An Observational, Laboratory-Based Study of Outbreaks of Middle East Respiratory Syndrome Coronavirus in Jeddah and Riyadh, Kingdom of Saudi Arabia, 2014

Christian Drosten,1,2,a Doreen Muth,1,a Victor M. Corman,1,2,a Raheela Hussain,3,a Malaki Al Masri,4 Waleed Haj Omar,5 Olfert Landt,6 Abdullah Assiri,4 Isabella Eckerle,1 Ali Al Shangiti,5 Jaffar A. Al-Tawfiq,7,8 Ali Albarrak,9 Alimuddin Zumla,4,10,11 Andrew Rambaut,12,13 and Ziad A. Memish4,14

1Institute of Virology, University of Bonn Medical Centre, 2German Centre for Infection Research, Hannover, Germany; 3Jeddah Regional Laboratory, 4Global Centre for Mass Gatherings Medicine, and 5Regional Laboratory, Ministry of Health, Riyadh, Kingdom of Saudi Arabia; 6Tib-Molbiol, Berlin, Germany; 7Johns Hopkins Aramco Healthcare, Saudi Aramco, Dhahran, Kingdom of Saudi Arabia; 8Indiana University School of Medicine, Indianapolis; 9Prince Sultan Military Medical City, Riyadh, Kingdom of Saudi Arabia; 10Division of Infection and Immunity, University College London, National Institute for Health Research Biomedical Research Centre, University College London Hospitals National Health Service Foundation Trust, and 11Institute of Evolutionary Biology, University of Edinburgh, Centre for Infection, Immunity and Evolution, University of Edinburgh, United Kingdom; 12Fogarty International Center, National Institutes of Health, Bethesda, Maryland; and 13Alfaisal University, Riyadh, Kingdom of Saudi Arabia

(See the Editorial Commentary by Leitmeyer on pages 378–80.)

Background. In spring 2014, a sudden rise in the number of notified Middle East respiratory syndrome coronavirus (MERS-CoV) infections occurred across Saudi Arabia with a focus in Jeddah. Hypotheses to explain the outbreak pattern include increased surveillance, increased zoonotic transmission, nosocomial transmission, and changes in viral transmissibility, as well as diagnostic laboratory artifacts.

Methods. Diagnostic results from Jeddah Regional Laboratory were analyzed. Viruses from the Jeddah outbreak and viruses occurring during the same time in Riyadh, Al-Kharj, and Madinah were fully or partially sequenced. A set of 4 single-nucleotide polymorphisms distinctive to the Jeddah outbreak were determined from additional viruses. Viruses from Riyadh and Jeddah were isolated and studied in cell culture.

Results. Up to 481 samples were received per day for reverse transcription polymerase chain reaction (RT-PCR) testing. A laboratory proficiency assessment suggested positive and negative results to be reliable. Forty-nine percent of 168 positive-testing samples during the Jeddah outbreak stemmed from King Fahd Hospital. All viruses from Jeddah were monophyletic and similar, whereas viruses from Riyadh were paraphyletic and diverse. A hospital-associated transmission cluster, to which cases in Indiana (United States) and the Netherlands belonged, was discovered in Riyadh. One Jeddah-type virus was found in Riyadh, with matching travel history to Jeddah. Viruses isolates representing outbreaks in Jeddah and Riyadh were not different from MERS-CoV EMC/2012 in replication, escape of interferon response, or serum neutralization.

Conclusions. Virus shedding and virus functions did not change significantly during the outbreak in Jeddah. These results suggest the outbreaks to have been caused by biologically unchanged viruses in connection with nosocomial transmission.

Keywords. MERS-coronavirus; outbreak; nosocomial transmission; virus isolation; transmission infection control.

Received 27 June 2014; accepted 25 August 2014; electronically published 16 October 2014.

© The Author 2014. Published by Oxford University Press on behalf of the Infectious Diseases Society of America. All rights reserved. For Permissions, please e-mail: journals.permissions@oup.com.
DOI: 10.1093/cid/ciu812
The Middle East respiratory syndrome coronavirus (MERS-CoV) was discovered in 2012 and has since been found to cause sporadic cases and small case clusters of severe acute respiratory illness [1]. All cases occurred in the Arabian peninsula or had epidemiological links to the region. The total number of notified cases since 2012 was 199 as of 25 March 2014 [2]. From the end of March through April 2014, an exponential increase of new cases occurred in Saudi Arabia with a focus in Jeddah, causing conjecture about potential changes in fundamental epidemiological parameters [3]. Hypotheses to explain the outbreak pattern include increased surveillance, increased zoonotic transmission, increasing nosocomial transmission, and changes in viral transmissibility, as well as false-positive results due to laboratory errors. The latter option caused concern about the validity of the overall case count notified to the World Health Organization [3].

To fully appreciate the extensive outbreak in Jeddah, it will be necessary to reconstruct transmission chains and dissect the epidemiology in such a way that fundamental epidemiological parameters can be inferred. Although these analyses may take considerable time, health authorities are in urgent need of information to guide potential alterations of preventive measures and travel recommendations. Virological studies can provide valuable insight into virulence and transmissibility even in absence of detailed clinical or epidemiological information. Moreover, the trend in numbers and nature of requests received in the diagnostic laboratory can provide helpful insight into the general situation at point of care.

During the outbreak in Jeddah, all reverse transcription polymerase chain reaction (RT-PCR) testing was centrally performed by the Jeddah Regional Laboratory (JRL). JRL is a reference facility within the laboratory network of the Saudi Ministry of Health that serves the Jeddah region and provides confirmatory MERS-CoV testing for all Ministry of Health laboratories across the Kingdom of Saudi Arabia. Here we provide direct insight into laboratory results from JRL and performed a thorough analysis of the outbreak-associated virus along with functional studies of virulence and immune escape in cell culture. We compare Jeddah-derived viruses with viruses occurring elsewhere in the country during the same time period.

MATERIALS AND METHODS

RT-PCR and Sequencing

All procedures followed protocols described previously [4–6]. JRL used LightMix kits (Tib-Molbiol) containing premixed primers and probe for the upE and ORF1A assays to minimize the risk of reagent-based contamination and detection artifacts [4]. Primers for viral genome sequencing are available upon request.

Virus Isolation

Samples were inoculated in VeroB4 cells seeded at 3 × 10⁵ cells/mL in 24-well plates 16 hours prior to infection, for 1 hour at 37°C. Cells were incubated at 37°C and checked daily for cytopathogenic effects. Every 2 days, cell culture supernatant was sampled and tested by real-time RT-PCR for increase of MERS-CoV-specific viral RNA. PCR-positive wells were harvested and used for the production of virus stocks. Virus stocks were quantified by plaque titration on VeroB4 cells as described earlier [7].

Virus Growth Kinetics

A549 cells (ATCC CCL-185) were seeded at 2 × 10⁵ cells/well in 24-well plates 16 hours prior to infection. At 1, 8, 24, 48, and 72 hours postinfection, supernatants were sampled, and the increase of MERS-CoV-specific viral RNA was quantified by real-time RT-PCR [7].

Plaque Titration and Neutralization Assay

VeroB4 cells were seeded at 1.5 × 10⁵ cells/well in 24-well plates 16 hours prior to titration. Cells were overlaid after infection with 500 µL Avicel (FCM BioPolymer) at a final concentration of 1.2% in Dulbecco’s modified Eagle’s medium [8]. Three days postinfection, cells were fixed in 6% formaldehyde and stained with crystal violet solution. For neutralization assay [9, 10], 25 plaque-forming units of MERS-CoV were preincubated with diluted serum for 1 hour at 37°C.

RESULTS

Laboratory Performance and Overall Diagnostic Results

Case identification and notification during the outbreak in Jeddah was mainly based on laboratory testing. To obtain insight into laboratory testing during the outbreak, the sample reception list in JRL was analyzed (Figure 1). There was a striking increase of diagnostic requests during April, which was mainly caused by samples from Jeddah (Figure 1A). From 1 January to 28 April 2014, JRL received 6285 samples for RT-PCR testing for MERS-CoV. Of these samples, 5828 were received since 26 March, the date when the first case in the Jeddah outbreak was tested. This suggests a 36.8-fold increase of the monthly workload in April. The maximal number of samples received in a single day was 481. Almost half of all positive testing samples during the Jeddah outbreak (82 of 168) stemmed from King Fahd Hospital (KFH). The rate of samples with positive tests from KFH seemed to increase earlier than in other hospitals in the city (Figure 1B). Over the course of 4 weeks in April, the fraction of positive RT-PCR results in samples from Jeddah
as well as samples from all cities did not vary significantly (Supplementary Table 1). Although the laboratory entry list did not identify the symptom status of patients, it indicated by presence of a patient identifier code whether cases were in hospital or likely part of a contact investigation (Table 1). There was a marked increase of contact investigations in Jeddah vs other locations. Expectedly, the proportion of samples with low viral loads (indicated by high cycle threshold [Ct] values) was high in contact investigations (Figure 1C and 1D). Studies of reliability of laboratory procedures did not reveal any evidence for generic background contamination in the laboratory (Supplementary Data 1).

Viral Genome Sequence and Phylogeny

Seven viruses from the Jeddah outbreak were entirely sequenced and compared with full-length or subtotal genome sequences available in April 2014 in GenBank (Supplementary Table 2). An analysis of major reading frames across the genome, taking into account additional spike gene sequences (KM027263-KM027276), suggested no unique amino acid changes in relevant protein domains (Supplementary Data 2).

All viruses pertaining to the Jeddah outbreak clustered in 1 phylogenetic clade (Figure 2). Seventeen partial genome sequences were determined from samples obtained from Riyadh, Al-Kharj, and Madinah during March and April 2014 for comparison. These partial sequences comprised the entire structural protein genes of the MERS-CoV genomes, approximately 8.7 kb in length. As shown in Figure 2, viruses from Riyadh fell into 6 different positions, 1 of which (clade 2) may constitute a human-to-human transmission cluster, to which also the exported cases to Indiana (United States) as well as the Netherlands belong (Supplementary Table 3) [14, 15]. Another virus from Riyadh clustered with Jeddah-type viruses. This patient originated from Jeddah and had visited his sick son in KFH in Jeddah before his trip to Riyadh.

To better evaluate the diversity of viruses circulating in Jeddah, single-nucleotide polymorphisms (SNPs) were studied (Table 2). All samples except 1 had the same combination of
SNPs. The deviating sample was taken on 22 April and had a double peak in 1 SNP that was confirmed twice by repetition of RT-PCR and sequencing. Further partial sequencing of this virus did not yield any other double peaks, suggesting the ongoing formation of quasispecies as described before [16], rather than simultaneous infection with 2 viruses. The sequences

Figure 2. Phylogenetic tree inferred using MrBayes [11] for the concatenated coding regions of 105 Middle East respiratory syndrome coronavirus genomes or partial genomes sampled from humans and camels. We employed a codon position-specific general time reversible (GTR) substitution model with $\gamma$-distributed rates among sites. Displayed is the majority consensus of 10,000 trees sampled from the posterior distribution with mean branch lengths. Posterior support is shown for nodes where $<0.90$. Sequences sampled from camels are denoted with a yellow circle, those from humans with a green circle. Sequences new to this study are labeled in bold. The cluster comprising viruses isolated from the Jeddah/Makkah hospitals in April 2014 are highlighted with a red box and those from the Prince Sultan Military Medical City, Riyadh, in March–April 2014 are highlighted in blue. For comparison, the Al-Hasa 2013 hospital outbreak [12] is highlighted in yellow and the 2013 Hafr-Al-Batin community outbreak [13] in green.
from a US patient and a patient in Riyadh with known travel histories to Jeddah had Jeddah-typical SNP patterns (Table 2). In contrast, viruses detected in Jeddah 1 month and 5 months before the outbreak did not cluster with the Jeddah-type outbreak viruses. A virus detected in Riyadh (SA2014_158) was related to camel viruses sharing a recent common ancestor with Jeddah-type outbreak viruses, but was distinct in its SNP pattern.

**Virus Infection Studies**

To study potential alterations in virus functions, 16 clinical samples from Jeddah with projected viral loads of ≥5 × 10^6 copies per sample were selected and inoculated in Vero B4 cells. Five viral isolates were obtained. Because the replication phenotype of all viruses was highly similar in preliminary experiments, 1 isolate termed MERS-CoV Jeddah_10306 was fully sequenced and chosen for further study (GenBank accession number KM027260; Supplementary Table 2). For comparison, virus was isolated from patients in a hospital-associated cluster in Riyadh, and an isolate termed MERS-CoV Riyadh_683 was chosen and sequenced (GenBank accession number KM027262; Supplementary Table 3). The original viral isolate EMC/2012 [1] was compared as well.

Single-step growth curves were done on Vero cells by inoculation with high multiplicities of infection (MOI) of 1 infectious dose per cell, which will reveal gross differences such as in the viruses’ capacity to enter cells. As shown in Figure 3A, there were no relevant differences in replication between the 3 viral strains. Because Vero cells derived from rhesus monkey kidney tissue might not optimally reflect the target tissue of MERS-CoV infection, A549 cells derived from a human alveolar epithelial carcinoma (non-small-cell lung cancer) were used in parallel. Results of 1-step growth curves were highly similar (Figure 3B).

Because differences in the viruses’ adaptation to replicate in primate cells may not become obvious in 1-step growth curves, replication trials were repeated in parallel in both cell lines using a reduced MOI of 0.01 that causes a prolonged course of replication with multiple rounds of infection in culture. No relevant difference in replication was seen between any of the 3 viral isolates in Vero and A549 cells (Figure 3C and 3D).

The type I interferon system is among the most efficient innate antiviral defenses. As MERS-CoV EMC/2012 was shown to be highly susceptible against type I interferon, infection trials were done in Vero cells pretreated with interferon alfa to induce an antiviral state prior to infection at MOI = 0.01. Even though Vero cells are known to induce an efficient antiviral state
upon external IFN stimulus, no differences between the 3 viral strains were seen (Figure 3E).

Antibody functions provide a laboratory correlate of adaptive immunity. As viruses may differ in their robustness against neutralizing antibodies, all 3 viruses were subjected to plaque reduction neutralization assays using serum of a MERS patient with known antibody titer [6]. No relevant differences in the reduction of viral plaques depending on serum dilution were seen with any virus (Figure 3F).

Viral Loads
Viral load data reflect clinical virus excretion, which cannot be modeled in cell culture. Ct values as a surrogate of viral loads were compared between samples from Jeddah and other cities.
Mean Ct values in Jeddah and elsewhere were not significantly different (30.4 and 31.4, respectively). However, the frequency distributions and median values suggested a pronunciation of lower viral load samples in Jeddah. Within Jeddah, Ct values in KFH (n = 82) did not differ from those in any other hospitals (n = 108). All samples from Jeddah tested during April were categorized by week of reception and plotted as shown in Figure 4C. There was a subjective trend toward lower Ct values by the third week. However, these points were identified as outlier values, and mean viral loads did not differ significantly in any of the weeks of April according to analysis of variance (F = 0.82, P = .48). One of those outlier samples with a very low Ct value, encountered on 20 April 2014, yielded the isolate of MERS-CoV C10306, which has been entirely sequenced without any evidence for significant mutations, and which was studied in above-described cell culture experiments without any evidence for increased virulence.

DISCUSSION

The unprecedented increase in new cases of MERS-CoV infections during spring 2014 has caused concern in the public health community worldwide. Our initial sequence analyses communicated during the ongoing outbreak provided a preliminary idea of the molecular epidemiology, with outbreak viruses forming a homogeneous, monophyletic clade [17]. Paraphyly of concurrent viruses is expected when infections are independently acquired from a diversified source population such as expected in animal reservoirs. In Riyadh, concurrently circulating viruses were indeed distributed across at least 6 different clades, suggesting that these infections resulted from increased zoonotic activity or introduction of human viruses from other regions. One larger virus cluster was observed in Riyadh, associated with a specific hospital, suggesting nosocomial transmission (clade 2). The patient exported to Indiana had worked in this hospital, whereas the cases in the Netherlands were hospitalized in Madinah but not Riyadh [14, 15]. This suggests unnoticed transmission links such as infected patients transferred between hospitals, or acquisition from common zoonotic sources.

Interestingly, one of the viruses seen in Riyadh resembled camel viruses in close relationship to Jeddah-type strains. These viruses may have been widely distributed in camels by late 2013 to early 2014, as they were detected in Taif (southeast of Jeddah) and in Qatar on the eastern Arabian Peninsula [16, 18]. Viruses encountered in Jeddah shortly before the outbreak such as Jeddah-1 or Jeddah_C6664 were clearly distinct, suggesting that

Figure 4. Virus shedding in patients. Cycle threshold (Ct) values during the outbreak in Jeddah. A and B. Frequency distribution of Ct values in Jeddah vs other cities. C. Ct values during the outbreak in Jeddah by week, starting on 26 March 2014.
the outbreak might have been initiated by the introduction of Jeddah-type viruses into camels in the region. The monophyly and similarity of outbreak viruses favors the idea that the subsequent transmission took place in humans. The regional restriction of outbreak viruses matches our earlier observation of low transmissibility between humans in nonnosocomial settings such as household contact clusters [19]. Despite a documented transmissibility between humans in nonnosocomial settings such as household contact clusters [19]. Despite a documented transmissibility between humans in nonnosocomial settings such as household contact clusters [19]. Despite a documented transmissibility between humans in nonnosocomial settings such as household contact clusters [19]. Despite a documented transmissibility between humans in nonnosocomial settings such as household contact clusters [19]. Despite a documented transmissibility between humans in nonnosocomial settings such as household contact clusters [19]. Despite a documented transmissibility between humans in nonnosocomial settings such as household contact clusters [19]. Despite a documented transmissibility between humans in nonnosocomial settings such as household contact clusters [19]. Despite a documented transmissibility between humans in nonnosocomial settings such as household contact clusters [19]. Despite a documented transmissibility between humans in nonnosocomial settings such as household contact clusters [19]. Despite a documented transmissibility between humans in nonnosocomial settings such as household contact clusters [19].

In conclusion, our investigations suggest a predominance of human-to-human transmission during the Jeddah outbreak without evidence for modification of viral shedding, replication, or immune escape. A coincident increase of cases in Riyadh was the result of multiple, independent sources with some phylogenetic evidence of nosocomial spread. Contact tracing by RT-PCR should be restricted to defined groups of patients to avoid an overload on the healthcare system. Retrospective serological tests may provide a valid alternative to RT-PCR testing of contacts [19].
Supplementary Data

Supplementary materials are available at Clinical Infectious Diseases online (http://cid.oxfordjournals.org). Supplementary materials consist of data provided by the author that are published to benefit the reader. The posted materials are not copyrighted. The contents of all supplementary data are the sole responsibility of the authors. Questions or messages regarding errors should be addressed to the author.

Notes

Acknowledgments. This study was part of a public health intervention under the authority of the Ministry of Health of the Kingdom of Saudi Arabia.

Disclaimer. Tib-Molbiol had no influence in the decision to use the reagents mentioned in this study. The work does not make any comparisons of these reagents with products provided by competing commercial or non-commercial entities.

Financial support. C. D. acknowledges support from the European Commission (www.emperie.eu/emp; contract number 223498) and ANTIGONE (contract number 278976), infrastructural support from the German Centre for Infection Research, the German Ministry for Research and Education, and the German Research Council (grant number 01KIO701 and DR 772/3-1). I. E., D. M., and V. M. C. acknowledge grant and Education, and the German Research Council (grant number 01KIO701 and DR 772/3-1). The work does not make any comparisons of these reagents with products provided by competing commercial or non-commercial entities.

Potential conflicts of interest. O. L. is CEO of Tib-Molbiol, a company providing some of the reverse transcription polymerase chain reaction reagents used in this study. All other authors report no potential conflicts.

All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

References


