

According to the microbiological classification, 14 patients had a multibacillary form (positive smear) and 1 patient had a paucibacillary form (negative smear). Clinical signs suggested multibacillary leprosy (>5 patches or lesions on the patient's skin) for 15 patients and paucibacillary leprosy (1–5 patches or lesions on the skin) for 2 patients. The median time between diagnosis and treatment was 6 days (range 0–20 days). Four patients had a severe disability with a grade 2. Overall, 15 patients had lepromatous leprosy and 2 had tuberculoid leprosy.

Although elimination of leprosy was achieved in La Réunion, the implementation of a leprosy surveillance system enabled us to highlight an autochthonous circulation of *Mycobacterium leprae*, leading to a cluster of cases recently diagnosed in the southwestern part of the island. During the investigation of this cluster, it was noticed that most of the doctors were unaware of the existence of leprosy in La Réunion or of the disease's clinical signs. Incidence of leprosy could therefore be largely underestimated because of this lack of knowledge, and actions to raise awareness among health care professionals will be established to improve the detection and rapid treatment of patients.

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Vaccinia Virus Zoonotic Infection, São Paulo State, Brazil

To the Editor: Since 1999, vaccinia virus (VACV) has been isolated frequently from dairy cattle and humans (1–3). During bovine vaccinia outbreaks, VACV can be transmitted to farmers and those who milk cows; it frequently causes lesions on the hands and forearms. Bovine vaccinia causes economic losses and affects public health services in Brazil (1–4). One of the first VACV viruses isolated during Brazilian bovine vaccinia outbreaks was Araçatuba virus (ARAV), which was collected in São Paulo State, and since that time, other VACVs have been isolated in this state (2,5,6).

The circulation of VACV in São Paulo forests was described in the 1960s and 1970s, although such isolates seem to be phylogenetically distinct from ARAV and other VACVs that currently circulate in Brazil (7). Although VACV in several Brazilian states has been reported (1–3), the intrastate spread of VACV concerns veterinary and medical authorities and presents a challenge to the sanitary barriers and prophylactic measures implemented to date. We report 2 zoonotic bovine vaccinia outbreaks in the midwestern region of São Paulo State, Brazil.

The Institutional Ethics and Animal Welfare Commission from the Faculdade de Medicina Veterinária e Zootecnia—Universidade Estadual Paulista Júlio de Mesquita Filho/Campus de Botucatu approved this study. In 2009 and 2010, exanthematic outbreaks were reported in rural areas of Itatinga (23°6'7"S, 48°36'57"W) and Torre de Pedra (23°14'38"S, 48°11'42"W) counties, respectively. Between the 2 outbreaks, lesions were observed on the teats and udders of 10 lactating cows. The lesions appeared

as macules, evolved into vesicles, pustules, and ulcers and healed after 2–3 weeks. Lesions developed on the hands and arms of the milkers after occupational contact with sick animals. The milkers also described headache, lymphadenopathy, and fever.

Specimens from 7 scabs and 1 vesicle were collected for virus identification by laboratory assays. After DNA extraction (InvitexDNA, Berlin, Germany), the samples were subjected to a specific orthopoxvirus PCR for the amplification of the A56R gene of vaccinia virus (8). A fragment of ≈ 950 bp was amplified from 5 exanthematic lesions. Two milk samples collected from sick cows were also positive for

A56R. Parapoxvirus DNA was not detected in any collected sample (9). Material from the bovine and human exanthematic lesions induced characteristic poxvirus cytopathic effects in baby hamster kidney cells. In addition, 13 of the 18 collected bovine serum specimens were positive for orthopoxvirus according to a plaque reduction neutralization test and an ELISA (4). Human serum specimens were negative for orthopoxvirus by the plaque reduction neutralization test but positive by IgM ELISA, indicating the occurrence of an acute infection process (4).

A56R-PCR amplicons from 2 exanthematic lesions and 2 milk samples were sequenced in both orientations by using the Mega-BACE-

sequencer (GE Healthcare, Little Chalfont, UK). Optimal alignment of our samples and other orthopoxvirus A56R gene sequences with ClustalW (www.ncbi.nlm.nih.gov/pmc/articles/PMC308517) by using MEGA3.1 (www.megasoftware.net) showed that a signature deletion was present in the sequences of several Brazilian VACV isolates (1–3). Three of the 4 sequenced amplicons exhibited 100% identity: the milk samples and a lesion collected from a same county. VACV samples from Itatinga and Torre de Pedra showed high identity with ARAV (2) and other Brazilian VACVs, including the Cantagalo (1) and Mariana viruses (10). A phylogenetic tree based on the A56R gene was constructed with the neighbor-joining method, 1,000 bootstrap replicates, and the Tamura 3-parameter model (MEGA3.1) (Figure). VACVs from Itatinga and Torre de Pedra clustered with several VACVs isolated during bovine vaccinia outbreaks. The A56R sequences obtained in this study were deposited in GenBank (accession no. It1446645).

We describe a new zoonotic outbreak of bovine vaccinia in São Paulo State, Brazil. Our molecular data suggest that this outbreak was caused by a VACV that is genetically related to viruses isolated in previous years, including ARAV, which was isolated in 1999 (2). The emergence and reemergence of this virus in previously bovine vaccinia-free microregions of São Paulo State suggest that VACV could have adapted to a specific microbiome and that the virus may be circulating not only in cattle and humans but also in some wild reservoir (10). Although genetic and ecologic studies of Brazilian VACVs have advanced in the past several years, little has been achieved in terms of bovine vaccinia prevention and control. Therefore, bovine vaccinia surveillance and public communication are critical in areas where VACV circulates.

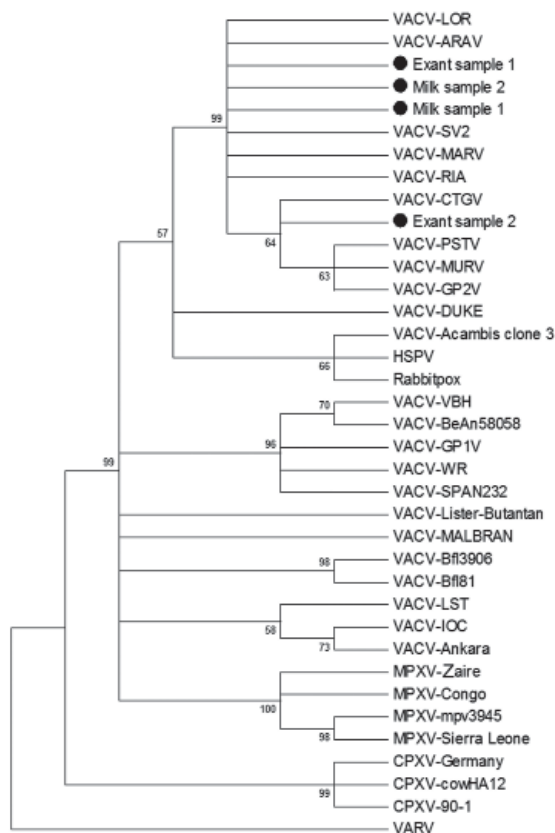


Figure. Consensus bootstrap phylogenetic tree based on the nucleotide sequences of the A56R-hemagglutinin gene of vaccinia virus. The tree was constructed with hemagglutinin sequences by using the neighbor-joining method with 1,000 bootstrap replicates and the Tamura 3-parameter model in MEGA3.1 software (www.megasoftware.net). Bootstrap values $>50\%$ are shown. Nucleotide sequences were obtained from GenBank. Black dots indicate the vaccinia virus (VACV) analyzed in this study. HSPV, horsepoxvirus; VARV, variola virus; CPXV, cowpoxvirus; MPXV, monkeypoxvirus.

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Mumps Vaccine Effectiveness Against Orchitis

To the Editor: Yung et al. reported in the April 2011 issue of *Emerging Infectious Diseases* on the epidemiologic characteristics of the nationwide mumps outbreak in England and Wales in 2004–2005 (1). The associated effect of disease was considerable, with >43,000 reported cases and >2,600 hospitalizations. Compared with the prevaccine era, the average age of infection was higher, with infection occurring mostly in older teenagers and young adults (2). Older age at infection is associated with a higher risk of certain complications, particularly orchitis (3). Yung et al. reported that among

cases of mumps, previous mumps measles rubella (MMR) vaccination offered considerable protection against orchitis, meningitis, and hospitalization (1).

In the Netherlands, mumps vaccination, using a 2-dose schedule with the MMR vaccine against measles, mumps, and rubella, was introduced in 1987, including catch-up vaccination of 3 birth cohorts (1983–1985). From birth cohort 1985 onwards, the coverage of the first and second dose of MMR has been consistently >92% (4). This coverage led to immediate control of mumps, with mumps related hospitalization dropping from 390 cases in 1987 to 11 in 1990 (5).

However, a major reemergence of mumps in the Netherlands occurred during August 2007–May 2009, when a large genotype D mumps outbreak affected mainly unvaccinated persons with a religious objection to vaccination (6). Subsequently, a genotype G outbreak of mumps started at the end of 2009, affecting mainly vaccinated adolescents. The outbreak started among university students in different cities, with a sudden increase in transmission after a large party for students in early 2009 (7).

The Dutch Centre for Infectious Disease Control advised Municipal Health Services in January 2011 to recommend MMR vaccination for university students who were unvaccinated or who had received only 1 dose of vaccine in the past. This policy was further implemented in the new academic year that began in August 2011. Information regarding the effectiveness of previous MMR vaccination against mumps complications is needed to support this policy and to predict the effect on mumps-related disease.

To study this policy, we analyzed mumps notifications in the Netherlands during December 1, 2009–June 14, 2011. Notifications include information about vaccination