

historical information of the *V. cholerae* ST75 strains they studied; and our colleagues in the Biobank Section of Taiwan Centers for Disease Control for providing *V. cholerae* isolates.

This study was funded by the Ministry of Health and Welfare, Taiwan (grant no. MOHW108-CDC-C-315-122129).

About the Author

Mr. Tu is a research associate in the Centers for Disease Control, Ministry of Health and Welfare, Taiwan. His expertise includes systems biology, computational biology, and machine learning, including developing *Vibrio cholerae* core genome multilocus sequence typing profiling pipelines for the organization.

References

1. World Health Organization. Cholera Annual Report 2017. *Wkly Epidemiol Rec.* 2018;93:489–500.
2. Mutreja A, Kim DW, Thomson NR, Connor TR, Lee JH, Kariuki S, et al. Evidence for several waves of global transmission in the seventh cholera pandemic. *Nature.* 2011;477:462–5. <https://doi.org/10.1038/nature10392>
3. Lippi D, Gotuzzo E, Caini S. Cholera. *Microbiol Spectr.* 2016;4.
4. Yen CH. A recent study of cholera with reference to an outbreak in Taiwan in 1962. *Bull World Health Organ.* 1964;30:811–25. [10.1128/microbiolspec.PoH-0012-2015](https://doi.org/10.1128/microbiolspec.PoH-0012-2015)
5. Taiwan National Infectious Disease Statistics System [cited 2019 Feb 1]. <https://nidss.cdc.gov.tw>
6. Luo Y, Octavia S, Jin D, Ye J, Miao Z, Jiang T, et al. US Gulf-like toxigenic O1 *Vibrio cholerae* causing sporadic cholera outbreaks in China. *J Infect.* 2016;72:564–72. <https://doi.org/10.1016/j.jinf.2016.02.005>
7. Okada K, Na-Ubol M, Natakathung W, Roobthaisong A, Maruyama F, Nakagawa I, et al. Comparative genomic characterization of a Thailand-Myanmar isolate, MS6, of *Vibrio cholerae* O1 El Tor, which is phylogenetically related to a “US Gulf Coast” clone. *PLoS One.* 2014;9:e98120. <https://doi.org/10.1371/journal.pone.0098120>
8. Greig DR, Schaefer U, Octavia S, Hunter E, Chattaway MA, Dallman TJ, et al. Evaluation of whole-genome sequencing for identification and typing of *Vibrio cholerae*. *J Clin Microbiol.* 2018;56:e00831–18. <https://doi.org/10.1128/JCM.00831-18>
9. Watve SS, Chande AT, Rishishwar L, Mariño-Ramírez L, Jordan IK, Hammer BK. Whole-genome sequences of 26 *Vibrio cholerae* isolates. *Genome Announc.* 2016;4:e01396–16. <https://doi.org/10.1128/genomeA.01396-16>
10. Kaper JB, Bradford HB, Roberts NC, Falkow S. Molecular epidemiology of *Vibrio cholerae* in the U.S. Gulf Coast. *J Clin Microbiol.* 1982;16:129–34.

Address for correspondence: Chien-Shun Chiou, Centers for Disease Control, Central Region Laboratory, 5F, 20 Wen-Sin South 3rd Rd, Taichung City 40855, Taiwan; email: nipmcs@cdc.gov.tw

Diabetes Mellitus, Hypertension, and Death among 32 Patients with MERS-CoV Infection, Saudi Arabia

Khalid H. Alanazi, Glen R. Abedi, Claire M. Midgley, Abdulrahim Alkhamis, Taghreed Alsaqer, Abdullah Almoaddi, Abdullah Algwizani, Sameeh S. Ghazal, Abdullah M. Assiri, Hani Jokhdar, Susan I. Gerber, Hail Alabdely, John T. Watson

Author affiliations: Ministry of Health, Riyadh, Saudi Arabia (K.H. Alanazi, A. Alkhamis, T. Alsaqer, A. Almoaddi, A. Algwizani, S.S. Ghazal, A.M. Assiri, H. Jokhdar, H. Alabdely); Centers for Disease Control and Prevention, Atlanta, Georgia, USA (G.R. Abedi, C.M. Midgley, S.I. Gerber, J.T. Watson)

DOI: <https://doi.org/10.3201/eid2601.190952>

Diabetes mellitus and hypertension are recognized risk factors for severe clinical outcomes, including death, associated with Middle East respiratory syndrome coronavirus infection. Among 32 virus-infected patients in Saudi Arabia, severity of illness and frequency of death corresponded closely with presence of multiple and more severe underlying conditions.

First described in 2012, infection with Middle East respiratory syndrome coronavirus (MERS-CoV) has been reported worldwide. More than 2,200 cases have been reported to the World Health Organization, and more than one third have resulted in death (1).

Certain underlying conditions, including diabetes mellitus (DM), hypertension, chronic cardiac disease, and chronic renal disease, are recognized risk factors for illness and death caused by infection with MERS-CoV (2,3). We further explored this relationship among MERS patients admitted to a referral hospital in Riyadh, Saudi Arabia, during August 1, 2015–August 31, 2016. Enrollment criteria and data collection methods have been described (4).

We considered persons with a medical history of DM as having documented DM and persons with multiple recorded periods of hyperglycemia during hospitalization as having possible DM (4). We similarly identified patients with hypertension or chronic kidney disease (CKD) by using documentation in the medical chart. We defined cardiovascular disease as having documentation of coronary artery disease or a history of heart failure or stroke. We considered patients with cardiovascular disease or CKD to have chronic organ dam-

age (COD). We performed statistical analysis by using SAS version 9.4 (<https://www.sas.com>) and Microsoft Excel (<https://www.microsoft.com>).

Of 33 enrolled patients, medical history was available for 32 through medical charts. Underlying disease status among the 32 patients were no DM, hypertension, or COD (n = 11); DM without hypertension or COD (n = 5); DM and hypertension without COD (n = 5); and DM or hypertension with COD (n = 11). Of the 21 patients who had DM, 19 had DM documented in the medical chart, and 2 had possible DM, with random glucose readings >350 mg/dL during hospitalization. All 15 patients with hypertension had concomitant DM (Figure; Appendix Table, <https://wwwnc.cdc.gov/EID/article/26/1/19-0952-App1.pdf>). Of the 11 patients who had COD, 8 had cardiovascular disease, 1 had CKD, and 2 had cardiovascular disease and CKD. Of the 10 patients who had cardiovascular disease, 5 had a history of coronary disease, 3 had a history of heart failure, and 4 had a history of stroke; of the 3 patients with a history of heart failure, 1 also had coronary disease and 1 had a history of stroke.

Age was associated with presence of DM (mean 59 years vs. 30 years; $p < 0.0001$, by *t*-test), hypertension (mean 64 years vs. 36 years; $p < 0.0001$ by *t*-test), and cardiovascular disease (median 66 years vs. 41 years; $p < 0.0001$ by *t*-test). Sex was not significantly associated with DM (68% of patients with DM were male vs. 45% of patients without DM; $p = 0.2159$ by χ^2 test), hypertension (67% of patients with hypertension

were male vs. 59% of patients without hypertension; $p = 0.6474$ by χ^2 test, or cardiovascular disease (60% of patients with cardiovascular disease were male vs. 64% of patients without cardiovascular disease; $p = 0.8439$ by χ^2 test).

Of the 32 patients, 21 survived until discharge, including 8 who required supplemental oxygen during hospitalization. Eleven died in the hospital, all of whom required ventilatory support. Case-patients with multiple and more severe underlying conditions generally had worse clinical course and outcomes than those without these conditions (Figure; Appendix Table). Of the 11 case-patients with no DM or hypertension, 100% survived, as did all patients with DM but without hypertension or COD. In comparison, 2 (40%) of 5 with DM and hypertension but without COD died, and 9 (82%) of 11 with DM or hypertension and with COD died (Appendix Table).

In a previous study (5), DM, chronic lung disease, heart disease, and smoking were identified as underlying health conditions and behaviors associated with primary infection with MERS-CoV. Alqatani et al. reported that DM, hypertension, cardiac disease, renal disease, and bronchial asthma were frequent underlying conditions associated with death of MERS-CoV-infected patients and also found that the risk for death increased for patients with multiple comorbidities (3). We found that DM, hypertension, and COD co-occurred frequently in MERS-CoV-infected patients, and severity of illness and frequency

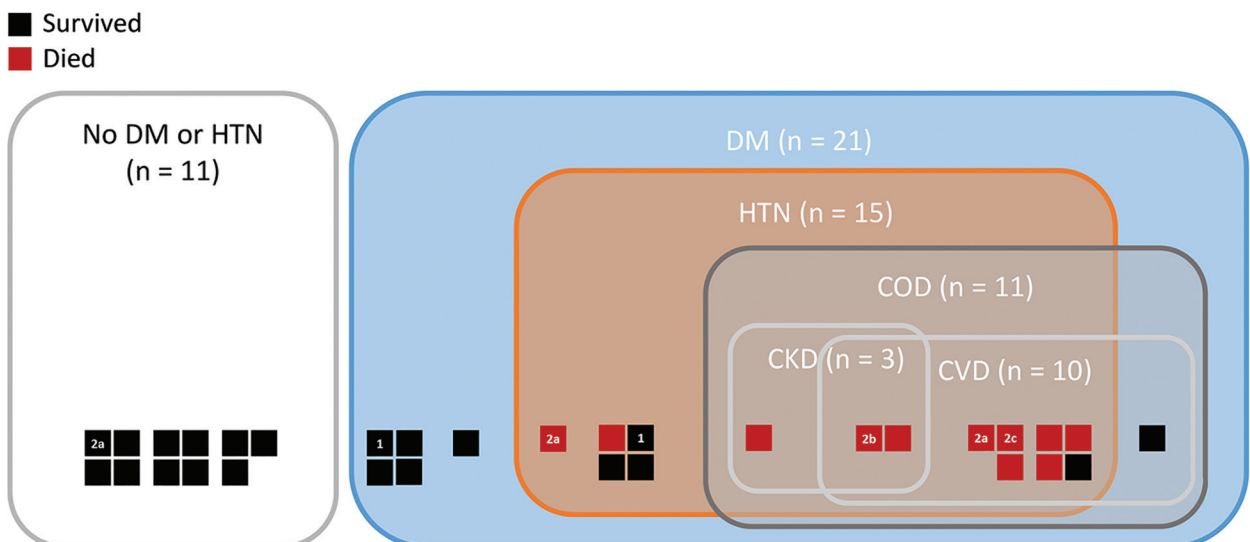


Figure. Characteristics of 32 case-patients infected with Middle East respiratory syndrome coronavirus, by underlying condition and survival status, Saudi Arabia. 1, DM defined as hyperglycemia recorded during hospitalization (n = 2). 2a, chronic lung disease in 1 patient with no DM or HTN who survived, 1 patient with DM and HTN but no COD who died, and 1 patient with CVD and not CKD who died. 2b, epilepsy in 1 patient with CVD and CKD who died. 2c, uterine cancer in 1 patient with CVD and not CKD who died. COD, chronic organ damage; CKD, chronic kidney disease; CVD, cardiovascular disease; DM, diabetes mellitus; HTN, hypertension.

of death were higher for patients with multiple and more severe underlying conditions. Further studies are necessary to better clarify the mechanisms that lead to severe outcomes among these patients.

For case-patients infected with MERS-CoV, the presence and compounding of underlying conditions, including DM, hypertension, and, ultimately, COD, corresponded with an increasingly complicated clinical course and death. These findings indicate that increased clinical vigilance is warranted for patients with multiple and severe underlying conditions who are suspected of being infected with MERS-CoV.

About the Author

Dr. Alanazi is director general of infection prevention and control at the Ministry of Health, Riyadh, Saudi Arabia. His research interests include prevention and control of infectious diseases in the healthcare setting.

References

1. World Health Organization. Regional office for the Eastern Mediterranean. MERS situation update; October 2018 [cited 2019 Oct 30]. <http://www.emro.who.int/pandemic-epidemic-diseases/mers-cov/mers-situation-update-october-2018.html>
2. Assiri A, Al-Tawfiq JA, Al-Rabeeh AA, Al-Rabiah FA, Al-Hajjar S, Al-Barrak A, et al. Epidemiological, demographic, and clinical characteristics of 47 cases of Middle East respiratory syndrome coronavirus disease from Saudi Arabia: a descriptive study. *Lancet Infect Dis*. 2013;13:752–61. [https://doi.org/10.1016/S1473-3099\(13\)70204-4](https://doi.org/10.1016/S1473-3099(13)70204-4)
3. Alqahtani FY, Aleanizy FS, Ali El Hadi Mohamed R, Alanazi MS, Mohamed N, Alrasheed MM, et al. Prevalence of comorbidities in cases of Middle East respiratory syndrome coronavirus: a retrospective study. *Epidemiol Infect*. 2018;Nov 5:1–5.
4. Al-Abdely HM, Midgley CM, Alkhamis AM, Abedi GR, Lu X, Binder AM, et al. Middle East respiratory syndrome coronavirus infection dynamics and antibody responses among clinically diverse patients, Saudi Arabia. *Emerg Infect Dis*. 2019;25:753–66. <https://doi.org/10.3201/eid2504.181595>
5. Alraddadi BM, Watson JT, Almarashi A, Abedi GR, Turkistani A, Sadran M, et al. Risk factors for primary Middle East respiratory syndrome coronavirus illness in humans, Saudi Arabia, 2014. *Emerg Infect Dis*. 2016;22:49–55. <https://doi.org/10.3201/eid2201.151340>

Address for correspondence: Glen R. Abedi, Centers for Disease Control and Prevention, 1600 Clifton RD NE, Mailstop A34, Atlanta, GA 30329-4027, USA; email: gabedi@cdc.gov

Influenza D Virus of New Phylogenetic Lineage, Japan

Shin Murakami, Ryota Sato, Hiroho Ishida, Misa Katayama, Akiko Takenaka-Uema, Taisuke Horimoto

Author affiliations: University of Tokyo, Tokyo, Japan (S. Murakami, H. Ishida, M. Katayama, A. Takenaka-Uema, T. Horimoto); Yamagata Livestock Hygiene Service Center, Yamagata, Japan (R. Sato)

DOI: <https://doi.org/10.3201/eid2601.191092>

Influenza D virus (IDV) can potentially cause respiratory diseases in livestock. We isolated a new IDV strain from diseased cattle in Japan; this strain is phylogenetically and antigenically distinguished from the previously described IDVs.

Influenza D virus (IDV; family *Orthomyxoviridae*) is one of the possible bovine respiratory disease complex (BRDC) causative agents. IDVs are detected in and isolated from cattle in many countries in North America, Asia, Europe, and Africa (1–4). In addition, both IDV RNAs and specific antibodies have been detected in many animal species (1,5,6). To date, IDVs have been phylogenetically classified into 3 lineages: D/OK, D/660, and Japanese lineages. We isolated a new IDV strain from cattle in Japan with respiratory disease, whose hemagglutinin-esterase-fusion (HEF) gene did not belong to the known phylogenetical lineages.

At a herd in Yamagata Prefecture in northern Japan, 15 Holsteins (37.5% of bred cattle in the herd) had respiratory signs develop during January 6–10, 2019 (Appendix Table 1, <http://wwwnc.cdc.gov/EID/article/26/1/19-1092-App1.pdf>). We collected nasal swab samples from 9 of 15 cows on January 7 and 10. All samples subjected to IDV-specific real-time reverse transcription PCR (RT-PCR) (7) were found positive. We also subjected these samples to RT-PCR analyses specific for bovine viral diarrhoea virus 1 and 2, infectious bovine rhinotracheitis virus, bovine parainfluenza virus 3, bovine respiratory syncytial virus, bovine coronavirus, bovine rhinitis A virus, *Mycobacterium bovis*, *Mycoplasma bovis*, *Mycoplasma dispar*, *Ureaplasma diversum*, and *Mycoplasma bovirhinis*. All samples were found negative for these pathogens except for the sample from cow no. 5, which was positive for *M. dispar*. Despite these cows receiving antimicrobial drug treatment, we isolated *Mannheimia haemolytica* from 7 of them (nos. 1–5, 7, 8); cow no. 5 died on January 7. Taken together, these