Peste des Petits Ruminants Virus in Heilongjiang Province, China, 2014

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During March 25–May 5, 2014, we investigated 11 outbreaks of peste des petits ruminants in Heilongjiang Province, China. We found that the most likely source of the outbreaks was animals from livestock markets in Shandong. Peste des petits ruminants viruses belonging to lineages II and IV were detected in sick animals.

Peste des petits ruminants (PPR) is a contagious disease that infects goats and sheep and has a case-mortality rate of ≈80% for acute cases. PPR virus (PPRV) is a member of the family Paramyxoviridae, genus Morbillivirus (1). The disease is present mainly in Africa, the Middle East, and the Indian subcontinent (2–8).

In July 2007, a PPR outbreak was reported in the Ngari region of southwestern Tibet, China. The outbreak was eliminated by using strict control measures. These measures included culling of all animals suspected to be infected; using a PPR vaccine (75/1 strain) (Tecon Animal Husbandry Bio-Technology Co. Ltd., Xinjiang, China) throughout Tibet and neighboring areas; and restriction of transport of animals (9).

On December 5, 2013, a new outbreak of PPR was reported in Huochoeng County in Xinjiang Province. PPR was also detected in Gansu, Inner Mongolia, Ningxia, Jiangxi, and Hunan Provinces by mid-March 2014.

Heilongjiang Province is the northernmost province of China (Figure 1, panel A). The total population of small ruminants in this province was ≈9 million in 2012 (http://www.stats.gov.cn), and nearly all ruminants were raised for meat or wool production. Sheep and goats were always kept separately, and registered flocks contained 120–6,000 animals (mean 434 animals). Before 2014, no PPR outbreaks had been documented in this region. We report outbreaks of PPR in 11 counties in Heilongjiang Province during 2014.

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Kit (QIAGEN, Valencia, CA, USA) according to the manufacturer’s instructions. PPRV was detected by using a reverse transcription PCR (RT-PCR) specific for the 3’ end of the nucleoprotein gene of PPRV; this RT-PCR yields an amplification product of 351 bp (12). PCR products were purified by using the QIA Quick Gel Extraction Kit (QIAGEN) and sequenced.

Multiple sequence alignment was performed by using ClustalX2.0 (13), and a phylogenetic tree was constructed by using the neighbor-joining method with MEGA6 (14). A bootstrap analysis of 1,000 replicates was performed to test the degree of branching.

Serologic analysis indicated that 17% (312/1887) of sampled animals and 76% (31/41) of imported flocks had antibodies against PPRV; all animals from Suichua, Yanshou, and Qing’an Counties were antibody negative (Table). A total of 29% (29/100) of local flocks in 5 counties (Zhaodong, Hulan, Huachuan, Nenjiang, and Baoqing) had antibody-positive animals, which suggests that transmission of PPRV between local and imported flocks had occurred in these areas.

RT-PCRs showed that 14% (39/285) of nasal swab samples and 89% (25/28) of tissue samples were positive for the nucleoprotein gene of PPRV; overall PPRV positive
rate was 20% (64/313) (Table). Combined results of serology and the molecular diagnostic tests indicated that 43% (60/141) of suspected flocks were positive for PPRV. Elevonic and the molecular diagnostic tests indicated that 43%

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Figure 2. Phylogenetic analysis of sequences of the 3’ ends of nucleoprotein genes of peste des petits ruminants virus (PPRV), Heilongjiang Province, China, March 25–May 5, 2014. The tree was constructed by using the neighbor-joining method in MEGA6 (14). Values along branches indicate bootstrap values of 1,000 replicates, and numbers on the right indicate lineages. Black dots indicate PPRV-positive samples isolated in this study. Scale bar indicates estimated number of substitutions per 20 nt.