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Contents

Summary of the Fortieth Meeting of the International Task Force for Disease Eradication (ITFDE)

October 28-29, 2025

The 40th meeting of the International Task Force for Disease Eradication (ITFDE)[1] was convened in a hybrid (in-person and virtual) format at The Carter Center (TCC) in Atlanta, GA, USA, on October 28-29, 2025, to discuss "the status of dracunculiasis (Guinea worm) eradication."

Global Guinea Worm Eradication Program Overview

Guinea worm disease (GWD), or dracunculiasis, is caused by the parasite *Dracunculus medinensis*. When emerging gravid female worms discharge their larvae into stagnant freshwater, the larvae can be consumed by tiny copepods ("water fleas"), which serve as intermediate hosts where the larvae develop from immature first-stage larvae (L1s) to infectious third-stage larvae (L3s). Definitive hosts, such as people or non-human animals, can ingest water or eat raw/under-cooked aquatic animals such as fish or frogs (or aquatic animal waste) containing infected copepods or viable infectious L3s and become infected with *D. medinensis*. When this occurs, L3s migrate within the host's body where they mate, and the female worms mature over the next 10-14 months before emerging through the definitive host's skin. Although contact with water soothes the host's pain, it also stimulates the worm to release thousands of L1s, continuing the transmission cycle.

The campaign to eradicate GWD began at the Centers for Disease Control and Prevention (CDC) in 1980, and GWD eradication was adopted as a subgoal for the International Drinking Water Supply and Sanitation Decade (1981-1990). The Carter Center began leading the global Guinea Worm Eradication Program (GWEP) in 1986, strengthening the coalition that includes ministries of health (MOH) in endemic countries, the World Health Organization (WHO), CDC, and the United Nations Children's Fund (UNICEF). Thousands of village volunteers and supervisory health staff reduced GWD cases in humans from an estimated 3.5 million annually in 1986 to only 15 cases in 2024,[2] preventing over 100 million infections and nearly 9.6 million years of suffering. These reductions were realized through health education, surveillance, filtration of unsafe water, copepod control with the organophosphate temephos (Abate®), containment of individual cases, and provision of safe drinking water. Guinea worm (GW) infections detected among domesticated dogs in Chad in 2012[3] and among domesticated cats and

[1] The ITFDE members are Dr Kashef Ijaz, The Carter Center (Chair), USA; Dr Fatima Barry, World Bank, USA; Mr. Simon Bland, Global Institute for Disease Elimination, United Arab Emirates; Dr Ibrahima Soce Fall, WHO, Switzerland; Dr Peter Figueroa, University of the West Indies, Jamaica; Dr Donald Hopkins, The Carter Center, USA; Dr Patrick Lammie, Task Force for Global Health, USA; Dr Kim Lindblade, independent consultant, Switzerland; Dr David Molyneux, Liverpool School of Tropical Medicine, United Kingdom; Dr Ana Morice, independent consultant, Costa Rica; Dr Rory Nefdt, UNICEF, USA; Dr William Schluter, Centers for Disease Control and Prevention, USA; Dr Faisal Sultan, Shaukat Khanum Memorial Cancer Hospital and Research Center, Pakistan; Dr Jordan Tappero, Bill & Melinda Gates Foundation, USA; and Dr Dyann Wirth, Harvard TH Chan School of Public Health, USA.

[2] Annual Dracunculiasis Surveillance Summary, 2024 in WER (2025) 100:165-191

[3] Eberhard M., Ruiz-Tiben E., Hopkins D.R., Farrell C., Toe F., Weiss A., Withers P.C., Jenks M.H., Thiele E.A., Cotton J.A., Hance Z., Holroyd N., Cama V.A., Tahir M.A., Mounda T. (2013) The peculiar epidemiology of dracunculiasis in Chad. *The American Journal of Tropical Medicine and Hygiene*. 90(1):61-70. doi: 10.4269/ajtmh.13-0554.

baboons (Ethiopia) in 2013 posed a new challenge for the GWEP. In addition to the human cases detected in 2024, the five remaining endemic countries reported 664 animal GW infections, mostly in dogs. As of October 2025, ten human cases of GWD and 674 animal GW infections were reported.[4]

Eradicating *D. medinensis* will require sustained political will, cross-border coordination, and One Health approaches addressing human, animal, and environmental-related issues. The 2025 World Health Assembly (WHA) Resolution on GW eradication (WHA 78.14) acknowledges the need to accelerate interventions, calling for sustained political will and financial commitment to achieve the goal. With the continued dedication of community volunteers, Ministries of Health (MoHs), the WHO, TCC, donors, and other partners, GW could become the first human disease to be eradicated without a vaccine.

Certification of Eradication

Reaching global eradication of *D. medinensis* requires the WHO to formally certify all countries worldwide as GW-free.[5] Eradication is defined as the permanent reduction to zero of the worldwide incidence of infection caused by a specific agent as a result of deliberate efforts, and the stage when intervention measures are no longer needed.[6] The WHO certification process begins at the national level when an endemic country documents at least three consecutive calendar years of zero indigenous human cases—and, where relevant, zero animal infections (i.e., elimination of transmission)—under a nationwide, functioning surveillance system, and submits a national dossier for review. An international certification team appointed by WHO then conducts an in-country assessment. The International Commission for the Certification of Dracunculiasis Eradication (ICCDE)[7] reviews the findings and makes a recommendation to WHO for certification of elimination. Once all countries are certified GW-free, WHO will undertake an additional three years of global surveillance before declaring eradication.[8] WHO would recommend to the WHA that eradication according to the criteria of certification has been achieved in all countries. The same hurdles to eliminating transmission also create setbacks for certification. Insecurity, population movement, and limited access can undermine the surveillance systems required both for certification and for maintaining certified status.[9]

Thus far, WHO has certified 200 countries, areas, and territories, representing 188 Member States, as free of *D. medinensis* transmission. The remaining endemic countries are at different points in the certification process. Sudan remains in the pre-certification stage until security conditions allow for the surveillance and inspection needed for certification. Cameroon was certified as free of GW transmission in 2007; however, since 2019 it has reported an increasing number of dog infections and isolated human cases near the border with Chad. WHO is in the process of reclassifying Cameroon as GW-endemic.

GWEP Research Agenda

Multiple simple yet effective interventions designed to intervene at various points of the GW life cycle facilitated a 99.9% reduction in GWD from 1986 to 2010 and appeared to reaffirm prior understandings of the parasite's natural history. As a result, there was little perceived need for robust and rigorous research into the parasite's biology and development of therapeutic interventions or diagnostics to detect early *D. medinensis* infection. However, recent changes in the relative incidence of infection among non-human definitive host species signaled an important shift in the epidemiological profile of GWD and necessitated a re-evaluation of the need for a more robust and focused GWEP research agenda.

A GW research gap analysis was conducted in 2020 to identify evidence gaps and research opportunities, and to prioritize related research initiatives. The current state of knowledge of five thematic areas was compared to prominent unknowns and vulnerabilities to identify evidence gaps and research opportunities. Following a subsequent review in 2023, the five thematic areas were re-envisioned to better align with GW's multiple-host pathogen system and to formalize five GWEP research agenda work streams and two cross-cutting initiatives.[10] These work streams

[4] As of January 30, 2026, 10 human cases and 683 animal infections were reported in 2025. The Carter Center (January 30, 20226) Guinea Worm Disease Reaches All Time Low: Only 10 Human Cases Reported in 2025. https://www.cartercenter.org/news/guinea-worm-announcement/

[5] Kovalenko, A. (n.d.). Eradication of Guinea Worm Disease Case Statement. Retrieved from https://www.who.int/docs/default-source/ntds/dracunculiasis/center-who-gw-case-statement2020.pdf?sfvrsn=5c00d407_4

[6] Dowdle, W.R. and Hopkins, D.R., eds., 1998. The Eradication of Infectious Diseases. New York: John Wiley & Sons. Dowdle, W.R., 1998. The principles of disease elimination and eradication. Bulletin of the World Health Organization, 76(2): 38-41.

[7] Kovalenko, A. (n.d.). Eradication of Guinea Worm Disease Case Statement. Retrieved from https://www.who.int/docs/default-source/ntds/dracunculiasis/center-who-gw-case-statement2020.pdf?sfvrsn=5c00d407_4

[8] Kovalenko, A. (n.d.). Eradication of Guinea Worm Disease Case Statement. Retrieved from https://www.who.int/docs/default-source/ntds/dracunculiasis/center-who-gw-case-statement2020.pdf?sfvrsn=5c00d407_4

[9] Sankara, D. (2025, October 28). Role of geospatial mapping in eradicating Guinea worm [PowerPoint slides]. World Health Organization.

[10] Delea, M. G., Sack, A., Eneanya, O. A., Thiele, E., Roy, S. L., Sankara, D., Ijaz, K., Hopkins, D. R., & Weiss, A. J. (2024). Slaying the Serpent: A Research Agenda to Expand Intervention Development and Accelerate Guinea Worm Eradication Efforts. *The American Journal of Tropical Medicine and Hygiene, 111*(3_Suppl), 12-25. Retrieved Nov 25, 2025, from https://doi.org/10.4269/ajtmh.23-0889

include diagnostics, enhanced surveillance, disease ecology, population genomics, and therapeutics. The two cross-cutting initiatives include modeling and implementation research. Each work stream has a defined scope of work and is supported by a technical working group of subject matter experts. The expanded research agenda aims to generate additional tools and resources to support national GWEPs and accelerate eradication efforts.

Diagnostics

Strategic development and deployment of novel GW diagnostic tools could play a decisive role in achieving eradication and certification. At present, no molecular test is available that can detect prepatent *D. medinensis* infection in humans or animals prior to worm emergence, creating a fundamental limitation for national programs. The GWEP has established a coordinated diagnostics portfolio designed to address this critical gap that focuses on two needs: (1) detection of past or prepatent GW infection and (2) environmental surveillance (ES).

Diagnostic development efforts are guided by two GW target product profiles (TPPs), which define the minimum and ideal performance characteristics required for tools to be programmatically useful. One TPP addresses diagnostics for detecting prepatent GW infection in animal hosts, while the second defines requirements for tools capable of detecting GW analytes in water and other environmental matrices.[11] Together, these TPPs ensure that innovation remains aligned with eradication, certification, and field implementation.

GWEP's diagnostics portfolio integrates serologic, antigen, and nucleic-acid–based approaches, each tailored to collectively support three core use cases: disease surveillance, diagnosis of prepatent infection, and environmental surveillance.[12] Rather than relying on a single test, the portfolio is designed to generate a complementary suite of tools that can be deployed according to available laboratory infrastructure, technical capacity, and programmatic objectives in endemic settings.[13]

Clinical Diagnostics

In 2025, the GWEP deployed a mobile enzyme-linked immunosorbent assay (ELISA)[14] in Chad to longitudinally test 800 dogs across four groups: dogs with confirmed GWD (positive controls), negative controls from a non-endemic district, and presumed negative adult dogs and naïve negative puppies, both from endemic areas.[15] Over the six-month study, seropositivity was observed in all groups except the negative controls, a pattern consistent with exposures missed through surveillance based on detection of emergent GWs. Seropositivity among presumed negative adults and naïve puppies suggests the presence of unreported or transient infections, as well as low-level early exposure in young dogs (though ongoing research is being conducted to determine if any readings are false positives caused by infection with closely related pathogens). These findings provide the first serological evidence of natural GW infection in dogs and underscore the limitations of relying exclusively on clinical case detection.

The next phase of clinical diagnostic deployment, scheduled for late 2026, will implement a two-step testing algorithm, in which all serologically positive animals undergo reflex nucleic acid testing (NAT). NATs are molecular assays that detect parasite DNA during active infection only, allowing programs to distinguish between active infection and prior exposure. This distinction would become critical if a therapeutic becomes available, as treatment should target active—not historical—infections. This serves as a practical decision point for triaging animals and prioritizing interventions. NATs also serve as a means of validating the results of serological tests, which are cheaper and can help target where more expensive, confirmatory NAT testing is needed.

Research partners are developing highly specific NATs capable of detecting extremely low levels of parasite genetic material in clinical samples, including Nanopore sequencing, which offers a portable, real-time platform well-suited for field deployment. Through comparative genomics and in-silico filtering, investigators have generated a curated panel of candidate molecular targets. Pilot hybrid-capture experiments screened 51 probes, yielding nine high-stringency markers that are specific to *D. medinensis*. These enrichment techniques, paired with Nanopore-based workflows, are approaching the sensitivity and specificity thresholds required for a prepatent diagnostic as outlined in the corresponding TPP.[16] In parallel, these efforts are informing the development of simpler, scalable NATs that can be integrated into routine surveillance.

[11] Target product profile to detect Dracunculus medinensis presence in environmental samples. Geneva: World Health Organization; 2024. License: CC BY-NC-SA 3.0 IGO.

[12] Van Loben Sels, J., *Carter Center Diagnostics Investment Strategy, Results from ELISA Deployment Study*. Presentation delivered at the 40th ITFDE on October 28, 2025.

[13] Meredith, L., Fletcher, N., Purves, K., Vasylyeva, T., & Kovalenko, A. (2025). Nanoworms: Nanopore-Based Approach for Novel Operationalization of Worm Observation And Rapid Monitoring With Sequencing. *The Guinea Worm Eradication Program (GWEP)*. Briefing Book - 40th ITFDE Meeting.

[14] Hakimi, H., Weerarathne, P., Saleh, M. N., Rech, R. R., Ngandolo, R., Tchindebet, P. O., Verocai, G. G. (2024). Assessing the performance of TRX and DUF148 antigens for detection of prepatent 3 Guinea worm (Dracunculus medinensis) infection in dogs. Retrieved from https://www.who.int/docs/default-source/ntds/dracunculiasis/center-who-gw-case-statement2020.pdf?sfvrsn=5c00d407_4

[15] Van Loben Sels, J., *Carter Center Diagnostics Investment Strategy, Results from ELISA Deployment Study*. Presentation delivered at the 40th ITFDE on October 28, 2025.

[16] Target product profile to detect prepatent Dracunculus medinensis infections in animals. Geneva: World Health Organization; 2024. License: CC BY-NC-SA 3.0 IGO.

Environmental Surveillance

Environmental DNA (eDNA) approaches are being developed for ES of GW genetic material in water sources, copepods, and aquatic animals/aquatic animal waste.[17, 18] eDNA methods offer the potential to identify contaminated matrices even in the absence of reported human or animal cases.[19] As such, ES provides a complementary tool for identifying transmission risk and verifying the absence of ongoing transmission. ES efforts also include targeting copepod intermediate hosts, which can help identify water sources requiring Abate® treatment and serve as internal controls for sampling and molecular processing.

Ongoing work involves evaluating field sampling strategies and molecular assays, including sampling water, copepods, and aquatic animals for qPCR-based detection of D. medinensis to inform the development of practical, programmatically deployable ES tools that can strengthen eradication efforts in the final stages.[20] The first field test of ES sampling methodology and molecular assays, including sampling water, copepods, and aquatic animals for qPCR-based detection of D. medinensis, is slated for summer 2026.

Intermediate Host Intervention Research

Abate® is used to treat water sources to suppress copepod densities and interrupt GWD transmission. Challenges with the use of Abate® include accurate dosing, treatment frequency, environmental modifiers of effectiveness, and potential copepod resistance. A high-resolution, one-month survey of 21 waterbodies conducted in four villages in Chad in July 2025, with sampling every three days, found that Abate® produced an average ~65% reduction in copepod density lasting approximately 14 days under these circumstances. A minimum duration of 14 days is important programmatically given it takes approximately 14 days for L1s to mature into infectious L3s in copepods. This shorter duration of effect (<14 days vs >14 days) may explain why a previous longer-term study with a 14-day sampling interval conducted among a small number of water sources in Chad did not detect a measurable effect of Abate®.[21]

Across waterbodies, greater proportional reductions were observed where turbidity and baseline copepod densities were high. However, laboratory experiments suggest the opposite pattern, with reduced Abate-related mortality when clay was added to otherwise clear water. The different reactions across contrived water conditions demonstrate substantial variation in Abate® efficacy and impact among Chadian copepod isolates.[22] These findings, though generated from small studies conducted in a localized geography, or using a single isolate of Chadian copepods, respectively, still underscore the importance of combining field and laboratory studies to interpret Abate® performance and highlight the influence of sampling design on the ability to detect treatment effects. Additional investigation is required to understand the external validity of the results and potential temephos resistance among copepod genera; related studies are currently in the design phase.

Population Genomics

Population genomic analyses are being used to understand the dynamics of GW populations over time and geography, including inferring transmission patterns and historical population expansion and/or contraction. As of October 2025, the mitochondrial genomes of over 20,000 individual GW specimens have been sequenced, the majority of which are from Chadian dogs, allowing for a conservative estimate of unique female lineages and historical population size because the mitochondrion is inherited only from the mother.[23] Hypervariable nuclear microsatellite loci are also sequenced, allowing for the more precise identification of individuals and first-order relationships (i.e., sibship and parent-offspring), which can identify distinct transmission events within a given year (siblings) and between consecutive years (parent-offspring) and at smaller geographical scales (individual villages).[24]

[17] Zhou, N., *Environmental Assay Development.* Presentation delivered at the 40th ITFDE on October 28, 2025.

[18] Beck, N., Shirai, J., Zhou, N., & Meschke, J. S. (2025). Innovative Sampling and Molecular Detection Methods for Guinea Worm eDNA and Copepods in the Environment. *The Carter Center -The Guinea Worm Eradication Program (GWEP).* Briefing Book - 40th ITFDE Meeting.

[19] Smalley, H., Keskinocak, P., Swann, J., Hanna, C., & Weiss, A. (2024). Potential Impact of a Diagnostic Test for Detecting Prepatent Guinea Worm Infections in Dogs. *The American Journal of Tropical Medicine and Hygiene*, 110(5), 953-960. Retrieved Nov 25, 2025, from https://doi.org/10.4269/ajtmh.23-0534

[20] Beck, N., Shirai, J., Zhou, N., & Meschke, J. S. (2025). Innovative Sampling and Molecular Detection Methods for GW eDNA and Copepods in the Environment. *The Carter Center -The GW Eradication Program (GWEP).* Briefing Book - 40th ITFDE Meeting.

[21] Civitello, D., *Cyclopoid Copepod Population Dynamics in Chad and Abate Efficacy and Effectiveness Studies.* Presentation delivered at the 40th ITFDE on October 29, 2025.

[22] Civitello, D., *Cyclopoid Copepod Population Dynamics in Chad and Abate Efficacy and Effectiveness Studies.* Presentation delivered at the 40th ITFDE on October 29, 2025.

[23] Ribado, J. V., Li, N. J., Thiele, E., Lyons, H., Cotton, J. A., Weiss, A., Tchindebet Ouakou, P., Moundai, T., Zirimwabagabo, H., Guagliardo, S. A. J., Chabot-Couture, G., & Proctor, J. L. (2021). Linked Surveillance and Genetic Data Uncovers Programmatically Relevant Geographic Scale of Guinea Worm Transmission in Chad. PLoS neglected tropical diseases, 15(7), e0009609. https://doi.org/10.1371/journal.pntd.0009609

[24] Guagliardo, S.A.J., Thiele, E., Unterwegner, K., Nanguita, N.N., Dossou, L., Ouakou, P.T., Zirimwabagabo, H., Ruiz-Tiben, E., Hopkins, D.R., Roy, S.L., Cama, V., Bishop, H., Sapp, S., Yerian, S. & Weiss, A.J. (2022). Epidemiological and Molecular Investigations of a Point-Source Outbreak of Dracunculus medinensis Infecting Humans and Dogs in Chad: a Cross-Sectional Study. Lancet Microbe, 3(2), e105-e112. DOI: 10.1016/S2666-5247(21)00209-3

This work has yielded key insights into the risk of GW transmission between humans and animals. Namely, worms collected from human and non-human hosts are the same species from common parasite populations, with no current evidence of a host-parasite compatibility barrier.[25, 26] High probability first-order relationships between worms collected from human and non-human hosts have been documented (both sibling and parent-offspring pairs), suggesting that both humans and animals are at risk of infection from the same parasite lineages. These findings indicate that animals and humans can pose transmission risk to each other.

In all endemic countries, genomic data are consistent with infections being missed by the respective national GWEP surveillance systems.[27] The genetic data cannot specify where missed infections are sustained, but the number of genetic variants observed each year, and the general rarity of first-order relationships between worms, are consistent with numerous undetected and/or uncontained infections each year. Counts of unique genetic lineages and sibling cohorts have been used to provide a baseline estimate of the minimum number of uncontained infections required to produce the genetic variation observed from one year to the next, but investigators are pursuing more rigorous modeling to better estimate the scope.[28]

Angola provides a useful warning of how the GW population can expand and persist when given the opportunity provided by appropriate transmission environments and the absence of robust surveillance systems. In all countries reporting multiple GW infections, GWD is sustained by endemic transmission. Angola appears unique, as its GW population seems to be the product of a population expansion from a limited initial population (though there are insufficient genetic data to distinguish whether the initial infections were imported or originated from a small endemic refuge population). A single mitochondrial lineage dominates in Angola even as sample sizes have increased, while all other endemic countries have levels of genetic variation consistent with long-term endemic GW transmission of numerous distinct lineages.[29–32]

Animal Research

Guinea worm infections in non-human animals were known historically, but were thought to be misdiagnoses, infections among dead-end hosts, or too limited to sustain transmission once human cases were eliminated. However, after dog infections detected in Chad during 2012 were confirmed as *D. medinensis*,[33] and data from genomic surveillance and investigations revealed that human and non-human animal hosts share common parasite populations,[34] it became apparent that interrupting transmission in animals is necessary for eradication.[35] Animal research is key to this goal and focuses on addressing outstanding questions related to transmission dynamics and improving animal surveillance and welfare. There are three main areas of animal research—studies related to: 1) domesticated animals, 2) Olive baboons (*Papio anubis*), and 3) wild carnivores.

Domesticated animal research includes examinations of co-infections to inform diagnostic specificity and improve welfare, as well as ongoing use of surveillance data to address gaps and improve programmatic activities. A new study will investigate domesticated dog and cat movement, home range size, and water sources shared with humans and baboons.[36] The study will use global positioning system (GPS) collars and behavioral observations of these animals in Ethiopia to identify potential transmission hot spots and inform programmatic actions.

[25] Durrant, C., Thiele, E.A., Holroyd, N., Doyle, S.R., Sallé, G., Tracey, A., Sankaranarayanan, G., Lotkowska, M.E., Bennett, H.M., Huckvale, T., Abdellah, Z., Tchindebet, O., Wossen, M., Logora, M.S.Y., Coulibaly, C.O., Weiss, A., Schulte-Hostedde, A.I., Foster, J.M., Cleveland, C.A., Cotton, J.A. (2020). Population Genomic Evidence that Human and Animal Infections in Africa Come from the Same Populations of Dracunculus medinensis. PLoSNTDs, 14(11), e0008623. DOI: 10.1371/journal.pntd.0008623.

[26] Thiele, E. A., Eberhard, M. L., Cotton, J. A., Durrant, C., Berg, J., Hamm, K., & Ruiz-Tiben, E. (2018). Population Genetic Analysis of Chadian Guinea worms Reveals that Human and Non-Human Hosts Share Common Parasite Populations. PLoS neglected tropical diseases, 12(10), e0006747.

[27] Thiele, E.A., *Guinea Worm Population Genomics Project Update – 2025*. Presentation delivered at the 40th ITFDE on October 29, 2025.

[28] Delea, M. G., Sack, A., Eneanya, O. A., Thiele, E., Roy, S. L., Sankara, D., Ijaz, K., Hopkins, D. R., & Weiss, A. J. (2024). Slaying the Serpent: A Research Agenda to Expand Intervention Development and Accelerate Guinea Worm Eradication Efforts. *The American Journal of Tropical Medicine and Hygiene*, 111(3_Suppl), 12-25. Retrieved Nov 25, 2025, from https://doi.org/10.4269/ajtmh.23-0889

[29] Thiele, E.A., *Guinea Worm Population Genomics Project Update – 2025*. Presentation delivered at the 40th ITFDE on October 29, 2025.

[30] Ribado, J. V., Li, N. J., Thiele, E., Lyons, H., Cotton, J. A., Weiss, A., Proctor, J. L. (2021a). Linked surveillance and genetic data uncovers programmatically relevant geographic scale of Guinea worm transmission in Chad. PLOS Neglected Tropical Diseases, 15(7). doi:10.1371/journal.pntd.0009609.

[31] Durrant, C., Thiele, E.A., Holroyd, N., Doyle, S.R., Sallé, G., Tracey, A., Sankaranarayanan, G., Lotkowska, M.E., Bennett, H.M., Huckvale, T., Abdellah, Z., Tchindebet, O., Wossen, M., Logora, M.S.Y., Coulibaly, C.O., Weiss, A., Schulte-Hostedde, A.I., Foster, J.M., Cleveland, C.A. … Cotton, J.A. (2020). Population genomic evidence that human and animal infections in Africa come from the same populations of Dracunculus medinensis. *PLoSNTDs*, 14(11), e0008623. DOI: 10.1371/journal.pntd.0008623.

[32] Thiele, E. A., Eberhard, M. L., Cotton, J. A., Durrant, C., Berg, J., Hamm, K., & Ruiz-Tiben, E. (2018). Population Genetic Analysis of Chadian Guinea Worms Reveals that Human and Non-Human Hosts Share Common Parasite populations. PLoS neglected tropical diseases, 12(10), e0006747

[33] Eberhard M.L., Ruiz-Tiben E., Hopkins D.R., Farrell C., Toe F., Weiss A., Withers P.C., Jenks M.H., Thiele E.A., Cotton J.A., Hance Z., Holroyd N., Cama V.A., Tahir M.A., Mounda T. (Nov 2013) The peculiar epidemiology of dracunculiasis in Chad. Am J Trop Med Hyg. 2014 Jan;90(1):61-70. doi: 10.4269/ajtmh.13-0554.

[34] Thiele, E. A., Eberhard, M. L., Cotton, J. A., Durrant, C., Berg, J., Hamm, K., & Ruiz-Tiben, E. (2018). Population genetic analysis of Chadian Guinea worms reveals that human and non-human hosts share common parasite populations. *PLoS neglected tropical diseases, 12*(10), e0006747. https://doi.org/10.1371/journal.pntd.0006747.

[35] Sack, A., *Overview of Guinea Worm Animal Research*. Presentation delivered at the 40th ITFDE on October 29, 2025.

[36] Sack, A., *Overview of Guinea Worm Animal Research*. Presentation delivered at the 40th ITFDE on October 29, 2025.

The next two areas of research both address GW transmission among wild animal hosts. Olive baboons, genets[37] (*Genetta* sp.), and African wildcats (*Felis lybica*)/domesticated cat hybrids are the only wildlife species that have been detected with emerged GWs. Un-emerged worms have been collected from dead wild animals or removed surgically and may indicate dead-end hosts, as it remains unclear whether the worms would have emerged over time.

In 2013, Olive baboons became the first wild animal hosts detected with GWD. In response, a multi-institutional team was established in 2018 to conduct research in Ethiopia with the objective of clarifying disease transmission dynamics among affected Olive baboons. Since 2024, 15 troops have been under active surveillance in both GW-endemic woredas (Gog and Abobo) of Ethiopia, and community surveillance is ongoing in surrounding areas.[38] The aims of the baboon research are to: 1) generate continuous sentinel surveillance data from high-risk troops, 2) define home ranges and water source use through weekly tracking and placement of GPS collars, and 3) collect blood samples to support diagnostic tool development. Research also involves trapping baboons to examine them for signs of GWD and removing suspected *D. medinensis* worms to reduce possible ongoing transmission potential and obtain genomic sequencing to inform population genomics work across hosts.[39] The decision to include a troop in active surveillance is based on historic infections in baboons, domesticated animals, and humans. Troops under surveillance can change based on program needs as new information becomes available. Ongoing human and domesticated animal surveillance and community surveillance are ongoing in areas at risk for GWD due to human movement or historic infection and serve as a baseline to determine whether baboon surveillance is needed in these areas.

Recent reports of two genets (one per year during 2023 and 2024; both in South Sudan) with emerged worms prompted concerns about the role of small carnivores in GWD transmission. It is unknown whether small wild carnivores can maintain transmission in the absence of human or domesticated animal transmission, as both genets were reported adjacent to human habitation, and genets as a species can thrive in peri-urban areas. To answer these questions, a new project to trap and place GPS collars on small carnivores in South Sudan is under development.

Modeling

Modeling can support GWEP planning, programmatic decision-making, and strategies to reduce infections. The GWEP employs two complementary modeling approaches for these purposes—spatio-temporal modeling and empirical forecasting.[40] Spatio-temporal modeling is used to map and forecast GW transmission hot spots. Incidence data are combined with geospatial, climatic, and socio-demographic data to produce detailed risk maps that guide surveillance, reveal environmental correlates of transmission, and illustrate variations in the spatial epidemiology of GW over a 13-year period (2012–2025) in Chad.[41] Empirical forecasting is used to develop novel, seasonally informed transmission models simulating the parasite's lifecycle. These models can project eradication timelines, assess current interventions, and evaluate potential surveillance tools under different implementation scenarios.[42]

TCC and the Gates Foundation's Institute for Disease Modeling implemented a forecasting modeling approach to gain insights into possible time to GW elimination in Chad. This work suggests that, with the absence of novel intervention tools, elimination could still be achieved, but with a long tail out to ~2050. Taking this further, the DEACON suite of models[43, 44] captures seasonal and long-term dynamics of canine infection using 2014–2019 canine data and project outcomes for 2020–2030 across varying levels of tethering adherence and Abate® performance. Early results indicate that, based on plausible assumptions of rates of adherence to known interventions, elimination of canine infections in Chad is achievable before 2030.[45]

[37] Guinea Worm Wrap-Up #320 "South Sudan: The Way Forward" p.3-4. May 2025.

[38] Mulugeta, s. Y., Sack, A., Alemayehu, F., Amenu, M., Tesfaye, J., & Demissie, K. (2025). Guinea Worm Disease Surveillance amongst Olive Baboons in Gambella, Ethiopia. The Carter Center . doi: https://thecartercenter.sharepoint.com/:b:/s/3a1ccd99-eb0a-4613-aff0-602f987bacc3/EZJOXl_w0EdGs6qNN2FZd-ABAdS1vJpFxQN73QsQzI9R2w?e=k7jryY

[39] Demessie, A.K., *Baboon Research in Ethiopia*. Presentation delivered at the 40th ITFDE on October 29, 2025.

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A systems-level simulation incorporating a two-step diagnostic approach—screening followed by a reflex test—further evaluated how diagnostics, tethering, Abate®, and potential therapeutics interact.[46]

Results demonstrated that:

- reductions in dog infections are more strongly influenced by proactive tethering coverage, duration of test-positive tethering, and testing frequency than by diagnostic sensitivity or specificity;
- improvements in Abate® effectiveness, determined by the fidelity of the intervention and how well it achieved desired outcomes, produced the largest reductions over time; and
- incorporating potential therapeutics into the model suggested that effective treatment could reduce or eliminate the need for prolonged test-positive tethering.[47]

Together, these findings highlight the value of combining enhanced interventions, novel diagnostics, and therapeutic interventions with modeling tools to guide programmatic decisions in the final stages of the eradication endgame.

Conclusions and Recommendations

1. The ITFDE noted continued progress towards GW eradication, with certification of 17 countries as free of *D. medinensis* transmission, including most recently the Democratic Republic of the Congo in 2022. Sudan may also be GW-free, but civil war has prevented the ICCDE from making a required certification assessment visit. The ITFDE reaffirmed the goal of eradication while acknowledging programmatic challenges, including geopolitical issues such as security challenges that prevent certification, and the discovery of multiple non-human animal definitive hosts, which were not evident earlier in the eradication campaign. Based on these challenges, global and national GWEPs should first target zero human infections.
2. The ITFDE expressed concern about the large increase in reported animal GW infections in Cameroon after the infection was rediscovered in that country. It also noted the need for stronger national political support for GWEPs, especially in Cameroon and Angola, and the urgent requirement for security, both in the small remaining endemic area of Mali as well as in CAR, the latter of which has implications for potential cross-border importation.
3. The ITFDE applauds the substantial progress being made on GW disease ecology, enhanced surveillance, population genomics, therapeutics, diagnostics, modeling, and implementation of research under the auspices of the robust GWEP research agenda.
4. While pursuing research to further accelerate the pathway to eradication through the development of novel tools for diagnosis of prepatent infection, environmental surveillance, and potential therapeutic interventions, the ITFDE recommends that the GWEP continue prioritizing genomics surveillance and other implementation work to arrest *D. medinensis* transmission.
5. Epidemiological issues regarding *D. medinensis* in domesticated and wild animals must be addressed. This includes defining the role, magnitude, and geographic range of wild animal infections, and further enhancing wildlife surveillance, including the use of species agnostic diagnostics.
6. Novel diagnostics and modeling tools should be advanced and evaluated for their potential to strengthen surveillance, refine intervention timing, and support decision-making. Tools should be suitable for field deployment in resource-limited settings and capable of detecting infections in wild and domesticated animals, including prepatent infections.
7. Genomic surveillance data should be incorporated into national program decision-making, including analysis of transmission patterns, missed infections, lineage structure, and host associations. Collaboration between research groups and national programs will be essential to ensure genomic findings are interpreted and applied effectively to guide targeted interventions. The ICCDE can also use this information to consider if and how to incorporate genomic surveillance data into certification criteria.

Certification and post-certification frameworks should be updated to reflect the changing epidemiology of GWD, especially the emergence of animal infections. New classifications related to GW elimination, decertification, and re-certification may be required. The WHO and the ICCDE should review emerging research and assess new surveillance tools relevant to revised certification criteria and post-certification monitoring. This will enable remaining endemic countries to begin planning and collecting biological and environmental specimens for future testing with validated tools that will be required for certification. ■

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WHO web sites on infectious diseases

Adolescent health	https://www.who.int/health-topics/adolescent-health#tab=tab_1
Avian influenza	https://www.who.int/health-topics/influenza-avian-and-other-zoonotic#tab=tab_1
Buruli ulcer	https://www.who.int/health-topics/buruli-ulcer#tab=tab_1
Child health	https://www.who.int/health-topics/child-health#tab=tab_1
Cholera	https://www.who.int/health-topics/cholera#tab=tab_1
COVID-19	https://www.who.int/health-topics/coronavirus#tab=tab_1
Dengue	https://www.who.int/health-topics/dengue-and-severe-dengue#tab=tab_1
Ebola virus disease	https://www.who.int/health-topics/ebola#tab=tab_1
Emergencies	https://www.who.int/emergencies/situations
Emergencies dashboard	https://extranet.who.int/publicemergency
Foodborne diseases	https://www.who.int/health-topics/foodborne-diseases#tab=tab_1
Global Health Observatory (GHO) data	https://www.who.int/data/gho
Global Influenza Surveillance and Response System (GISRS)	https://www.who.int/initiatives/global-influenza-surveillance-and-response-system
Global Outbreak Alert and Response Network (GOARN)	https://extranet.who.int/goarn/
Health topics	https://www.who.int/health-topics/
Human African trypanosomiasis	https://www.who.int/health-topics/human-african-trypanosomiasis#tab=tab_1
Immunization, Vaccines and Biologicals	https://www.who.int/health-topics/vaccines-and-immunization#tab=tab_1
Influenza	https://www.who.int/health-topics/influenza-seasonal#tab=tab_1
International Health Regulations	https://www.who.int/health-topics/international-health-regulations#tab=tab_1
International travel and health	https://www.who.int/health-topics/travel-and-health#tab=tab_1
Leishmaniasis	https://www.who.int/health-topics/leishmaniasis#tab=tab_1
Leprosy	https://www.who.int/health-topics/leprosy#tab=tab_1
Lymphatic filariasis	https://www.who.int/health-topics/lymphatic-filariasis#tab=tab_1
Malaria	https://www.who.int/health-topics/malaria#tab=tab_1
Middle East respiratory syndrome coronavirus (MERS-CoV)	https://www.who.int/health-topics/middle-east-respiratory-syndrome-coronavirus-mers#tab=tab_1
Neglected tropical diseases	https://www.who.int/health-topics/neglected-tropical-diseases#tab=tab_1
Onchocerciasis	https://www.who.int/health-topics/onchocerciasis#tab=tab_1
OpenWHO	https://openwho.org/
Outbreak news	https://www.who.int/emergencies/disease-outbreak-news
Poliomyelitis	https://www.who.int/health-topics/poliomyelitis#tab=tab_1
Rabies	https://www.who.int/health-topics/rabies#tab=tab_1
Schistosomiasis	https://www.who.int/health-topics/schistosomiasis#tab=tab_1
Smallpox	https://www.who.int/health-topics/smallpox#tab=tab_1
Soil-transmitted helminthiases	https://www.who.int/health-topics/soil-transmitted-helminthiases#tab=tab_1
Trachoma	https://www.who.int/health-topics/trachoma#tab=tab_1
Tropical disease research	https://tdr.who.int/
Tuberculosis	https://www.who.int/health-topics/tuberculosis#tab=tab_1
Weekly Epidemiological Record	http://www.who.int/wer
WHO Lyon Office for National Epidemic Preparedness and Response	https://www.who.int/about/structure/lyon-office
Yellow fever	https://www.who.int/health-topics/yellow-fever#tab=tab_1
Zika virus disease	https://www.who.int/health-topics/zika-virus-disease#tab=tab_1