avian influenza A(H5N1) virus, for which only 2 of the serum specimens we tested were positive (data not shown), but much lower than the seropositivity level for low pathogenicity avian influenza A(H9N2) virus; 3.4% of the samples tested were positive for A/Chicken/Hong Kong/G9/1997(H9N2)–like virus (data not shown). A previous US study has reported H6N2-positive antibodies in veterinarians (*9*). Our results and the veterinarian study indicate that the H6N2 virus could infect humans.

In our study, positive samples were detected in 19 of 22 provinces and in all tested worker populations, suggesting that the H6 virus has been broadly circulating in birds in China. Live poultry market exposure is the major risk factor for human infection with avian influenza H6 virus. The limitation of this study is that antigen selection may not accurately detect neutralization antibodies for different subtypes of H6 viruses. Surveillance of the H6 virus in birds and occupationally exposed populations should be strengthened for pandemic preparedness.

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References

1. Downie JC, Webster RG, Schild GC, Dowdle WR, Laver WG. Characterization and ecology of a type A influenza virus isolated from a shearwater. Bull World Health Organ. 1973;49(6):559-66.
2. Wang G, Deng G, Shi J, Luo W, Zhang G, Zhang Q, et al. H6 influenza viruses pose a potential threat to human health. J Virol. 2014;88:3953–64. http://dx.doi.org/10.1128/JVI.03292-13
3. Jiao P, Yuan R, Wei L, Jia B, Cao L, Song Y, et al. Complete genomic sequence of a novel natural recombinant H6N2 influenza virus from chickens in Guangdong, Southern China. J Virol. 2012;86:7717–8. http://dx.doi.org/10.1128/JVI.00963-12
4. Zhao G, Lu X, Gu X, Zhao K, Song Q, Pan J, et al. Molecular evolution of the H6 subtype influenza A viruses from poultry in eastern China from 2002 to 2010. Virol J. 2011;8:470. http://dx.doi.org/10.1186/1743-422X-8-470
5. Pepin KM, Wang J, Webb CT, Smith GJ, Poss M, Hudson PJ, et al. Multiannual patterns of influenza A transmission in Chinese live bird market systems. Influenza Other Respir Viruses. 2013;7:97–107. http://dx.doi.org/10.1111/j.1750-2659.2012.00354.x
6. Yuan J, Zhang L, Kan X, Jiang L, Yang J, Guo Z, et al. Origin and molecular characteristics of a novel 2013 avian influenza A(H6N1) virus causing human infection in Taiwan. Clin Infect Dis. 2013;57:1367–8. http://dx.doi.org/10.1093/cid/cit479
7. Gillim-Ross L, Santos C, Chen Z, Aspelund A, Yang CF, Ye D, et al. Avian influenza H6 viruses productively infect and cause illness in mice and ferrets. J Virol. 2008;82:10854–63. http://dx.doi.org/10.1128/JVI.01206-08
8. World Health Organization. Manual for the laboratory diagnosis and virological surveillance of influenza. Geneva: The Organization; 2011. p. 63–77.
9. Myers KP, Setterquist SF, Capuano AW, Gray GC. Infection due to 3 avian influenza subtypes in United States veterinarians. Clin Infect Dis. 2007;45:4–9. http://dx.doi.org/10.1086/518579

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Absence of MERS-Coronavirus in Bactrian Camels, Southern Mongolia, November 2014

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To the Editor: Middle East respiratory syndrome coronavirus (MERS-CoV) was first identified among humans in 2012 in Saudi Arabia (*1*). As of February 5, 2015, a total of 971 MERS cases and 356 associated deaths had been confirmed (*2*). Because MERS is a zoonotic disease, it is essential that the animal reservoirs and hosts that sustain virus circulation in nature be identified.

Seroepidemiologic and virologic studies have demonstrated evidence of MERS-CoV infection in dromedary camels (*Camelus dromedarius*) in the Arabian Peninsula (*3*), and viruses isolated from dromedaries appear capable of infecting the human respiratory tract (*4*). In some instances, MERS-CoV infection in dromedaries has preceded infection in humans (*5*), indicating that dromedaries are a natural host for MERS-CoV and a possible source of human infection. Thus, it is important to define the geographic range of MERS-CoV infection in camels and the species of camelids that are infected by MERS-CoV in nature.

Two species of camels exist: 1-hump dromedaries (*C. dromedarius*) and 2-hump Bactrian camels (*C. bactrianus*).

[1]These authors contributed equally to the article.

Dromedaries are common in hot desert terrains of the Arabian Peninsula, the Middle East, Afghanistan, central Asia, India, and parts of Africa. Bactrian camels are found in colder steppes of Mongolia, Central Asia, Pakistan, and Iran. Studies have demonstrated a high seroprevalence (>90%) of MERS-CoV in adult (≥5 years of age) dromedaries from the Middle East and from northern, eastern, and parts of central Africa (*6*), but whether MERS-CoV circulates among Bactrian camels is unknown.

To determine whether MERS-CoV is circulating among both species of camels, we studied apparently healthy Bactrian camel herds in southern Mongolia during November 24–30, 2014. We investigated 11 herds in Umnugovi Province (170 sampled animals) and 1 herd in the adjacent Dundgovi Province (30 sampled animals) (Table). A convenience sample was collected from each herd; younger animals were oversampled. Serum and nasal swab samples were collected from each animal. The nasal swab samples were placed in virus transport medium and later tested by real-time PCR targeting open-reading frame 1a and upstream of envelope protein gene, as previously described (*7*); all samples were negative for MERS-CoV RNA. The serum samples were tested for the presence of MERS-CoV antibody by using a validated MERS-CoV (strain EMC) spike pseudoparticle neutralization test (*8*); no samples were positive, indicating a lack of recent or past MERS-CoV infection. A random sample of 5 serum samples each from camels in Umnugovi and Dundgovi Provinces was tested by using a microneutralization test against bovine coronavirus (BCoV) as previously described (*8*); all 10 samples were positive (titer range 1:20–1:640).

The sampled animals included 127 camels ≥5 years of age from 12 herds across 2 provinces in southern Mongolia. Thus, the negative test results indicate that MERS-CoV is not circulating among Bactrian camels in southern Mongolia. The seroprevalence of MERS-CoV among adult dromedaries in the Middle East and Africa is typically >90%, so the lack of any serologic reactivity in camels from Mongolia implies that MERS-CoV infection does not infect Bactrian camels or that the geographic range of the virus does not extend to northeastern Asia. In contrast, infection with a BCoV-like coronavirus seems ubiquitous in Bactrian camels, as it is in dromedaries (*7*).

Dipeptidyl peptidase-4 (DPP4; cluster of differentiation 26) is the receptor for MERS-CoV. As deduced from the human DPP4–MERS-CoV spike protein structural model, the differences in the amino acids in DPP4 molecules of dromedary and Bactrian camel were found in 2 small regions far from the binding interface of DDP4 and MERS spike protein (*9*). The 15 aa of DPP4 critical for binding with MERS-CoV spike protein are conserved between dromedaries and Bactrian camels. Definitive evidence of susceptibility, or lack thereof, of Bactrian camels to MERS-CoV can be established only by experimental infection of these animals.

Even if Bactrian camels are susceptible to MERS-CoV infection, geographic separation may be an alternative explanation for the absence of MERS-CoV among camels in Mongolia. So far, Australia is the only country where dromedaries appear to be free of MERS-CoV; however, as with dromedaries elsewhere, dromedaries in Australia are infected by a BCoV-like virus (*8*). Dromedaries in Australia originated from Afghanistan; these camels were shipped to Australia in the early part of the twentieth century to work on railroad construction projects. There are 2 plausible explanations for the lack of MERS-CoV in Australia: the small numbers of adult animals that were transported from Afghanistan to Australia might not have been sufficient to introduce the virus into Australia or the virus might have been absent from dromedaries in Afghanistan.

Our study was limited by sample size and by the breadth of the study area. Mongolia has 21 provinces and ≈349,300 Bactrian camels, but we studied just 2 southern

Table. Collection sites of nasal swab and serum specimens from Bactrian camels tested for Middle East respiratory syndrome coronavirus, southern Mongolia, November 2014

Herd no.	Province, district	Age, y			No. sampled/no. total in herd
		≤1	2–4	≥5	
1	Umnugovi, Khankhongor	9	5	9	23/56
2	Umnugovi, Khankhongor	7	2	9	18/31
3	Umnugovi, Khankhongor	8	0	5	13/28
4	Umnugovi, Khankhongor	0	9	17	26/65
5	Umnugov, Bayan-Ovoo	0	7	8	15/27
6	Umnugovi, Bayan-Ovoo	0	1	16	17/70
7	Umnugovi, Bayan-Ovoo	0	0	4	4/9
8	Umnugovi, Bayan-Ovoo	0	2	9	11/33
9	Umnugovi, Bayan-Ovoo	0	0	10	10/54
10	Umnugovi, Bayan-Ovoo	1	5	7	13/36
11	Umnugovi, Bayan-Ovoo	0	8	12	20/24
12	Dundgovi, Khuld	0	9	21	30/58
Total		25	48	127	200/491

provinces and a total of 200 camels. Umnogovi Province has the largest, and Dundgovi Province the fifth largest, camel population in the country (≈113,000 and ≈28,000 animals, respectively). Further studies on the epidemiology of MERS-CoV infection in dromedaries and Bactrian camels from central Asia, China, and Mongolia are warranted.

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References

1. Zaki AM, van Boheemen S, Bestebroer TM, Osterhaus ADME, Fouchier RAM. Isolation of a novel coronavirus from a man with pneumonia in Saudi Arabia. N Engl J Med. 2012;367:1814–20. http://dx.doi.org/10.1056/NEJMoa1211721
2. World Health Organization. Middle East respiratory syndrome coronavirus (MERS-CoV): summary of current situation, literature update and risk assessment–as of 5 February 2015 [cited 2015 Feb 25]. http://www.who.int/csr/disease/coronavirus_infections/mers-5-february-2015.pdf?ua=1
3. Reusken CBEM, Haagmans BL, Müller MA, Gutierrez C, Godeke G-J, Meyer B, et al. Middle East respiratory syndrome coronavirus neutralising serum antibodies in dromedary camels: a comparative serological study. Lancet Infect Dis. 2013;13:859–66. http://dx.doi.org/10.1016/S1473-3099(13)70164-6
4. Chan RWY, Hemida MG, Kayali G, Chu DKW, Poon LLM, Alnaeem A, et al. Tropism and replication of Middle East respiratory syndrome coronavirus from dromedary camels in the human respiratory tract: an in-vitro and ex-vivo study. Lancet Respir Med. 2014;2:813–22. http://dx.doi.org/10.1016/S2213-2600(14)70158-4
5. Azhar EI, El-Kafrawy SA, Farraj SA, Hassan AM, Al-Saeed MS, Hashem AM, et al. Evidence for camel-to-human transmission of MERS coronavirus. N Engl J Med. 2014;370:2499–505. http://dx.doi.org/10.1056/NEJMoa1401505
6. Reusken CBEM, Messadi L, Feyisa A, Ularamu H, Godeke G-J, Danmarwa A, et al. Geographic distribution of MERS coronavirus among dromedary camels, Africa. Emerg Infect Dis. 2014;20:1370–4. http://dx.doi.org/10.3201/eid2008.140590
7. Chu DKW, Poon LLM, Gomaa MM, Shehata MM, Perera RAPM, Abu Zeid D, et al. MERS coronaviruses in dromedary camels, Egypt. Emerg Infect Dis. 2014;20:1049–53. http://dx.doi.org/10.3201/eid2006.140299
8. Hemida MG, Perera RA, Al Jassim RA, Kayali G, Siu LY, Wang P, et al. Seroepidemiology of Middle East respiratory syndrome (MERS) coronavirus in Saudi Arabia (1993) and Australia (2014) and characterisation of assay specificity. Euro Surveill. 2014;19: pii 20828.
9. Wang N, Shi X, Jiang L, Zhang S, Wang D, Tong P, et al. Structure of MERS-CoV spike receptor-binding domain complexed with human receptor DPP4. Cell Res. 2013;23:986–93. http://dx.doi.org/10.1038/cr.2013.92

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Oligella ureolytica Bacteremia in Elderly Woman, United States

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To the Editor: *Oligella ureolytica* is an aerobic gram-negative coccobacillus found as a commensal organism in human urinary tracts (*1*). Previously referred to as CDC Group IVe, this bacterium is not commonly encountered as a source of infection and is difficult to isolate by using conventional laboratory procedures (*2*). The few cases of pathogenic infection with *O. ureolytica* described in the literature have occurred in patients ranging in age from newborn to 89 years and from the varied locations of India, Turkey, Canada, and the United States (*3*–*7*). We report a case of *O. ureolytica* bacteremia in a patient in whom sepsis was diagnosed and review the current literature on this emerging pathogen.

A 66-year-old woman sought treatment in our emergency department for a fever of 100.7°F, femur fracture, and a right buttock stage III decubitus ulcer. She reported having fallen 4 days earlier, after which she was unable to walk and spent 4 days laying in her own urine and feces. Blood tests revealed an elevated leukocyte count of 24.4 × 10^9 cells/L (76% neutrophils, 2% bands), and urinalysis showed trace leukocyte esterase, +3 bacteria, and 5–10 leukocytes. Chest radiograph and head computed tomography images were unremarkable. Her electrocardiogram showed nonspecific ST wave changes. Samples from the patient's blood, urine, and wounds were collected while the patient was in the emergency department and were sent for culture.

Wound cultures showed growth of *Proteus mirabilis* and *Enterococcus* spp. The urine culture grew >100,000 CFU *Escherichia coli*. The first set of blood cultures grew *O. ureolytica* in aerobic and anaerobic bottles, but another set drawn 30 min later showed no growth. The blood cultures were processed by using the Bact/Alert 3D (bioMérieux, Marcy l'Etoile, France) and Gram stained. Identification was from the Vitek 2 compact system (bioMérieux). The *O. ureolytica* sample was sensitive to amikacin, ampicillin/sulbactam, ceftazidime, ceftriaxone, gentamicin, imipenem, levofloxacin, nitrofurantoin, trimethoprim/sulfamethoxazole, and chloramphenicol. No resistance was found.

Because of the unique bacteremia, further diagnostics were conducted. The results of chest, abdomen, and pelvic computed tomography scans were unremarkable. HIV