have regularly acquired specimens from such outbreaks and we can identify them in their records, such specimens could represent not only a treasure trove of biodiversity (*10*) but also an alternative source of pathologic specimens and infectious agent genomic material.

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The computational results of this work have been achieved by using the Life Science Compute Cluster of the University of Vienna (Vienna, Austria). Data from this study are available in the European Nucleotide Archive: sequencing reads, accession no. PRJEB67701; capture data, ERR12141761, accession nos. ERR12141763, ERR12141765, and ERR12141766; and shotgun data, accession nos. ERR1214809–811 and ERR1214826.

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Reference

1. Titanji BK, Tegomoh B, Nematollahi S, Konomos M, Kulkarni PA. Monkeypox: a contemporary review for healthcare professionals. Open Forum Infect Dis. 2022; 9:ofac310.
2. Patrono LV, Pléh K, Samuni L, Ulrich M, Röthemeier C, Sachse A, et al. Monkeypox virus emergence in wild chimpanzees reveals distinct clinical outcomes and viral diversity. Nat Microbiol. 2020;5:955–65. https://doi.org/10.1038/s41564-020-0706-0
3. Calvignac-Spencer S, Düx A, Gogarten JF, Leendertz FH, Patrono LV. A great ape perspective on the origins and evolution of human viruses. Adv Virus Res. 2021;110:1–26. https://doi.org/10.1016/bs.aivir.2021.06.001
4. Calvignac S, Terme J-M, Hensley SM, Jalinot P, Greenwood AD, Hänni C. Ancient DNA identification of early 20th century simian T-cell leukemia virus type 1. Mol Biol Evol. 2008;25:1093–8. https://doi.org/10.1093/molbev/msn054
5. de-Dios T, Scheib CL, Houldcroft CJ. An adagio for viruses, played out on ancient DNA. Genome Biol Evol. 2023;15:evad047.
6. Parker S, Buller RM. A review of experimental and natural infections of animals with monkeypox virus between 1958 and 2012. Future Virol. 2013;8:129–57. https://doi.org/10.2217/fvl.12.130
7. Peters JC. An epizootic of monkey pox at Rotterdam Zoo. Int Zoo Yearb. 1966;6:274–5. https://doi.org/10.1111/j.1748-1090.1966.tb01794.x
8. Bem RA, Domachowske JB, Rosenberg HF. Animal models of human respiratory syncytial virus disease. Am J Physiol Lung Cell Mol Physiol. 2011;301:L148–56. https://doi.org/10.1152/ajplung.00065.2011
9. Morris JA, Blount RE, Savage RE. Recovery of cytopathogenic agent from chimpanzees with coryza. Exp Biol Med. 1956;92:544–9. https://doi.org/10.3181/00379727-92-22538
10. Card DC, Shapiro B, Giribet G, Moritz C, Edwards SV. Museum genomics. Annu Rev Genet. 2021;55:633–59. https://doi.org/10.1146/annurev-genet-071719-020506

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Case of Human Orthohantavirus Infection, Michigan, USA, 2021

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Orthohantaviruses cause hantavirus cardiopulmonary syndrome; most cases occur in the southwest region of the United States. We discuss a clinical case of orthohantavirus infection in a 65-year-old woman in Michigan and the phylogeographic link of partial viral fragments from the patient and rodents captured near the presumed site of infection.

Orthohantaviruses are negative-sense, enveloped RNA viruses that are transmitted by host reservoirs, such as rodents, to humans. Human infection occurs through inhalation of aerosolized viral particles from host excreta, such as urine or feces, often in enclosed spaces during infestations. New World orthohantavirus infection results in hantavirus cardiopulmonary syndrome (HCPS), which consists of febrile illness with edema and respiratory failure (*1*). In the United States, most HCPS cases occur in the Southwest and have a ≈35% mortality rate (*2*).

The dominant orthohantavirus that causes HCPS in the United States is Sin Nombre virus (SNV), which is thought to be carried and transmitted by the western deer mouse (*Peromyscus sonoriensis*). New York virus (NYV) is another pathogenic variant of orthohantavirus that is found in white-footed deer mice (*Peromyscus leucopus*); cases occur primarily in the Northeast region of the country (*3*). Although multiple host reservoirs for orthohantaviruses are distributed throughout the United States, most human cases are caused by SNV (*4*,*5*).

In early May 2021, a previously healthy 65-year-old woman visited an emergency department in Washtenaw County, Michigan, USA, with febrile prodrome of 3–6 days, thrombocytopenia, mild transaminase elevation, and acute hypoxic respiratory failure of unclear etiology requiring intubation. An extensive infectious disease workup was conducted, and physicians initially ruled out such pulmonary pathogens as SARS-CoV-2, common respiratory viruses, fungal agents, and *Legionella* spp. The family was interviewed to obtain a travel and animal exposure history, which revealed that the patient had not traveled outside of Michigan in the previous year. The interview also confirmed that the patient had not consumed unpasteurized dairy or undercooked meat, had a mostly indoor dog, lived near a natural area but used trails/sidewalks, and had no known rodent infestation in the home. However, the spouse reported that the patient had spent time recently cleaning out a relative's home that had been uninhabited for 2 years and was infested with mice.

Table. Measurements, location, and quantitative PCR results from captured rodents at likely site of patient orthohantavirus exposure, Michigan, USA, 2021*

Sample ID	Species (common name)	Weight, g	Total length, mm	Tail length, mm	Hind foot length, mm	Ear size, mm	Age/sex	Location of capture	PCR+ tissue (Ct values)
YR-01	*Peromyscus leucopus* (white-footed mouse)	13.2	152	75	19.5	16.5	Subadult/M	Garage right front corner	Kidney (33, 33), BAF (35, 35)
YR-02	*Blarina brevicauda* (Northern short-tailed shrew)	18	115	27	15	2.5	Adult/F	Backyard	NA
YR-03	*P. leucopus*	21	174	86	20.5	17.5	Adult/F	Backyard	Kidney (39, 39), liver (38, 34)
YR-04	*Tamias striatus* (Eastern chipmunk)	84.5	221	75	33.5	18	Adult/F	Backyard	NA
YR-05	*T. striatus*	73.5	222	85	36.5	18	Adult/M	Backyard	NA
YR-06	*P. leucopus*	17	159	73	20.5	17	Subadult/M	Porch right back corner	NA
YR-07	*T. striatus*	90	225	83	35	14.5	Adult/F	Neighbor backyard, right side	NA
YR-08	*T. striatus*	91	224	83	35	19	Adult/F	Neighbor backyard, right side	NA
YR-09	*T. striatus*	88	227	93	34	15	Adult/F	Neighbor backyard, right side	NA
YR-10	*T. striatus*	94	202†	48†	36	18	Adult/M	Backyard	Lung (35, 35)
YR-11	*T. striatus*	58	214	85	36	14	Subadult/M	Backyard	NA
YR-12	*T. striatus*	49	196	72	37	17	Subadult/M	Backyard	Lung (39, 39)

*BAF, brown adipose fat; Ct, cycle threshold; ID, identification; PCR+, positive result determined by quantitative reverse transcription PCR.
†Bobbed tail.

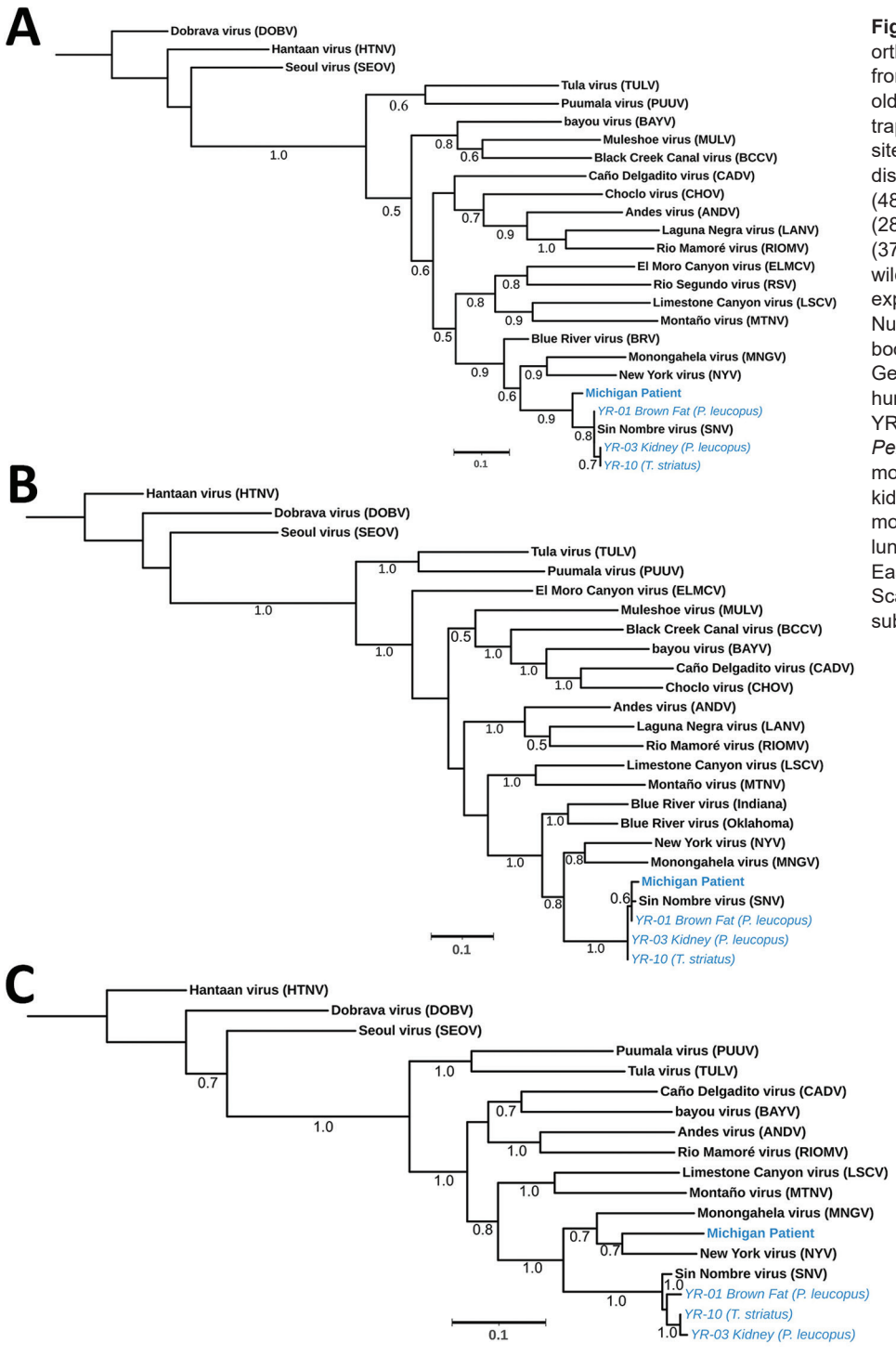

Figure. Phylogenetic analysis of orthohantavirus sequence fragments from samples taken from a 65-year-old woman in Michigan, USA, and trapped rodents from the likely site of exposure (blue text). Trees displaying the patient small fragment (481 bp) (A), medium fragment (283 bp) (B), and large fragment (377 bp) (C) were aligned against wild-caught rodents near site of exposure and reference sequences. Numbers along branches indicate bootstrap values of 500 replicates. GenBank accession numbers: human patient, OR428177–9; YR-01, brown adipose fat from a *Peromyscus leucopus* white-footed mouse, OR428180–2; YR-03, kidney tissue from a *P. leucopus* mouse, OR428183–5; and YR-10, lung tissue from a *Tamias striatus* Eastern chipmunk, OR428186–8. Scale bars indicate number of substitutions per site.

Results of a tickborne disease panel were negative, but hantavirus antibody testing performed at a commercial lab showed positive results for both IgM and IgG. The treating hospital notified the Michigan Department of Health and Human Services of a case of HCPS. Confirmatory hantavirus testing was arranged and confirmed with the Centers for Disease Control and Prevention, using serum samples collected from hospitalization.

Trapping was performed in and around the suspected site of exposure (relative's home) using Sherman folding traps (https://shermantraps.com;

94 trap nights), resulting in 12 rodents captured (12.8% trap success) under an approved animal-use protocol (*6*). Trapping was conducted 12 days after the patient was released from the hospital. Researchers observed signs of previous trapping efforts; 5 unusable *Peromyscus* mouse carcasses were found in snap traps in the residential basement. Signs of infestation were evident. Of the 12 trapped rodents, 3 (25%) were *P. leucopus* mice, 1 (8%) was a Northern short-tailed shrew (*Blarina brevicauda*), and 8 (67%) were Eastern chipmunks (*Tamias striatus*) (Table). The surrounding flora consisted of lawns, shrubs, and an evergreen windbreak near a public trail.

Using quantitative reverse transcription PCR, we screened lung, liver, brown fat, or kidney tissue from captured rodents and from a plasma sample of the patient obtained during hospitalization (*6*). Brown fat and kidney tissue from 2 *P. leucopus* mice and lung tissue from 2 *T. striatus* chipmunks tested positive for SNV. Three fragments were obtained from the patient sample, 1 for the short segment (480 bp), 1 for the medium segment (283 bp), and 1 for the large segment (377 bp). Similar fragments were also generated from 3 of the 4 infected rodents; all sequences are publicly available in GenBank (accession nos. OR428177–88). We compared fragments by using phylogenetic analysis against several known orthohantavirus reference sequences to determine potential identification. The partial sequences of SNV short and medium segments from the patient formed a phylogenetic lineage with SNV sequences from the rodents collected in or near the suspected site of exposure in Michigan. However, the patient's large fragment formed a lineage with NYV, suggesting that this species may be an SNV or NYV variant (Figure).

Previously, we identified the likely site of rodent-to-human SNV transmission in a patient case study (*6*). Here, we attempted a similar approach but were only able to generate partial sequences for the patient sample, which we compared with captured rodents. Orthohantavirus incubation periods can be up to several weeks after exposure (*7*), which may impact the timeliness of trapping efforts. We found infected *P. leucopus* mice and *T. striatus* chipmunks at the site of exposure, both of which have been reported to carry NYV or SNV; *P. leucopus* mice are susceptible and capable vessels for SNV replication after laboratory infection (*6*,*8*–*10*). This finding suggests that orthohantaviruses may not be as species host–restricted as previously thought. Further studies are warranted to clarify (or define) orthohantavirus species in Michigan to anticipate the risk for patient infection. Increasing surveillance and diagnostic efforts can enable prospective detection of circulating viruses.

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References

1. Nichol ST, Spiropoulou CF, Morzunov S, Rollin PE, Ksiazek TG, Feldmann H, et al. Genetic identification of a hantavirus associated with an outbreak of acute respiratory illness. Science. 1993;262:914–7. https://doi.org/10.1126/science.8235615
2. Akram SM, Mangat R, Huang B. Hantavirus cardiopulmonary syndrome. In: StatPearls [Internet]. Treasure Island (FL): StatPearls Publishing; 2024.
3. Hjelle B, Lee SW, Song W, Torrez-Martinez N, Song JW, Yanagihara R, et al. Molecular linkage of hantavirus pulmonary syndrome to the white-footed mouse, *Peromyscus leucopus*: genetic characterization of the M genome of New York virus. J Virol. 1995;69:8137–41. https://doi.org/10.1128/jvi.69.12.8137-8141.1995
4. Rollin PE, Ksiazek TG, Elliott LH, Ravkov EV, Martin ML, Morzunov S, et al. Isolation of black creek canal virus, a new hantavirus from *Sigmodon hispidus* in Florida. J Medical Virology. 1995;46: 35–39. https://doi.org/10.1002/jmv.1890460108
5. Ksiazek TG, Martin ML, Groves MG, Nichol ST, Peters CJ, Monroe MC, et al. Isolation, genetic diversity, and geographic distribution of Bayou virus (Bunyaviridae: hantavirus). Am J Trop Med Hyg. 1997;57:445–8. https://doi.org/10.4269/ajtmh.1997.57.445
6. Goodfellow SM, Nofchissey RA, Schwalm KC, Cook JA, Dunnum JL, Guo Y, et al. Tracing transmission of Sin Nombre virus and discovery of infection in multiple rodent species. J Virol. 2021;95:e0153421. https://doi.org/10.1128/JVI.01534-21
7. Vial PA, Valdivieso F, Mertz G, Castillo C, Belmar E, Delgado I, et al. Incubation period of hantavirus cardiopulmonary syndrome. Emerg Infect Dis. 2006;12:1271–3. https://doi.org/10.3201/eid1208.051127

8. Mills JN, Ksiazek TG, Ellis BA, Rollin PE, Nichol ST, Yates TL, et al. Patterns of association with host and habitat: antibody reactive with Sin Nombre virus in small mammals in the major biotic communities of the southwestern United States. Am J Trop Med Hyg. 1997;56:273–84. https://doi.org/10.4269/ajtmh.1997.56.273
9. Childs JE, Ksiazek TG, Spiropoulou CF, Krebs JW, Morzunov S, Maupin GO, et al. Serologic and genetic identification of *Peromyscus maniculatus* as the primary rodent reservoir for a new hantavirus in the southwestern United States. J Infect Dis. 1994;169:1271–80. https://doi.org/10.1093/infdis/169.6.1271
10. Quizon K, Holloway K, Iranpour M, Warner BM, Deschambault Y, Soule G, et al. Experimental infection of peromyscus species rodents with Sin Nombre virus. Emerg Infect Dis. 2022;28:1882–5. https://doi.org/10.3201/eid2809.220509

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Autochthonous Ascariasis, Mississippi, USA

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We describe a case of a 2-year-old child who expelled a single adult female *Ascaris lumbricoides* worm. The patient is from a rural county in Mississippi, USA, with no reported travel outside of the United States. The caregivers in the home practice good sanitation. Exposure to domestic pigs is the likely source of infection.

[1]These authors are co–first authors.

A reported increase of hookworm and strongyloidiasis transmission in rural Alabama, USA, in 2017 (*1*) has led to more interest in isolated cases of autochthonous transmission of soil-transmitted helminths in the southeastern United States. This increased transmission and interest led to several small- and large-scale surveys of soil-transmitted helminths and other parasitic diseases in Mississippi (*2*–*4*), Alabama (*5*), and Texas (*6*). No cases of ascariasis were identified in those surveys. However, highly endemic porcine ascariasis is present in some farmed pigs in the United States (*7*). Sporadic reports have been documented of autochthonous ascariasis cases and case clusters in northeastern states (*8*), and *Ascaris lumbricoides* roundworm–mediated Löffler syndrome (eosinophilic pneumonitis) has been reported in Louisiana over the past decade (*9*). Those autochthonous ascariasis cases represented spillover infections to humans from pigs. We describe a case of zoonotic ascariasis from New Albany in Union County, Mississippi.

A previously healthy 2-year-old girl was brought to her local pediatrician with complaints of abdominal cramping for 2 weeks, loose stools (without blood or mucous), and a decreased appetite. The family was originally from Mexico but had lived in the United States for 13 years. Neither the patient nor her twin sister had been outside of the United States. The family lived on a farm with pigs, and both children reportedly ate dirt from the house plants. The mother found a motile worm in the patient's diaper, filmed the worm, and then discarded the diaper and worm.

We identified the helminth from the video (Video, https://wwwnc.cdc.gov/EID/article/30/4/24-0176-V1.htm) as an adult female *A. lumbricoides* worm because of the characteristic size, shape, reddish-orange color, and a pointed rather than recurved tail. The patient was treated by her pediatrician with ivermectin (1 dose of a 3 mg tablet) because albendazole was not available and mebendazole was not covered by the patient's insurance. We performed automated complete blood counts by using an in-office hematology analyzer (without eosinophil count capacity). The patient was not anemic (hemoglobin 11.8 g/dL [reference range, for age 11–13.7 g/dL]; mean corpuscular volume 80.4 fL [reference range for age 75–86 fL]). We treated the family members as a precautionary measure. We obtained stool samples from the patient within 24 hours of treatment but detected no eggs on Kato–Katz microscopic smear. The patient did not expel any additional worms. We followed