

# Molecular Characterization of *Echinococcus vogeli* from Human Case, Colombia, 2024

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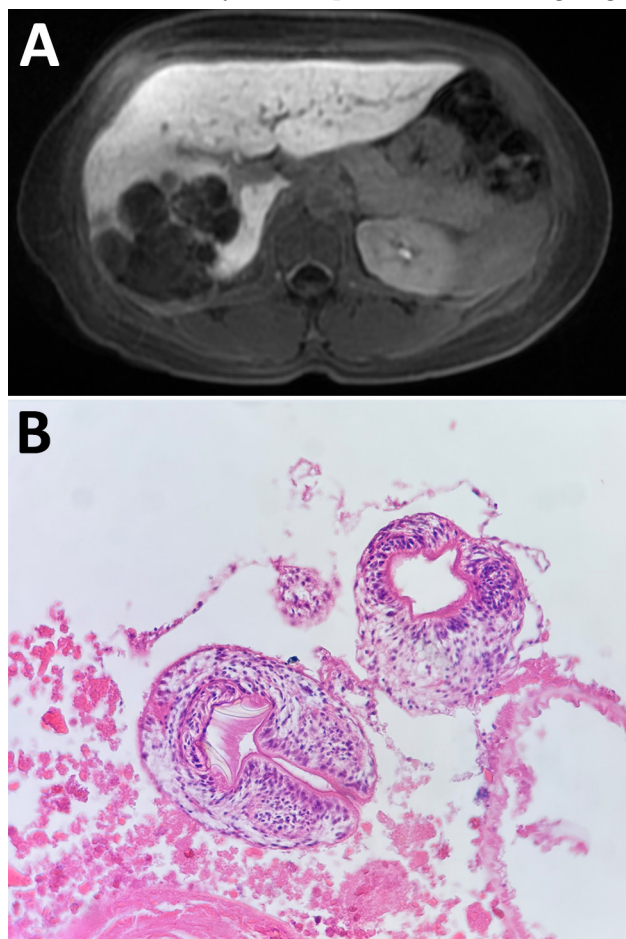
In Colombia, 35 confirmed cases of neotropical polycystic echinococcosis were reported during 1978–2018. In most cases, *Echinococcus vogeli* was identified by means of morphologic identification. We describe a case of *E. vogeli* echinococcosis in a woman, diagnosed through PCR, mitochondrial DNA sequencing, and molecular characterization

Human echinococcosis (also known as hydatidosis) is a zoonotic neglected disease caused by infection of cestode larval form of *Echinococcus* spp. tapeworms (1,2). At least 4 *Echinococcus* species are recognized as causes of human disease and have relevance in public health: *E. granulosus* causes cystic echinococcosis and is a cosmopolitan species; *E. multilocularis* produces alveolar echinococcosis and predominates in the northern hemisphere; and *E. vogeli* causes neotropical polycystic and *E. oligarthus* unicystic echinococcosis, both confined to tropical zones in Central and South America (1,2). Neotropical polycystic echinococcosis (NPE) affects mostly persons living in rural and sylvatic regions where the cycle of the *E. vogeli* tapeworm involves the paca (*Cuniculus paca*) as the intermediate host and the bush dog (*Speothus venaticus*) as the natural final host (2,3). Nevertheless, a proposed domiciliary transmission cycle posits that human infection occurs incidentally through fecal contamination by domestic hunting dogs (alternative final host) after they fed on paca viscera (2,4).

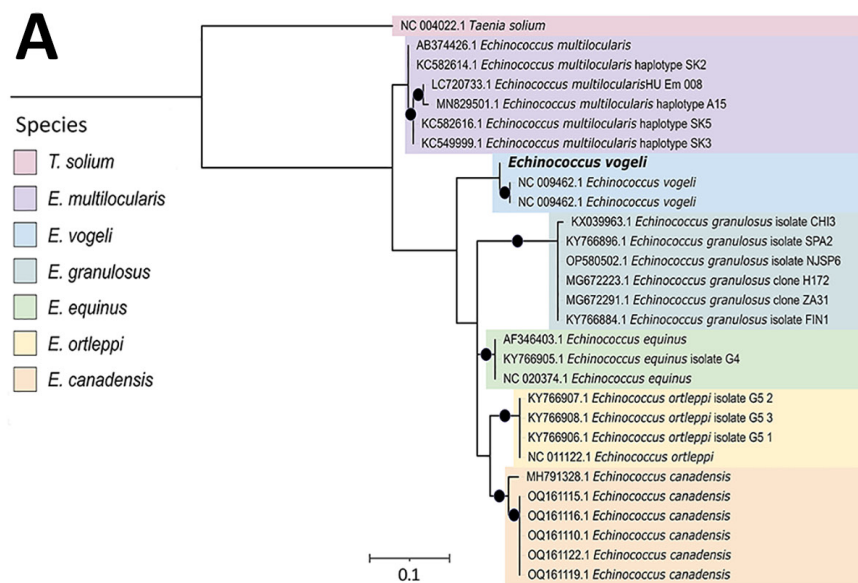
In Colombia, 35 confirmed cases of NPE were reported during 1978–2018 (2,5–7). In most of them,

*Echinococcus* spp. infection was identified by means of morphologic identification (2,5,6); in 1 case, the 2018 report, molecular detection identified the *E. vogeli* cytochrome c oxidase subunit 1 (*cox1*) mitochondrial gene without molecular characterization (7). Here, we present a case of *E. vogeli* echinococcosis in a woman in Colombia diagnosed through PCR, sequencing mitochondrial DNA, and molecular characterization. We obtained written consent from the patient to report on her case.

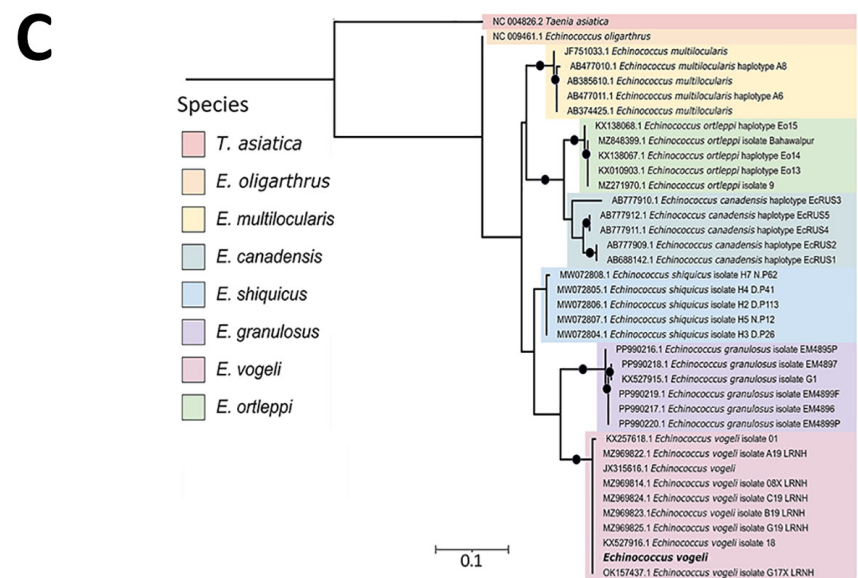
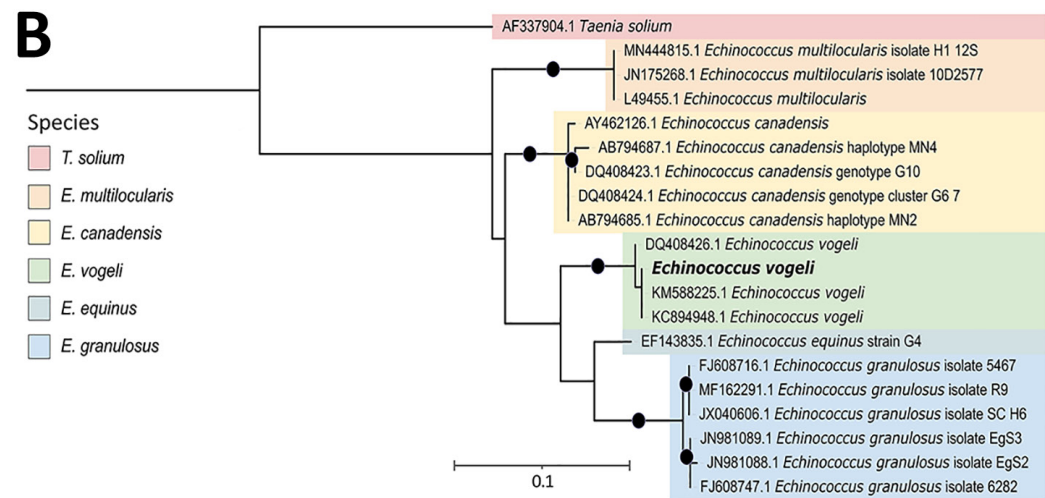
An otherwise healthy 50-year-old woman sought care at the emergency department of the Hospital Militar Central (Bogotá, Colombia) on September 23, 2024, after 8 days of epigastric and right hypochondrium pain; she did not have jaundice or other symptoms. As a child, she had lived in a rural region of Cesar Department (Colombian Caribbean region); she saw pacas often and always had kept domestic hunting dogs.



**Figure 1.** Neotropical polycystic echinococcosis in a woman, Colombia, 2024. A) Abdominal MRI scan showed hypodense, round polycystic vesicles, replacing right liver parenchyma with predominant peripheral calcifications and fat content. B) Protoscoleces of *Echinococcus* tapeworms with rostellar hooks. Hematoxylin & eosin staining; original magnification  $\times 4$ .



**Figure 2.** Phylogenetic reconstruction of the cytochrome b (A), 12S rRNA (B) and cytochrome c oxidase subunit 1 (C) genes of the *Taeniidae* family from consensus sequences obtained in study of *Echinococcus vogeli* infection in a human, Colombia, 2024. Bold text indicates strains from this study. Black dots indicate node support for bootstrap values >80. We used a maximum-likelihood approach to construct phylogenetic trees using IQ-TREE multicore version 1.6.12 (<https://iqtree.github.io/release/v1.6.12>). The best-fitting nucleotide substitution model for each gene was automatically selected by the software, and default parameters were applied. GenBank accession numbers are provided for reference sequences. Scale bar indicates substitutions per site.



Physical examination revealed a mild tenderness in right hypochondrium without peritoneal irritation signs. Serum liver function tests were without abnormality. Abdominal magnetic resonance imaging showed hypodense, round polycystic vesicles, replacing right liver parenchyma with predominant peripheral calcifications and fat content (Figure 1, panel A). Differential diagnoses were mucinous cystic neoplasm, hepatic liposarcoma, and hydatid cysts. We performed a total right segmental liver resection and cholecystectomy. The histopathological results of surgical liver specimen showed multiple cysts with *Echinococcus* protoscoleces (Figure 1, panel B). The patient received albendazole (200 mg 2×/d) for 1 month and was discharged.

We performed PCR on the liver histopathological sample, targeting the cytochrome b (Cob), 12S rRNA, and *cox1* genes, confirming the presence of *Echinococcus* sp. We sequenced the amplicons using Oxford Nanopore MinION (Oxford Nanopore Technologies, <https://nanoporetech.com>) and used those sequences for phylogenetic reconstruction. Phylogenetic analysis showed that the sequences we obtained of the 3 genes clustered with *E. vogeli* sequences downloaded from GenBank (Figure 2). Sequences from this study were deposited in GenBank (accession nos. PV243336, PV243987, and SUB15312175).

The clinical characteristics of NPE in patients depend on the location of the metacestode as well as the extent of invasion of tissues (2). The liver is the most frequently affected organ (2). Metacestodes could be found in the liver alone or with vesicles situated in the abdomen, in the liver and the lungs or pleural cavities, or only as calcified vesicles in the liver (2). Other organs involved included the diaphragm, spleen, pancreas, omentum, mesenteries, rectovesical pouch, ovaries, uterus, abdominal wall, psoas muscle, and vertebra (2). Before surgery, patients often receive misdiagnosis with a variety of disorders, including hepatic tumor, abscess, cirrhosis or cholecystitis, gall bladder cancer, mesenteric tumor, and costal chondrosarcoma (2).

Geographic origin of the patients is a crucial diagnostic clue for *E. vogeli* echinococcosis (2). They are typically born in or have lived for prolonged periods in rural tropical areas of Central or South America, particularly in regions with abundant wildlife (2). Familiarity with pacas and whether domestic dogs were fed viscera of pacas are characteristics that contribute to a correct diagnosis (2). Ultrasound fine-needle aspiration and histopathologic examination of surgical specimens can permit taxonomic identification through larval morphologic clues (protoscoleces,

hook shape and size, proportions of small and long blades) and are considered the standard, but definitive diagnosis is difficult when the hooks are absent (1–3). Since 2017, in Brazil, using molecular characterization of *E. vogeli* through *cox1* mitochondrial gene in samples from humans, domestic dogs, and pacas has suggested the presence of shared haplotypes among different populations of this cestode, reflecting the retention of ancestral polymorphisms (8–10).

In summary, our report highlights the value of molecular characterization of *E. vogeli* from histopathologic samples. Consistent with previous reports (2), we recommend that NPE be considered not as a medical curiosity but as a possible diagnosis of polycystic masses in humans from tropical zones in Central or South America.

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Dr. Morcillo Muñoz is an infectious diseases fellow at Universidad Nacional de Colombia in Bogotá, Colombia. His research interests primarily focus on neglected infectious diseases.

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## Seroprevalence of Rift Valley and Crimean-Congo Hemorrhagic Fever Viruses, Benin, 2022–2023

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We screened 650 febrile patients from Benin for Rift Valley fever and Crimean-Congo hemorrhagic fever viruses during 2022–2023. None were positive by reverse transcription PCR; 1.1% and 0.3%, respectively, had virus-specific IgG. False-positive results from malaria-associated antibodies likely reacting with histidine-tagged viral antigens mandate careful validation of serologic tests in malaria-endemic regions.

Rift Valley fever virus (RVFV; family Phenuiviridae) and Crimean-Congo hemorrhagic fever virus (CCHFV; family Nairoviridae) are arthropodborne viruses endemic to Africa and the Arabian Peninsula (1,2) and high-priority pathogens that can cause lethal hemorrhagic fever (2–4) (<https://www.who.int/publications/m/item/WHO-BS-2023-2449>). In West Africa, RVFV and CCHFV are considered endemic in Senegal and Mauritania (1,2); regional circulation seems likely in Guinea, Burkina Faso, Ghana, and Nigeria (2). In Benin, CCHFV antibodies were reported in humans in 1981, but RVFV and CCHFV epidemiology remains unknown (1,2). Both RVFV and CCHFV infect diverse animals reared as livestock (3). Benin has been undergoing changes in traditional cattle farming, including increased herd sizes and sedentarization (5), which may intensify RVFV and CCHFV circulation. We collected serum samples for routine diagnostic examinations for RVFV and CCHFV in 7 hospitals located across ≈700 km and 3 ecozones in Benin (Appendix Table, Figure, <https://wwwnc.cdc.gov/EID/article/31/8/25-0020-App1.pdf>).

We investigated serum samples from 650 febrile patients (mean age 26.7 [interquartile range 18–34] years; 70.3% female, 29.7% male) who were seen during December 2022–January 2023. We analyzed samples for acute RVFV and CCHFV infection using PCR-based methods and had no positive results (Appendix). However, we detected IgG by using commercially available ELISA kits (RVFV, competitive ELISA; ID.Vet, <https://bioadvance.life/en/id-vet-2>; CCHFV, indirect ELISA; Euroimmun, <https://www.euroimmun.com>) with viral nucleoproteins as antigens. We confirmed CCHFV ELISA results by using a CCHFV immune complex capture IgG ELISA (Panadea Diagnostics, <https://www.panadea-diagnostics.com>) and RVFV and CCHFV ELISA results by indirect IgG immunofluorescence assays (IFAs).