(*9*). The TMB-2–producing *A. soli* strain that we isolated came from a blood culture, indicating that *A. soli* is a potential cause of bloodstream infections or bacteremia. *A. soli* has also been detected in lice and keds of domestic animals (*10*), indicating that *A. soli* may inhabit natural environments and that injuries and bites by arthropods might present a risk for invasive infections. Isolates of *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 *A. soli* strains.

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Spread of Vaccinia Virus to Cattle Herds, Argentina, 2011

To the Editor: Since 1999, several zoonotic outbreaks of vaccinia virus (VACV) infection have been reported in cattle and humans in rural areas of Brazil. The infections have caused exanthematous lesions on cows and persons who milk them, and thus are detrimental to the milk industry and public health services (*1*,*2*). In Brazil during the last decade, VACV outbreaks have been detected from the north to the extreme south of the country (*1*–*4*). Because Brazil shares extensive boundaries with other South American countries, humans and cattle on dairy and beef-producing farms in those countries may be at risk of exposure to VACV. To determine if VACV has spread from Brazil to Argentina, we investigated the presence of VACV in serum samples from cattle in Argentina.

During 2011, we obtained serum samples from 100 animals (50 dairy and 50 beef cattle) on farms in Córdoba, Corrientes, Entre Ríos, and Santa Fe Provinces in Argentina (online Technical Appendix, panel A, http://wwwnc.cdc.gov/EID/article/20/9/14-0154-Techapp1.pdf). No VACV cases had been reported in humans or cattle in these provinces. However, Corrientes Province borders the Brazilian state of Rio Grande do Sul, where VACVs (Pelotas 1 and Pelotas 2 viruses) were isolated during an outbreak affecting horses in 2008 (*2*).

To determine the presence of neutralizing antibodies in the serum samples, we used an orthopoxvirus 70% plaque-reduction neutralization test as described (*4*). On the basis of previous studies that detected viral DNA in serum samples (*4*–*6*), we used real-time PCR to amplify the highly conserved orthopoxvirus vaccinia growth factor (*vgf*) gene DNA (P.A. Alves, unpub. methods).

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 orthopoxvirus, 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 from beef and 2 from dairy cattle) 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

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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*

Province	Cattle type	No. farms sampled	No. serum samples tested	No. positive samples, by level of NU/mL against orthopoxvirus†					No. (%) positive by real-time PCR	
				100	200	400	800	Total (%)	*vgf*	HA
Córdoba	Dairy	1	25	0	0	1	0	1 (4.0)	2 (8.0)	0
Santa Fe	Dairy	1	25	3	0	0	0	3 (12.0)	0	0
Corrientes	Beef	>2‡	8	0	1	1	0	2 (25.0)	1 (12,5)§	1 (12,5)§
Entre Ríos	Beef	5	42	2	2	1	1	6 (14.3)	2 (4,8)	1 (2,4)§
Total	Dairy and beef	>9	100	5	3	3	1	12 (12.0)	5 (5.0)	2 (2.0)

*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.

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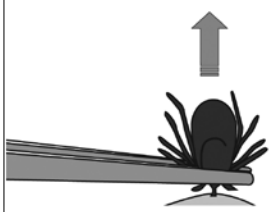
How to Correctly Remove a Tick

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.



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1600 Clifton Road NE, Atlanta, GA 30333
Telephone: 1-800-CDC-INFO (232-4636)
TTY: 1-888-232-63548
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

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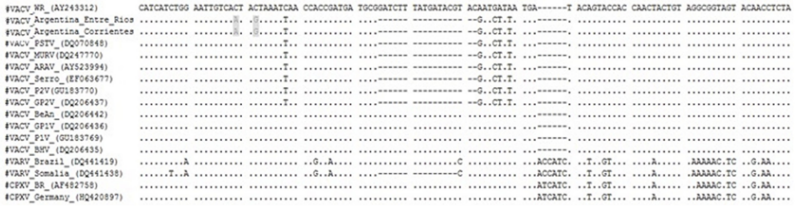
Spread of Vaccinia Virus to Cattle Herds, Argentina, 2011

Technical Appendix

A

B

C



D

	VACV WR	VACV Argentina Entre Rios	VACV Argentina Corrientes	VACV PSTV	VACV MURV	VACV ARAV	VACV Serro	VACV P2V	VACV GP2V	VACV BeAn	VACV GP1V	VACV P1V	VACV BHV	VARV Brazil	VARV Somalia	CPXV BR	CPXV Germany
VACV WR (AY243312)																	
VACV Argentina Entre Rios	93,6																
VACV Argentina Corrientes	93,6	100															
VACV PSTV (DQ070848)	95,5	98,2	98,2														
VACV MURV (DQ247770)	95,5	98,2	98,2	100													
VACV ARAV (AY523994)	95,5	98,2	98,2	100	100												
VACV Serro (EF063677)	95,5	98,2	98,2	100	100	100											
VACV P2V (GU183770)	95,5	98,2	98,2	100	100	100	100										
VACV GP2V (DQ206437)	95,5	98,2	98,2	100	100	100	100	100									
VACV BeAn (DQ206442)	100	93,6	93,6	95,5	95,5	95,5	95,5	95,5	95,5								
VACV GP1V (DQ206436)	100	93,6	93,6	95,5	95,5	95,5	95,5	95,5	95,5	100							
VACV P1V (GU183769)	100	93,6	93,6	95,5	95,5	95,5	95,5	95,5	95,5	100	100						
VACV BHV (DQ206435)	100	93,6	93,6	95,5	95,5	95,5	95,5	95,5	95,5	100	100	100					
VARV_Brazil(DQ441419)	78,2	71,8	71,8	73,6	73,6	73,6	73,6	73,6	73,6	78,2	78,2	78,2	78,2				
VARV Somalia (DQ441438)	77,3	70,9	70,9	72,7	72,7	72,7	72,7	72,7	72,7	77,3	77,3	77,3	77,3	99,1			
CPXV BR (AF482758)	81,8	75,5	75,5	77,3	77,3	77,3	77,3	77,3	77,3	81,8	81,8	81,8	81,8	96,4	95,5		
CPXV Germany (HQ420897)	81,8	75,5	75,5	77,3	77,3	77,3	77,3	77,3	77,3	81,8	81,8	81,8	81,8	96,4	95,5	100	

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.