horses and 1 from *Cx. tarsalis* mosquitoes. Notably, our sequence is distantly related to GQ287646, which was isolated from *Culex* spp. mosquitoes in Chaco, Argentina. The nucleotide sequence of the positive control VEEV-Tc83 is correctly placed in the VEEV clade.

Clinical and laboratory findings showed that the illness described here was compatible with viral encephalitis. Using a generic RT-PCR assay on an early CSF sample, we amplified a partial sequence (NSP4 gene) of an alphavirus. Phylogenetic analyses showed that the patient's sequence grouped with sequences from WEEV, with high statistical support. A second RT-PCR assay on the NSP1 gene enabled us to obtain an amplification of 208 bp, which is consistent with the expected size for WEEV. Therefore, we concluded that the fatal disease was likely caused by WEEV. Since the 1970s, to our knowledge, the presence of WEEV (or other alphaviruses) in Uruguay has not been documented. Moreover, no recent reports have been made of genome detection of WEEV in encephalitis cases in the region.

Although the case described here may be rare, the etiology of many viral encephalitides in Uruguay remains unknown. Serologic studies in horses and studies to detect arboviruses in mosquito populations are being conducted to investigate the status of arbovirus infections in Uruguay.

Acknowledgments

We thank José C. Russi for his invaluable scientific advice and encouragement during all the stages of this work and Gabriela Algorta for her help and interest in our research.

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DOI: 10.3201/eid1705.101068

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Widespread Availability of Artemisinin Monotherapy in the United States

To the Editor: Artemisinin-based combination therapies are recommended as first line treatments for *Plasmodium falciparum* malaria in most areas of the world. The article by Shahinas et al. (*1*) describes a patient who had *P. falciparum* malaria after returning from Nigeria. Her isolate had an elevated 50% inhibitory concentration to artemisinin derivatives. She had obtained artesunate in Nigeria and took it weekly for malaria prophylaxis, which might have contributed to the relative resistance found.

In 2009, one artemisinin-based combination therapy (artemether/lumefantrine) became available for use in the United States. However, it is not widely appreciated that artemisinin is actually available in the United States as an herbal supplement for over-the-counter purchase (*2*). It is marketed for general health maintenance and for treatment of parasitic infections and cancers (Figure), although as with other supplements it is not intended to diagnose, treat, cure, or prevent any disease. As in the patient described by Shahinas et al., widespread use

Figure. Bottle of artemisinin, available over-the-counter as an herbal supplement.

of artemisinin or its derivatives as monotherapies could potentially lead to progressively increasing resistance in *P. falciparum* malaria (*3*). Studies in western Cambodia, where artemisinin monotherapy has been available for many years, have revealed in vivo artesunate resistance, with markedly decreased parasite clearance times (*3*). Progressive spread of artemisinin resistance could have disastrous consequences for the global control of malaria. Thus, minimally regulated use of potent compounds in dietary supplements has the potential for major public health implications.

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DOI: 10.3201/eid1705.101532

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Yersinia pestis DNA Sequences in Late Medieval Skeletal Finds, Bavaria

To the Editor: We read with interest the report by Wiechmann et al. that, in the investigation of late medieval plague, partial sequencing of the *Yersinia pestis* pPCP1 plasmid yielded the observation of a 3-T homopolymeric tract which differed from the 5-T homopolymeric tract of the Orientalis *Y. pestis* CO92 type strain (*1*). This observation was unexpected because previous data from multispacer sequence typing and *glp* D gene sequencing yielded only the Orientalis biotype in cases of ancient plague (*2*).

Using suicide PCR (*3*), we therefore further investigated pPCP1 in 10 negative control dental pulp specimens and 60 specimens collected from 1 Justinian Orientalis plague site (*2*), 2 Black Death Orientalis sites, and 2 additional medieval plague sites. All negative controls remained negative; 14 (23%) of 60 plague specimens yielded a PCR product, and 7 interpretable sequences yielded a 3-T homopolymeric tract in all cases.

We further tested a *Y. pestis* isolate collection comprising 2 Antiqua, 6 Medievalis, and 4 Orientalis strains. No amplification was obtained in DNA-free PCR mix and 5 *Y. enterocolitica*–negative control isolates, whereas sequencing yielded a 3-T homopolymeric tract in all 12 *Y. pestis* isolates.

BLAST analysis (http://blast.ncbi.nlm.nih.gov/blast.cgi) indicated that the 5-T homopolymeric tract has been found only once in the *Y. pestis* CO92 strain (*4*) and in none of 22 modern and 11 ancient sequences (Table). This 5-T homopolymeric tract is therefore CO92 strain specific and not a marker for the Orientalis biotype. This pPCP1 plasmid sequence, located into a noncoding region of the 3′ extremity of the plasmid, is characterized by several homopolymeric tracts of poly (A) and poly (T), including the 1 herein investigated. Instability of the T-stretches has been reported in bacterial genomes (*5*) as being hot spots for mutations (*5*).

Therefore, in our assessment, the data reported for the late medieval Bavaria burial (*1*) do not support that deaths of persons buried in this site resulted from a non-Orientalis plague. Typing modern or ancient *Y. pestis* strains should not rely on poly (A) and poly (T) homopolymeric tracts sequencing.

This study was funded by Unité de Recherche sur les Maladies Infectieuses et Tropicales Emergentes, Unité Mixte de Recherche, Centre National de la Recherche Scientifique 6236.

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DOI: 10.3201/eid1705.101777