(9). The TMB-2–producing \textit{A. soli} strain that we isolated came from a blood culture, indicating that \textit{A. soli} is a potential cause of bloodstream infections or bacteremia. \textit{A. soli} has also been detected in lice and keds of domestic animals (10), indicating that \textit{A. soli} may inhabit natural environments and that injuries and bites by arthropods might present a risk for invasive infections. Isolates of \textit{Acinetobacter} species, particularly those recovered from blood culture, should be identified to species type to enable further evaluation of the clinical significance of carbapenem-resistant \textit{A. soli} strains.

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The opinions expressed by the authors contributing to this journal do not necessarily reflect the opinions of the Centers for Disease Control and Prevention or the institution with which the authors are affiliated.
To amplify the hemagglutinin (HA) gene DNA from the serum samples, we used real-time PCR with primers as described by de Souza Trindade et al. 2008 (7). The HA PCR products were directly sequenced in both orientations by using specific primers and capillary electrophoresis (Genetic Analyzer 3130; Applied Biosystems, Grand Island, NY, USA). We used ClustalW (http://www.clustal.org) and MEGA4 software (http://megasoftware.net/) to align nucleotide sequences and construct a phylogenetic tree (neighbor-joining method, 1,000 bootstraps) from the obtained HA fragment.

Of the 50 dairy cattle samples, 4 (8.0%) had neutralizing antibodies against orthopoxvirus; of these, 3 (75.0%) had titers of 100 neutralizing units (NU)/mL, and 1 (25.0%) had a titer of 400 NU/mL. Of the 50 beef cattle, 8 (16.0%) had antibodies to orthopoxivirus, 1 (12.5%) of which had a titer of 800 NU/mL. Most of the positive samples were from cattle in Corrientes and Entre Ríos Provinces (Table).

Of the 100 serum samples, 5 (3.0%) were positive for vgf by real-time PCR. HA DNA was amplified from 2 of the 3 vgf PCR–positive beef cattle samples; plaque-reduction neutralization test results were also positive for the 2 samples (Table).

Alignment of the HA fragment nucleotide sequence of the isolates from Argentina showed that the sequence was highly similar to that of the homologous gene of VACV isolates from Brazil. Furthermore, the sequences showed a signature deletion that is also present in the sequences of VACV isolates from Brazil. Compared with sequences for other VACV isolates, those from Argentina had 2 polymorphisms (online Technical Appendix, panel C). The HA sequences from the isolates from Argentina demonstrated 100% identity among themselves and exhibited higher identity with group 1 (98.2% identity) versus group 2 (93.6% identity) isolates from Brazil (online Technical Appendix, panel D). In the phylogenetic tree based on the HA nucleotide sequences (online Technical Appendix, panel B), the VACVs from Argentina clustered with several group 1 VACVs detected during outbreaks in Brazil.

Although no outbreaks of exanthematous VACV infection have been described in cattle or humans in Argentina, we detected neutralizing antibodies against orthopoxvirus and detected VACV DNA in serum samples from cattle in the country. Most of the seropositive samples were from cattle in Entre Ríos Province, which shares a border with Uruguay, and Corrientes Province, which shares a border with Rio Grande do Sul State in Brazil, where Pelotas VACVs have been isolated (2).

We believe that the seropositive cattle in this study may have been exposed to VACV, the only orthopoxvirus known to be circulating in South America (1–4,8–10). Despite veterinary surveillance efforts of border control organizations, VACV control may be hampered by the circulation of infected rural workers and the misdiagnosis of VACV infection; misdiagnoses occur because VACV lesions resemble those of other exanthematous diseases. Moreover, peridomestic rodents have been hypothesized to act as VACV hosts, and could facilitate the spread of VACV in border areas (10).

In addition, we could not rule out the circulation of autochthonous VACV in Argentina, but this is a less likely explanation. Our findings suggest that cattle herds in areas of Argentina near the border with Brazil may be exposed to VACV from Brazil and, thus, may be at risk for VACV infection. Further research is needed to determine the risk factors for VACV infection and to assess the circulation of VACV in South America.

### Acknowledgments

We thank João Rodrigues dos Santos, Ângela Sana Lopes, Ilda Gama, and colleagues from the Laboratório de Vírus for their excellent technical support.

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### Table. Diagnosis of Orthopoxvirus infection in beef and dairy cattle during a study of the spread of vaccinia virus to cattle herds, Argentina, 2011

<table>
<thead>
<tr>
<th>Province</th>
<th>Cattle type</th>
<th>No. farms sampled</th>
<th>No. serum samples tested</th>
<th>No. positive samples, by level of NU/mL against orthopoxivirus†</th>
<th>No. (%) positive by real-time PCR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Córdoba</td>
<td>Dairy</td>
<td>1</td>
<td>25</td>
<td>0 0 1 0 1 (4.0)</td>
<td>2 (8.0)</td>
</tr>
<tr>
<td>Santa Fe</td>
<td>Dairy</td>
<td>1</td>
<td>25</td>
<td>3 0 0 0 3 (12.0)</td>
<td>0</td>
</tr>
<tr>
<td>Corrientes</td>
<td>Beef</td>
<td>&gt;2‡</td>
<td>8</td>
<td>0 1 1 0 2 (25.0)</td>
<td>1 (12.5)§</td>
</tr>
<tr>
<td>Entre Ríos</td>
<td>Beef</td>
<td>5</td>
<td>42</td>
<td>2 2 1 1 6 (14.3)</td>
<td>2 (4.8)</td>
</tr>
<tr>
<td>Total</td>
<td>Dairy and beef</td>
<td>&gt;9</td>
<td>100</td>
<td>5 3 3 1 12 (12.0)</td>
<td>5 (5.0)</td>
</tr>
</tbody>
</table>

†HA, hemagglutinin gene DNA; NU, serum dilution at which 70% plaque reduction per mL occurs; vgf, orthopoxvirus vaccinia growth factor gene DNA.

†Determined by plaque-reduction neutralization test.

‡Samples were obtained from several farms in Corrientes Province.

§Animal was also positive by plaque-reduction neutralization test.
Ana Paula Moreira Franco-Luiz, Alexandre Fagundes-Pereira, Galileu Barbosa Costa, Pedro Augusto Alves, Danilo Bretas Oliveira, Cláudio Antônio Bonjardim, Paulo César Peregrino Ferreira, Giliane de Souza Trindade, Carlos Javier Panei, Cecília Mónica Galosi, Jônatas Santos Abrahão, and Erna Geessien Kroon


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How to Correctly Remove a Tick

1. Grasp the tick firmly and as closely to the skin as possible. With a steady motion, pull the tick’s body away from the skin. Do not be alarmed if the tick’s mouthparts remain in the skin. Cleanse the area with an antiseptic.

2. For more information please contact: Centers for Disease Control and Prevention

1600 Clifton Road NE, Atlanta, GA 30333

Telephone: 1-800-CDC-INFO (232-4636)
TTY: 1-888-232-6354
Web: www.cdc.gov/Lyme

Cerebellitis Associated with Influenza A(H1N1)pdm09, United States, 2013

To the Editor: Central nervous system (CNS) manifestations of influenza are uncommon, especially in adults (1,2), and influenza-associated cerebellitis is exceedingly rare: 8 cases have been reported (3–7; online Technical Appendix). We describe a case of cerebellitis caused by influenza A(H1N1)pdm09 in an adult woman.

The 37-year-old female patient who sought medical care in Florida, United States, on January 5, 2013, described a 4-day history of intermittent fever of 38.5°C, generalized fatigue, diffuse headache, mild nonproductive cough, 3 episodes of vomiting, and decreased oral intake. On January 4, she experienced acute onset of ataxia and dysarthric speech with slurred pronunciation. She reported no contact with sick persons, recent travel, or exposure to pets or birds. She had a medical history of asthma since childhood, controlled by using montelukast tablets and inhaled steroids. The patient denied having ever received an influenza vaccination.

The patient appeared ill; her oral temperature was elevated at 38.3°C, but other vital signs were within normal limits (blood pressure 109/70 mm Hg; pulse rate 88 beats/minute; respiratory rate 15 breaths per minute; and oxygen saturation 98% at room air). Mucosal membranes appeared normal. No neck stiffness or palpable lymph nodes were noted. Results of heart examination were normal. Lungs were clear to auscultation, and the abdomen was soft, indicating no hepatosplenomegaly or palpable masses. No rash was seen. The neurologic examination revealed normal mental status but moderate ataxic dysarthria. Her cranial nerves were intact, and motor strength was 5/5 throughout. Results of a sensory
Spread of Vaccinia Virus to Cattle Herds, Argentina, 2011

Technical Appendix
Technical Appendix Figure. A) Map with black dots indicating the 4 provinces where blood samples were collected for the study of the spread of vaccinia virus (VACV) to cattle herds, Argentina, 2011. B) Phylogenetic tree based on nucleotide sequences of orthopoxvirus hemagglutinin (HA) gene. The tree was constructed with HA sequences by using the neighbor-joining method with 1,000 bootstrap replicates and the Tamura 3-parameter model in MEGA4 (http://megasoftware.net/). Bootstrap values are represented on branches and only values >90% are shown. Nucleotide sequences were obtained from GenBank. Scale bar represents 0.02 substitutions per nucleotide position. C) Nucleotide sequence of the VACV Argentina A56R (HA) gene compared with homologous sequences from several other orthopoxviruses. The samples from Argentina showed 2 polymorphisms (C–A and C–G) in comparison with other VACV isolates. D) A56R (HA) gene nucleotide identity matrix. The analysis involved 17 nt sequences. Evolutionary analyses were conducted in MEGA4.