

vaccinia and AIDS-associated complications that culminated in death of the recruit 18 months after vaccination.

In patients without underlying disease, cowpox infections manifest as self-healing diseases. However, in the absence of vaccination and among a population with increased numbers of immunocompromised persons, the risk for human poxvirus infections is increasing. Early diagnosis is essential for differentiating cowpox from illnesses and skin reactions with similar signs and symptoms, such as smallpox, monkeypox, generalized vaccinia virus infection, disseminated herpes zoster and herpes simplex virus infections, drug-associated eruptions, erythema multiforme, enterovirus infections, secondary syphilis, scabies, insect bites, impetigo, and molluscum contagiosum. The oral drug tecovirimat (previously known as ST-246), as well as cidofovir, CMX-001 (an antiviral substance), and vaccinia immune globulin, should be considered for use as postexposure therapeutic treatment for orthopoxvirus disease (10).

## References

1. Olson VA, Laue T, Laker MT, Babkin IV, Drosten C, Shchelkunov SN, et al. Real-time PCR system for detection of orthopoxviruses and simultaneous identification of smallpox virus. *J Clin Microbiol.* 2004;42:1940–6. <http://dx.doi.org/10.1128/JCM.42.5.1940-1946.2004>
2. Lawn R. Risk of cowpox to small animal practitioners. *Vet Rec.* 2010;166:631. <http://dx.doi.org/10.1136/vr.c2505>
3. Pelkonen PM, Tarvainen K, Hynninen A, Kallio ER, Henttonen K, Palva A, et al. Cowpox with severe generalized eruption, Finland. *Emerg Infect Dis.* 2003;9:1458–61. <http://dx.doi.org/10.3201/eid0911.020814>
4. Czerny CP, Eis-Hübinger AM, Mayr A, Schneeweis KE, Pfeiff B. Animal poxviruses transmitted from cat to man: current event with lethal end. *Zentralbl Veterinarmed B.* 1991;38:421–31.
5. Blackford S, Roberts DL, Thomas PD. Cowpox infection causing a generalized eruption in a patient with atopic dermatitis. *Br J Dermatol.* 1993;129:628–9. <http://dx.doi.org/10.1111/j.1365-2133.1993.tb00500.x>
6. Hönlinger B, Huemer HP, Romani N, Czerny CP, Eisendle K, Höpfl R. Generalized cowpox infection probably transmitted from a rat. *Br J Dermatol.* 2005;153:451–3. <http://dx.doi.org/10.1111/j.1365-2133.2005.06731.x>
7. Haase O, Moser A, Rose C, Kurth A, Zillikens D, Schmidt E. Generalized cowpox infection in a patient with Darier disease. *Br J Dermatol.* 2011;164:1116–8. <http://dx.doi.org/10.1111/j.1365-2133.2011.10226.x>
8. Dabrowski PW, Radonic A, Kurth A, Nitsche A. Genome-wide comparison of cowpox viruses reveals a new clade related to variola virus. *PLoS ONE.* 2013;8:e79953. <http://dx.doi.org/10.1371/journal.pone.0079953>
9. Redfield RR, Wright DC, James WD, Jones TS, Brown C, Burke DS. Disseminated vaccinia in a military recruit with human immunodeficiency virus (HIV) disease. *N Engl J Med.* 1987;316:673–6. <http://dx.doi.org/10.1056/NEJM198703123161106>
10. Duraffour S, Andrei G, Snoeck R. Tecovirimat, a p37 envelope protein inhibitor for the treatment of smallpox infection. *IDrugs.* 2010;13:181–91.

Address for correspondence: Hermann Meyer, Neuherbergstrasse 11, 80937 Munich, Germany; email: hermann1meyer@bundeswehr.org

## Absence of Middle East Respiratory Syndrome Coronavirus in Camelids, Kazakhstan, 2015

Eve Miguel,<sup>1</sup> Ranawaka A.P.M. Perera,<sup>1</sup> Almagul Baubekova, Véronique Chevalier, Bernard Faye, Nurlan Akhmetsadykov, Chun Yin Ng, François Roger, Malik Peiris

Author affiliations: Centre de Coopération Internationale en Recherche Agronomique pour le Développement, CIRAD, AGIRs, Montpellier, France (E. Miguel, V. Chevalier, B. Faye, F. Roger); The University of Hong Kong, Hong Kong, China (R.A.P.M. Perera, C.Y. Ng, M. Peiris); LLP Antigen Research and Production Enterprise Antigen, Almaty, Kazakhstan (A. Baubekova, N. Akhmetsadykov); Food and Agriculture Organization of the United Nations Camel Project, AlKharj, Saudi Arabia (B. Faye)

DOI: <http://dx.doi.org/10.3201/eid2203.151284>

**To the Editor:** Middle East respiratory syndrome coronavirus (MERS-CoV) acquired from animals causes severe pneumonia in humans, with some chains of human-to-human transmission, leading to large outbreaks. MERS-CoV is a cause of concern for global public health. The only natural host of MERS-CoV identified so far is the dromedary camel (*Camel dromedarius*) (1,2), and transmission from camels to humans has been documented (3). The geographic distribution of MERS-CoV in dromedaries extends beyond the Arabian Peninsula (where human cases have been reported) to North and East Africa (where human cases have not been reported) (2,4). However, MERS-CoV from a camel in Egypt and MERS-CoV from a human were phenotypically similar in tropism and replication competence in ex vivo cultures of the human respiratory tract (5).

Our previous study demonstrated no evidence of MERS-CoV infection in Bactrian camels in Mongolia (6). The question whether MERS-CoV is endemic in camelids in Central Asia remains unanswered. MERS-CoV RNA was detected in swab samples from camels in Iran, which had been imported from Pakistan; however, where the infection was acquired is unclear (7).

In Asia, Kazakhstan is of particular interest because large populations of 2 major camelid species overlap: 90% Bactrian (Kazakh breed including 3 ecotypes) and ≈10% dromedary (Arvana breed from Turkmenistan) and their hybrids (8). To determine whether MERS-CoV is present in camelids in Kazakhstan, we conducted a seroepidemiologic survey.

During February–March 2015, blood was collected from 550 female camels (455 dromedary, 95 Bactrian)

<sup>1</sup>These authors contributed equally to this article.

(Figure) in 2 regions, Almaty and Shymkent, which differ in camelid density (0.034 and 0.20 camels/km<sup>2</sup>, respectively; <http://www.stat.gov.kz>). Dromedaries were sampled in the cities/villages of Kyzylorda (105 animals from 2 herds), Zanakorgan (35 animals from 1 herd), Sholakkorgan (110 animals from 2 herds), and Akshiy (205 animals from 4 herds). Bactrian camels were sampled in Sholakkorgan (40 animals from 1 herd) and Kanshengel (55 animals from 1 herd) (Figure). For dromedary camels, mean age was 6.1 years (SD 3–7 years) and mean herd size was 53.6 animals (SD 31–70); for Bactrian camels, mean age was 6.5 years (SD 5–8 years) and mean herd size was 48.6 animals (SD 40–55). Serum samples were tested for MERS-CoV antibodies at a screening dilution of 1:20 by using a validated MERS-CoV (strain EMC) spike pseudoparticle neutralization test (9). Positive and negative controls were included in each run. Absence of positivity for any sample indicated a lack of recent or past MERS-CoV infection.

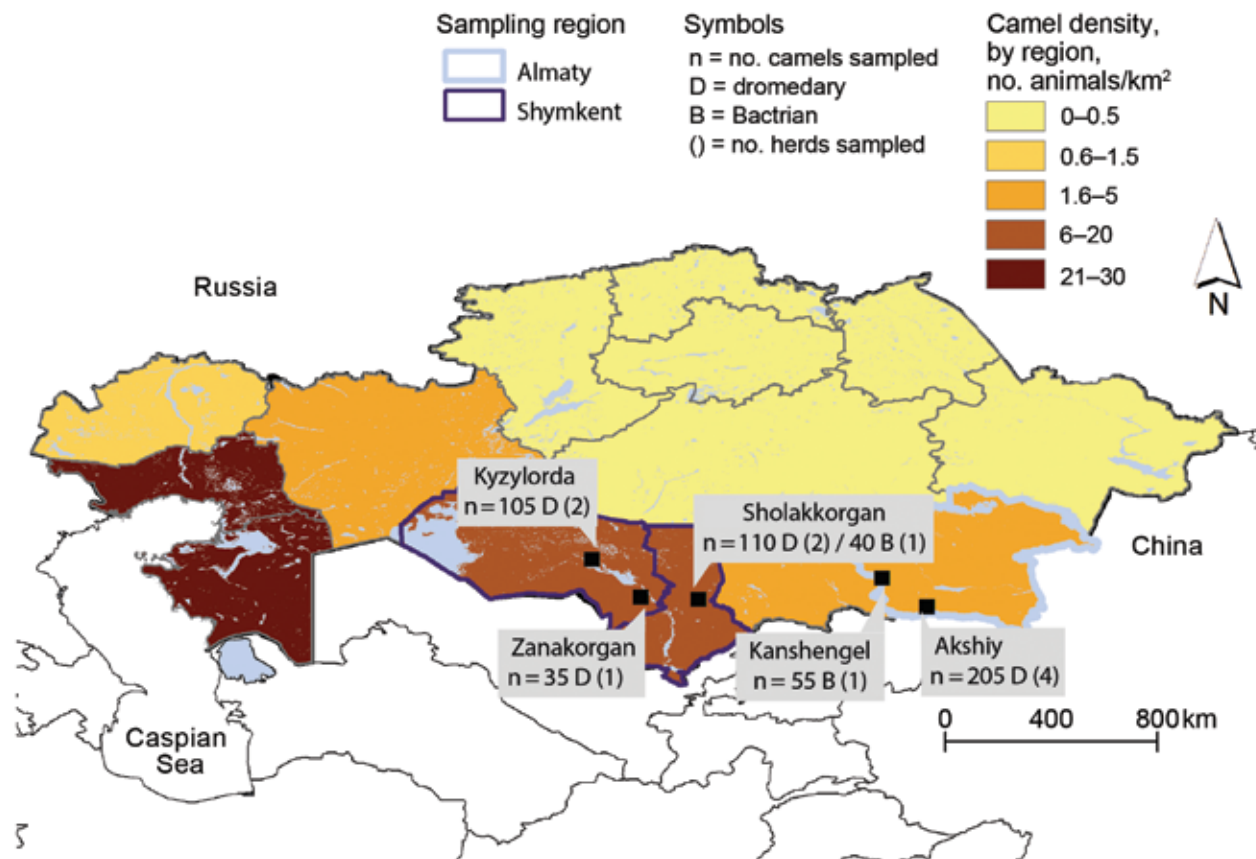
Two randomly selected samples each from dromedaries from Kyzylorda, Zanakorgan, and Akshiy and Bactrians from Sholakkorgan and Kanshengel were tested for neutralizing antibody to bovine coronavirus (9). All 10 samples

were seropositive, as has been reported for Bactrian camels in Mongolia and the Middle East (6,9).

Given the uniformly high seroprevalence of MERS-CoV infection among dromedaries in Africa and the Arabian Peninsula, the lack of infection in dromedaries in southern Kazakhstan was surprising. Because genetically diverse MERS-CoV from Africa remains antigenically conserved with viruses from the Arabian Peninsula, the lack of antibodies is probably not explained by antigenically divergent strains (9). Feral dromedaries in Australia, which originated from animals imported from Afghanistan or Pakistan during 1840–1907, are also seronegative for MERS-CoV (10). In contrast, bovine-like coronavirus seems to be present in dromedaries everywhere (including Kazakhstan and Australia).

Our study was limited by sample size and by geographic coverage. Of the ≈180,000 camels in Kazakhstan, we studied camelids from only 2 of the 13 provinces. No samples were collected from the western part of the country near Turkmenistan, where dromedaries are also common.

Dromedaries are clearly a natural host of MERS-CoV. However, the finding that MERS-CoV is not endemic in dromedaries in all geographic regions suggests the



**Figure.** Density of camelids in Kazakhstan (extracted from the Ministry of National Economy of the Republic of Kazakhstan Committee on Statistics, Department of Statistics; <http://www.stat.gov.kz>) and specimen collection for detection of Middle East respiratory syndrome virus, by species and region, 2015.

possibility that dromedaries may not be the ultimate natural reservoir (i.e., the long-term host of a pathogen of an infectious disease). Topography (i.e., mountain chains) may limit camel movements from the Middle East or Africa to Central Asia, although such interchange certainly occurred centuries ago as a consequence of the silk-trade routes through southern Kazakhstan. The only known recent imports to Kazakhstan are dromedaries (Arvana breed), brought from Turkmenistan for cross-breeding with Bactrians to improve milk production (8). The findings that MERS-CoV is not universally endemic in dromedaries raises the hypothesis that certain species of bats or some other animal, the environment, or both, may constitute a maintenance community and be the true natural reservoir of MERS-CoV and that the virus spills over to camels and is maintained within camels for varying periods of time. Further studies on the epidemiology of MERS-CoV infection among camelids from central Asia are warranted.

This work was supported by a research grant from the US National Institute of Allergy and Infectious Diseases, National Institutes of Health, Department of Health and Human Services (contract no. HHSN272201500006C) and a commissioned grant from the Health and Medical Research Fund, Food and Health Bureau, Government of the Hong Kong Special Administrative Region.

## References

1. Reusken CB, Haagmans BL, Müller MA, Gutierrez C, Godeke GJ, 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](http://dx.doi.org/10.1016/S1473-3099(13)70164-6)
2. Perera RA, Wang P, Gomaa MR, El-Shesheny R, Kandeil A, Bagato O, et al. Seroepidemiology for MERS coronavirus using microneutralisation and pseudoparticle virus neutralisation assays reveal a high prevalence of antibody in dromedary camels in Egypt, June 2013. *Euro Surveill*. 2013;18:pii=20574. <http://dx.doi.org/10.2807/1560-7917.ES2013.18.36.20574>
3. Memish ZA, Cotten M, Meyer B, Watson SJ, Alshahafi AJ, Al Rabeeah AA, et al. Human infection with MERS coronavirus after exposure to infected camels, Saudi Arabia, 2013. *Emerg Infect Dis J*. 2014;20:1012–5.
4. Reusken CB, Messadi L, Feyisa A, Ularumu H, Godeke GJ, 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>
5. Chan RW, Hemida MG, Kayali G, Chu DK, Poon LL, 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](http://dx.doi.org/10.1016/S2213-2600(14)70158-4)
6. Chan SM, Damdinjav B, Perera RA, Chu DK, Khishgee B, Enkhbold B, et al. Absence of MERS-coronavirus in Bactrian camels, southern Mongolia, November 2014. *Emerg Infect Dis*. 2015;21:1269–71. <http://dx.doi.org/10.3201/eid2107.150178>
7. World Organisation for Animal Health. Infection with coronavirus in camels, Iran [cited 2015 Oct 11]. [http://www.oie.int/wahis\\_2/public/wahid.php/Reviewreport/Review?page\\_refer=MapFullEventReport&reportid=16411](http://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=16411)
8. Knoll EM, Burger P. The encounter between Bactrian and dromedary camels in Central Asia. In: Faye B, Konuspayeva G, editors. *Camels in Asia and North Africa: interdisciplinary perspectives on their past and present significance*. Vienna (Austria): Austrian Academy of Sciences Press. 2012. p. 27–33, photos p. 248–250.
9. 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. <http://dx.doi.org/10.2807/1560-7917.ES2014.19.23.20828>
10. Cramer G, Durr PA, Barr J, Yu M, Graham K, Williams OJ, et al. Absence of MERS-CoV antibodies in feral camels in Australia: implications for the pathogen's origin and spread. *One Health*. 2015;1:76–82.

Address for correspondence: Eve Miguel, CIRAD, AGIRs, Avenue Agropolis, 34398 Montpellier CEDEX 5, France; email: eve.miguel@cirad.fr

## Novel Reassortant Avian Influenza A(H5N1) Virus in Human, Southern Vietnam, 2014

**Ikuyo Takayama,<sup>1</sup> Nguyen Trung Hieu,<sup>1</sup> Masayuki Shirakura, Mina Nakauchi, Seiichiro Fujisaki, Hitoshi Takahashi, Shiho Nagata, Nguyen Thanh Long, Takato Odagiri, Masato Tashiro, Tsutomu Kageyama**

Author affiliations: National Institute of Infectious Diseases, Tokyo, Japan (I. Takayama, M. Shirakura, M. Nakauchi, S. Fujisaki, H. Takahashi, S. Nagata, T. Odagiri, M. Tashiro, T. Kageyama); Pasteur Institute, Ho Chi Minh City, Vietnam (N.T. Hieu, N.T. Long)

DOI: <http://dx.doi.org/10.3201/eid2203.151360>

**To the Editor:** The first case of human infection with highly pathogenic avian influenza A(H5N1) virus in Vietnam was reported in December 2003 (1), and >120 human cases were confirmed through 2013, with a high case-fatality rate (2). In 2013, clade 2.3.2.1a/c H5N1 viruses circulated widely in poultry across the country, although clade 1.1.1/1.1.2 H5N1 viruses predominated in poultry from the Mekong Delta region to central Vietnam (3,4).

In 2014, two cases of human infection with A(H5N1) virus were identified in southern Vietnam. One case was associated with a clade 1.1.2 reassortant virus, A/Vietnam/14012902/2014 (Global Initiative on Sharing

<sup>1</sup>These first authors contributed equally to this article.