received 5 doses. Five respondents were prescribed 3, 4, or 6 doses (online Technical Appendix Table 2). This finding indicates large inconsistencies in the PEP prescribing practices in this region of Kenya, a pattern that is similar in other parts of East Africa (*6*).

Respondents bore all medical costs without subsidy. Direct medical costs were ≈$2 $500 (US) per bite victim, and indirect medical costs were ≈$4 $100. The average cost of obtaining a single dose of PEP ranged from $8 to $120 (Table; online Technical Appendix Table 2).

All respondents had heard of rabies. Nine (82%) knew it was transmitted to humans through a bite from a rabid dog, and 4 (36%) knew that rabies among dogs could be prevented through vaccination.

During 2014, at least 3 suspected human rabies deaths and 4 domestic animal deaths were associated with this cluster. Postbite care, including PEP, is a heavy economic burden on this community, moreso because rabies vaccine is not always locally accessible. Dog vaccination rates are low in this region and rabies in suspected animals is rarely definitively diagnosed, increasing risks for human rabies virus exposures and the economic burden of PEP administration. We recommend implementation of regular and comprehensive mass dog vaccination campaigns, in line with Kenya's National Rabies Elimination Strategy (*7*), and further detailed studies on the epidemiology of rabies in this ecosystem, which supports human, wildlife, and domestic dog populations.

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Generalized Cowpox Virus Infection in a Patient with HIV, Germany, 2012

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To the Editor: In October 2012, a 35-year-old man with clinical category C HIV infection was admitted to the intensive care unit at the University of Duisburg–Essen, Essen, Germany. The man had severe respiratory distress syndrome with septic shock, and he was infected with hepatitis B and C viruses and Epstein-Barr virus. Standard infection-control procedures were followed: the patient was placed in a single room; healthcare providers wore personal protective equipment (gown, face shield, mask, and gloves); and a closed system was used for endotracheal suctioning.

Physical examination of the patient revealed multiple skin lesions on his right forearm and right leg. In the following days, more skin lesions appeared on his abdomen and head. The skin lesions were inflamed macules with central livid, hemorrhagic ulceration (1–2 cm in diameter) and raised edges. Kaposi sarcoma was suspected initially, but on hospital day 5, a skin biopsy showed large intracellular eosinophilic inclusion bodies pathognomonic for infection with cowpox virus (family *Poxviridae*, genus *Orthopoxvirus*). To confirm the diagnosis of cowpox virus infection, we conducted biopsies of 3 skin lesions on hospital day 7. Despite antimicrobial drug and supportive therapy, the patient died that day from septic shock.

The 3 biopsy samples obtained on hospital day 7 were cultured on African green monkey kidney (MA104) cells, and within 2 days, many plaques were observed. DNA extracted from homogenates and virus isolated from the biopsy material were tested by orthopoxvirus real-time PCR (*1*); results were positive for all 6 samples. We confirmed the presence of cowpox virus DNA in all samples by sequencing the hemagglutinin gene.

Serum obtained from the patient on day 2 after admission, when the first lesions were noted, was also positive for

orthopoxvirus DNA by real-time PCR (*1*); approximately 50 genome copies were detected, corresponding to a cycle threshold of 29.7. No orthopoxvirus-specific IgG was detected by immunofluorescence assay; this lack of detection is in agreement with observations that orthopoxvirus antibodies can first be detected in the pustular stage of disease but not as early as the macular stage (http://www.bt.cdc.gov/agent/smallpox/smallpox-biological-weapon-abstract.asp). The patient was born after the cessation of mandatory smallpox vaccination, so vaccine-induced IgG is unlikely.

Generalized cowpox virus infection in humans is atypical; the disease usually manifests as a single painful, ulcerated vesiculopustular lesion, which subsequently forms a scar, accompanied by malaise, fever, and long-lasting, painful local lymphadenopathy. However, in immunocompromised persons and persons with eczema, a generalized (and lethal, in at least 1 case) smallpox-like infection can develop (*2*–*7*). Phylogenetic analysis, based on the hemagglutinin gene, of the cowpox isolate from this study (GenBank accession no. KT182068) (Figure) revealed a close relationship with cowpox viruses isolated from humans in Germany during 1990 and 2009 (*8*). This group of viruses forms a distinct clade that is closer to taterapox, camelpox, and variola (smallpox) viruses than to another clade that contains other strains of cowpox virus and vaccinia and monkeypox viruses. Previous reports have postulated the existence of at least 2 species of cowpox virus (*8*).

Cattle were initially incorrectly presumed to be cowpox virus reservoirs; today, wild rodents are considered to be the true reservoirs. Cowpox virus is transmitted to humans by direct contact with infected animals, mainly cats, which become infected when hunting small rodents. The incubation period is typically 7–12 days. The source of infection for the patient in our study remains unclear; interviews with his family revealed no previous contact with pet animals.

Vaccinia virus, another orthopoxvirus, is known to have induced a generalized infection in a 19-year-old military recruit after smallpox vaccination; the recruit had HIV infection, but this was not known before vaccination (*9*). Satellite ulcers at the site of inoculation and a widespread, disseminated pustular rash resulted in disseminated

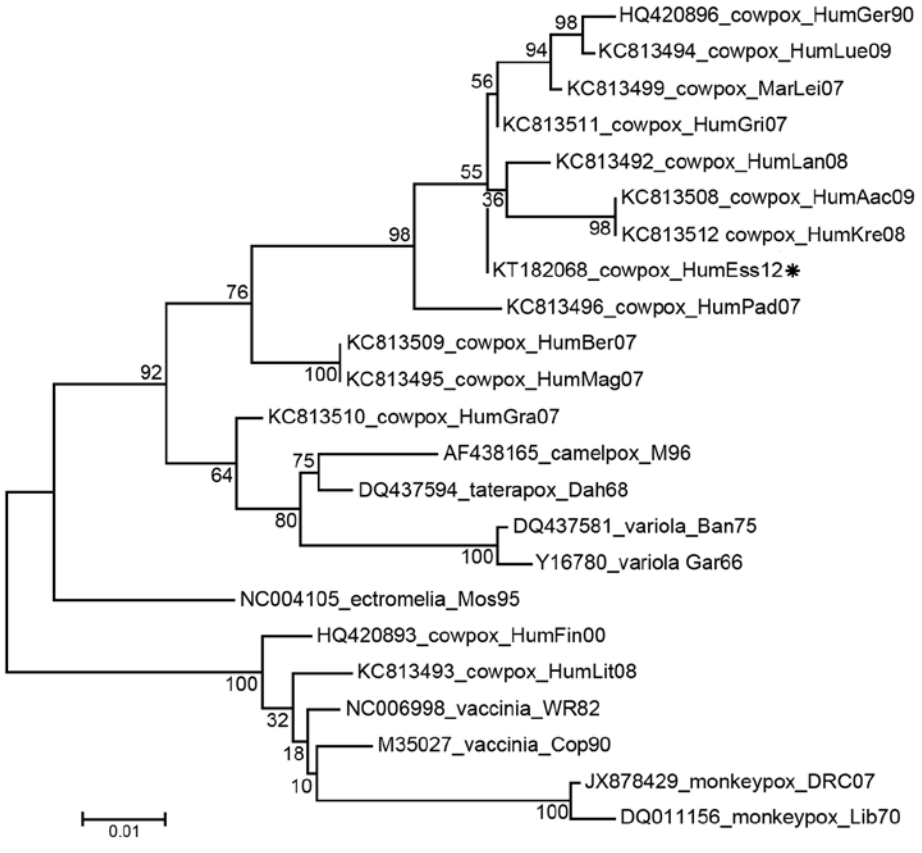

Figure. Evolutionary relationships of cowpox virus isolated from a 35-year-old man with HIV infection treated in the intensive care unit at the University of Duisburg–Essen, Essen, Germany (KT182068_HumEss12, asterisk), other human isolates of cowpox virus, and other orthopoxviruses. The evolutionary history was inferred by using the maximum-likelihood method. The percentage of trees in which the associated taxa clustered together is shown next to the branch nodes. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 23 nt sequences (GenBank accession numbers are indicated). All positions containing gaps and missing data were eliminated; the final dataset had 772 positions. Evolutionary analyses were conducted in MEGA6 (http://www.megasoftware.net). Aac, Aachen; Ban, Bangladesh; Ber, Berlin; Cop, Copenhagen; Dah, Dahomey; DRC, Democratic Republic of Congo; Ess, Essen; Fin, Finland; Gar, Garcia; Ger, Germering; Gra, Graz; Gri, Grimmen; Hum, human; Kre, Krefeld; Lan, Landau; Lei, Leipzig; Lib, Liberia; Lit, Lithuania; Lue, Luedenscheid; Mag, Magdeburg; Mar, Patagonian mara (*Dolichotis patagonum*); Mos, Moscow; Pad, Paderborn; WR, Western Reserve. Scale bar indicates the number of nucleotide changes per site.

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*).

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

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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)

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