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the kidneys is clearly consistent with sickled erythrocytes causing vascular congestion and infarction, thus contributing to the patient's death.

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Human Brucellosis, Inner Mongolia, China

To the Editor: Brucellosis is one of the most common zoonotic diseases worldwide (1). The disease is caused by Brucella spp. and mainly transmitted from its animal reservoirs to humans by direct contact with infected animals or through the ingestion of raw milk or unpasteurized cheese (2). Human brucellosis has a wide spectrum of clinical manifestations, which can vary from subclinical infection with seroconversion to a full-blown clinical picture of fever; osteoarticular involvement; sweating; constitutional symptoms; and hepatic, cardiac, central nervous system, or ocular involvement (2-4). Although controlled in many industrialized countries, the disease remains endemic to many parts of the world, including Spain, Latin America, the Middle East, parts of Africa, and Asia (5). In the People's Republic of China, human brucellosis was highly endemic from the mid-1950s well into the 1970s, but then incidence decreased until the mid-1990s. However, incidence has increased sharply in China since 1995 (6), and the Inner Mongolia Autonomous Region is the most severe endemic focus; most reports of the disease occurred during 1999–2008. National and local public health authorities are concerned about the increasing incidence of the disease in this province. Here we report the epidemic characteristics that existed in this region during 1999–2008.

Human brucellosis is a reportable disease in China; suspected or confirmed cases must be reported to local and provincial Centers for Disease Control and Prevention (CDC) and then to Chinese CDC (CCDC) through the National Notifiable Disease Surveillance System. To meet case definitions, disease in persons must be accompanied by clinical signs and must be confirmed by serologic tests or isolation in accordance with the case definition of the World Health Organization (1,7).

We obtained the National Notifiable Disease Surveillance System data that were confirmed by the Chinese CDC from Inner Mongolia CDC. A total of 43,623 cases were reported during 1999-2008, of which 70.7% occurred in male patients; the difference in incidence between sexes was significant by χ^2 test ($\chi^2 = 581.9$, p<0.00001). A total of 28,237 (64.7%) reported cases occurred in persons 30-59 years of age, male (70.2%) and female (29.8%). However, 658 patients (396 boys) were <10 years of age, and 497 patients (333 men) were >70 years of age. The number of cases peaked in 2008, with 7,645 and 3,460 cases in male and female patients, respectively. The epidemic peaked in March-August, with 74.8% reported cases during the study period. The number of reported cases in 2008 was 25.6× the number reported in 1999. The highest proportion of cases (55.9%) occurred among persons engaged in agricultural activities (planting, animal husbandry) in rural areas; the next highest proportion was in shepherds (29.2%), who depend only on their herds to satisfy their nutritional needs. The number of cases sharply increased from 37 and 16 in 2001 to 315 and 308

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in 2008 among housekeepers and students, respectively. In this province, B. melitensis was the most common pathogen, although B. abortus prevailed in certain regions. During our epidemiologic investigation, the number of agriculture workers who were inexperienced in animal husbandry increased suddenly and quickly; thus the trade and transportation of unquarantined and unvaccinated animals rose sharply. This situation most likely led to easier transmission to humans by direct contact with infected animals than had occurred previously. The results of our investigation indicate that the main risk factors associated with this outbreak were occupation (agriculture worker, shepherd, butcher, slaughterhouse worker, and cattle dealer) and risky practices (handling of ruminant abortions, skinning of stillborn lambs and kids, and crushing the umbilical cord of newborn lambs and kids with teeth) and certain dietary preferences (consuming unpasteurized and unboiled milk and fresh cheese) (W. Guo, pers. comm.).

Our results show that the annual incidence of the disease varied greatly from 0 to 818.52/100,000 at county levels during the study period (Figure). The largest incidence of the disease occurred in Abaga County in the center of Inner Mongolia. The spatial distribution of the disease clustered in the northeastern (Hulunbeir) and central (Xilinguole) districts. Hence, future public health planning and resource allocation should focus on Hulunbeir and Xilinguole, and active surveillance should be strengthened in these high-risk districts.

We report the epidemic features of human brucellosis in a province in China. This information will be helpful to establish strategies for prevention, surveillance, and management of human brucellosis in China and in other countries where the disease is endemic.

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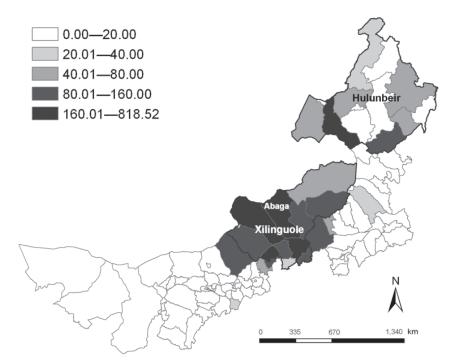


Figure. Annualized average incidence of human brucellosis, Inner Mongolia Autonomous Region, People's Republic of China, 1999–2008.

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Multiple Serotypes of Bluetongue Virus in Sheep and Cattle, Israel

To the Editor: In September 2008, the Israeli Veterinary Field Services were notified of uncharacteristic disease on a dairy farm near the border with Lebanon in Rosh Ha Nikra, (online Appendix Figure, www.cdc.gov/ EID/content/16/12/2003-appF.htm). In November, blood samples were obtained from 5 cows, 4 of which were recovering from signs of infection with bluetongue virus (BTV). Virus isolation was conducted at the Kimron Veterinary Institute, Bet Dagan, Israel. One isolate (ISR2008/03) was sent to the World Animal Health Organisation Bluetongue Reference Laboratory at the Institute for Animal Health (IAH), Pirbright, UK, for further characterization. BTV-16 was identified by using serotype-specific real-time reverse transcription-PCR (RT-PCR) for genome segment 2 (Seg-2). BTV-16 has been detected in Israel and is considered endemic, along with BTV serotypes 2, 4, 6, and 10 (1).

Ten additional blood samples and 1 spleen sample subsequently obtained from affected cattle on the farm were sent to IAH. All samples were tested for BTV by serogroup-specific realtime RT-PCR specific for Seg-1. Six samples (including 1 from the spleen) were positive for BTV. Serotype-specific real-time RT-PCR showed that 2 blood samples contained BTV-16 and 1 blood sample contained BTV-4 and BTV-16. The amount of BTV RNA in the remaining 3 RT-PCR-positive samples was low, and attempts to identify serotype were unsuccessful. Virus from the spleen was isolated in an insect cell line (KC cells from Culicoides sonorensis midge embryos, CRL 1660; American Type Culture Collection, Manassas, VA, USA), and the virus was serotyped as BTV-8 by RT-PCR.

BTV-4 was isolated from bovine blood obtained in October 2008 from a farm in Zde Eliahu, 100 km east of Rosh Ha Nikra. However, this animal was co-infected with BTV-24, which has been found at numerous sites in Israel (online Appendix Figure). BTV-24 was isolated at IAH from samples obtained from sheep and cattle showing clinical signs of disease. BTV-4, BTV-16, and BTV-24 all reemerged in Israel during 2009, the mortality rate was up to 80% on 1 sheep farm infected with BTV-24 (2). An outbreak in Hatzafon in November 2009 was confirmed as BTV-5 by serotype-specific real-time RT-PCR.

To determine origins of BTV strains causing these outbreaks, we sequenced Seg-2 of the BTV-4 (Zde Eliahu) and BTV-8 and BTV-16 (ISR2008/02, ISR2008/13, and ISR2008/03) isolates from Israel. BTV-16 ISR2008/03 had >99% nt sequence identity (2,935 bp) with BTV-16 (GRE1999/13) isolated in Greece in 1999 but was distinct from BTV-16 (OMN2009/02) recently isolated in Oman. BTV-8 isolate ISR2008/13 had >99% nt sequence identity (2,939 bp) with the northern European strain of BTV-8 (NET2006/04). This finding indicates that the BTV-8 isolate from Israel (ISR2008/13) belongs to the same lineage as BTV-8 from northern Europe (NET2006/04) and may have been introduced into Israel during importation of BTV-8–positive animals from northern Europe.

BTV-4 isolate ISR2008/02 had >99% nt sequence identity (2,926 bp) with BTV-4 (DQ191279) isolated in Israel in 2001, which suggests that this serotype has either continued to circulate or has reemerged. BTV-24 (ISR2008/05) belongs to a western topotype. However, few nucleotide sequences are available for comparison of BTV-24 Seg-2 regions. BTV-5 has not been isolated; therefore, no sequence data are available.

Although BTV-2, BTV-4, BTV-6, BTV-10, and BTV-16 are considered endemic to Israel, clinical signs of disease are uncommon. We report clinical signs of infection in cattle in Israel caused by BTV-8 and BTV-24. We also report active circulation of 5 BTV serotypes (BTV-4, BVT-5, BTV-8, BTV-16, and BTV-24) during 2008–2009. Multiple serotypes were isolated on 3 farms containing sheep that had clinical signs of BT (farm 1: BTV-4 and BTV-24, farm 2: BTV-8 and BTV-24, and farm 3: BTV-4, BTV-8, and BTV-24). BTV-4, BTV-8, and BTV-16 were also isolated from cattle at Rosh Ha Nikra. Identification of multiple cocirculating BTV serotypes increases the likelihood of genome segment reassortment, which could potentially lead to increased virulence. Whole genome sequencing of isolates from these farms is in progress to determine whether any of these isolates are reassortants, as has been observed in Italy (3)

Our study indicates that BTV-8 strains from Israel and northern Europe (4-6) are closely related and share a recent common origin. The strain from Israel may represent an extension of the outbreak in Europe. Use of inactivated virus vaccines has dramatically decreased the number of cases caused by virulent BTV-8 in Europe (7), which suggests that a similar campaign might be effective in Israel. However, the BTV-24 strain from Israel appears to be highly virulent in