Rate of Evolution (substitution per site per year)</th>
<th>Result</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>JX80059.2 (EN8/2012)</td>
<td>60 yr, KSA Male</td>
<td>Jeddah, KSA</td>
<td>Infected cell culture (putative on admission)</td>
<td>Roche 454; Sanger#</td>
<td>30,119bp; 1,006 fold</td>
<td>NR</td>
<td>NR</td>
<td>NR</td>
<td>1.28</td>
</tr>
<tr>
<td>KC94050.2 (En8/12)</td>
<td>49 yr, Qatari Male admitted to hospital in Qatar and London</td>
<td>KSA, Qatar</td>
<td>Deep tracheal aspirate (18 DPO)</td>
<td>Sanger#</td>
<td>30,111bp; 2-11 fold</td>
<td>JX80059, KC69704</td>
<td>a. 1.0x10^-7, 5.0x10^-7; b. 3.35x10^-7; (Influenza A’ H1N1: 2x10^-3 SARS-CoV)</td>
<td>NR</td>
<td>2.29</td>
</tr>
<tr>
<td>KC67074 (En8/12)</td>
<td>49 yr, Qatari Male admitted to hospital in Qatar and London</td>
<td>KSA, Qatar</td>
<td>Sputum (16 DPO)</td>
<td>Illumina MiSeq; BEAST</td>
<td>30,112bp; 4,444 fold</td>
<td>JX80059, KC69704</td>
<td>a. 1.0x10^-7, 5.0x10^-7; b. 3.35x10^-7; (Influenza A’ H1N1: 2x10^-3 SARS-CoV)</td>
<td>NR</td>
<td>2.29</td>
</tr>
<tr>
<td>HPA/England/2013</td>
<td>60 yr UK male</td>
<td>United KSA</td>
<td>Throat swab</td>
<td>Sanger#</td>
<td>30,042bp; 2-11 fold</td>
<td>NR</td>
<td>NR</td>
<td>NR</td>
<td>12</td>
</tr>
<tr>
<td>KF192507 (Munich/Abu Dhabi)</td>
<td>73 yr male, admitted in UAE and transferred to Germany</td>
<td>Abu Dhabi, UAE</td>
<td>BAL (12 DPO)</td>
<td>Roche 454; Sanger#; PhyML</td>
<td>30,132bp</td>
<td>NR</td>
<td>NR</td>
<td>NR</td>
<td>13,23</td>
</tr>
<tr>
<td>KC85821 (Esen/A)</td>
<td>45 yr Qatari male admitted to hospital in Qatar and transferred to Germany</td>
<td>Doha, Qatar</td>
<td>BAL</td>
<td>Roche 454; Sanger#; PhyML</td>
<td>5,130bp (partial)</td>
<td>JX80059, KC69704, KF192507, KC776174, England2</td>
<td>1.6x10^-7</td>
<td>NR</td>
<td>13,23</td>
</tr>
<tr>
<td>KF186567, KF186564, KF186565 (Al-Hasa, KSA, 1/2013)</td>
<td>HCoV, patient “H”, patients from Al Hasa Outbreak</td>
<td>Eastern KSA</td>
<td>Throat swab/sputum (throat aspirate/BAL)</td>
<td>Illumina MiSeq; PhyML; BEAST</td>
<td>30,117bp</td>
<td>NR</td>
<td>NR</td>
<td>Aug 2011 (Nov 2009–Apr 2012)</td>
<td>15</td>
</tr>
<tr>
<td>KC776174 (Jordan/Amman, 6/2012)</td>
<td>Zanzibar hospital, Jordan</td>
<td>Jordan</td>
<td>Bronchial wash</td>
<td>NR</td>
<td>30,030bp</td>
<td>NR</td>
<td>NR</td>
<td>NR</td>
<td>13</td>
</tr>
<tr>
<td>All above, plus</td>
<td>All above, plus French patient</td>
<td>All above, plus Dubai</td>
<td>All above</td>
<td>BEAST</td>
<td>NR</td>
<td>JX80059, KC69704, KF192507, KC776174, England2, KF186564, Dubai</td>
<td>1.5 x 10^-7</td>
<td>June 2011 (Sept 2010–Nov 2011)</td>
<td>12</td>
</tr>
<tr>
<td>KF600012 – KF60056</td>
<td>Cases in Al-Ahsa, Riyadh, Buraeidh, Bish, and Haf-Al-Batin</td>
<td>KSA</td>
<td>Tracheal aspirate, nose-pharyngeal swab, throat swab, respiratory swab, or unknown source</td>
<td>Illumina MiSeq; PhyML</td>
<td>13 complete (up to 30,115) and 8 partial; &gt;3,000 fold</td>
<td>All available except JX80059 and KC776174</td>
<td>6.3x10^-6</td>
<td>July 2011 (July 2007–June 2012)</td>
<td>27</td>
</tr>
</tbody>
</table>

Notes: # Sanger density sequencing; PhylML, Phylogenetic Estimation Using Maximum Likelihood; BEAST, Bayesian Evolutionary Analysis by Sampling Trees; DPO, Days post onset of symptoms; NR, Not reported; BAL, bronchoalveolar lavage.

**MERS-CoV – Host Interactions**

The S protein of coronaviruses is responsible for binding to the host cell receptor. The DPP4 (dipeptidyl peptidase 4, also known as CD26)\textsuperscript{40-41}, has been identified as the functional cellular receptor for MERS-CoV, in contrast to the angiotensin-converting enzyme 2 (ACE2), used by the SARS-CoV\textsuperscript{42} and hCoV-NL63. DPP4 homologues permitting MERS-CoV infection are present in a variety of bat, pig, civet and rabbit cell lines, whereas cell lines of canine, feline, rodent, chicken and insect origin were not susceptible\textsuperscript{42-43}.

DPP4 is an exopeptidase and is involved in the regulation of chemokine and cytokine responses and in glucose metabolism\textsuperscript{44}. Upon binding, the viral entry of MERS-CoV involves virus-cell fusion, which can be either activated by type II transmembrane serine proteases TMPRSS2 or mediated by low pH and endosomal cathepsins\textsuperscript{45}. The receptor-binding domain (RBD) in the S
protein responsible for binding to DPP4 has also been mapped. The RBD-S interaction falls within residues 358-662 of the S1 domain, where antibodies to this domain were observed to efficiently neutralize infection\textsuperscript{45-46,47}. Crystal structures of this binding interface showed a homologous core subdomain but much variation in the external receptor binding motif region, compared with that of SARS-CoV\textsuperscript{41}.

In humans, DPP4 is primarily expressed on the epithelial cells in kidney, small intestine, liver and prostate, and on activated leukocytes\textsuperscript{13-40}. MERS-CoV has been shown to infect non-ciliated bronchial epithelium, bronchiolar epithelial cells, alveolar epithelial cells, endothelial cells, and lung ex vivo organ cultures at least as well as SARS-CoV\textsuperscript{40-48,49,50}. Receptor preference and underlying tissue tropism may influence the severity of highly pathogenic coronaviruses compared with HCoV-229E infection, which is usually milder and has limited infectivity of these lower respiratory tract cells. However, cellular tropism does not completely account for severity of disease.

Cell-based studies have shown that MERS-CoV, like other coronaviruses, evades innate immune recognition, perhaps accounting for the high proportion of cases observed with severe disease\textsuperscript{46,18-48,49}. However, MERS-CoV was observed to have higher sensitivity to pegylated interferon treatment, compared with SARS-CoV. This has been hypothesized to be due to the lack of a SARS-CoV ORF6 homologue in MERS-CoV, which has been shown to inhibit the nuclear translocation of p-STAT1 and activation of downstream antiviral genes\textsuperscript{28-51}. MERS-CoV was observed to induce a massive dysregulation of the host cellular transcriptome to a much greater extent and in a shorter time after infection than SARS-CoV, resulting in profound apoptosis of surrounding cells\textsuperscript{17,49,50}. This involves the greater suppression of the antigen presentation pathway in MERS-CoV compared with SARS-CoV. This phenomenon suggests that SARS-CoV and MERS-CoV may activate different cellular mechanisms for viral replication and infection, and may delay the adaptive response in the infected host, particularly the immunocompromised patients\textsuperscript{17}.

### Discussion and gaps in knowledge

Much has been learned about the MERS-CoV and the disease syndrome it causes in humans since the first case was reported in September 2012, but many critical questions remain unanswered. From the time of the first cases reported to WHO, it was suspected that the virus was of animal origin and subsequent observations since that time have reinforced this view. Current evidence suggests that the virus is most closely related genetically to viruses found in a number of species of old world and new world insectivorous bats\textsuperscript{1,28-29,30,31,32,33,34}. The finding of a gene fragment in a Saudi bat\textsuperscript{54}, which is homologous with that of viruses from humans, suggests that bats may be the ultimate reservoir of virus; however, it is very possible that another intermediate animal reservoir could be involved, as was the case with SARS and with Nipah virus in Malaysia. Serological data suggest infections with MERS-CoV or a closely related virus in camels, however the virus itself has not been detected in camels\textsuperscript{36-35}. Currently, all known cases have a direct or indirect link to the Middle East. Although surveillance is more limited in some parts of the world, large clusters like those seen in Al Hasa, KSA and Zarqa, Jordan have not been observed elsewhere. This apparent restriction of transmission from non-human sources to one area of the world may provide clues to the source of exposures. The most likely explanations are either a restriction in the range of the putative host species or exposures related to human behaviours that occur only in the area. Regardless of the reservoir, however, the primary question to be answered is the route of transmission from animal to human. Sporadic and index cases provide the best opportunity for identifying exposures of interest as these are the infections most likely acquired from non-human exposures. The high predominance of older individuals among these cases could be a clue to exposures and demands further investigation using structured case-control studies\textsuperscript{53}.

The recent increase in numbers of sporadic cases associated with a change in the proportion of male and female cases is concerning. While it could represent changes in surveillance strategies, it may also signal a change in the behaviour of the virus, an expansion of the reservoir, or changes in human exposures.

It is now clear that the virus does transmit from person to person. However, sustained human-to-human transmission has not been observed. The relative ease with which outbreaks have been extinguished without resorting to overly aggressive isolation and quarantine measures and the limited secondary transmission around clusters, suggest that transmission of virus may be readily stopped.

Genetic sequence data indicate that multiple independent introductions into human populations have occurred. In addition, modelled estimates of $R_0$ suggest that $R_0$ is <1, though the upper range of estimates may slightly exceed 1\textsuperscript{22-26}. Reports of mild and asymptomatic cases discovered through investigations and testing of contacts of confirmed cases, suggest that the focus on severe disease as a surveillance strategy may miss significant numbers of milder or asymptomatic cases\textsuperscript{52}. The importance of these milder cases in transmission, however, is uncertain and needs to be assess with seroepidemiologic studies\textsuperscript{54}. Evidence from SARS, however, suggests that asymptomatic cases did not transmit infection\textsuperscript{55}. It appears likely that the presence of comorbid conditions, particularly when found in high concentrations such as in HCS, can facilitate transmission.

The basic clinical appearance and course of severe cases seen since the earliest reports has not substantially changed; however, it is now clear that milder and even asymptomatic presentations do occur and that the case-fatality rate is lower than observed. The acute renal failure observed in many cases, especially those reported early on, has been primarily associated with hemodynamic compromise, suggesting that it is likely a secondary process. However, receptors for the virus do occur in renal tissue and viral RNA has been detected at low titres in urine. It is important to note that although the primary site of
infection has been the respiratory tract, approximately one-third of patients have experienced gastrointestinal symptoms and low titres of virus have been detected in faeces. While generally this is not likely useful for diagnostic purposes, this finding supports current recommendations for adding contact precautions in HCS and may have implications for infection control in the community. The observed differences in proportion of cases that are severe between primary (index/sporadic) and secondary cases is likely a reflection of the surveillance strategy that focuses on severe disease for identifying primary cases and the additional case-finding carried out around them. However, the possibility that the virulence of the virus is different when transmitted from humans than it is when transmitted from non-human sources cannot be excluded based on available evidence. The presence of a pre-existing chronic medical condition likely increases the chance of severe outcome and death.

At this time, treatment for MERS-CoV remains supportive. A number of licensed pharmaceuticals have been tested in vitro and testing is currently underway in vivo; however, the lack of an appropriate animal model is hampering these efforts. Clinical observation of patients infected with MERS-CoV and experience with other infectious diseases suggest that high-dose corticosteroids are not effective in management of the disease and may be contraindicated for other reasons. Considerable controversy exists about the value of high-dose corticosteroids in the management of ARDS. There is substantial evidence of harm, and no evidence of benefit, from high-dose corticosteroids when used for SARS and influenza A(H1N1)pdm09. For this reason, WHO guidance does not recommend the systemic use of high-dose corticosteroids for MERS-CoV treatment, with a few exceptions limited to, for example, patients with asthma or vasopressor refractory shock. It may be that convalescent sera holds some promise until an effective pharmaceutical can be identified. If indeed convalescent sera proves efficacious, specific human monoclonal antibodies may also be considered. Sharing of clinical information and case-management experience is critical to better understand the natural history of disease for MERS-CoV and improve management guidance. In addition to infection prevention and control measures aiming to minimize transmission of MERS-CoV, attention should be paid to rigorous implementation of safe practices to prevent acquisition of bacterial and fungal pathogens associated with health care.

Many critical questions about MERS-CoV and its related disease remain. First among these is the nature of the exposures that result in human infection. Although an animal reservoir of the virus is the most likely hypothesis, the route of transmission could be either direct or indirect contact with the reservoir or an intermediate host, including consumption of a contaminated food product, or contact with a contaminated fomite. Thus far, spread among humans appears to be relatively easy to extinguish with conventional infection control measures and has not required the aggressive measures that were used to contain SARS. Prevention of transmission from the putative animal reservoir to humans is the critical step needed to halt the ongoing spread of this virus. The answer to how to achieve this and other remaining questions requires formal, structured, multinational collaborative research studies, including the development and implementation of effective surveillance strategies.

Members of the MERS-CoV Research Group

Mohammad Mousa Abdallat
Ministry of Health
Amman, Jordan

Fekri Abroug
Intensive Care Department
Fattouma Bourguiba Hospital
Monastir, Tunisia

Said H.S. Al Dhahry
Department of Laboratory Medicine
Hamad Medical Corporation
Doha, Qatar

Mohd Mohd Alhajri
Supreme Council of Health
Doha, Qatar

Rafat Al-Hakeem
Public Health Directorate
Farida Ismail Al Hosani
Health Authority Abu Dhabi
United Arab Emirates

Sultan Mohammed Abdalla Al Qasrawi
Communicable Disease Directorate
Ministry of Health
Amman, Jordan

Hamad Eid Al-Romaihi
Supreme Council of Health
Doha, Qatar

Abdullah Assiri
Public Health Directorate
Ministry of Health
Riyadh, Saudi Arabia

J Kenneth Baillie
The Roslin Institute
University of Edinburgh
Edinburgh, Scotland

Peter Karim Ben Embarek
Food Safety and Zoonoses
World Health Organization
Geneva, Switzerland

Afif Ben Salah
Institut Pasteur de Tunis
Tunis, Tunisia

Benjamin Blümel
Department of Infectious Disease Epidemiology
Robert Koch Institute
Berlin, Germany

Thomas Briese
Center for Infection and Immunity and Department of Epidemiology
Columbia University
Mailman School of Public Health
New York, New York, USA

Udo Buchholz
Department of Infectious Disease Epidemiology
Robert Koch Institute
Berlin, Germany

Sebastien Bruno Francois Cognat
Support to IHR Capacity Development
World Health Organization
Geneva, Switzerland

Gabriel N. Defang
Head, Viral & Zoonotic Diseases Research Program
NAMRU3 – U.S. Naval Medical Research Unit No. 3, Cairo, Arab Republic of Egypt

Stéphane De La Rocque
IHR Monitoring, Procedures and Information
World Health Organization
Geneva, Switzerland

Isabella Donatelli
National Influenza Centre
Department of Infectious, Parasitic and Immune-Mediated Diseases
Istituto Superiore di Sanità
Roma, Italy

Christian Drosten
Institute of Virology
University of Bonn Medical Centre
Bonn, Germany

Patrick Anthony Drury
Global Alert and Response Operations
World Health Organization
Geneva, Switzerland

Sergey Romualdovich Eremin
AMR, Infection Control and Publications
World Health Organization
Geneva, Switzerland

Neil M. Ferguson
MRC Centre for Outbreak Analysis and Modelling
Department of Infectious Disease Epidemiology
Imperial College London
London, United Kingdom

Arnaud Fontanet
Emerging Diseases Epidemiology Unit
Institut Pasteur
Pierre B.H. Formenty  
Control of Epidemic Diseases  
World Health Organization  
Geneva, Switzerland

Ron A.M. Fouchier  
Department of Virology  
Erasmus MC  
Rotterdam, Netherlands

Christine Qiuhan Gao  
Biodefence Centre  
Singapore Armed Forces  
Singapore

Erika Garcia  
Global Alert and Response Operations  
World Health Organization  
Geneva, Switzerland

Susan I. Gerber  
Division of Viral Diseases/ Epidemiology Branch  
National Center for Immunization and Respiratory Diseases  
Centers for Disease Control and Prevention  
Atlanta, USA

Benoît Guery  
Maladies Infectieuses  
CHRU  
Lille, France

Bart L. Haagmans  
Viroscience Lab  
Erasmus MC  
Rotterdam, Netherlands

Aktham Jeries Haddadin  
National Laboratories Directorate  
Ministry of Health  
Amman, Jordan

Maxwell Charles Hardiman  
IHR Monitoring, Procedures and Information  
World Health Organization  
Geneva, Switzerland
Lisa E Hensley  
National Institutes of Health  
Frederick, Maryland, USA  

Stéphane Alexandre Louis Hugonnet  
Global Alert and Response Operations  
World Health Organization  
Geneva, Switzerland  

David SC Hui  
The Chinese University of Hong Kong  
Department of Medicine & Therapeutics  
Prince of Wales Hospital  
Hong Kong, SAR  

Nicolas Isla  
Global Alert and Response Operations  
World Health Organization  
Geneva, Switzerland  

William B. Karesh  
Executive Vice President for Health and Policy  
EcoHealth Alliance  
New York, New York, USA  

Marion Koopmans  
National Institute of Public Health and the Environment  
Bilthoven, Netherlands  

Anna Kuehne  
Department of Infectious Disease Epidemiology  
Robert Koch Institute  
Berlin, Germany  

W. Ian Lipkin  
Center for Infection and Immunity  
Columbia University  
New York, New York, USA  

Ali R. Mafi  
Pandemic and Epidemic Diseases  
World Health Organization Regional Office for the Eastern Mediterranean  
Cairo, Egypt  

Mamunur Malik  
Pandemic and Epidemic Diseases  
World Health Organization Regional Office for the Eastern Mediterranean  

PLOS Currents Outbreaks
Jean-Claude Manuguerra
Laboratory for urgent response to biological threats
Institut Pasteur
Paris, France

Ziad Memish
Deputy Minister of Health
Ministry of Health
Riyadh, Saudi Arabia

Anthony Wayne Mounts
Global Influenza Programme
World Health Organization
Geneva, Switzerland

Elizabeth Mumford
Food Safety and Zoonoses
World Health Organization
Geneva, Switzerland

Langoya Opoka
Pandemic and Epidemic Diseases
World Health Organization Regional Office for the Eastern Mediterranean
Cairo, Egypt

Ab Osterhaus
Viroscience Lab, Erasmus MC
Rotterdam, Netherlands

Christopher John Oxenford
Support to IHR Capacity Development
World Health Organization
Geneva, Switzerland

Junxiong Pang
Centre for Infectious Disease Epidemiology and Research
Saw Swee Hock School of Public Health
National University of Singapore
Genome Institute of Singapore
Singapore

Richard Pebody
Respiratory Diseases Department
Centre for Infectious Disease Surveillance and Control
Public Health England


Correspondence

Anthony W. Mounts
Global Influenza Programme, World Health Organization, Geneva, Switzerland
Email: mountsa@who.int; Telephone: +41227911062

The opinions expressed in this article are those of the authors and members of the working group and do not necessarily reflect those of the institutions or organizations with which they are affiliated.

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