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Natural *Trichuris trichiura* Infections in Endemic Hydromyini Rodents, Papua New Guinea, 2019–2023

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Screening of 874 wild mammals in Papua New Guinea during 2019–2023 identified *Trichuris* whipworm infections in multiple rodent species. Mitochondrial and nuclear markers identified 8 *Trichuris trichiura* infections. Those findings broaden the recognized host range of this human soil-transmitted helminth and raise questions regarding wildlife involvement in its transmission ecology.

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The *Trichuris trichiura* whipworm is a soil-transmitted helminth that infects ≈500 million persons worldwide (*1*). Despite environmental transmission through infective eggs, *T. trichiura* is generally considered to be maintained exclusively by humans and nonhuman primates (*2*). Although whipworms infect a wide range of mammalian hosts, including rodents (*3*,*4*) and marsupials (*5*), *Trichuris* species whipworms generally are considered host-specific, and experimental studies show that *T. trichiura* does not readily establish patent infections in rodents or other nonprimate hosts (*1*; K.A. Stark et al., unpub. data, https://doi.org/10.1101/2025.05.09.653168). All major soil-transmitted helminths, including *T. trichiura*, are endemic in Papua New Guinea (*7*; J.L. Scott, master's thesis, James Cook University, 2023). We investigated *Trichuris* whipworm infections in wild mammals in Papua New Guinea and unexpectedly identified *T. trichiura* in multiple endemic rodents.

We sampled mammals during 2019–2023 at 19 localities across 2 mountain systems and 3 lowland sites (Appendix 1 Figure 1, https://wwwnc.cdc.gov/EID/article/32/12/26-1101-App1.pdf). We examined the cecum and colon of 874 animals for whipworms (Appendix 1; Appendix 2 Table, https://wwwnc.cdc.gov/EID/article/32/12/26-1101-App2.xlsx). The Ethical Committee of the Faculty of Science, University of South Bohemia approved the animal research protocol (approval no. 2019-1).

Rodents in Papua New Guinea come from 2 major murine lineages: Rattini, which includes endemic and introduced *Rattus* species, and Hydromyini, an endemic Australo–Papuan adaptive radiation occupying diverse ecologic niches. Of the 874 tested animals, 43 marsupials tested negative for whipworms, although the small sample distributed across multiple taxa precludes inference regarding their susceptibility. Sixteen rodents harbored *Trichuris* spp. whipworms: 7 *Rattus niobe* rats and 9 Hydromyini rodents representing 7 species (Table). The 7 infections in *R. niobe* rats occurred at a single location, whereas infections in Hydromyini rodents were distributed among several locations and host lineages.

Because morphologic species delimitation within *Trichuris* is difficult, we genetically characterized worms from 11 infected rodents (Appendix 1). The mitochondrial genomes of 8 specimens shared 97.5%–97.7% nucleotide identity with a human-derived *T. trichiura* reference sequence from Ecuador (GenBank accession no. AP017704) (Appendix 1 Table 2). Each

Table. Whipworm infections and molecular identification in wild mammals in study of natural *Trichuris trichiura* infections in endemic Hydromyini rodents, Papua New Guinea, 2019–2023

Host group	Genus	No. examined	No. *Trichuris*-positive	No. molecularly characterized	No. identified as *T. trichiura*
Rattini	*Rattus*	491	7	2	0
Hydromyini	*Hydromys*	6	1	1	0
	Hyomys	2	1	1	1
	Mallomys	15	2	2	2
	Pogonomys	12	3	3	3
	Uromys	11	2	2	2
	Other Hydromyini genera*	294	0	0	0
Marsupialia	All genera†	43	0	0	0
Total		874	16	11	8

*Other Hydromyini genera consisted of *Abeomelomys*, *Anisomys*, *Coccymys*, *Leptomys*, *Lorentzimys*, *Macruromys*, *Melomys*, *Microhydromys*, *Paramelomys*, *Protochromys*, and *Pseudohydromys*.
†Marsupials consisted of *Cercartetus*, *Dactylopsila*, *Dorcopsulus*, *Echymipera*, *Microperoryctes*, *Murexia*, *Petaurus*, *Phalanger*, *Phascolosorex*, *Pseudochirops*, and *Pseudochirulus*. Complete individual-level sampling data are provided in Appendix 2 (https://wwwnc.cdc.gov/EID/article/32/12/26-1101-App2.xlsx.

genome represented a distinct mitochondrial haplotype. Maximum-likelihood phylogenetic analysis placed all 8 genomes within the *T. trichiura* clade (100% bootstrap support) (Figure), together with isolates from humans and nonhuman primates. Those isolates clustered within a subclade containing isolates from Asia and South America, and the closest relatives were derived from human infections in Ecuador and Honduras. Independent analysis of the nuclear internal transcribed spacer 2 marker corroborated their identification, placing the same 8 specimens within *T. trichiura* (100% bootstrap support) (Appendix 1 Figure 2). The remaining 3 characterized specimens, from 2 *R. niobe* rats and 1 *Hydromys chrysogaster* rakali, clustered within divergent rodent-associated *Trichuris* lineages.

The 8 *T. trichiura* infections occurred in 6 Hydromyini species (*Hyomys goliath* rats, *Mallomys hercules* rats, *Pogonomys macrourus* mice, *P. loriae* mice, *Uromys caudimaculatus* rats, and *Uromys* spp. rats) at 4 locations on both mountain systems and across the 2019, 2020, and 2023 sampling periods. Those hosts represent distinct Hydromyini phylogenetic lineages and include terrestrial and scansorial species, suggesting that infection is not restricted to a single host lineage or ecology.

Worm burdens varied among infected rodents; of note, 122 worms were recovered from 1 *M. hercules* rat. Adult female worms containing developed eggs were observed (Appendix 1 Figure 3), providing evidence of reproductive maturation in naturally infected Hydromyini rodents. However, we did not assess egg viability or subsequent transmission; our findings therefore do not establish transmission competence or reservoir status.

The occurrence of *T. trichiura* worms in several Hydromyini species expands the recognized natural host range of a parasite generally associated with humans and nonhuman primates. Repeated spillover from humans remains possible because environmentally resistant *T. trichiura* eggs provide opportunities for cross-species exposure. However, detection in several rodent species at multiple locations in different years and with distinct mitochondrial haplotypes raises the possibility of circulation among wild rodents. Hydromyini are broadly distributed across New Guinea and neighboring regions (*7*), suggesting that this host association might not be restricted to the sampled populations in Papua New Guinea. If rodents produce viable and infectious eggs, they could also be a source of infection for humans. That possibility is particularly relevant because 5 of the 8 *T. trichiura*–infected rodents were obtained through hunter-assisted sampling. Wild rodents are commonly hunted for food in Papua New Guinea, providing an interface between humans and native forest rodents (*8*). That practice increases human–rodent contact and could enable parasite transmission between the two. Distinguishing those transmission pathways will require assessing the infectivity of rodent-derived eggs and comparing *T. trichiura* populations from sympatric humans and wildlife.

Our findings identify an unexpected nonprimate component of *T. trichiura* ecology. From a One Health perspective, if infected rodents contribute to environmental contamination with viable eggs, transmission could persist outside treated human populations, potentially complicating prevention and control efforts. Our study highlights the need to consider wildlife when investigating *T. trichiura* transmission in endemic settings.

Mitochondrial and internal transcribed spacer 2 ribosomal DNA sequences of whipworms and representative host cytochrome b sequences were submitted to GenBank (accession nos. PZ173638–PZ173648, PZ188518–PZ188528, and PZ184053–PZ184067). Alignments and tree files were deposited in Zenodo (https://doi.org/10.5281/zenodo.22846525).

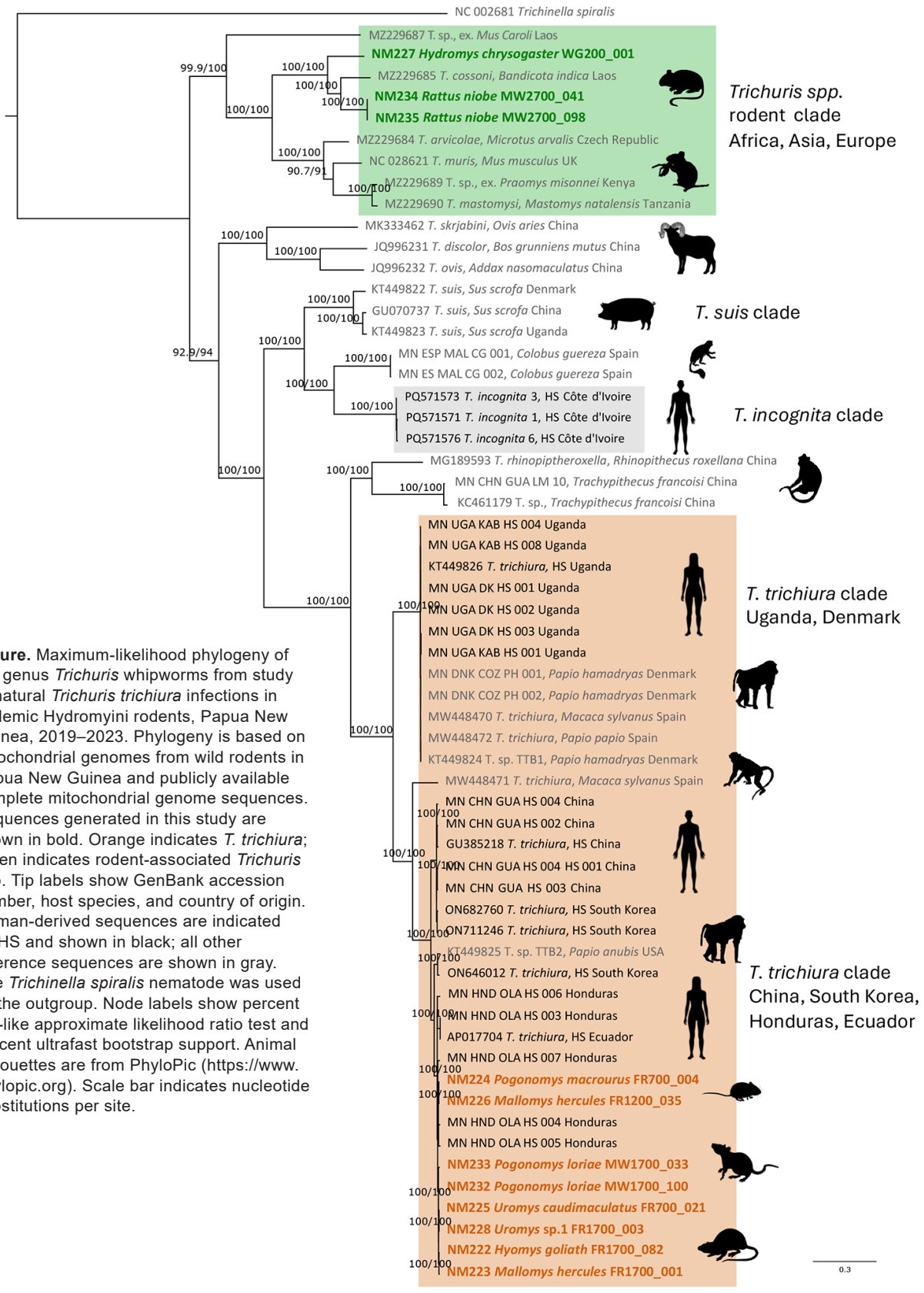


Figure. Maximum-likelihood phylogeny of the genus *Trichuris* whipworms from study of natural *Trichuris trichiura* infections in endemic Hydromyini rodents, Papua New Guinea, 2019–2023. Phylogeny is based on mitochondrial genomes from wild rodents in Papua New Guinea and publicly available complete mitochondrial genome sequences. Sequences generated in this study are shown in bold. Orange indicates *T. trichiura*; green indicates rodent-associated *Trichuris* spp. Tip labels show GenBank accession number, host species, and country of origin. Human-derived sequences are indicated by HS and shown in black; all other reference sequences are shown in gray. The *Trichinella spiralis* nematode was used as the outgroup. Node labels show percent SH-like approximate likelihood ratio test and percent ultrafast bootstrap support. Animal silhouettes are from PhyloPic (https://www.phylopic.org). Scale bar indicates nucleotide substitutions per site.

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F.V. and D.S.O. conducted the field sampling; F.V. genotyped the hosts; J.G.B., A.R., and D.Č. designed the study; N.M. dissected the samples; N.M. and A.R. performed the preliminary morphometric analyses; N.M. and A.B. carried out the laboratory work; N.M. and J.G.B. analyzed the genetic data and performed the statistical and phylogenetic analyses; D.Č. and V.N. secured funding; V.N., D.Č., A.R., and J.G.B. supervised the work; J.G.B. drafted the manuscript; and all authors read and approved the final version of the manuscript.

About the Author

Dr. Moradpour is a veterinarian in Brno, Czech Republic. Her research focuses on the taxonomy, phylogeny, and evolution of parasitic helminths, particularly nematodes, in wildlife hosts.

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