This case highlights 2 issues: the unknown epidemiology of CHIKV in Africa and the difficulty of diagnosing one arboviral infection during an outbreak of another arboviral infection. Further research is necessary to elucidate the true extent of CHIKV in African countries and to understand the public health implications of co-infection and co-distribution of multiple arboviruses.

This work was supported by a grant from the National Center for Global Health and Medicine (27-6001).

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Puumala Virus in Bank Voles, Lithuania

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DOI: http://dx.doi.org/10.3201/eid2301.161400

Little is known about the presence of human pathogenic Puumala virus (PUUV) in Lithuania. We detected this virus in bank voles (Myodes glareolus) in a region of this country in which previously PUUV-seropositive humans were identified. Our results are consistent with heterogeneous distributions of PUUV in other countries in Europe.

Puumala virus (PUUV) (family Bunyaviridae) is an enveloped hantavirus that contains a single-stranded trisegmented RNA genome of negative polarity (I). PUUV harbored by the bank vole (Myodes glareolus) is the most prevalent human pathogenic hantavirus in Europe (2). A high population density of bank voles can lead to disease clusters and possible outbreaks of nephropathia epidemica, a mild-to-moderate form of hantavirus disease (3).

In contrast to the Fennoscandian Peninsula and parts of central Europe (4,5), little is known about the epidemiology of PUUV in Poland and the Baltic States. Recent investigations confirmed the presence of PUUV in certain parts of Poland (5,6). A molecular study of bank voles in Latvia identified 2 PUUV lineages (Russian and Latvian) (7). In Estonia, serologic and molecular screening provided evidence of the Russian PUUV lineage (8). For Lithuania, a previous serosurvey indicated the presence of PUUV-specific antibodies in humans from 3 counties (online Technical Appendix Figure 1, http://wwwnc.cdc.gov/EID/article/23/1/16-1400-Techapp1.pdf). However, molecular evidence of PUUV in humans or in voles is lacking (9).

We report a molecular survey of rodent populations in Lithuania at 5 trapping sites, including 2 sites in counties where PUUV-specific antibodies were previously detected in humans (online Technical Appendix Figure 1). A total of 134 bank voles, 72 striped field mice (Apodemus agrarius), and 59 yellow-necked field mice (A. flavicollis) were captured during 2015. Three trapping sites (Juodkrantė, Elektrėnai, and Lukštas) were located in forests at or near

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a cormorant colony, and 2 trapping sites (Žalginiai and Rusnė) were located in a wet forest and flooded meadows. All applicable institutional and national guidelines for the care and use of animals were followed.

For PUUV detection, we extracted RNA from bank vole lung tissue samples by using the Qiazol Protocol (QIAGEN, Hilden, Germany) and conducting screening by using a small segment RNA–specific reverse transcription PCR (RT-PCR) and primers Pu342F and Pu1102R (6). We detected PCR products for 5 (LT15/164, LT15/165, LT15/166, LT15/174, and LT15/201) of 45 bank voles from the Lukštas trapping site. All 9 striped field mice and 2 yellow-necked field mice from Lukštas showed negative results for the PUUV RT-PCR.

We amplified the complete nucleocapsid protein–encoding region for 3 of the 5 samples positive by RT-PCR with 3 primer pairs: PuNCRS (5′-TAGTAGTAGACTCCTTGAA-3′)/Pu255R (5′-TGGACACAGCATCTGCCA-3′), Pu40F (5′-CTGGAATGATGACTTAAC-3′)/Pu393R (5′-TATGTTAATGTCCTTGATTG-3′), and Pu1027F (5′-ATGTCATGTTAGGTCA-3′)/Pu1779R (5′-TCAGCATTTGAGTTAGT-3′). RT-PCR products were directly sequenced by using the BigDye Terminator Version 1.1 Cycle Sequencing Kit (Applied Biosystems, Darmstadt, Germany). We deposited the sequences of the 5 samples in GenBank under accession nos. KX757839, KX757840, KX757841, KX751706, and KX751707 (Figure; online Technical Appendix Figure 2).

The 3 nucleocapsid protein–encoding nucleotide sequences showed identities of 98.2%–99.8%, and the 3 deduced nucleocapsid protein amino acid sequences showed identities of 99.8%–100% (online Technical Appendix Table). We found the highest similarity of the 3 nucleotide and corresponding amino acid sequences for the PUUV strain from Latvia (Jelgava1/Mg149/2008; JN657228): nucleotide sequence 89.8%–90.4% and amino acid sequence 99.8%–100% (online Technical Appendix Table).

We generated phylogenetic trees by using MrBayes 3.2.6 software (http://mrbayes.sourceforge.net/download.php) and MEGA6 software (http://www.megasoftware.net/). The optimal substitution model was calculated by using jModelTest 2.1.4 (https://code.google.com/p/jmodeltest2). The Bayesian tree was based on transition model 2 with invariant sites and gamma distribution and 4 million generations. For maximum-likelihood analysis, the Kimura 2-parameter model and 1,000 bootstrap replicates were used. Posterior probabilities are indicated before slashes, and bootstrap values are indicated after slashes. Scale bar indicates nucleotide substitutions per site. ALAD, Alpe-Adrian lineage; CE, Central European lineage; DAN, Danish lineage; FIN, Finnish lineage; HOKV, Hokkaido virus; LAT, Latvian lineage; N-SCA, North-Scandinavian lineage; RUS, Russian lineage; S-SCA, South-Scandinavian lineage.

To evaluate a potential association of PUUV with evolutionary lineages of the bank vole, we determined vole cytochrome b gene sequences, deposited them in GenBank

![Figure. Phylogenetic tree based on complete nucleocapsid gene sequences of Puumala virus (PUUV) strains from Lithuania (LT), Latvia (Jelgava1), and other PUUV clades. Tula virus (TULV) was used as the outgroup. The tree was generated by Bayesian and maximum-likelihood analysis using MrBayes 3.2.6 (http://mrbayes.sourceforge.net/download.php) and MEGA6 software (http://www.megasoftware.net/). The optimal substitution model was calculated by using jModelTest 2.1.4 (https://code.google.com/p/jmodeltest2). The Bayesian tree was based on transition model 2 with invariant sites and gamma distribution and 4 million generations. For maximum-likelihood analysis, the Kimura 2-parameter model and 1,000 bootstrap replicates were used. Posterior probabilities are indicated before slashes, and bootstrap values are indicated after slashes. Scale bar indicates nucleotide substitutions per site. ALAD, Alpe-Adrian lineage; CE, Central European lineage; DAN, Danish lineage; FIN, Finnish lineage; HOKV, Hokkaido virus; LAT, Latvian lineage; N-SCA, North-Scandinavian lineage; RUS, Russian lineage; S-SCA, South-Scandinavian lineage.](https://www.cdc.gov/eid/content/23/1/159-Figure1.png)
to evaluate the geographic distribution and temporal fluctuation of PUUV in bank vole populations in Lithuania.

Acknowledgment

We thank Nicole Reimer for generating Technical Appendix Figure 1.

P.S. was supported by a stipend from the Erasmus Programme.

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Loiiasis in US Traveler Returning from Bioko Island, Equatorial Guinea, 2016

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DOI: http://dx.doi.org/10.3201/eid2301.161427

The filarial parasite Loa loa overlaps geographically with Onchocerca volvulus and Wuchereria bancrofti filariae in central Africa. Accurate information regarding this overlap is critical to elimination programs targeting O. volvulus and W. bancrofti. We describe a case of loiiasis in a traveler returning from Bioko Island, Equatorial Guinea, a location heretofore unknown for L. loa transmission.

Loiiasis (African eye worm disease) is caused by infection with Loa loa, a parasitic vector-borne filarial worm endemic to 10 countries in central and western Africa, including Equatorial Guinea (1). The worm, spread by the bite of Chrysops dimidiata and C. silacea flies, is of public health concern because of its geographic overlap with Onchocerca volvulus and Wuchereria bancrofti worms, which cause onchocerciasis and lymphatic filariasis, respectively (2). Mass drug administration programs for onchocerciasis and lymphatic filariasis often include ivermectin, which can cause serious and occasionally fatal adverse neurologic reactions in persons with high levels of circulating L. loa microfilariae (3). To avoid such reactions, an accurate picture of the geographic distribution of L. loa infection is needed. Given the importance of epidemiologic data in the management of filarial infections, we report a case of loiiasis in a US woman who had traveled to Equatorial Guinea.

In May 2016, a 25-year-old woman sought care in Winston-Salem, North Carolina, USA, for fatigue, swelling of her left ankle, right knee pain, and intensely pruritic skin lesions on her lower extremities. She had lived on Bioko Island, Equatorial Guinea, during October 2015–March 2016 while studying local wildlife. On Bioko Island, she frequented local water sources to bathe and wash clothes and consistently took atovaquone/proguanil for malaria prophylaxis. She did not spend time on Equatorial Guinea’s mainland or travel to other nations in central or western Africa. Her flight from the United States to Bioko Island connected in Ethiopia; she did not leave the airport.

Symptoms developed soon after her return to North Carolina in late March 2016. Laboratory evaluations