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Comparative Analysis of Risk Factors Associated with Guinea Worm Disease in Five Endemic Countries

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This is to certify that the doctoral dissertation by

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has been found to be complete and satisfactory in all respects,
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Walden University
2025

Abstract

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By

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MPH, University of Liverpool, 2011

BS Med Tech, Adventist University of the Philippines, 2009

Dissertation Submitted in Partial Fulfillment

of the Requirements for the Degree of

Doctor of Philosophy

PhD in Public Health, Major in Epidemiology

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Abstract

Guinea worm disease (GWD) has persisted in a small number of endemic countries despite decades of eradication efforts. Ongoing GWD transmission in these countries underscores the need to examine behavioral, environmental, and surveillance-related drivers. The purpose of this quantitative study was to assess associations among risk factors, including dog tethering, pond treatment with Abate, and community awareness, and GWD incidence. The study also examined the relationship between climate-related environmental factors and GWD case distribution, as well as the influence of awareness levels on GWD rumor reports. Guided by the PRECEDE–PROCEED framework, this retrospective secondary analysis used data from national eradication programs (2012–2023), with a total sample size of N = 784. Statistical methods included multiple linear regression, negative binomial regression, Pearson correlations, spatial analysis (bivariate Moran's I, LISA), and time-series forecasting. Dog tethering was significantly associated with increased reported Guinea worm disease (GWD) cases. This is likely due to responsive interventions in areas where transmission is high. However, environmental variables were not significant predictors of GWD case counts, but spatial clustering revealed geographic heterogeneity. Higher awareness was associated with fewer GWD rumors ($\beta = .459$, $p < .001$), suggesting that effective communication may reduce misinformation. Forecasts indicated that without intensified interventions, transmission may persist beyond 2030 in some countries. This study may promote positive social change by informing targeted interventions and improving surveillance.

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Dedication

I want to dedicate this to my parents for their unwavering love, encouragement, and sacrifices have been the foundation of my journey. Their belief in my potential has fueled my determination, and I am forever grateful for the values and strength they have instilled in me.

I also want to dedicate this to my husband for his constant support, understanding, and patience have been my anchor throughout this academic pursuit. His belief in my dreams and the sacrifices he made alongside me are immeasurable. This achievement is as much his as it is mine.

To my precious children, they are my inspiration and the driving force behind every late night and early morning spent on this dissertation. Their resilience and understanding during this challenging time have touched my heart. I dedicate this work to them, with the hope that it inspires them too to pursue their dreams fearlessly.

This dissertation is a testament to the love and support of my incredible family. Thank you for being my pillars of strength, my cheerleaders, and my motivation. I couldn't have done it without you.

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I am profoundly grateful to my parents, Erlinda Agua and Andres Agua Jr, whose love, encouragement, and sacrifices have been the driving force behind my academic pursuits. Their belief in me has been a constant source of inspiration, and I am thankful for the values they have instilled in me.

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Table of Contents

List of Tables

List of Figures

Chapter 1: Introduction to the Study

Introduction

Dracunculiasis is one of the neglected tropical diseases, the first parasitic disease targeted for eradication and the second disease to be eradicated after smallpox in 1979 (World Health Assembly [WHA], 1980). It was intended to be the second disease after rinderpest that affects animals that will be eradicated (Mariner et al., 2012). However, dracunculiasis has not yet been eradicated. Dracunculiasis, also known as guinea worm disease, is caused by *Dracunculus medinensis*, a large nematode, also known as the "fiery serpent" in the Old Testament (Groove, 1900). There is no medicine nor vaccine for dracunculiasis, unlike smallpox and rinderpest which were declared eradicated in 1979 and 2011 respectively (Biswas et al., 2013; Breman, 2021; FAO, OIE, 2022). In the 1940s estimated 48 million were affected while estimated 10 million in 1976, 3.5 million in 1986, and 13 in 2023 (Stoll, 1947; Watts, 1987; World Health Organization [WHO], 1982, 2023a). The disease was reported to be in Egypt, Democratic Republic of Congo, the Islamic Republic of Iran, India, Pakistan, Saudi Arabia, Benin, Burkina Faso, Ghana, Cote d'Ivoire, Cameroon, Central African Republic, Niger, Nigeria, Mauritania, Uganda, Kenya, Senegal, Togo, and Yemen, and is currently endemic in Angola, Chad, Ethiopia, Mali, Sudan and South Sudan (Biswas et al., 2013; WHO, 2022a).

The International Drinking Water Decade was launched in 1980s with the goal of providing improved access to safe water and provided opportunity to eliminate the disease (Brieger & Otusanya, 1997; WHA, 1980). A concerted effort by several stakeholders, including The Carter Center, UNICEF, the United States Centers for

Disease Control and Prevention (CDC), the World Health Organization (WHO), and Member States of the World Health Assembly (WHA), led to the passage of several resolutions and the establishment of strategies to eradicate dracunculiasis. Additionally, efforts were made to interrupt transmission. In 2019, WHO set a goal to eradicate dracunculiasis in both humans and animals by 2030 (WHA, 1989, 1991; WHO, 2021b). The eradication strategies included improving access to safe water supply, surveillance and early detection, case management and containment, health education and social mobilization, vector control and certifying countries free of dracunculiasis (WHA, 1991). It was believed that the disease could be eradicated, as the worm emerging from the skin could easily be recognized and the only known reservoir was human — until infections in animals were reported (Cairncross et al., 2002; Hopkins et al., 2021; Muller, 1982; Watts, 1987). This study described the current epidemiology of the disease in endemic countries and provided a comparative analysis of the risk factors associated with Guinea worm disease in four of five endemic countries.

Background

In 2017, the disease was only endemic in four countries—Chad, Ethiopia, Mali, and South Sudan—out of the 20 countries that were endemic in the 1980s. Additionally, one country that was recently endemic, Angola, had not reported cases since the early 1980s, and another country, Sudan, was in the precertification stage (WHO, 2023b). The World Health Organization certified 188/194 member states as free of dracunculiasis (WHO, 2023b). The Democratic Republic of Congo was the most recent country to be certified free of dracunculiasis in 2022 (WHO, 2023b, 2023c). Chad reported cases in

2010 after eight years of reporting zero-case reporting (WHO, n.d.). Ethiopia and Mali reported consistently low number of cases, while South Sudan continued to report sporadic cases. Angola never reported cases historically but detected its first human infection in 2018 and was officially declared endemic in 2020 (WHO, 2020a, 2020b, 2021). Muller (1982) and Caincross et al. (2002) argued that humans were the only definitive hosts of *Dracunculus medinensis.* In 2012, 27 dogs infected with *D. medinensis* were found and reported in Chad, and the number increased annualy and peaked in 2019 (WHO, 2015, 2020). Studies show that the *D. medinensis* in human is genetically indistinguishable from the *D. medinensis* in animal within the same geographical population of *D. medinensis,* which implies that the parasite was indigenous and maintained through local transmission involving human and animal hosts (Durrant et al., 2020; Thiele et al., 2018).

Despite of the progress in the reducing disease, a significant gap in understanding the behavioral, environmental, and programmatic determinants influencing the persistence of Guinea worm disease (GWD) transmission. Specifically, the relationships among dog tethering, water treatment, community awareness, climatic factors, and spatial patterns had not been fully examined in endemic settings.

This study was conducted to address this knowledge gap with multi-country retrospective surveillance data from 2012–2023 to analyze the associations between these variables and disease outcomes. The findings were intended to inform targeted, context-specific interventions towards global certification objectives.

Problem Statement

Although substantial progress was made, the total number of global cases has plateaued in the double digits since 2015, with transmission persisting in five endemic countries since 2018 (WHO, 2023b). This stagnation was concerning given the 2030 target set by the World Health Organization (WHO) to certify all countries as free of dracunculiasis, as outlined in the NTD Road Map 2021–2030 (WHO, 2021b). Dracunculiasis, a disease of poverty, continued to affect populations in remote and underserved areas where access to safe water sources, health education, and disease surveillance is limited (Cairncross et al., 2002; The World Bank, 2023a).

The relevance of the problem is underscored by the United Nations Sustainable Development Goals (SDGs), particularly SDG 3.3, which called for ending epidemics of NTDs, and SDG 6.1, which focused on achieving universal and equitable access to safe drinking water by 2030 (United Nations, 2015). Efforts to eliminate Guinea worm disease therefore, intersected with broader global health and development goals, emphasizing the importance of addressing health equity, strengthening surveillance systems, and promoting behavioral and environmental interventions in endemic areas.

Recent evidence revealed emerging challenges, including an increase in animal infections— particularly among dogs in Chad—and the reappearance of human cases in areas previously believed to be transmission-free (Durrant et al., 2020; Thiele et al., 2018). These developments complicated the eradication strategies, which were originally designed based on the assumption that *D. medinensis* exclusively infected humans.

Despite active surveillance and control programs, a meaningful gap remains in the research literature. Most existing studies are descriptive, single-country, or human-centric, lacking an integrated analysis across multiple endemic countries and host species. This study addresses that gap by using retrospective data from national eradication programs (2012–2023) to examine behavioral, environmental, and programmatic predictors of both human and animal Guinea worm infections. By identifying common risk factors across settings, the findings aim to inform more adaptive, data-driven eradication strategies and support continued progress toward global certification and sustainable health equity.

Purpose of the Study

This quantitative correlational study aimed to investigate the relationship between specific behavioral, environmental and programmatic factors and the incidence of guinea worm disease across five endemic countries. The identified independent risk factors encompass dog tethering practices, pond treatment with Abate, community knowledge about the disease, awareness of rewards for reporting, and village access to safe water sources. This analysis sought to clarify how these factors collectively influence the incidence of Guinea worm disease.

A primary objective of this research was to assess whether achieving zero global cases or infections of guinea worm disease by 2027 and subsequent certification by 2030 was feasible, given current behavioral, environmental, and surveillance trends. The dependent variable was the number of reported human and animal GWD cases, and

covariates such as country and month of emergence were considered to account for geographic and seasonal variation.

Furthermore, the study endeavored to explore the role of awareness—specifically focusing on the reward system and knowledge about the disease—in the reporting of rumors using the number of rumors as a secondary dependent variable. Understanding how these awareness factors influenced the dissemination of information about the disease can contributed to the refinement of reporting mechanisms and community engagement strategies.

By analyzing multi-year surveillance data (2012–2023), the study aimed to generate actionable evidence to guide effective interventions, improve rumor reporting systems, and contribute to Guinea worm disease eradication efforts. The study's findings aimed to inform policy decisions, enhance surveillance systems, and accelerate progress toward global certification.

Research Questions and Hypothesis

Research Question 1: Does the theory of change explain the association between the dog tethered, ponds treated with abate, and people's awareness about the disease and reward, village access to safe water sources, and guinea worm disease (in humans and animals)?

$H_0$1: The theory of change does not explain the association between the dog tethered, ponds treated with abate, and people's awareness about the disease and reward, village access to safe water sources, and guinea worm disease (in humans and animals)?

H_a1: The theory of change explain the association between the dog tethered, ponds treated with abate, and people's awareness about the disease and reward, village access to safe water sources, and guinea worm disease (in humans and animals)?

Research Question 2: What is the relationship between environmental factors (climate, temperature, water supply) and guinea worm cases or infection?

$H_0$2: There is no relationship between environmental factors and the number of guinea worm cases or infections.

H_a2: The environmental factors have a relationship with the number of guinea worm cases or infections.

Research Question 3: What is the relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about guinea worm disease/infection reported?

$H_0$3: There is no relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about Guinea worm disease/infection reported.

H_a3: There is a relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about Guinea worm disease/infection reported.

Theoretical and/or Conceptual Framework for the Study

Theoretical Framework

This study was grounded in the Theory of Change (ToC) framework, which integrated both causal theory—focusing on the determinants of outcomes—and action theory, which explained how interventions influenced those determinants and led to desired results (Gielen et al., 2008; Jones & Rosenberg, 2018). Program theory, often represented as a logic model, identified the pathways through which inputs (e.g., activities, resources) led to outputs and long-term outcomes. This approach provided a foundation for evaluating health programs such as the Guinea Worm Eradication Programme (GWEP), where cause-and-effect assumptions guided the assessment of interventions and their impact (Bickman, 1987).

A specific application of program theory used in this study was the PRECEDE–PROCEED model, which was an example of logic model, developed by Green and Kreuter (1999), offered a structured, phased approach for planning and evaluating public health programs. The PRECEDE and PROCEDE models, among other theoretical models, provided an appropriate framework for this research. The strategies implemented in affected communities were based on the on PRECEED-PROCEED Model (Green et al., 2022). Appropriate theoretical models were crucial for determining whether the expected outcome could be achieved based on determinants (inputs and activities). Health programs, such as the Guinea-Worm Eradication Programme (GWEP), involved a set of planned activities over a defined period to accomplish specific goals—in this case, eradication of dracunculiasis.

This study was grounded in the PRECEDE–PROCEED model, which included two interrelated frameworks: PRECEDE (Predisposing, Reinforcing, and Enabling Constructs in Educational Diagnosis and Evaluation), which guided the identification of behavioral and environmental factors influencing health outcomes, while PROCEED (Policy, Regulatory, and Organizational Constructs in Educational and Environmental Development) which focused on implementation and evaluation. (Green & Kreuter, 1999; Gielen et al., 2008).

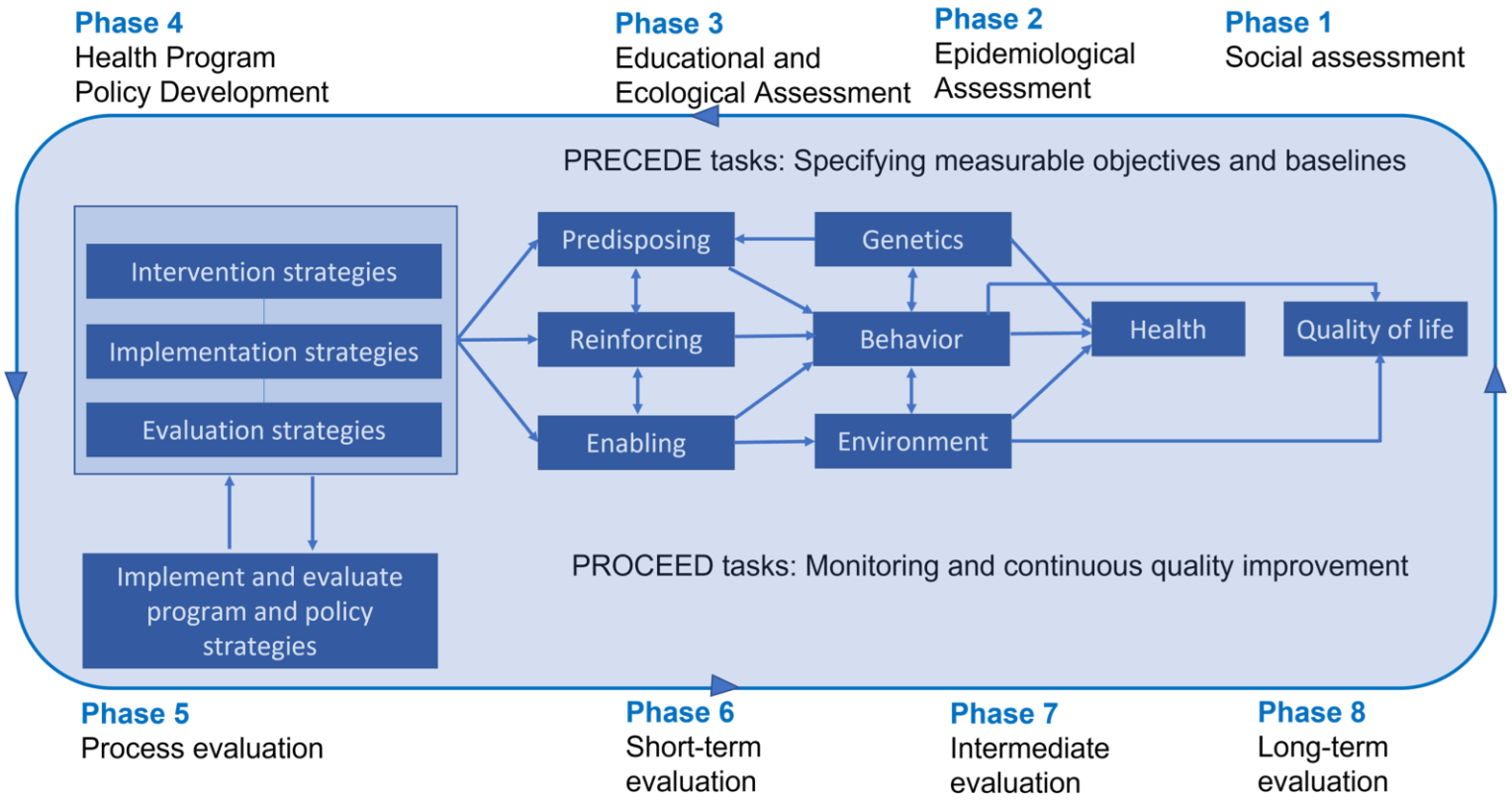
This model comprised of eight structured phases: 1. social assessment; 2 epidemiological, behavioral and environmental assessment, 3. educational and ecological assessment including predisposing factor, enabling and reinforcing factors; 4. administrative policy assessment; 5 implementations; 6. process evaluation; 7 outcome evaluations or intermediate evaluation; and 8 impact evaluations or long-term evaluation (Gielen et al., 2008). This study focused specifically on phase 2, 3, 7 and 8, which supported the identification of determinants and evaluation of program outcomes. The theoretical propositions underlying this framework posited that interventions targeting modifiable behavioral and environmental risk factors—when supported by enabling and reinforcing structures—could lead to measurable reductions in Guinea worm disease. These assumptions directly supported the study's research questions, which examined: (1) the association between community-level interventions (e.g., dog tethering, pond treatment, awareness) and Guinea worm cases, (2) the influence of environmental conditions (e.g., temperature, water access) on transmission, and (3) the relationship between awareness and rumor reporting. The social and epidemiological assessment on

relied on literature reviews and analysis of available secondary data on the number of human cases and Guinea worm infections.

These theoretical principles aligned with the conceptual framework presented below, which defined the key variables and their interrelationships.

Figure 1

Generic representation of PRECEED and PROCEDE model, adapted from "Health Promotion and Planning, Implementation and Evaluation. Creating Behavioral, Environmental and Policy" Change (Green et al., 2022)



Conceptual Framework

This study was grounded in the conceptualization of Guinea worm disease (GWD) persistence as a multifactorial phenomenon, shaped by a combination of behavioral, environmental, and programmatic determinants. The central concept underlying the study was that GWD transmission was influenced not only by biological and ecological conditions but also by community behaviors, health education, and the effectiveness of intervention strategies such as dog tethering, water source protection, and reward-based surveillance.

A growing body of research over the past decade highlighted the re-emergence of GWD in settings where environmental conditions supported transmission and behavioral practices (such as consumption of untreated water or untethered dog movement) contributed to ongoing infections (Boyce et al., 2020; Eberhard et al., 2014; Durrant et al., 2020). Studies also demonstrated the critical role of community awareness and incentive-based reporting systems in enhancing surveillance sensitivity and reducing rumor-related delays in detection (Hopkins et al., 2018). These findings supported the need for integrated approaches that examined how multiple risk factors interacted to influence outcomes—especially in the context of recent increases in animal infections and challenges to eradication goals.

The key concepts in this framework included:

- behavioral factors (e.g., dog containment, awareness about the disease and rewards),

- environmental factors (e.g., surface water occurrence, temperature, precipitation), and
- programmatic elements (e.g., water source protection, Abate® pond treatment, surveillance systems).

The logical connection among these elements was that programmatic interventions aimed to modify behavioral and environmental conditions, which in turn influenced transmission outcomes (cases, infections, or rumors). These relationships formed the basis for the study's hypotheses and informed the selection of variables and analytical methods.

This framework aligned with the study's approach by guiding the investigation of associations between defined risk factors (independent variables) and GWD outcomes (dependent variables), both quantitatively and spatially. It also informed the development of operational definitions for variables used in secondary data analysis and supported the interpretation of findings in light of eradication program strategies. This framework complemented the PRECEDE–PROCEED model that grounds the overall program logic and intervention design. A more detailed exploration of the conceptual and empirical literature supporting this framework was presented in Chapter 2.

Nature of the Study

This study adopted a quantitative, exploratory, and descriptive design using a retrospective cohort approach. It utilized secondary epidemiological data collected from the national Guinea worm eradication programs between 2012 and 2023. A retrospective design was appropriate because it allowed analysis of an existing cohort of affected

populations over time to evaluate associations between exposures (risk factors) and outcomes (Bruce et al., 2008) This approach supported the investigation of temporal patterns and associations using already reported surveillance data.

The independent variables included dog tethering practices (binary), pond treatment with Abate® (percentage), awareness of the disease and reward (percentage), and access to safe water (percentage). Environmental variables, such as precipitation, temperature, and surface water occurrence, were also treated as independent predictors. The dependent variables were the number of reported Guinea worm disease cases (human and animal combined) and the number of reported rumors. Covariates included the country and month of emergence, both of which may have influenced disease outcomes due to seasonal and geographic variability.

The study applied descriptive, inferential, and spatial statistical techniques. Descriptive analysis summarized key indicators. Negative binomial regression was used to test associations between independent variables and disease outcomes. Spatial analyses—including Global Moran's I and LISA (Local Indicators of Spatial Association)—were conducted to explore clustering and geographic heterogeneity. Forecasting techniques were also used to model future case trends. These analyses collectively addressed the study's three research questions and tested the hypotheses derived from the theoretical and conceptual frameworks. A detailed methodology, including data sources, variable coding, and analysis procedures, was provided in Chapter 3.

Definitions of Key Terms and Study Variables

The following terms were defined based on authoritative sources, primarily the World Health Organization (WHO), the WHO Collaborating Center for Dracunculiasis Eradication, and relevant eradication program partners (World Health Organization [WHO], 2015b). These definitions were operationalized for the purposes of this study, with coding and analytic treatment described further in Chapter 3.

Independent Variables

*Dog tethering reported (binary):*Indicates whether dog tethering was reported in the village. Tethering refers to the practice of physically restraining dogs to prevent water source contamination by infected animals (Eberhard et al., 2014). Coded as 1 = Yes; 0 = No.

*Awareness about reward for reporting (Level 1–3):*The percentage of individuals aware of the cash reward offered for reporting human or animal Guinea worm infections, stratified by endemicity level (WHO, 2025b).

Village-level monthly mean temperature: The average surface air temperature (°C) recorded monthly at the village level, extracted from historical gridded climate datasets (e.g., CRU TS4.08).

Village-level monthly total precipitation: The total amount of rainfall (mm) recorded monthly at the village level, obtained from gridded precipitation datasets (e.g., CRU TS4.08).

Mean surface water occurrence within 10-meter buffer: The average proportion of months (1984–2020) in which surface water was present within a 10-meter radius of the village, based on satellite-derived water occurrence data (Pekel et al., 2016)

Dependent Variable

Dracunculiasis case: A case of guinea-worm disease is a person exhibiting a skin lesion with emergence of a Guinea worm, and in which the worm is confirmed in laboratory as *D. medinensis*. That person is counted as a case only once during the calendar year, i.e. when the first worm emerges from that person. Infection refers to animal exhibiting worm emergence from the skin (WHO, 2016; WHO Collaborating Center for Dracunculiasis Eradication, 2023) .

Dracunculiasis infection (animal): An infection of guinea worm is an animal exhibiting a skin lesion with emergence of a Guinea worm, in which the worm is confirmed in the laboratory as *D. medinensis* and counted only once per calendar year.

Total number of cases. The combined count of confirmed human and animal infections per year.

Rumor of Guinea worm disease: Any information about an alleged case or infection of Guinea worm disease or (dracunculiasis) obtained from any source (WHO, 2023d).

Covariates

Month of emergence (seasonality): The calendar month (1–12) in which the first sign of worm emergence was reported for a human or animal case. Used to model potential seasonal transmission patterns.

Country: The national program from which data were reported, representing one of the six endemic or formerly endemic countries included in the study.

Other Key Terms

Global eradication: The confirmed absence of absence of manifestation of dracunculiasis in man and animal worldwide.

Local eradication: The confirmed absence of absence of manifestation of dracunculiasis in man and animal in geographical unit (e.g. country).

Endemic for dracunculiasis: Presence of indigenous transmission of dracunculiasis.

Formerly endemic for dracunculiasis: Countries that had indigenous transmission but have reported zero cases for at least 3 consecutive years.

Recently freed for dracunculiasis: Countries or areas that have been recently free from dracunculiasis for at least one year.

At risk village: A village bordering an endemic villages or sharing water sources with one.

Containment of case: The process of completely stopping dracunculiasis transmission from an infected person. A contained case is detected guinea-worm disease before or within 24 hours of worm emergence, and the village volunteer manages the case by cleaning and bandaging the affected skin until the worm is removed, and providing health education to discourage contamination of water sources; and verified and validated by a supervisor within 7 days; and ABATE used to treat potential

contaminated water sources (WHO Collaborating Center for Dracunculiasis Eradication, 2023).

Vector control: Application of Abate or larvicide within 7 days of emergence of worm in the potential sources of water contaminated by the patient (CDC, Global 2000, UNICEF, & WHO, n.d.).

Villages under active surveillance: Villages with endemic dracunculiasis or those at high risk of importation are those that are actively being monitored. Active surveillance involves daily home inspections by village volunteers, supported by supervisors, looking for people or animals displaying signs of dracunculiasis (Hopkins et al., 2021).

Imported case: A human or animal infection acquired outside the village or location where it was detected, often linked to contaminated water sources or travel. This typically occurs as a result of ingesting contaminated water, traveling, or coming into contact with a paratenic host (Hopkins et al., 2021).

Limitations of the Study

Limitations Related to Study Design and Methodological Weaknesses

This study was subject to several limitations related to its retrospective and observational design, secondary data use, and reliance on externally sourced datasets—all of which may have influenced internal and external validity. Specifically, these limitations may have reduced internal validity through selection and measurement bias and limited external validity due to reduced generalizability.

First, the retrospective and observational nature of the study limited control over the original data collection process. All data were obtained from external sources, such as national ministries of health and surveillance systems, which varied in completeness, consistency, and standardization. The heterogeneity of these data sources—including incomplete monthly climate records, inconsistent case reporting, and differing indicator definitions—could have reduced analytical power and limited comparability of results across time and countries (Baldwin et al., 2022; Sürücü & Maslakci, 2020).

Second, key variables related to programmatic activities, awareness levels, and environmental exposures were often aggregated at national or annual levels. Such aggregation may have obscured local heterogeneity and led to ecological fallacies, thereby limiting the detection of associations at the village level (Karki et al., 2021).

Third, because this was a secondary data analysis, the study relied on pre-existing datasets with predefined variables and quality control protocols that were not originally tailored to the research questions. This compromised construct validity by weakening the alignment between theoretical constructs and measured indicators. For example, inconsistent definitions of awareness or case detection across countries and years may have hindered uniform measurement of these constructs (Sürücü & Maslakci, 2020).

Fourth, the study could not control for multiple unmeasured confounding variables—such as socioeconomic status, cultural practices, mobility, and healthcare access—that may have influenced both exposures and outcomes. The inability to adjust for such confounders compromised internal validity by introducing alternative explanations for the findings and reduced external validity across diverse contexts.

Fifth, the environmental variables were generated from gridded remote sensing data using a 10-meter buffer around villages. Although this allowed for spatially detailed analysis, it introduced potential spatial mismatches and exposure misclassification due to challenges like the modifiable areal unit problem (MAUP) and microscale variability (Guagliardo et al., 2020).

Sixth, due to the non-experimental nature of the study, causal inferences could not be drawn. Observed associations (e.g., between dog tethering and case counts) may have reflected reverse causation or programmatic responsiveness rather than causal mechanisms.

Seventh, the PRECEDE–PROCEED model, while used to frame the analysis, may have had limited utility in capturing complex ecological or sociopolitical drivers of Guinea worm transmission (Gielen et al., 2008).

Finally, generalizability was limited to the five African countries included in the sample. Results could not be extrapolated to other contexts with different socio political, environment, or epidemiological profiles (Creswell, 2009; Jones et al., 2020).

Furthermore, unmeasured or context-specific interactions may have affected the interpretation of relationships between Abate use, awareness, and disease outcomes. Several forms of bias could have influenced study findings.

Biases That Could Influence Study Outcomes

First, selection bias may have resulted from incomplete or inconsistent reporting of cases or rumors in retrospective surveillance data, potentially distorting case distributions (Creswell, 2009; Jones et al., 2020).

Second, awareness and knowledge data were self-reported, introducing potential recall bias, social desirability bias, and framing effects. Although responses were stratified by endemicity levels to reduce misclassification, within-group variability may have been obscured, further compounding ecological bias.

Third, the use of rumor reporting as a proxy indicator for community engagement and surveillance sensitivity was limited. The study could not verify whether rumors corresponded to confirmed cases, which constrained the interpretability of this variable as an outcome measure.

Fourth, some datasets—such as monthly climate data—were incomplete across the full study period and were either imputed or case-wise excluded, which may have affected model robustness and statistical power, particularly for village-level or time-series regressions.

Measures to Address Limitations

Despite these limitations, several strategies were employed to enhance analytical rigor. The study applied a triangulated integration of spatial, behavioral, environmental, and programmatic data—an approach aligned with integrated public health surveillance strategies (Clark et al., 2025; Moraga & Alahmadi, 2025; Tula et al., 2024). This multi-source design reduced dependency on any single dataset and mitigated construct validity threats by enabling cross-validation. For example, the use of remote sensing facilitated standardized measurement of environmental exposures across countries and time, addressing data heterogeneity (Teitelbaum et al., 2024). Similarly, stratification of awareness data by endemicity helped contextualize participant responses and partially

offset self-report bias. The analytical framework emphasized methodological transparency, allowing for reproducibility and clarity in how limitations were addressed. Although some limitations—especially unmeasured confounding and limited construct validity—remained, the study's integrative approach and transparency supported internal validity and analytical robustness.

Although observational studies involving mixed data sources face persistent challenges—including data quality limitations, confounding, and constraints on causal inference—carefully chosen analytic strategies can mitigate these limitations and yielded credible, context-sensitive findings. Triangulation, particularly across quantitative and qualitative data, was widely recognized for its ability to strengthen internal validity and deepen interpretive insights (Creswell, 2009, 2014, 2018). While not constituting a mixed-methods design, the strategic integration of diverse data types aligns with principles of methodological triangulation, as formalized in phased analytic procedures. In epidemiological research, triangulation across statistical and design-based methods—such as those proposed by Hammerton and Munafò (2021) and Treur et al. (2024)—serves to reduce bias and reinforce causal interpretations. Transparency was further promoted through explicit reporting frameworks and visualization tools such as joint displays, which supported systematic integration and are endorsed by Creswell (2014), Guetterman et al. (2015) and Johnson et al. (2019). Moreover, domain-specific literature highlighted the value of stratified analytic approaches, including principal stratification, which enhanced the reliability and contextual relevance of observational findings.

Collectively, these strategies underscored the methodological rigor achievable through thoughtful data integration and transparency.

Assumptions

This study was guided by a set of underlying assumptions that, while not empirically tested within the scope of the research, were necessary to provide context and ensure meaningful interpretation of the results. These assumptions are grounded in general public health principles, prior programmatic knowledge, and the realities of retrospective analysis in endemic settings.

In any research based on retrospective, multi-country surveillance data, several assumptions were necessary to support the validity and interpretability of the findings. In this study, the assumptions outlined below were essential for enabling spatial comparisons, interpreting intervention effects, and modeling relationships between environmental, programmatic, and behavioral variables and Guinea worm disease occurrence. Without these assumptions, the ability to draw meaningful conclusions from secondary data sources and program records would have been substantially limited.

Accuracy of Historical Surveillance Data.

It was assumed that the epidemiological data provided by the Ministries of Health in Chad, Ethiopia, Mali, South Sudan, and Angola accurately reflected the true burden and distribution of Guinea worm disease during the study period. The validity of the spatial and statistical analyses depended on the reliability and consistency of these routine surveillance datasets. This assumption aligned with the practice of using national

program data for retrospective epidemiologic analyses, as seen in prior work on Guinea worm surveillance (Hopkins et al., 2022).

Consistency of Transmission Pathways

The study assumed that the biological transmission cycle of *Dracunculus medinensis* was largely consistent across the five study countries. While localized differences in intermediate hosts or animal reservoirs (e.g., domestic dogs) may have existed, the core mechanism of waterborne transmission remained stable. This assumption enabled cross-country comparisons of environmental and behavioral risk factors. Previous research described unique but fundamentally related transmission patterns in Chad (Eberhard et al., 2014; Thiele et al., 2018), reinforcing the importance of considering both consistency and localized nuances.

Stability of Environmental and Climatic Conditions.

It was assumed that major climate anomalies or sudden environmental disruptions (e.g., flooding, drought, or land-use change) did not occur in a way that would disproportionately affect transmission dynamics in certain regions during the study period. Although seasonal and interannual variability was modeled, no large-scale ecological shocks were accounted for. This assumption was consistent with past approaches to climate–disease modeling in endemic settings (Molyneux et al., 2017; WHO, 2023a)

Equitable Health Service Delivery

The study assumed that Guinea worm program activities—such as community surveillance, case detection, health education, and vector control—were implemented

with relative equity within districts. This was necessary to ensure that observed differences in disease outcomes could be attributed to environmental and behavioral factors, rather than uneven service delivery. Similar assumptions have been made in program evaluation contexts where intervention coverage was expected to be uniform within implementation units (Cairncross et al., 2002; WHO, 2021a)

Cultural and Behavioral Continuity

It was also assumed that cultural beliefs, health-seeking behaviors, and community awareness about Guinea worm disease remained relatively stable during the study period. This assumption was especially important in analyzing data related to awareness campaigns, rumor surveillance, and uptake of preventive behaviors. While such behaviors can evolve over time, previous studies showed that shifts were often gradual unless catalyzed by major events (Hotez, 2020).

Consistency in Intervention Implementation

The study assumed that key control interventions—such as dog tethering and the application of Abate® to water sources—were implemented consistently during the study period and followed standard program guidelines. This assumption supported the analysis of intervention impact on disease incidence. Prior studies of program monitoring in Chad reported variation in implementation intensity but overall consistency in protocol (Guagliardo et al., 2020)

Socioeconomic and Political Stability

Finally, it was assumed that no major socioeconomic or political disruptions (e.g., conflict, mass displacement, or economic collapse) occurred that would significantly alter

access to water, healthcare, or disease surveillance systems. This assumption was common in studies that aimed to isolate environmental or programmatic determinants of disease (Biswas et al., 2013; WHO/UNICEF, 2022).

Scope and Study Delimitations

This study was designed with practical and conceptual boundaries that shaped its scope, focus, and applicability. These delimitations were necessary to maintain methodological clarity, ensure data quality, and align with the research objectives focused on Guinea worm disease transmission in endemic African countries.

Temporal and Analytical Scope

The study was restricted to the period from 2012 through 2023, based on the availability of surveillance and environmental data submitted by the Ministries of Health in Chad, Ethiopia, Mali, South Sudan, and Angola. This timeframe allowed for a comprehensive analysis of temporal trends and environmental influences on disease incidence. However, data beyond 2023 were not included, limiting the study's ability to assess recent or emerging changes in transmission dynamics. This restriction presented may have affected internal validity, as findings could not account for programmatic or ecological changes that occurred after the study period.

Focus of the Research Problem

The analysis concentrated on village-level variables that were theoretically and empirically linked to Guinea worm transmission, including dog tethering, pond treatment with Abate® insecticide, community awareness about the disease and rewards, access to safe water, and environmental conditions (temperature, precipitation, and surface water

occurrence). These variables were chosen based on their relevance to known risk factors and their availability in the dataset. However, individual- and household-level influences such as cultural beliefs, health-seeking behavior, and socioeconomic status were not included due to data limitations. As a result, this narrower analytic lens may have limited the internal comprehensiveness of the study.

Population Inclusion and Exclusion

The study included only villages from the five endemic countries where complete epidemiological and environmental data were available. Villages lacking sufficient surveillance or environmental data were excluded from analysis, which could have introduced selection bias. This exclusion could have limited external validity, as findings may not fully represent villages with limited data infrastructure or underreporting — settings where Guinea worm disease may have persisted unnoticed.

Conceptual Framework Boundaries

The study was guided by the PRECEDE–PROCEED model, which provided a structured framework for understanding health behaviors and the implementation of public health interventions. While alternative frameworks such as the Health Belief Model or the Social Ecological Model could have added depth to behavioral analysis, they were not incorporated in order to maintain analytic focus and consistency with the primary study objective (Green et al., 2022).

Programmatic and Stakeholder Exclusions

Although the Guinea worm eradication effort was strongly supported by The Carter Center, the World Health Organization, and the Bill & Melinda Gates Foundation,

the study did not evaluate the financial, operational, or strategic contributions of these stakeholders. The decision to exclude these programmatic dimensions was made to maintain focus on epidemiological and environmental determinants of disease transmission. Although, acknowledging these partners was essential, their activities were outside the analytic scope of this investigation.

Generalizability of Findings

Due to the use of secondary data, the exclusion of underreported areas, and the focus on village-level rather than household-level predictors, the generalizability of findings was limited. Results may be most applicable to similarly endemic, data-rich settings and may not fully translate to regions experiencing conflict, population displacement, or gaps in surveillance systems. Nonetheless, the study offered valuable insights that could inform targeted surveillance and intervention strategies in comparable settings.

Significance of Study

This study had the potential to make meaningful contributions to knowledge, practice, policy, and positive social change in the domains of epidemiology, public health, and global disease eradication by 2030 (WHO, 2021a).

Advancement of Knowledge in the Discipline

This research advanced the theoretical and empirical understanding of GWD by providing an integrated analysis of behavioral, environmental, spatial, and programmatic data. In doing so, it contributed to the epidemiological literature on disease surveillance and eradication strategies in the context of neglected tropical diseases (NTDs). The use of

a structured framework (e.g., the PRECEDE–PROCEED model) also contributed to theoretical discourse by illustrating its application in ecological and cross-sectoral analyses (Gielen et al., 2008).

Additionally, by employing geospatial analysis and remote sensing data, this study highlighted innovative methods for identifying environmental determinants of GWD and targeting high-risk areas—thus broadening methodological approaches within spatial epidemiology (Boyce et al., 2020).

Contribution to Practice and Policy

The study provided actionable evidence to inform national programs, WHO, and international partners engaged in the eradication of GWD. By identifying key risk factors and contextual limitations, the findings supported more targeted interventions, improved resource allocation, and refined surveillance strategies (Aldrich et al., 2015; Vaivada et al., 2022). It also helped address critical operational gaps by highlighting the strengths and weaknesses of current data systems and programmatic approaches (Jansen et al., 2010; Vaivada et al., 2022).

Furthermore, comparative analyses across multiple endemic countries generated insights that may have informed cross-border strategies and supported harmonized eradication policies suited to varying sociopolitical and ecological contexts (Drobnič, 2014).

Implications for Positive Social Change

This research held promise for fostering positive social change by addressing upstream determinants of health, such as access to safe drinking water and public health

education. Through its analysis of community-level vulnerabilities and awareness, the study supported the development of locally responsive and culturally sensitive health interventions that enhanced community well-being and resilience (Dhar et al., 2022; Ede et al., 2014; Pellegrino et al., 2022; Simeon et al., 2020).

Moreover, the findings aligned with global health and development frameworks—particularly Sustainable Development Goal (SDG) 3.3, which targeted the end of epidemics of neglected tropical diseases, and SDG 6.1, which aimed to ensure universal access to safe and affordable drinking water (United Nations, 2015). By contributing evidence toward these goals, the study reinforced the interconnectedness of disease control, social equity, and development.

In summary, this study offered a multifaceted contribution—advancing epidemiological knowledge, informing practice and policy, and promoting social justice. Its integrative, cross-disciplinary approach addressed critical gaps in GWD eradication and aligned with broader efforts to improve health outcomes and equity in underserved populations.

Summary

This chapter introduced the study's focus on identifying behavioral and environmental risk factors associated with dracunculiasis (Guinea worm disease) in five endemic countries—Chad, Ethiopia, Mali, South Sudan, and Angola. It emphasized the ongoing challenges to eradication and the need for innovative, evidence-based strategies to meet the 2030 target. The research problem and rationale were clearly articulated,

highlighting the study’s potential contributions to public health knowledge, policy, and positive social change in affected communities.

The chapter also presented the study's theoretical framework, the PRECEDE–PROCEED model, as a basis for exploring how programmatic, behavioral, and ecological factors influenced transmission. Key assumptions, limitations, and delimitations of the study were discussed to provide transparency and contextualize the findings.

Chapter 2 provides a comprehensive literature review, examining the pathophysiology and epidemiology of dracunculiasis, its associated risk factors, and environmental determinants. The chapter outlines the search strategy used and identifies key gaps in the literature that this study aimed to address.

Chapter 2: Literature Review

Introduction

Dracunculiasis (Guinea worm disease) remained a persistent public health challenge, particularly in marginalized and rural communities lacking access to safe drinking water. Despite decades of eradication efforts, residual transmission continued, posing a barrier to achieving global eradication. The purpose of this study was to identify predictors associated with the reduction of human and animal Guinea worm infections to support strategic interventions in endemic and at-risk regions.

The health and socioeconomic consequences of dracunculiasis were well-documented. Affected individuals often suffered from severe pain, temporary disability lasting several weeks, and long-term complications, such as joint damage and secondary infections. The adverse effects of dracunculiasis had been documented such as absentees of school-aged children, loss of income due to a disability, and excruciating pain caused by this disease (Cairncross et al., 2002; Smith et al., 1989; World Health Organization [WHO], 2025). Historically known as “the disease of the empty granary,” the infection peaked during harvest seasons and had a disproportionate impact on rural agricultural populations . It primarily affected the marginalized population, most vulnerable, remote and poor population as it was also called the disease of empty granary and had limited or no access to at least basic safe water sources (Brieger & Otusanya, 1997; Cobbina et al., 2010; Gyapong & Boakye, 2016; Henderson & Feeney, 1988; Ruiz-Tiben & Hopkins, 2006; WHO, 1995).

Risk factors associated with dracunculiasis may have changed with the shifts in the epidemiology of the disease. The current literature highlighted substantial progress in reducing human cases from millions in the 1980s to just 14 in 2023, yet underscored a troubling rise in animal infections, particularly in domestic dogs in Chad (Centers for Disease Control and Prevention, 2024; WHO, 2024). These emerging patterns suggested a shift in transmission dynamics and emphasized the need for an updated analysis of behavioral and environmental risk factors. Studies increasingly pointed to animal reservoirs and persistent water source contamination as critical challenges to final eradication (Wang, 2002)

Aligned with the WHO NTD Roadmap 2021–2030 (Burki, 2022) this study compared risk factors across Chad, Ethiopia, Mali, South Sudan, and Angola to identify predictors of residual transmission. Wang et al. (2023) found that combining near-universal dog tethering with pond treatment using Abate® could have eliminated animal transmission within five years. This research supported the inclusion of these interventions, alongside environmental factors such as precipitation and surface water proximity, in the study's analytical framework.

The dependent variable was the number of reported Guinea worm cases and infections in both humans and animals. Independent variables included behavioral, programmatic, and environmental factors, allowing for a comprehensive analysis to guide national eradication programs.

This chapter presented the literature review and was organized into the following sections: (a) search strategy, (b) lifecycle and pathophysiology of *Dracunculus*

medinensis, (c) global epidemiology and implications of the disease, (d) current interventions, including successes and challenges, (e) an overview of biological, environmental, and socioeconomic risk factors, and (f) the theoretical foundation for the study, grounded in the PRECEDE–PROCEED model.

This study compared the epidemiology of the disease in the remaining endemic countries and risk factors associated with dracunculiasis at this stage of the dracunculiasis eradication. The NTD roadmap 2021-2030 set new target to certify all countries by 2030, and countries committed to it (Burki, 2022). This study examined predictors of reducing the number of cases of guinea worm disease and animal guinea worm infection to zero. The dependent variable was the number of Guinea worm disease cases/infections and the independent variables included risk factors such as the proportion of dog tethered, proportion of treated ponds, access to safe water sources and environmental factors such as climate, temperature, and water sources. This information was expected to help policymakers determine what intervention were needed to achieve the dracunculiasis elimination by 2030.

In this chapter, search strategy and relevant literature on dracunculiasis and its various risk factors and determinants were presented. Key areas reviewed included the review of lifecycle of dracunculiasis, global epidemiology of the dracunculiasis, impact of dracunculiasis to the community, intervention strategies, and their successes and limitations. The risk factors included the biological, environmental, and socioeconomic determinants. Finally, the chapter described the PRECEDE–PROCEED theoretical model as the foundational model chosen for the study.

Literature Search Strategy

The literature search strategy was carried out using the following databases and search engine MEDLINE, EMBASE, CINAHL, PUBMED, the Cochrane Library, Thoreau, PMC, WHO Publications and CDC. The search was also conducted using Walden University Library. The review covered literature published between 1980 and 2024, including both seminal sources and recent peer-reviewed studies. Seminal literature published prior to 2010 was included to capture foundational knowledge on the lifecycle of *Dracunculus medinensis*, historical eradication strategies, and early epidemiological patterns, particularly those relevant to the initial global response.

The search keywords used were *dracunculiasis OR "guinea-worm disease" OR "guinea worm disease", dracunculiasis risk factor, dracunculiasis eradication, lifecycle of dracunculiasis, dracunculiasis in animal, epidemiology of* (Perini et al., 2020) *dracunculiasis and environment, dracunculiasis and Rumor reporting, dracunculiasis and prediction.* Approximately 878 peer-reviewed journals articles were found using the key word "*dracunculiasis"* was used, 271 when "*dracunculiasis eradication"* were used. 71 when "*dracunculiasis* and *water source"*, 10 using *"dracunculiasis eradication* and *water"*, 4 using the keywords "*impact on dracunculiasis* and *water",* 2 articles were found upon using the key word "*dracunculiasis* and *dog tethering,"* 11 articles with "*dracunculiasis* and *Abate," 7* found with "*dracunculiasis* and *reward"*. Only a few articles were published on the impact of interventions.

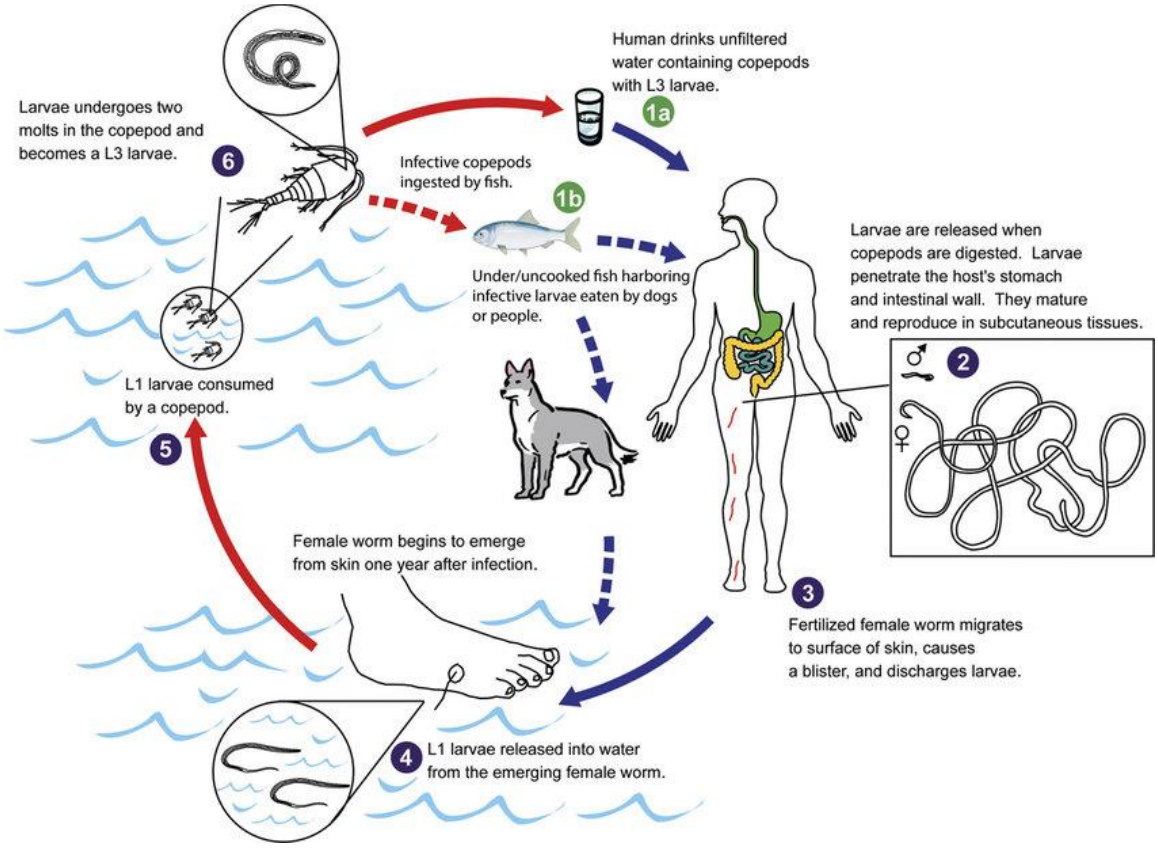
Dracunculiasis Pathophysiology

A person becomes infected by accidentally drinking water containing crustaceans or copepods infected with third stage larvae of *Dracunculus medinensis* (Fedchenko, 1870). *Mesocyclops*, *Thermocyclops*, and *Macrocyclops* are the most common species in Africa (Muller, 1982). Copepods or water fleas are mostly found in freshwater ponds, lakes, or shallow water, surface water, step wells, or cistern (Belcher, 1985). The first-stage larvae or embryo is not infective to man unless it is swallowed by copepod, the embryo can stay for 3 days to 5 days at 24^{o}C in water and must find copepod, and able to survive inside a copepod for 30 days making copepod an intermediate host of *D. medinensis* (Leiper, 1907; Muller, 1982; Tayeh et al., 2017; Perini et al., 2020; Islam et al., 2023). The embryo in the copepod molted twice to become a mature third-stage embryo, in 14 days in a temperature above 21^{o}C, which became infective to humans once swallowed and released into the stomach (Muller, 1982; Islam et al., 2023). The copepod can ingest 15-20 embryos. The copepod was immediately killed in the stomach due to hydrochloric acid or gastric juice and the embryos released into the stomach and penetrated the stomach lining to the connective tissue. After 6 months of ingesting the copepod, the male worm fertilized the female worm and died. The gravid female worm, which has between 1.4 to 3 million embryos, can grow to about 70 to 120 cm long and 0.2 cm wide and it migrated mostly to lower extremities, excretes toxic substance causing blister, itching, burning, and worm emergence after 6 to 12 months after infection, some scholars reported 10 to 14 months after ingestion (Muller., 1982; MacKenzie, 2010;

CDC, 2015; Biswas et al., 2013). Below is the illustration of the lifecycle of dracunculiasis.

Figure 2

Life Cycle of Dracunculus Medinensis in Human and Dog Adapted from Eberhard et al., 2014



When a person entered drinking water sources to relieve the pain, millions of embryos were released, restarting the cycle. An individual can have more than one worm; 21 worms in one person were reported in 2012 (Rao, 1982; WHO, 2014;). The site where the worm appeared could become inflamed, reddish, and tender, and the patient could

experience debilitating and excruciating pain. Patients could die from secondary infection or septicemia.

Alternate Pathways

Previous literature indicated that humans were the only reservoir and definitive host (Biswas et al., 2013; Cairncross et al., 2002; Muller, 1982; Watts, 1987). However, the lifecycle of dracunculiasis was observed to have changed when animal infections with *D. medinensis* were reported in Chad in 2012 (WHO, 2015). Infection was also reported among cats, wild cats and baboons (Beyene et al., 2017; Cleveland et al., 2018; Hopkins et al., 2022; WHO, 2023b). Several studies showed that the worm *D. medinensis* worm in humans was indistinguishable from the worm found in animals (Boyce et al., 2020; Cleveland et al., 2018; Eberhard et al., 2014; Galán-Puchades, 2019; Pellegrino et al., 2022; Thiele et al., 2018). However, studies suggested that dogs may not have become infected directly from ingesting infected copepods in drinking water but from a paratenic host, such as frogs and fish (Box, 2021; Cleveland et al., 2017). Cyclops are natural food for fish and aquatic animals. The dog either ate uncooked fish guts with L3 larvae or consumed an aquatic animal such as frogs (Box, 2021; CDC, 2015).

Implications of Dracunculiasis Eradication

Dracunculiasis is rarely fatal. However, people affected by this disease suffer from pain and disability and some have secondary infections. The people affected by the disease were mostly farmers, hunters, and housewives in the rural areas who did not have formal education (Mojoyinola & Blinkhorn, 2013). The patient could be disabled for 70 days which prevented the person from working and led to an economic loss of 11.7

million man-days annually if the disease had not been eliminated in India (Rao, 1982). This translated into nine months of work for farmers or $20 million per year if the disease was not eliminated in Nigeria (World Health Assembly [WHA], 2010). Cromwell et al., 2018 argued that if disease eradication was not initiated, about 2 million disability life years (DALYs) could have occurred from 1990 to 2016. Eradicating this disease would alleviate the suffering caused to men, women, and children in the most vulnerable and impoverished populations. The disease had an impact on the economic and social well-being of the person affected (Mojoyinola & Blinkhorn, 2013).

Eradication Strategy

Eradication strategies were aligned on breaking the cycle or interrupting transmission based on its life cycle (Biswas et al, 2013; Cairncross, Muller, & Zagaria, 2002; Leiper, 1907; Tayeh et al., 2017; Watts, 1987; WHA, 1991). The disease could be transmitted by drinking unsafe water sources therefore, supplying safe water sources in the community was expected to break the cycle. Dracunculiasis eradication was an indicator of the success of the International Water Decade in 1980s (WHA, 1981). In the early years of dracunculiasis eradication, the strategies focused on surveillance, early detection and containment of every case, provision of health education, and behavior change of patients not to enter water sources, provision of safe water sources and alternative ways of preventing people from ingesting the cyclops by using pipe filters and cloth filters, and by treating contaminated water with Abate (Biswas et al., 2013; Hopkins & Ruiz-Tiben, 1991; Kelly-Hope & Molyneux, 2021; Miri et al., 2010; WHO, 1996). However, with animal infections reported in Chad, Ethiopia, Mali and South Sudan, new

strategies became necessary to interrupt transmission among animals (Hopkins et al., 2022; WHO, 2022a).

Limitation of Current Strategy

The eradication of guinea worm disease faced numerous challenges that were categorized into distinct areas (Hopkins et al., 2022). Firstly, resource constraints presented a formidable hurdle, as limited financial and human resources may obstruct the comprehensive implementation of eradication strategies (Molyneux et al., 2020). This limitation could impede widespread interventions, monitoring efforts, and community engagement initiatives. Moreover, the geographical landscape poses a significant challenge, particularly concerning access to remote areas where guinea worm disease is prevalent. Difficulties in reaching these locations may have hindered the timely delivery of crucial healthcare services, interventions, and educational programs as observed in other eradication program like polio eradication (Kisanga et al., 2019).

Cultural and societal factors also played a pivotal role in the effectiveness of eradication strategies (Roberts, 2023). Deeply rooted cultural practices and societal beliefs could have influenced the acceptance of preventive measures, leading to resistance to behavioral changes and posing substantial challenges. Additionally, weak healthcare infrastructure in endemic regions was a critical limitation, potentially restricting the capacity to diagnose, treat, and prevent guinea worm disease effectively (Biswas et al., 2013; Roberts, 2023).

Inadequate disease surveillance systems further complicated eradication efforts, with the potential for underreporting or delayed reporting of cases (Lemma et al., 2020).

Timely and accurate information is indispensable for the success of eradication initiatives (Guagliardo et al., 2020; Hughes et al., 2020; Karki et al., 2021). Environmental factors, including changes in climate and water sources, may have affected the life cycle of the Guinea worm, influencing its prevalence, and adding complexity to adaptation strategies (Cobbina et al., 2010; National Water, 2023; Caretta et al., 2002).

Political instability in certain regions could also have posed a substantial obstacle to guinea worm eradication. Regions experiencing civil unrest may struggle to implement and sustain long-term eradication programs, disrupting healthcare services and hindering community engagement efforts (Kelly-Hope & Molyneux, 2021; Pellegrino et al., 2022; Rubenstein et al., 2021). Effective eradication requires seamless intersectoral coordination across health, water, sanitation, and education sectors. Limited collaboration among these sectors may impede the success of integrated strategies.

Educational barriers contributed to the challenges, with insufficient awareness and education about guinea worm disease and preventive measures hindering community participation (Madon et al., 2018; Pellegrino et al., 2022). A lack of understanding about the disease can result in non-compliance (e.g., patient drinking unsafe water source) with recommended interventions. Finally, the lack of adequate research and innovation poses a limitation, as insufficient exploration of new technologies or innovative approaches may hinder the development of more effective strategies (Horta & Mok, 2020). Embracing new scientific advancements is crucial for overcoming these persistent challenges. It is important to recognize that these limitations are context-dependent, emphasizing the need for a tailored and context-specific approach to Guinea worm disease eradication.

Epidemiology of the Disease

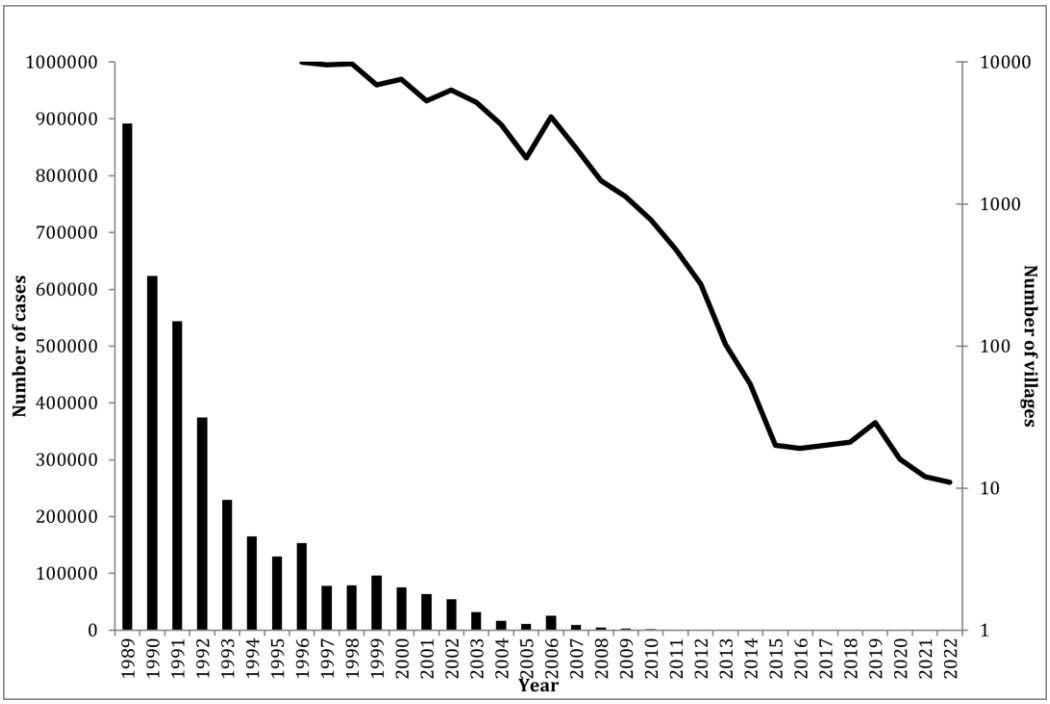
Progress was made from 1.89 million reported cases in 1989 in 20 endemic countries in 1980s—which became 21 after separation of Sudan and South Sudan in 2011, and 22 after Angola reported its first case in 2018—to only five endemic countries in 2020 (WHO, 2013; 2021). Twelve new cases were reported from three of five endemic countries —Chad (6), Ethiopia (1), South Sudan (5). A 99% reduction in the number of cases was reported in 2022 compared with 1989(WHO, 2023b). Of the 194 member states, six countries remain to be certified including Angola, Chad, Ethiopia, Mali, Sudan, and South Sudan (WHO, 2023b, 2023c). The Democratic Republic Congo, which had its last cases in 1950s, was certified free of dracunculiasis recently (WHO, 2023b). In the Neglected Tropical Diseases (NTD) roadmap 2030, one of the targets is to eradicate dracunculiasis which is also aligned to Sustainable Development Goals (SDGs) of eliminating NTDs by 2030 (WHO, 2023e).

Based on published data in the Global Health Observatory (WHO, 2022b) and recent *Weekly Epidemiological Record* (2023), which were received from the Ministry of Health, Chad reported six cases in 2022 compared with 640 cases in 1994 (World Health Organization, 2022; 2023). Ethiopia reported one case in 2022 compared with 1,252 cases in 1994. Mali reported zero cases in 2022 compared with 4,838 cases in 1994. South Sudan reported five cases in 2022 compared with 1,028 in 2011. All four endemic countries had reduced the number of cases by 99%. Compared with 2021, Chad reported eight cases, Ethiopia reported one case, Mali reported two cases, and South Sudan reported four cases. This represented a 25% reduction for Chad and a 100% reduction for

Mali, while South Sudan had experienced a 25% increase. Losio & Mushayabasa (2018) argued that disease severity could be measured using the basic reproduction number $R_{0,}$ which defined the number of secondary infections resulting from a single infection. They also demonstrated that if R_0 was more than one, the disease would persist and if less than one then the disease can be eradicated (Losio & Mushayabasa, 2018).

Figure 3

Annual Number of Dracunculiasis Cases and Villages Reporting Cases 1989–2022 Adapted from WHO, 2023b.

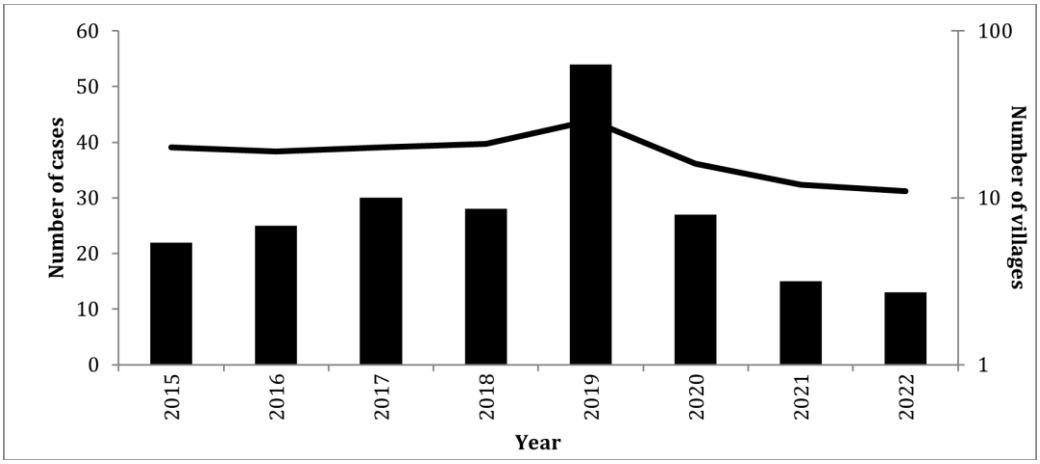


Note. The number of villages is plotted on a logarithmic scale.

Figure 4 shows mostly stabled number of dracunculiasis cases in humans.

Figure 4

Annual Number of Cases Since the Global Number of Cases Was Below 100



Note. The number of villages is plotted on a logarithmic scale.

Eradication Stages

Dracunculiasis eradication has three stages: the intervention stage, precertification stage, and certification stage (WHO, 1996). The intervention stage required all endemic countries to implement activities to interrupt transmission. Intervention included surveillance, case detection and containment, health education, and vector control. No medicines can be used to prevent or treat dracunculiasis; therefore, all interventions were related to the containment of the case (Biswas et al., 2013). A case could only be contained if the patient was detected within 24 hours of worm emergence, if the patient did not enter any water sources, if the patient immediately received health education, if the patient's wound was properly managed, and if the vector control, such as abating, was used within seven days of worm emergence in any water sources that may have been contaminated by the patient (CDC, Global 2000, UNICEF, WHO, n.d.). The first country that interrupted transmission—or the year in which the last indigenous case was reported

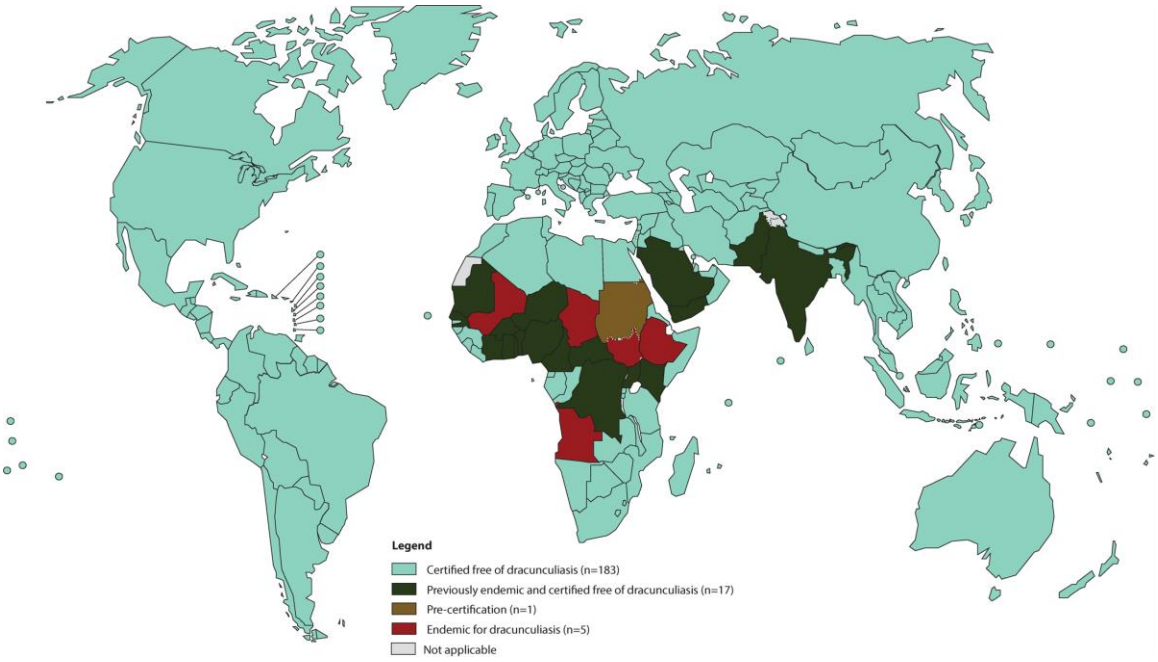
— was Pakistan in 1993, followed by Kenya in 1994; India in 1996; Cameroon, Senegal and Yemen in 1997; Central African Republic in 2001; Uganda in 2003; Benin and Mauritania in in 2004; Burkina Faso, Togo, Cote d'Ivoire in 2006; Niger and Nigeria in 2008; Ghana in 2010; and Sudan in 2013 (Biswas et al., 2013; WHO, 2000, 2009, 2022)

The confirmed absence of the emergence of adult worms —meaning a reduction in the number of cases to zero will indicate an interruption of transmission of the disease and requires three years of continued zero-case reporting (WHO, 2025b). The precertification stage last three years, during which surveillance should continue and an awareness campaign about the disease and the reward for reporting should be established. Sudan has reported zero cases since 2013; however, in 2017, three probable cases of dracunculiasis were reported, and the worm was not properly managed (WHO, 2022a).

After three years of zero-case reporting, the country will be moved to the certification stage, where it will be evaluated and verified to determine whether it has interrupted the transmission and whether the health system has the capacity to detect and respond to any case of dracunculiasis. An International Certification Team visited, verified, and evaluated the formerly endemic countries based on the submitted country report and presented evidence and findings to International Commission for Certification of Dracunculiasis Eradication (ICCDE) (WHO, 2000). The ICCDE then makes recommendations to WHO. The WHO certified 200 countries, areas, and territories, including 188 Member States of WHO (WHO, 2023b).

Figure 5

Certification Status of Dracunculiasis Eradication, 2023



Challenges to Dracunculiasis Eradication

With many countries certified free of dracunculiasis, a number of challenges have emerged with each country related to eradication strategies. One of the challenges is the animal reservoir, specifically among dogs in Chad, Mali, Ethiopia and South Sudan (Eberahard, 2014; Molyneux & Sankara, 2017; WHO, 2022a). Several infections of *D. medinensis* in dogs were reported in early 1950-1980, however, at that time, dogs were assumed to be accidentally infected from where human got infected (Muller, 1982). However, the number of infected dogs has increased since 2012, it is no longer considered an accidental infection. Pakistan, a country certified free of dracunculiasis, reported a dog with *D. medinensis* in 2001 (Muhammad et al., 2005). Another challenge is insecurity and conflict. Kelly-Hope and Molyneux (2021) quantified conflicts from

2000 to 2020 in Mali (n =2,556; 13 events per 100 000 population), South Sudan (n= 2,143;19.4 events per 100 000 population), Ethiopia (n=1490, 1.3 events per 100 000 population) , Chad (n=421, 2.6 per 100 000 population and Angola (n=222, 0.7 events per 100 000 population). According to Global Peace Index (GPI) for 2013 to 2016, Chad, Ethiopia, South Sudan and Mali were identified as having very low levels of peace (Du et al., 2018).

Risk Factors

Access to Safe Water Sources

Eradication of dracunculiasis was an indicator of success of the International Water Decade in 1980s (WHA, 1981). Access to clean and safe water sources for the remaining countries — Chad, Mali, Ethiopia and South Sudan — remained a challenge (Beyene et al., 2017). Several authors studied the association of drinking water sources and dracunculiasis. The disease was reported as prevalent in areas using pond water during the dry season (Belcher et al., 1975), in shallow ponds used at the onset of rainy season (Steib & Mayer, 1988), and in locations where small ponds were more accessible than alternate water sources (Tayeh, 1998). The disease was also found to be prevalent in low-water-level ponds from receding rivers during the dry season (Galán-Puchades, 2019). Consumption of contaminated water sources remained the primary pathway for dracunculiasis in human; the use of secondary water sources (ponds outside home) was associated with increased prevalence (Liu et al., 2020). Ede et al. (2014) reported that having access to at least two functional potable water sources such as boreholes located close to households, reduced the reliance on of pond water. Miri et al. (2010) found that

provision of safe water sources to community was the most desired intervention. In 2020, 90% of global population had access to at least basic water sources, while only 15.8% had access to safely managed drinking water sources (UNICEF, 2020).

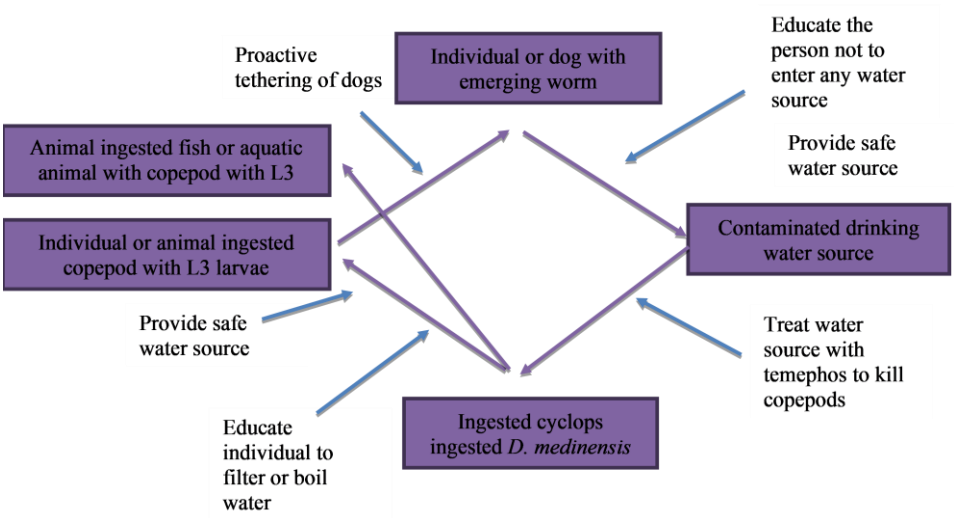
Copepod

Copepod is very important factor in the life cycle of *D. medinensis* (Muller, 1982); therefore, it is important to know at what point to conduct vector control strategies to break the cycle (see Figure 4). The vector control strategies in dracunculiasis eradciation are chemical (e.g. killing the copepods with larvicide such as Abate® [temephos]), thermal(e.g. heating or boiling) or mechanical (e.g. using filters) (Muller, 1970; Tayeh et al., 1996; Miri et al., 2010; WHO, 1989). Abate® is highly toxic to copepod and is considered safe for human consumption at a dosage of less than1mg/L (WHO, 1989). Losio and Mushayabasa (2018) argued that optimal control of the pathogen could lead to its eradication in the environment; similarly without effective control of the pathogen, the disease will persist. Infected copepods were obseved to become sluggish (Muller, 1970). Tayeh et al. (1996) argued that the use of cloth filter was effective when given freely and accompained by health education on the used of monofilament filter. One challenge in using Abate® was measuring the ponds, determine the correct dosage, and identify appropriate water sources (Miri et al., 2010). Grunert et al. (2022) confirmed that superior efficacy of Abate® against copepods. Abate® imobilized copepods, thereby killing them; and once the copepod died, the larva also died (Muller, 1970; Tayeh et al., 2017; Grunert et al., 2022). Application of Abate® to driking water sources was considered only in the presence of dracunculiasis in the village, the

estimated volume was known, water was not flowing, and the presence of barrier that kept people from entering (WHO, 1989). It was critical to treat potential water sources contaminated approximately one month before the emergence of worm (WHO, 1989).

Figure 6

Simple Life Cycle of D, Medinensis, and Point of Intervention to Break the Cycle



Surveillance

An international campaign to eradicate dracunculiasis has been underway, making surveillance essential to detect and contain any individual cases in endemic countries as well as in nations where the environmental factors favor local disease transmission (WHO, 1999).

Reward

A country was certified free of dracunculiasis only when all the cases are reported, including zero-case reporting (WHO, 1996). Eradication will take place only when the pathogen is eliminated globally. Before smallpox was officially certified as

eradicated in 1980, a global reward of 1000 USD was launched to ensure that any case of smallpox will be reported (Breman, 2021). Similar strategy was implemented in countries not yet certified free of dracunculiasis. A reward system was established to increase the sensitivity of surveillance, a reward system was established in every country (see Table 1) (Biswas et al., 2013; Guagliardo et al., 2020).

Table 1

Reward in Countries Endemic and in Precertification Stage (WHO, 2023b)

Country	Reward for voluntary reporting human cases	Reward for owner of dog reported guinea worm infection
Angola	USD 450	
Chad	50,000 CFA (~USD 100)	10,000 CFA (~USD 20)
Ethiopia	20,000 ETB (~USD 360)	1,000 ETB (~USD 40)
Mali	200,000 CFA (~USD 400)	10,000 CFA ((~USD 20)
South Sudan	50,000 SSP (~USD 380)	10 000 SSP (~USD 75)
Sudan	50,000 SDG (~USD 100)	50,000 SDG (~USD 100)

There is no global reward system that currently in place for reporting dracunculiasis. However, communities with increased knowledge about the reward were associated with higher number of infected dogs (Rubenstein et al., 2021). Countries have evaluated awareness of the community about the reward (WHO, 2022a). The ICCDE has set that at least 80% of the population in endemic district knew about the reward for voluntary reporting and 50% of general population (WHO, 2015b). Rewards has been given to the patient, informant and/or health worker (WHO, 2022a).

Rumor Reporting

A rumor of dracunculiasis is defined as any information of alleged case of dracunculiasis from any sources (WHO, 2023d). A rumor is identified having the signs and symptoms of dracunculiasis including a blister, itching, inflammation or hanging

worm. The implementation of reward system and rumor registration, and investigation of rumors of dracunculiasis has improved case detection (Breman, 2021; Senyonjo et al., 2021). In 2021, the number of rumors reported was 117,171 from Angola, Chad, Ethiopia, Mali and South Sudan, however, only 49 and 12 rumors were reported from Sudan and Democratic Republic of Congo respectively (WHO, 2022a). No study found on the correlation between rumor reporting and dracunculiasis cases nor the number of cases can be detected from n number of rumors. Rumor reporting was sometimes used in syndromic surveillance whereas the health system collects information on signs and symptoms even before the emergence of worm (Hughes et al., 2020).

Animal Infection

Animal have become reservoir host posing a challenge to eradication of dracunculiasis (Hopkins et al, 2022). Around 128 *D. medinensis* specimens were collected from remaining endemic countries, and study found that the *D. medinensis* in human and animal were indistinguishable (Thiele et al., 2018). Recent studies showed that the way dogs or cats drank water suggested that they were unlikely to ingest copepods (Crompton & Musinsky, 2011), however, Garrett et al., (2020) found in dog drinking trial that dogs can ingest copepods and higher ingestion rates. Dracunculiasis has been identified as food borne zoonosis (Cleveland et al., 2017; Galán-Puchades, 2019; Box, 2021). Studies suggested that infected animals became infected from eating uncooked fish guts containing infected cyclops (McDonald et al., 2020). However, a study conducted in Ethiopia found that dogs were unlikely to be infected by eating paratenic or aquatic hosts but were more likely infected through the water that was

provided to the dogs, age, and health conditions of the dog (Wilson-Aggarwal et al., 2021).

In Chad, although dogs were tethered, some owners provided water from natural sources or ponds. Cleveland et al. (2020) found that metal containers shortened the survival of copepods to 4h to 6h, compared to plastic containers under the same environmental condition in Chad (temperature range of 33-45^{o}C) (Cleveland et al., 2020). This is likely due to the fact that metal is good conductor of heat. Dog population size was a predictor of *D. medinensis* infection; the higher the population, the more the likelihood the chance of getting the dog infected (Richards et al., 2020).

Seasonality of the Disease

In the study using stochastic agent-based simulation with 2014–2017 data on infected dogs in Chad, the transmission dynamics were understood to start from April to August and peaks in June (Perini et al., 2020). In recent study, dog population, geographic, climate, and surveillance data were important predictors of dracunculiasis infection in Chad (Richards et al., 2020). Richards et al. (2020) argued that climatic and geographic factors played a role on the dracunculiasis infection despite of variation found. Environmental factors included precipitation and temperature (Perini et al., 2020; Richards et al., 2020). Perini et al. (2020) found that infectivity was highest in the months preceding the peak of rainy season and during the peak of heat wave. In Mali's Sahelian zone, cases occurred during the rainy season and residual ponds in the dry season (Desfontaine & Prod'Hon, 1982). The remaining five endemic countries may exhibit five different seasonal patterns. Some studies found that climate change have

found that climate change has affected the precipitation (rainfall) (Tabari, 2020; Zhang et al., 2022).

However, the question remains: Can the disease be eradicated by 2030, and what intervention needed to scale up to reach this goal, as the target has been pushed back repeatedly — from 1991 to 2015, then to 2020, and now to 2030 (The Lancet, 2019; WHO, 2021a).

Climate

The Köppen Climate Classification system (commonly referred to as the Köppen system) was developed by climatologist Wladimir Köppen and has been widely utilized by scientists to classify climates worldwide (Daniels, 2022). The system organizes climates into five primary types (A, B, C, D, E) based on average temperature and rainfall patterns. These types encompassed characteristics like moist tropical, dry, continental, and cold climates. Subcategories were identified by lowercase letters within parentheses, offering distinctions in factors such as moisture levels and seasonal variations. The classifications are as follows (Daniels, 2022):

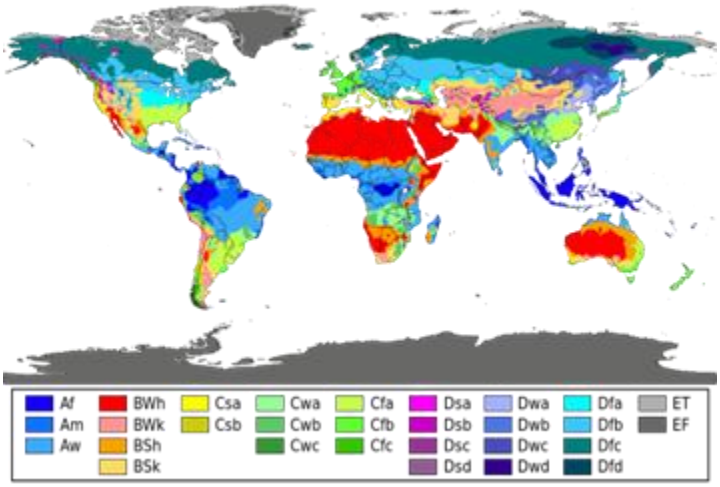
- Moist Tropical Climates (Type A):
    - Consistently high temperatures and substantial rainfall year-round.
- Dry Climates (Type B):
    - Minimal precipitation and a significant daily temperature range.
    - Subgroups: Semiarid or steppe (S) and arid or desert (W).
- Temperate Climates (Type C):
    - Moderate temperatures with distinct seasons.

    - Subgroups: Dry-summer subtropical or Mediterranean (Cs) and wet-summer subtropical or maritime (Cw).

- Continental Climates (Type D):
    - Located in the interiors of large land masses.
    - Notable seasonal variations and low rainfall.
- Cold Climates (Type E):
    - Regions with permanent ice and tundra, with above-freezing temperatures for four months.
- Additional Subgroups:
    - Designated by a second, lowercase letter within parentheses indicating seasonal distinctions.
        - "(f)" subgroup: Moist climate with consistent rainfall throughout the year, no distinct dry season (commonly associated with A, C, and D climates).
        - "(m)" subgroup: Rainforest climate despite a brief dry period during the monsoon cycle, exclusively applying to A climates.
        - "(s)" subgroup: Presence of a dry season in the summer hemisphere.
        - "(w)" subgroup: Presence of a dry season in the winter hemisphere.

Figure 7

Updated World Map of the Köppen-Geiger Climate Classification (Peel et al., 2007)



Theoretical Foundation

Green and Kreuter (1999) initially developed the PRECEDE model in the 1970s and later added the PROCEED component in 1991. Although PRECEDE-PROCEED model is a tool for designing, implementing, and evaluating health behavior change, interventions, in the propose study, the model served as a framework that will identify intervention strategies and factors that contribute to the final outcome—the reduction of new cases and animal infection — which ultimately leads to certification of the country (Bk & Glanz (2005).The model will be applied as a framework to determine the association of factors/predictors (PRECEDE) and outcome (reduction of dracunculiasis cases) and impact (eradication of dracunculiasis) (PROCEED).

PRECEED Phase

PRECEED has four phases, as adapted from Community Tool Box. (University of Kansas, 2014).

Phase 1: Social Assessment

Determine the desired outcome and impact. Improving quality of life by eradicating dracunculiasis (WHA, 1989) is the desired impact and reduction of cases to zero is the desired outcome. Dracunculiasis eradication is indicator of success of the International Water Decade in 1980s (WHA, 1981) and then indicator of success of Sustainable Development Goal (SDG) 6 (ensure access to water and sanitation for all) and SDG 3 (ensure health lives and promote well-being for all at all ages) (United Nation, n.d.).

Phase 2: Epidemiological Assessment

Identify the issues or factors (behavioral, lifestyle or environmental factors) that might influence the outcome or the ultimate goal. There are behavioral factors like drinking unsafe water sources or entering water sources during the emergence of worm and tethering of dogs (Biswas et al., 2013; McDonald et al., 2020). Environmental factors like water, climate, temperature and dog population (Desfontaine & Prod'Hon, 1982; Perini et al., 2020; Richards et al., 2020). Genetics are not covered by this study. Behavioral and environmental factors will be explored in this study.

Phase 3: Educational and Ecological Assessment

Three main factors are identified: Predisposing factors refers to person's knowledge, value, attitude, beliefs; enabling factors refers to skills, resources or barriers;

and reinforcing factors refers to reward or satisfaction that can affect, facilitate or hinder changes (Green et al., 2022).

Predisposing factors included community awareness about the disease and prevention,

Enabling factors included access to safe water sources, water sources treated with abate, training of health workers,

Reinforcing factors included (reward system or providing reward for reporting)

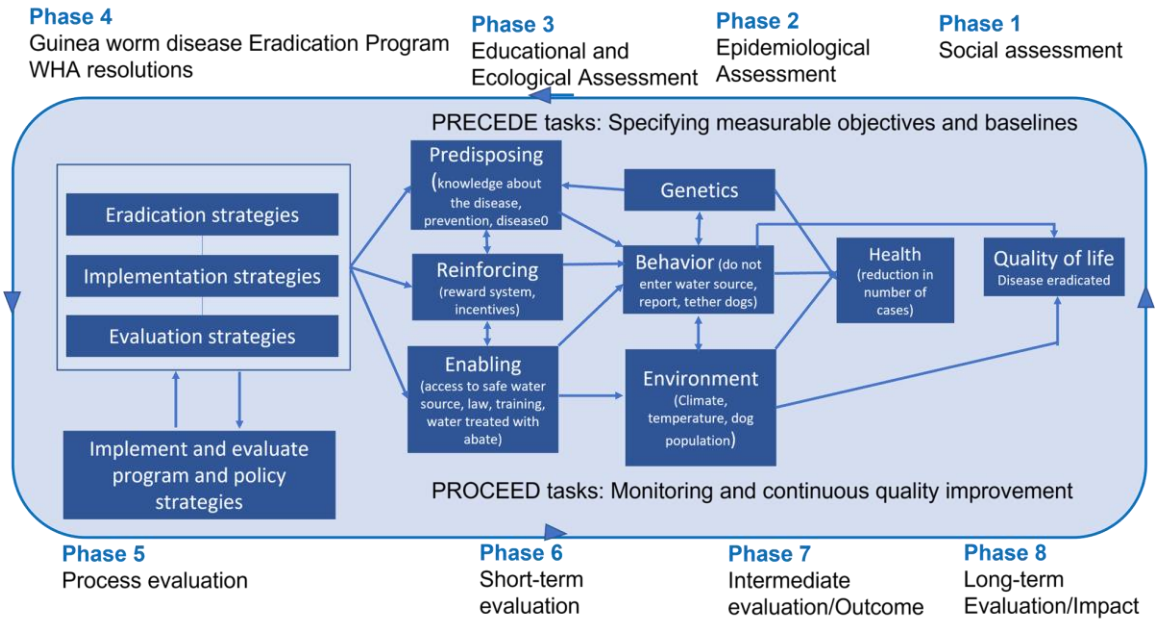
Phase 4: Identifying Policy Factors that can Influence the Outcome.

PROCEED Phase

PROCEED determines if the intervention is really working to the desired outcome—the reduction of the number of cases to zero—and desired impact—eradication of dracunculiasis. Evaluation strategies to determine the outcome or impact will include methods such as variance, regression, comparative analysis and descriptive statistics (Green et al., 2022). Below is the illustration of the model to this study. The factors are not limited to the factors mentioned in this illustration.

Figure 8

Guinea Worm Disease Eradication Adapted the PRECEDE and PROCEED Model (Green et al., 2022)



Summary and Conclusions

The literature review synthesized key themes related to the burden, pathophysiology, and epidemiology of dracunculiasis, with emphasis on the global and country-specific context of the remaining endemic countries. Studies documented the devastating health and socioeconomic consequences of the disease, as well as the progress made through eradication efforts. The review highlighted the effectiveness of surveillance, health education, safe water access, and vector control strategies such as the application of Abate®. The persistence of dracunculiasis in marginalized communities, particularly in Chad, Ethiopia, Mali, South Sudan, and Angola, remains a central concern.

A major theme across the literature was the emergence of animal reservoirs, particularly dog infections, as a significant barrier to eradication. Although several studies confirmed the biological indistinguishability of *D. medinensis* in humans and animals, the mechanisms of transmission in animals are not yet fully understood (Eberhard et al., 2014; Guagliardo et al., 2020; Richards et al., 2020). Moreover, limited evidence exists on the effectiveness of interventions such as dog tethering and reward systems in reducing transmission Another critical gap identified in the literature was the lack of comprehensive studies linking behavioral, programmatic, and environmental risk factors—such as awareness of the disease and reward system, application of larvicide, access to safe water, and exposure to environmental variables (temperature, precipitation, and surface water)—to the number of human and animal Guinea worm cases. Additionally, the relationship between rumor reporting and confirmed case detection remains underexplored, despite significant investments in awareness campaigns.

Although individual studies addressed some of these factors independently, few comparative or integrated analyses were conducted across multiple endemic countries using structured theoretical frameworks. Furthermore, cross-national evaluations that incorporated spatial analysis and environmental predictors were notably absent in the existing literature.

This study addresses these critical gaps by applying the PRECEDE–PROCEED model as a guiding theoretical framework to analyze associations between behavioral, ecological, and programmatic factors and disease outcomes. It extends the existing body of knowledge by integrating secondary surveillance data with environmental variables,

enabling a multi-country comparative analysis grounded in epidemiological and spatial methodologies.

The findings from this study aim to support targeted intervention strategies and inform global eradication efforts by identifying key predictors of Guinea worm transmission. The transition to Chapter 3 presents the research design, data sources, variable definitions, and statistical procedures used to examine these relationships using quantitative, inferential, and geospatial methods.

Chapter 3: Research Method

Introduction

The purpose of this quantitative study was to examine the relationship between risk factors, environmental factors, and Guinea worm disease in Angola, Ethiopia, Chad, Mali, and South Sudan. Appropriate statistical analyses were conducted to determine the influence of different factors on Guinea worm disease and to assess whether these factors predicted the likelihood of achieving elimination targets by 2030, as outlined in the Neglected Tropical Diseases (NTD) Roadmap 2021–2030 (World Health Organization [WHO], 2021). This study provided additional knowledge intended to contribute to the reduction of Guinea worm disease cases and infections and supported the achievement of the NTD Roadmap targets and milestones for Guinea worm disease (WHO, 2021b).

This chapter describes the research methods used in this study. It begins with an explanation of the research design and rationale, including the study population and sampling procedures. The following sections provide a description and assessment of the secondary data sources, including the study settings across the five endemic countries. Ethical approval processes are discussed, followed by the data analysis plan which outlines the procedures for data assessment, extraction, descriptive and inferential statistics, and secondary time series forecasting analysis. Threats to validity and a discussion of the study's limitations are also presented. The chapter concludes with a summary of the key methodological components.

Research Design and Rationale

This study used an epidemiological research study design and employed a quantitative approach, based on the positivist paradigm, with descriptive and correlational designs to determine relationships between variables (Creswell, 2009; Park et al., 2020; Bruce et al., 2008; Wang, 2002). The aim of the study, which fell under the umbrella of epidemiological research, was to assess the risk factors connected to the prevalence of dracunculiasis and to recommend preventive public health measures. The ultimate goal was to reduce the number of cases to zero and thereby achieve the objective of eradication. Epidemiological research also aims to assess the effectiveness of health policies (Aldrich et al., 2015). The results of this epidemiological research contributed to the improvement of strategies and the development of health policies.

Quantitative research used numbers, graphs, and maps to express data on Guinea worm disease patterns in the population, describing variations over time, place, and individuals (Creswell, 2009; Bruce et al., 2008). This was a descriptive study design that intended to describe the population affected by the disease, as well as the disease pattern, prevalence, and incidence rates of dracunculiasis (Wang, 2002). Causal inference aimed to identify the etiologic agents or determinants of dracunculiasis, using a correlational design to determine the relationship of the risk factors to dracunculiasis and to compare patterns among the five endemic countries (Creswell, 2009; Wang, 2002). This study did not intend to test cause-and-effect relationships between variables; otherwise, an experimental design would have been used (Creswell, 2009). Secondary data were used

to explore associations between risk factors and Guinea worm disease, employing a quantitative correlational design. (Creswell, 2009).

Retrospective methods gather data from the past, using data collected by others (Creswell, 2009; Bruce et al., 2008). This study used secondary data from 2012 to 2023. A retrospective approach was more appropriate for this research because the number of people affected by the disease was lower compared to when Guinea worm disease was endemic in 20 countries during the 1980s. The study focused on a cohort of villages affected by dracunculiasis.

Secondary data, including epidemiological data on human cases and infected animals, surveillance data, awareness survey data, and environmental data previously collected by others, were obtained and analyzed in this study (Little, 2013). Compared to primary research, which would have required the researcher to travel and collect new data over time, secondary research saved time and resources (Creswell, 2009; Little, 2013). However, it was recognized that each type of research approach has its own benefits and limitations.

Methodology

The secondary data used in this study were derived from routine surveillance data collected by the Ministries of Health of the five remaining endemic countries (Angola, Ethiopia, Chad, Mali, and South Sudan) (Guagliardo et al., 2020; The Carter Center [TCC], 2023; WHO, 2023b). The included secondary datasets consisted of demographic data, line listings of cases, line listings of infected animals, villages under surveillance, district surveillance data, line listings of rumors, surveys on the level of awareness, and

environmental data. The quantitative data included in these datasets were collected during the period from 2012 to 2023 (WHO, 2022a, 2022b, 2023b, 2024).

Population

All available samples in the secondary data were used in this study. The population used in previous studies included people and animals affected by dracunculiasis (Guagliardo et al., 2020; TCC, 2023; WHO, 2023b).

Sampling Procedures

The population and sample size used in each dataset analyzed in this study were carefully examined and documented. The secondary data used in this study were originally collected for other purposes (Little, 2013). Secondary data on dracunculiasis from the five remaining endemic countries were sampled from the global database maintained by the WHO. This study utilized secondary data from 2012, the first year that animal infections were reported in Chad—through 2023 (Liu et al., 2020). The study used secondary data on infections and cases of guinea worm disease from 2012 to 2023.

The currently endemic countries had both published and unpublished surveillance data on dracunculiasis, which were submitted by their respective National Guinea Worm Disease Eradication Programmes (NGWEP) (TCC, 2023; WHO, 2023b). The national programs combined active and passive surveillance strategies, with a focus on village-based monitoring and reporting. While offering rewards generated rumors that may have helped discover unrecognized transmission, there was limited evidence supporting the effectiveness of this strategy (Senyonjo et al., 2021; Guagliardo et al., 2020).

Description and Assessment of Secondary Source

Study Setting

Chad

Geography and Security Challenges: Chad is a landlocked Sahelian country located in central Africa. Despite its geographical positioning, the nation faces significant security challenges. These include border conflicts and the adverse impacts of climate change, as indicated by The World Bank (2023a).

Refugees and Socioeconomic Challenges: Chad is home to more than 450,000 refugees, a situation that poses challenges to the country's efforts in areas such as poverty reduction, addressing stunting, and maternal mortality rates. This humanitarian concern underscores the complexity of the challenges Chad is addressing (The World Bank, 2023a).

Population and Growth: The 2022 Revised World Population Prospects reveal that Chad sustains a population of approximately 18.3 million people, with a population growth rate of 3.2% (WHO, 2023e). The country's demographics play a crucial role in its socioeconomic dynamics.

Poverty and Economic Conditions: Chad grapples with substantial economic and social hurdles. About 42.3% of the population lives below the national poverty line, while nearly 31% live in extreme poverty, earning less than $2.15 per day. The nation also faces a relatively low literacy rate at 27% and an unemployment rate of 1.1%, as reported by the World Development Indicators database (2021a) and the International Labor Organization (2023).

Health and Mortality: Chad's health indicators paint a challenging picture. The life expectancy at birth is 53 years, with a crude death rate of 13 per 1,000 people. The under-5 mortality rate is particularly high at 110.5 deaths per 1,000 live births. These statistics, sourced from the World Development Indicators database (2021a) and the WHO(n.d.), reveal health-related issues that need attention.

Health Expenditure: According to the World Health Organization's Global Health Expenditure database (2023c), 59% of Chad's total health spending in 2020 came from out-of-pocket expenses. This indicates a reliance on individual payments for healthcare, which can have wider implications for health services accessibility and affordability.

Economic Outlook and Challenges: Chad's economic outlook is marked by uncertainty. Factors such as fluctuating oil prices, political instability, security risks, climate-related shocks, food security issues, and social discontent pose risks to the nation's economic stability. In 2021, Chad's economy contracted by 1.2%, but recovery is anticipated in 2022. Inflation is also expected to rise to 5.3% due to global food and energy price fluctuations, according to The World Bank (2023a).

Water Supply Disparities: Access to basic water supply is uneven between rural and urban areas in Chad. In 2022, only 41.15% of the rural population had access, while 60.27% of the urban population enjoyed the same privilege, as reported by WHO/UNICEF (2022). Furthermore, there are disparities within the poorest segments of the population, with only 22.4% of the poorest rural population having access to basic

water supply in 2022, and 22.8% among the poor population in 2017 (WHO/UNICEF, 2022).

Neglected Tropical Diseases: Chad is home to 13 neglected tropical diseases, including dracunculiasis, as reported by the WHO (2023). These diseases present public health challenges that require attention and resources for control, prevention and elimination.

Ethiopia

Population and Economic Situation: Ethiopia, the second most populous nation in Africa, is home to approximately 126 million people, according to data from the WHO (2023). Despite its large population, the country faces economic challenges, with a per capita gross national income of $1,020 as reported by The World Bank (2023b). Nevertheless, Ethiopia has experienced notable economic growth, with a 6.4% growth rate in FY2021/22.

Economic Growth and Challenges: The country's economic growth has had positive impacts on poverty reduction and human development indicators. However, Ethiopia still grapples with key challenges such as reducing conflicts, mitigating the effects of COVID-19, addressing food insecurity, and improving human capital. These challenges are critical aspects of the nation's development trajectory, as highlighted by The World Bank (2023b).

Poverty and Socioeconomic Indicators: Ethiopia's socioeconomic situation includes 29.6% of the population living below the national poverty line, with 30.8% living on less than $2.15 per day. The country also faces an unemployment rate of 3.9%,

with a literacy rate of 52%. These statistics are sourced from The World Bank (2023b), the International Labor Organization [ILO] (2023), and UNESCO Institute for Statistics (2022).

Health and Mortality: Ethiopia's health indicators show a crude death rate of 7 per 1,000 people, a life expectancy at birth of 60 years, and a mortality rate of 47 per 1,000 live births for children under five, according to data from the World Development Indicators database (2021b). These indicators provide insights into the nation's health status and challenges.

Health Expenditure: In 2020, out-of-pocket costs accounted for 33% of current health spending in Ethiopia, as indicated by the WHO's Global Health Expenditure database (2023c). This implies that a significant portion of healthcare expenses is borne directly by individuals, which can impact healthcare accessibility and affordability.

Disparities in Water Supply: Access to basic water supplies in Ethiopia exhibits disparities, with only 24.2% of the poorest rural population having access in 2017. Access increases to 31.0% among the poor and 37.8% among the rich. However, there has been some improvement, with 36.41% of those living in rural areas and 44.66% of those in cities having access in 2022, according to WHO/UNICEF (2022).

Neglected Tropical Diseases: Ethiopia is endemic for 12 neglected tropical diseases, including dracunculiasis, (WHO, 2023e). These diseases pose public health challenges and require concerted efforts for control and prevention.

Mali

Population and Poverty: Mali, a Sahelian nation in West Africa, is home to approximately 21.9 million people. A significant portion of its population faces socioeconomic challenges, with 44.6% living below the national poverty line and 14.8% in extreme poverty. Additionally, 3.5% of the population is unemployed, while the literacy rate stands at 31%. These statistics are based on data from The World Bank (2023b), the ILO (2023), and the UNESCO Institute for Statistics (2022).

Health and Mortality: In Mali, the health and mortality indicators are as follows: The crude death rate is 9 per 1,000 people, the life expectancy at birth is around 60 years, and the mortality rate for children under five is 97 per 1,000 live births. These figures, reflecting the nation's health profile, are sourced from the World Development Indicators database (2021b) and the United Nations Population Division (2022).

Health Expenditure: In 2020, out-of-pocket expenses constituted a significant portion of health spending in Mali, accounting for 29% of the total, according to the WHO's Global Health Expenditure database (2023f). This highlights the financial burden on individuals seeking healthcare.

Disparities in Water Supply: Disparities in access to clean water are evident in Mali. In 2022, only 74.4% of people in rural areas had access to a water supply, compared to a higher rate of 94.7% among those in urban areas, as reported by WHO/UNICEF. In 2017, 48.7% of the poorest rural population had access to clean water, underscoring the need for improved water infrastructure and services (WHO/UNICEF, 2022).

Neglected Tropical Diseases: Mali is endemic for 12 neglected tropical diseases, including dracunculiasis, according to the WHO (2023b). Addressing these diseases is essential for public health and the well-being of the population.

South Sudan

South Sudan, which became the world's youngest nation on July 9, 2011, has faced significant challenges, including civil war outbreaks in 2013 and 2016, exacerbating the humanitarian crisis (World Bank, 2023d). The country had a population of 11.1 million in 2022, as reported by the WHO (2023b). Disturbingly, in 2016, an alarming 67.33% of the population was living in extreme poverty, with an even higher 82.3% living below the national poverty line (World Bank, 2023e). Health indicators reveal a crude death rate of 11 per 1,000 people, a life expectancy at birth of 55 years, and a mortality rate for children under five of 99 per 1,000 live births (United Nation Population Division, 2022; World Development Indicators database, 2021a). Access to safe drinking water remains a pressing issue, with only 60% of the population having access to unsafe water sources, such as surface water and unprotected wells, as of 2020 (World Bank, 2023f).

Guinea Worm Disease Eradication Program: The National Guinea Worm Disease Eradication Programme (NGWEP) has been established in several countries, including Chad (CGWEP reestablished in 2012), Ethiopia (EDEP in 1993), Mali (1991), South Sudan (2011), and recently in Angola (Beyene et al., 2017; Rubenstein et al., 2021; TCC, 2023; WHO, 2023b). The scope of this study begins with data from the first reported animal infection in Chad (Guagliardo et al., 2020; WHO, 2022a, 2022b, 2023b).

Each NGWEP has established village-based surveillance in endemic villages. The village under active surveillance is defined as villages that had cases in the last 3 years or sharing water sources with the endemic village (Rubenstein et al., 2021). The intervention strategies in these endemic countries focus on villages under active surveillance, emphasizing reporting and awareness at all levels (Guagliardo et al., 2020). When an individual presents symptoms of Guinea worm disease, they report to either a village volunteer or a Guinea worm officer. The officer conducts an investigation, collects and preserves specimens, and sends them for laboratory confirmation to the United States Center for Disease Control and Prevention, a WHO Collaborating Center for Dracunculiasis Eradication (CDC, 2015; WHO, n.d.; Guagliardo et al., 2020).

Description and Assessment of Secondary Database

The primary data collected by the National Guinea Worm Eradication Programs (NGWEPs) were intended for surveillance purposes, employing a prospective study design with a multi-stage sampling method to collect dracunculiasis data and a cross-sectional survey among households. Data were obtained from the following sources: line listing of dracunculiasis cases, line listing of animals infected by dracunculiasis, aggregated dracunculiasis data by villages under active surveillance, aggregated surveillance data by district, aggregated data on rumors of dracunculiasis, aggregated data of households aware of the reward for reporting dracunculiasis, and climate data (Guagliardo et al., 2020; WHO, 2023a). A Case Investigation Form (CIF) was used to collect information about each patient affected by dracunculiasis (Guagliardo et al., 2020). The CIFs were compiled into line listings at the national level, and these line

listings were submitted by NGWEPs to WHO on the 20th of each subsequent month (WHO, 2023b, 2023d). The line listings contained a subset of the information included in the CIFs.

Although line listing formats varied slightly between countries, core variables consistently captured included age, sex, ethnicity, date of worm emergence, location or village where the case was detected, importation status, containment status, whether the patient contaminated a water source, and whether Abate treatment was applied. Aggregated dracunculiasis data by village contained information about the number of human dracunculiasis cases, number of infected dogs, number of rumors, number of water sources eligible for Abate treatment, number of water sources treated with Abate, number of dogs tethered, and number of households aware of the reward system.

The sampling frame included data submitted by NGWEPs and compiled into the Global Guinea Worm Database at WHO. This dataset included both unpublished and published data, with publicly available information disseminated through the Weekly Epidemiological Record and the Dracunculiasis Eradication Portal (WHO, 2022a, 2022b) All cases reported from the five endemic countries were included in the study.

The Validity of Data Collection Tool and Processes

WHO developed standard operating procedures which includes the data collection tools for collecting information about the cases, rumor registers, and the standard questionnaire for evaluating awareness of the community (WHO, 2015b). The questionnaires were adopted in endemic and formerly endemic countries. The method for

assessing awareness of community about the dracunculiasis and reward has been adopted during the external evaluation in Kenya, DRC, Sudan (unpublished report).

Secondary Data Storage and Protection

The identifiable data were anonymized, and numerical codes were assigned to villages. The data were encrypted and password protected. It were stored on a secure server at the World Health Organization (WHO). The health ministries agreed to WHO's data sharing policy, ensuring the ethical and secure use of data. WHO implemented measures to protect privacy and confidentiality while also avoiding stigmatization and exclusion (World Health Organization, 2018).

Because this study used secondary, de-identified surveillance data, no direct recruitment of human participants occurred. Therefore, informed consent and participant withdrawal procedures were not applicable. The researcher currently works in the WHO Guinea Worm Eradication Programme but maintained analytical independence and followed all institutional protocols to mitigate potential conflicts of interest. In line with WHO and Walden University data management policies, the datasets will be retained securely for five years following study completion and then permanently deleted using standard data destruction procedures.

Ethical Approval Process

Necessary clearance was obtained from the World Health Organization (WHO) for the use of de-identified archival data. Written permission was sought and obtained from the Director of the Global Neglected Tropical Diseases (NTD) Programme and the Team Leader of the Guinea Worm Disease Eradication Program. Prior to the

commencement of the study, approval was also requested from, and granted by, the Walden University Institutional Review Board (IRB), under approval number 04-02-24-0353232.

Because this study used only archival, de-identified surveillance data, there was no direct recruitment of participants. As such, no ethical concerns arose regarding recruitment, consent, or withdrawal from the study. The data used did not contain personal identifiers, and villages were coded numerically to preserve confidentiality. All data were encrypted, stored on WHO's secure server, and accessible only to authorized personnel.

Data will be retained for five years following the completion of the study and then permanently deleted, in accordance with institutional data retention policies. The researcher holds a professional role within WHO's Guinea Worm Eradication Programme but conducted this research independently to avoid any conflict of interest. No incentives were provided or received in association with this study.

Data Analysis Plan

Data Assessment and Extraction

The accessibility and appropriateness of all variables were evaluated for the available database. Variables were assessed for their level of measurement, and recoded where necessary to match the requirements of the research questions and planned analyses. The raw line listings were aggregated to appropriate units of analysis, and multiple datasets (e.g., aggregated surveillance data by village, aggregated animal infection data) were linked using location identifiers and contextual variables. A working

data file containing only the relevant variables was created, as recommended by Little (2013). This approach minimized data handling errors and ensured analytic consistency. The finalized working dataset was imported into IBM SPSS Statistics (Version 28.01) for further data cleaning, descriptive statistics, and inferential analyses.

Additionally, spatial datasets, including climate and surface water occurrence data, were extracted and processed to align with village-level locations. Monthly temperature and precipitation data were derived from historical climate data available through the World Bank Climate Knowledge Portal (World Bank, 2023h), utilizing zonal statistics techniques (ESRI, 2021). Surface water occurrence data were obtained from high-resolution satellite imagery provided by the Joint Research Centre's (JRC) Global Surface Water dataset (Pekel et al., 2016), accessed through the Google Cloud Storage platform (JRC, 2021). Spatial extraction and sampling were conducted using Geographic Information System (GIS) software—ArcGIS Pro (ESRI, 2021) and QGIS (QGIS Development Team, 2022)—to ensure precise geographic alignment across datasets. Extracted variables were matched with village identifiers, and spatial accuracy was validated through coordinate verification and projection checks. The resulting integrated spatial-environmental dataset was subsequently merged with epidemiological and programmatic data, creating a unified dataset suitable for comprehensive statistical and spatial analyses (Anselin et al., 2022)

Research Questions and Hypothesis

Research Question 1: Does the theory of change explain the association between the dog tethered, ponds treated with abate, and people's awareness about the disease and

reward, village access to safe water sources, and guinea worm disease (in humans and animals)?

$H_0$1: The theory of change does not explain the association between the dog tethered, ponds treated with abate, and people's awareness about the disease and reward, village access to safe water sources, and guinea worm disease (in humans and animals)?

H_a1: The theory of change explain the association between the dog tethered, ponds treated with abate, and people's awareness about the disease and reward, village access to safe water sources, and guinea worm disease (in humans and animals)?

Research Question 2: What is the relationship between environmental factors (climate, temperature, water supply) and guinea worm cases or infection?

$H_0$2: There is no relationship between environmental factors and the number of guinea worm cases or infections.

H_a2: The environmental factors have a relationship with the number of Guinea worm cases or infections.

Research Question 3: What is the relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about reporting guinea worm disease/infection?

$H_0$3: There is no relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about Guinea worm disease/infection reporting.

H_a3: There is relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about Guinea worm disease/infection reporting.

Study Variables

Table 2 presents the study variables examined in this research, categorized by variable type, specific variable name, and corresponding level of measurement. These variables were selected based on the conceptual framework and the study objectives to explore environmental, behavioral, and programmatic factors influencing Guinea worm disease transmission.

Table 2

Study Variables

Variable Type	Variable	Level of Measurement
Outcome (Dependent) Variables	Number of Guinea worm cases (human, monthly village-level)	Count (Discrete)
	Total Guinea worm cases (human + animal, annual country-level)	Count (Discrete)
	Number of rumors of Guinea worm disease	Count (Discrete)
Predictor (Independent) Variables	Dog tethering reported (binary: 1 = yes, 0 = no)	Categorical (Binary)
	Awareness about Guinea worm disease (Level 1, 2, 3)	Ratio/Continuous (%)
	Awareness about reward for reporting (Level 1, 2, 3)	Ratio/Continuous (%)
	Village-level monthly mean temperature	Continuous (Interval)
	Village-level monthly total precipitation	Continuous (Interval)
	Mean surface water occurrence within 10-meter buffer	Continuous (Ratio)
Covariates	Month of emergence (seasonality)	Categorical (12 months)
	Country	Categorical (6 countries)

According to Pearl (2009), Directed Acyclic Graphs (DAGs) offer a robust method to visually represent causal assumptions. Directed Acyclic Graphs are widely utilized in epidemiological research to clarify relationships among variables and control for confounding (Hernán & Robins, 2020). A directed acyclic graph (DAG) was developed to illustrate the hypothesized relationships among the study variables. As shown in Figure 9, environmental, behavioral, and spatial factors were theorized to influence the number of reported Guinea worm disease cases at the village or country level. The DAG was used to guide model building, clarify potential pathways of association, and inform covariate selection for multivariate and spatial analyses (Hernán & Robins, 2020). This conceptual framework reflected the integrated, multi-dimensional approach adopted in the study. Baseline risk factors, including prior human cases and animal infections, dog ownership status, and surveillance activity (active versus passive),

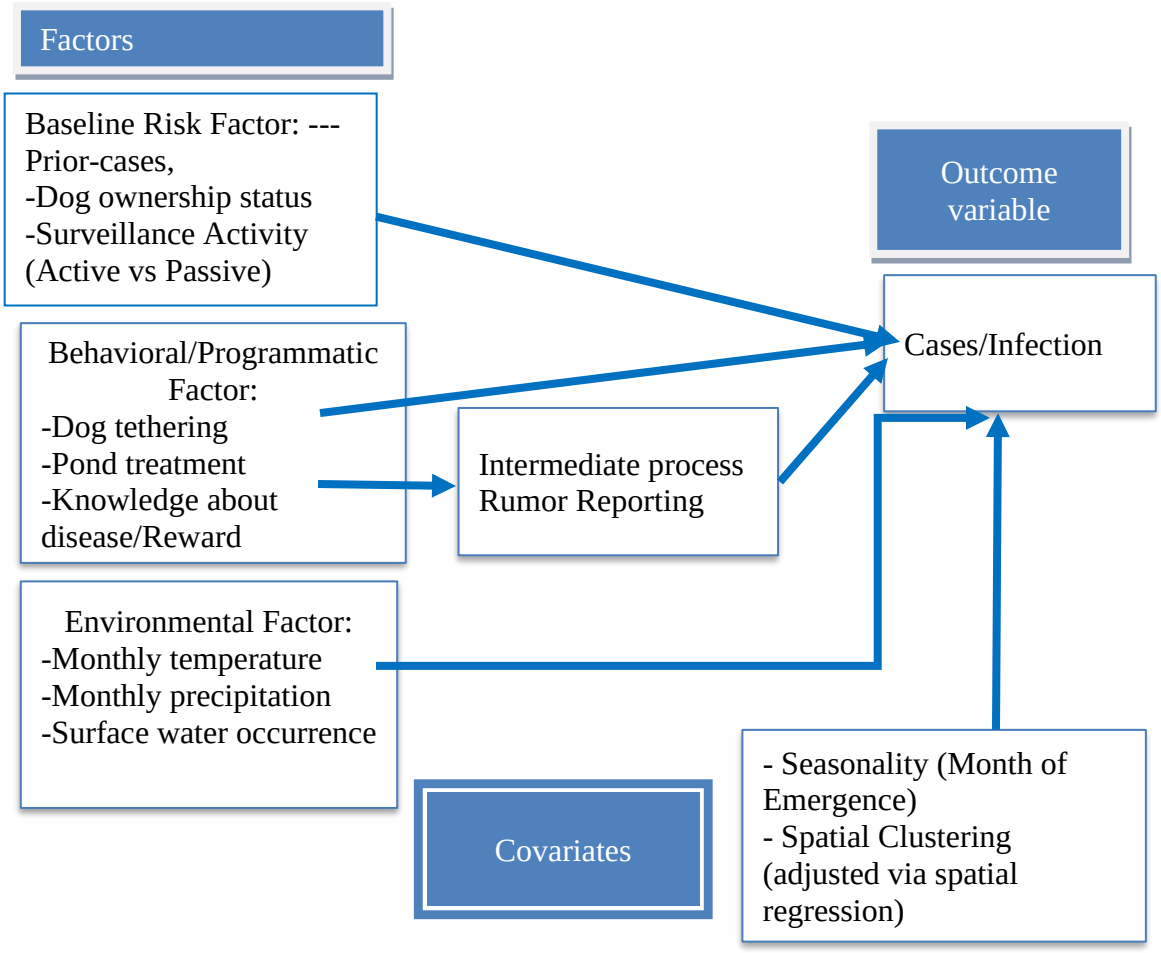
are hypothesized to influence the risk of Guinea worm disease (GWD) transmission. Behavioral and programmatic interventions—specifically dog tethering, pond treatment with Abate, and awareness about Guinea worm disease and reward programs—are expected to directly affect infection risk, as well as indirectly through the intermediate process of rumor reporting, which serves as an early indicator of transmission activity. Environmental factors, including monthly temperature, precipitation, and surface water occurrence, are also modeled as independent predictors of transmission risk. To account for potential confounding effects, seasonality (month of emergence) and spatial clustering (identified through spatial analysis and adjusted using spatial regression models) are included as covariates.

The data analysis plan was designed to address the study's research questions through a combination of descriptive and inferential statistical techniques. Descriptive statistics were used to summarize the distribution and characteristics of the variables. Inferential statistics were conducted to examine relationships and test hypotheses derived from the study's theoretical framework.

The analysis for Research Question 1 (RQ1) was grounded in the theory of change, which posited that dog tethering practices, pond treatment with abate, community awareness about the disease and rewards, and access to safe water sources would be associated with reduced Guinea worm disease occurrence in humans and animals. Inferential analyses for RQ1 tested these associations using appropriate statistical modeling techniques, accounting for the count nature and distributional characteristics of the data.

Figure 9

Directed Acyclic Graph (DAG) of Baseline, Environmental, Behavioral, and Spatial Predictors of Guinea Worm Disease Cases



Research Questions 2 (RQ2) and 3 (RQ3) explored environmental and behavioral factors influencing Guinea worm disease incidence and rumor reporting, respectively. Regression modeling, spatial analysis, and correlation analyses were conducted as detailed in the sections below.

All analyses were performed at a significance level of $p < .05$, with 95% confidence intervals reported. When assumptions for parametric tests were violated, non-parametric or alternative modeling approaches were employed.

Descriptive Statistics

The study employed descriptive statistics tailored to the level of measurement of variables. Mean, standard deviation, median, and interquartile ranges described continuous variables (e.g. number of cases, infections, environmental parameters such as temperature and precipitation). Percentages and frequencies summarized categorical data (e.g. dog tethering status, pond treatment status, awareness levels). Visualizations, including histograms, boxplots, frequency tables, and time series plots, illustrated data distributions and temporal trends effectively.

Time series analysis use stochastic methods to identify trends, seasonality, and patterns, leveraging exponential smoothing (Holt-Winters) and ARIMA modeling, with parameters selected based on ACF/PACF analysis and AIC criteria (Wei, 2013). Cross-country comparisons involved descriptive analyses of means and standard deviations for key variables, highlighting significant variations and commonalities.

Inferential Statistics

Inferential statistical analyses were conducted to address each research question based on the study's theoretical and empirical framework. The analytical approach was based on the generalized linear model (GLM) framework, allowing for flexibility in modeling both continuous and count-based outcomes. The analysis for Research Question 1 (RQ1) was grounded in the theory of change, positing that dog tethering practices, pond treatment with abate, awareness about the disease and rewards, and access to safe water sources would be associated with reductions in Guinea worm disease incidence. Research Questions 2 (RQ2) and 3 (RQ3) examined environmental and behavioral factors related to disease occurrence and rumor reporting.

All statistical analyses were conducted using a significance level of $p < .05$, with 95% confidence intervals reported. Where assumptions of parametric tests were not met, non-parametric alternatives were considered.

To address Research Question 1, a multiple linear regression analysis was conducted using national-level program data. The dependent variable—the number of Guinea worm disease cases (human and animal combined)—was log-transformed to meet normality and linearity assumptions required for regression analysis. Independent variables included the percentage of dogs tethered, proportion of ponds treated with Abate, awareness scores, and access to improved water sources Assumptions of linearity, normality of residuals, homoscedasticity, multicollinearity, and independence of errors were evaluated using residual plots, variance inflation factors (VIF), and the Durbin–Watson statistic (Walden University, 2023; Wang, 2002). The log transformation

addressed the skewed distribution of case counts and helped stabilize variance across predictor levels. This modeling approach aligned with the study's theory of change by testing whether programmatic interventions were statistically associated with changes in reported Guinea worm cases.

Secondary Time Series Forecasting Analysis

In addition to the association analyses, a secondary time series forecasting analysis was conducted to explore the future trajectory of Guinea worm disease incidence in key endemic countries. This supplementary analysis aimed to provide dynamic projections of future case counts alongside the cross-sectional findings, offering insights into whether current intervention trajectories are sufficient to achieve the 2030 transmission interruption goal.

Time series forecasting methods were applied to model historical trends and predict future case counts (IBM Corp., 2021; Wei, 2013). The Expert Modeler function in SPSS was employed, which automatically identifies and selects the optimal forecasting model based on data characteristics, including autoregressive integrated moving average (ARIMA) or exponential smoothing models. This approach minimized model selection bias, maximized forecast accuracy, and accommodated the limited number of annual observations available for each country.

Model specifications varied by country. For example, a simple exponential smoothing model was selected for Chad, whereas an ARIMA(0,0,0) model was used for Mali. Models were evaluated using fit statistics including stationary R-squared, root mean square error (RMSE), mean absolute percentage error (MAPE), and the Bayesian

information criterion (BIC). Forecasts included 95% confidence intervals to account for uncertainty.

Together, these dual analytical strategies—cross-sectional association analyses and dynamic time series forecasting—offered a robust understanding of both the existing relationships among key intervention factors and the projected trends in Guinea worm disease burden (IBM Corp., 2021; Wei, 2013).

Research Question 2 employed a combination of negative binomial regression and spatial analysis techniques to explore the relationship between environmental factors — specifically temperature, precipitation, and surface water occurrence— and the number of Guinea worm cases or infections. Negative binomial regression was selected due to the count nature of the dependent variable and the presence of overdispersion, which violates the assumptions of traditional Poisson regression.

Spatial analysis was conducted to examine the geographic distribution of both environmental factors and Guinea worm disease cases. This included assessing spatial autocorrelation using Global Moran's I, identifying local spatial clusters using Local Indicators of Spatial Association (LISA), and modeling spatial dependencies through spatial regression techniques (e.g., Spatial Lag and Spatial Error Models). This mixed-method spatial-statistical approach provided a comprehensive understanding of the environmental determinants of Guinea worm disease, incorporating both statistical significance and spatial distribution. Understanding of the environmental determinants of Guinea worm disease, accounting for both statistical significance and geographic patterns.

Research Question 3 (RQ3) focused on examining the relationship between awareness and knowledge about Guinea worm disease and the number of reported rumors or suspected cases. After initial descriptive and correlational analyses, a multiple linear regression model was conducted with the number of rumors as the dependent variable and awareness variables as predictors. Where appropriate, model diagnostics and transformations were applied to meet GLM assumptions.

For all inferential statistical tests, a significance level of $p < .05$ and a 95% confidence interval were used to determine whether to reject or retain the null hypothesis (Bruce et al., 2008). In addition, analysis of variance (ANOVA) was also conducted to compare mean awareness levels across different endemicity categories (e.g., endemic, at-risk, and non-endemic areas), assuming interval-scale data and approximate normality within groups (Walden University, 2023).

Descriptive statistics, including frequencies, means, and standard deviations, were used to summarize the awareness variables and rumor counts prior to regression analysis. As with other analyses, a significance threshold of $p < .05$ and a 95% confidence interval were used for hypothesis testing.

Power Analysis

This study analyzed all available country-year observations for RQ 1 (N = 24). Because the sample size was fixed, an a-priori calculation to determine the “required” N was not applicable. Instead, following recommended practice (Cohen, 1988; Faul et al., 2009), a post-hoc (observed-power) analysis after estimating the multiple-regression model.

Using G*Power 3.1 (test family: *F* tests → Linear multiple regression, fixed model, R^2 deviation from 0), the following inputs were entered:

$\alpha = .05$

observed $R^2 = .534$

total sample size N = 24

number of predictors k = 4

G*Power returned an effect size $f^2 = 1.15$, non-centrality parameter $\lambda = 27.48$, critical $F(4, 19) = 2.90$, and achieved power $(1 - \beta) = .974$. A power level well above the conventional .80 benchmark suggests that the nonsignificant coefficients for awareness, safe-water access, and Abate treatment are unlikely to be Type II errors attributable to insufficient sample size.

Because post-hoc power is algebraically determined by the observed effect size, it should be interpreted descriptively rather than as additional evidence of validity (Hoenig & Heisey, 2001). Nevertheless, reporting these values enhances transparency about the sensitivity of the analysis with the available data.

Figure 10

Post Hoc Power Analysis Results for Multiple Linear Regression Model (N = 24)

F tests – Linear multiple regression: Fixed model, R^2 deviation from zero
Analysis: Post Hoc. Compute achieved power, given α, sample size and effect size
Input parameters

Parameter	Value
Effect size f^2	1.145
α error probability	0.05
Total sample size	24
Number of predictors	4

Output parameters

Parameter	Value
Non-centrality parameter λ	27.48
Critical F (4, 19)	2.8951
Numerator *df*	4
Denominator *df*	19
Achieved power (1 – β)	0.9736

These statistics correspond to a post-hoc power analysis for a fixed-effects multiple-regression model (R^2 deviation from zero) with the specified inputs.

Threats to Validity

Internal validity may have been affected by the customization of case definitions and reporting tools to local settings within countries, despite the existence of standard definitions for cases of dracunculiasis and rumors and the use of standardized tools. Some countries defined rumors as suspected cases, while others combined the number of human case rumors with infected animal rumors. It was important to utilize a codebook when working with secondary data to ensure consistency (Little, 2013).

External validity may have been impacted by under coverage bias and underreporting of dracunculiasis to the surveillance system, limiting the generalizability of the results (Creswell, 2009). Another threat to external validity was sampling bias, which could have occurred if data were only reported from specific areas, particularly in countries where the disease was less prevalent. Limitations also included inherent problems with data quality and completeness associated with surveillance and secondary data sources, such as non-response bias and the inaccessibility of individual case investigation forms.

Statistical conclusion validity may have been threatened by potential violations of model assumptions, including overdispersion in count data and spatial autocorrelation, which were addressed by using negative binomial regression and spatial regression models. Construct validity threats included possible misalignment between proxy indicators (e.g., awareness proportions or water access) and actual community-level practices. These threats were minimized by using validated WHO tools and consistent data extraction protocols. Moreover, while secondary data are often susceptible to publication or reporting biases, recent evidence suggests that such biases may not systematically affect the timing or quality of published results in similar contexts (Olsson & Sundell, 2023).

Summary

Chapter 3 of this research study outlined the research methodology and design used to examine the relationship between risk factors, environmental variables, and Guinea worm disease in Angola, Chad, Ethiopia, Mali, and South Sudan. The study

employed a quantitative approach grounded in epidemiological research principles to better understand the factors influencing the prevalence and persistence of Guinea worm disease. The research design was retrospective, utilizing secondary data collected from 2012 to 2023, during which these countries continued their efforts toward disease eradication. This chapter outlined the data sources, research questions, hypotheses, and statistical methods used for data analysis.

The study used secondary data collected by the National Guinea Worm Disease Eradication Programs (NGWEP) in the five endemic countries. Data sources included demographic information, case listings, data on infected animals, environmental data, and awareness survey results. The study focused on evaluating the relationship between various risk factors, such as dog tethering, pond treatment with Abate, and community awareness, and the incidence of Guinea worm disease in humans and animals. It also examined the impact of environmental factors, such as climate and water supply, on the number of cases. The data analysis plan included descriptive statistics, negative binomial regression, time series analysis and forecasting, and spatial regression analysis.

A post hoc justification for statistical power was also included, noting that an a priori power analysis was not feasible due to the retrospective nature of the study. Instead, the study relied on effect size, sample size, and statistical significance values to assess the adequacy of the analyses. The research acknowledged potential threats to internal and external validity, including variations in case definitions across local settings, underreporting, sampling bias, and data quality limitations inherent in secondary surveillance datasets.

IBM SPSS Statistics was used for statistical analyses, while QGIS, ArcGIS Pro, and GeoDa were employed for spatial analyses. The results of these analyses are presented in Chapter 4.

Chapter 4: Results

Introduction

The purpose of this chapter is to present the findings of the quantitative analyses conducted to address the three research questions guiding this study. This research aimed to investigate the relationship between selected behavioral, programmatic, and environmental risk factors and the incidence of Guinea worm disease across five endemic countries between 2012 and 2023. The study also examined the role of awareness and knowledge—particularly regarding reward systems and disease recognition—in shaping rumor reporting patterns, with the broader aim of informing strategies toward the eradication of Guinea worm disease by 2030.

The following research questions and hypotheses guided the analysis:

Research Question 1: Does the theory of change explain the association between the dog tethered, ponds treated with abate, and people's awareness about the disease and reward, village access to safe water sources, and guinea worm disease (in humans and animals)?

H_o1**:** The theory of change does not explain the association between the dog tethered, ponds treated with abate, and people's awareness about the disease and reward, village access to safe water sources, and guinea worm disease (in humans and animals).

H_a1**:** The theory of change explain the association between the dog tethered, ponds treated with abate, and people's awareness about the disease and reward,

village access to safe water sources, and guinea worm disease (in humans and animals).

Research Question 2: What is the relationship between environmental factors (climate, temperature, water supply) and guinea worm cases or infection?

H_o2**:** There is no relationship between environmental factors and the number of guinea worm cases or infections.

H_a2**:** The environmental factors have a relationship with the number of Guinea worm cases or infections.

Research Question 3: What is the relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about reporting guinea worm disease/infection?

H_o3**:** There is no relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about Guinea worm disease/infection reporting.

H_a3**:** There is a relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about Guinea worm disease/infection reporting.

This chapter is organized by research question. Each section presents the descriptive statistics, assumption testing, and inferential statistical results related to the respective hypothesis. Results are presented using APA-style tables and figures, with supplemental materials provided in the appendices as necessary. Interpretation of the findings and their broader implications is reserved for Chapter 5.

Data Analysis

Analyses were conducted using SPSS, QGIS, ArcGIS Pro and GeoDa. Research Question 1 was analyzed using multiple linear regression applied to national-level data to evaluate associations proposed by the theory of change. Research Question 2 used negative binomial regression models at the village-month scale to assess the impact of environmental variables (temperature, precipitation, and surface water occurrence), followed by spatial regression using Spatial Lag and Spatial Error Models in GeoDa to account for spatial autocorrelation. Research Question 3 was assessed using descriptive statistics, Pearson correlations, and multiple linear regression to determine the associations between awareness and knowledge variables and the volume of rumor reports.

The results for each question are presented in sequence, including the relevant statistical outputs. Collectively, the findings provide an empirical foundation for understanding the multidimensional drivers of Guinea worm disease in support of eradication strategies.

Data Collection and Sample Characteristics

Time Frame and Data Sources

The data used in this study were obtained from archival program datasets compiled by the Guinea Worm Eradication Program (GWEP) and partner organizations between 2012 and 2023. These data included annual and monthly village-level case records, program implementation indicators (such as tethering, Abate use, awareness), and environmental covariates (e.g., temperature, precipitation, water occurrence)

extracted using GIS tools. No direct recruitment or survey participation was conducted for this dissertation. Therefore, response rates are not applicable.

Data Collection and Sample Statistics

For research question 1, the analysis was conducted at the country-year level, where each row in the dataset represents a country's aggregated program indicators for a specific year. The countries included in the analysis were Angola, Cameroon, Chad, South Sudan, Mali, and Ethiopia. For each country, village-level data on Guinea worm cases were aggregated annually, and the total number of cases (both human and animal) was computed as the outcome variable. This variable was log-transformed (log_totalcases) to improve normality and satisfy statistical assumptions.

The predictors included four national-level indicators derived from programmatic data: (1) a binary indicator for dog tethering (coded as 1 if any dog tethering activity was reported in that year and country, and 0 otherwise), (2) the proportion of water sources treated with Abate (pond_abate_pct), (3) the mean awareness level regarding the disease and the reward system (awareness_mean), and (4) the percentage of villages with access to safe water (village_safe_water_pct).

The final analytical dataset included 24 records (i.e., 24 country-year combinations) with complete data on the dependent variable and all four predictors. Although the small sample size limits statistical power and the ability to detect modest effects, the analytical approach was appropriate given the rarity of the disease and the limited number of endemic countries with confirmed transmission during the study

period. The design aligns with the objective of assessing how national-level programmatic efforts relate to transmission outcomes over time.

For research question 2. this analysis used village-level monthly data on human Guinea worm disease cases across Chad, Ethiopia, Mali, and South Sudan, covering the period from January 2012 to December 2023. The dataset includes 722 villages and over 72,000 village-month records. Each row represents the number of reported human GWD cases in a specific village during a specific month.

Environmental Predictor Variables

- Temperature (temp_val): average monthly temperature extracted via zonal statistics over a 10m buffer around each village.
- Precipitation (precip_val): average monthly rainfall derived similarly.
- Water presence (water_mean_occurrence): average surface water occurrence extracted from JRC Global Surface Water raster layers.

Missing climate values for 2021–2023 were imputed using village-level monthly means from 2012–2020. The analysis excluded animal infections and focused only on human cases. A total of 814 village-month observations with at least one reported human Guinea worm disease (GWD) case were included in the analysis. After merging and imputing missing values, complete data were available for 718 observations across all predictors. Given the large analytic sample (N = 718) and the small standard errors of the coefficients, the study was well-powered to detect even modest environmental effects on monthly Guinea-worm incidence. The absence of statistically significant predictors,

together with a pseudo-$R^2 \approx 0$, therefore most plausibly reflects genuine lack of association at the temporal and spatial scales analyzed, rather than insufficient power.

The data used to answer Research Question 3 were drawn from village-level reports collected across endemic and at-risk areas from 2012 to 2023. The analytic sample included variables capturing community awareness about Guinea worm disease, awareness of the reward system, and the number of rumors reported. These variables were compiled from national surveillance systems and programmatic reports submitted by endemic countries to the World Health Organization (WHO).

The final dataset included 232 village-month records with non-missing values for the dependent variable (RUMORS) and the three awareness-related predictors: awareness_1 (Level I: endemic areas), awareness_2 (Level II: at-risk areas), and awareness_3 (Level III: formerly endemic or never endemic areas). These awareness indicators represented the proportion of surveyed individuals within each village who correctly identified the reward for reporting a case or expressed knowledge of Guinea worm disease symptoms.

Descriptive statistics for the analytic sample indicated a mean of 2.96 rumors reported per village-month (SD = 5.33, range: 0–41). Mean awareness levels varied by endemicity level: awareness_1 had a mean of 0.71 (SD = 0.18), awareness_2 had a mean of 0.65 (SD = 0.21), and awareness_3 had a mean of 0.51 (SD = 0.23). All continuous predictors were examined for normality; while rumor counts were positively skewed, the use of a multiple regression accounted for this distributional characteristic.

Missing data were minimal and primarily due to incomplete survey submissions in selected years. Cases with missing values for any of the awareness variables or outcome were listwise deleted from regression analyses. All data were de-identified and used in accordance with WHO surveillance and ethical standards for secondary data analysis.

Results

Research Question 1

Research Question 1: Does the theory of change explain the association between the dog tethered, ponds treated with abate, and people's awareness about the disease and reward, village access to safe water sources, and guinea worm disease (in humans and animals)?

$H_0$1: The theory of change does not explain the association between the dog tethered, ponds treated with abate, and people's awareness about the disease and reward, village access to safe water sources, and guinea worm disease (in humans and animals)?

H_a1: The theory of change explain the association between the dog tethered, ponds treated with abate, and people's awareness about the disease and reward, village access to safe water sources, and guinea worm disease (in humans and animals)?

This section presents the results of the statistical analyses conducted to examine whether the theory of change (TOC) explains the association between dog control practices, vector control (abate application), community awareness, and access to safe

water with the number of reported Guinea worm disease cases (in humans and animals combined) at the country level from 2012 to 2023.

Descriptive Statistics

Descriptive statistics were computed for all variables included in the multiple regression model for Research Question 1. These included the log-transformed total number of Guinea worm cases (log_totalcases) and the four independent variables: dog tethering (Tethering_dummy), awareness of the disease and reward system (awareness_mean), proportion of villages with access to safe water (village_safe_water_pct), and proportion of water sources treated with Abate (pond_abate_pct).

Table 3 presents the measures of central tendency, dispersion, and shape of the distribution for each variable. The mean of log-transformed total cases was 1.19 (SD = 0.94), with values ranging from 0.00 to 3.31. The mean of the awareness variable was 0.67 (SD = 0.18), while the mean percentage of access to safe water was 54.13% (SD = 26.38%). The mean coverage of Abate treatment was 32.91% (SD = 39.97%). The binary indicator for dog tethering had a mean of 0.18 (SD = 0.39), indicating that only a small proportion of country-year records reported implementing this intervention.

Skewness and kurtosis values were inspected to evaluate the normality of the variable distributions. Most variables showed moderate skewness and kurtosis, with the exception of the raw (non-transformed) total cases variable ranged from 0 to 2,030, with a mean of 161.92 (SD = 387.33), which was highly positively skewed (Skewness = 3.11, Kurtosis = 10.34), justifying its log transformation prior to regression analysis. The log-

transformed dependent variable (log-transformed total cases), which had a mean of 1.19 (SD = 0.94), showed improved symmetry and distribution (Skewness = 0.73, Kurtosis = -0.41). On average, 67.33% of respondents were aware of Guinea worm disease and rewards (mean awareness score, SD = 0.18), and 54.13% of households had access to safe water sources (safe water access, SD = 0.26). Ponds treated with abate accounted for 32.91% (ponds with abate, SD = 0.40). Dog tethering was practiced in 18.18% of cases (dog tethering, SD = 0.39). The valid sample size with complete data across all variables was 24.

Table 3

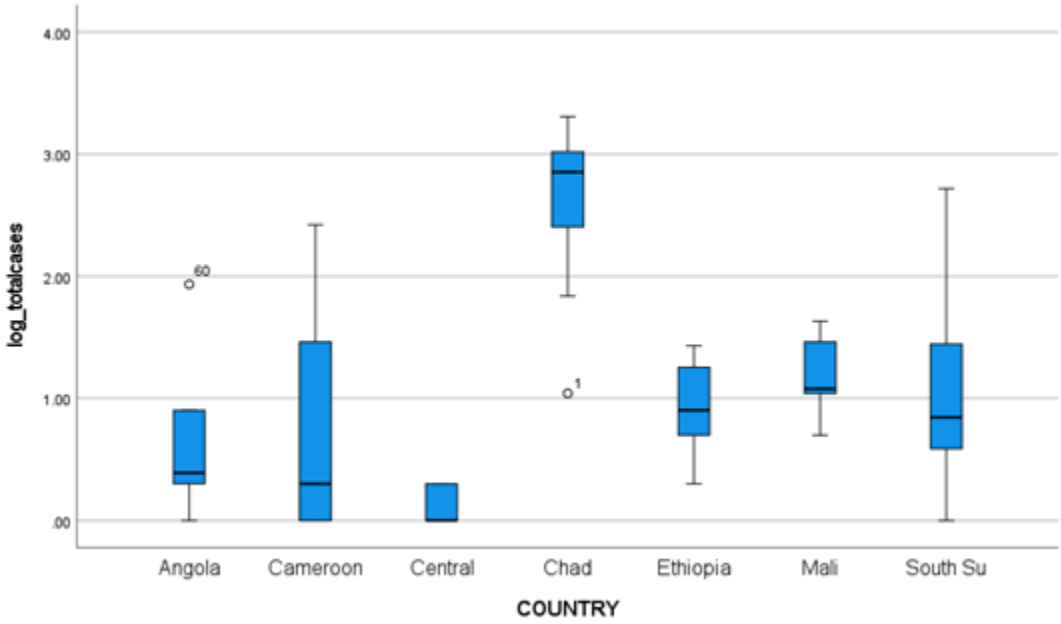
Descriptive Statistics for Variables Used in Research Question 1 Variables

Variable	N	Min	Max	Mean	SD	Skewness	Kurtosis
Log-transformed total cases	66	0.00	3.31	1.194	0.937	0.729	-0.408
Mean awareness score	42	0.33	0.92	0.673	0.176	-0.429	-0.970
Safe water access (%)	32	0.01	0.97	0.541	0.264	-0.172	-1.141
Ponds treated with abate (%)	40	0.00	1.00	0.329	0.400	0.729	-1.289
Dog tethering (1=yes, No=0)	66	0.00	1.00	0.182	0.389	1.689	0.877
Total cases (raw)	66	0.00	2030	161.92	387.33	3.113	10.340

Note. Valid N (listwise) = 24. M = mean; SD = standard deviation

Figure 11

Boxplot Showing the Distribution of Log-Transformed Total Guinea Worm Cases by Country (N = 66).



A preliminary examination of the log-transformed total Guinea worm cases by country is presented in Figure 11. The box represents the interquartile range, the line within the box indicates the median, and the whiskers represent the range. Dots indicate outliers. Chad exhibited the highest median number of cases, with a relatively narrow interquartile range, suggesting a concentration of high case counts. In contrast, the Central African Republic displayed consistently low values. Outliers were observed in Angola, Cameroon, and Chad. These patterns indicate substantial variability in case distribution across countries, justifying further regression analysis.

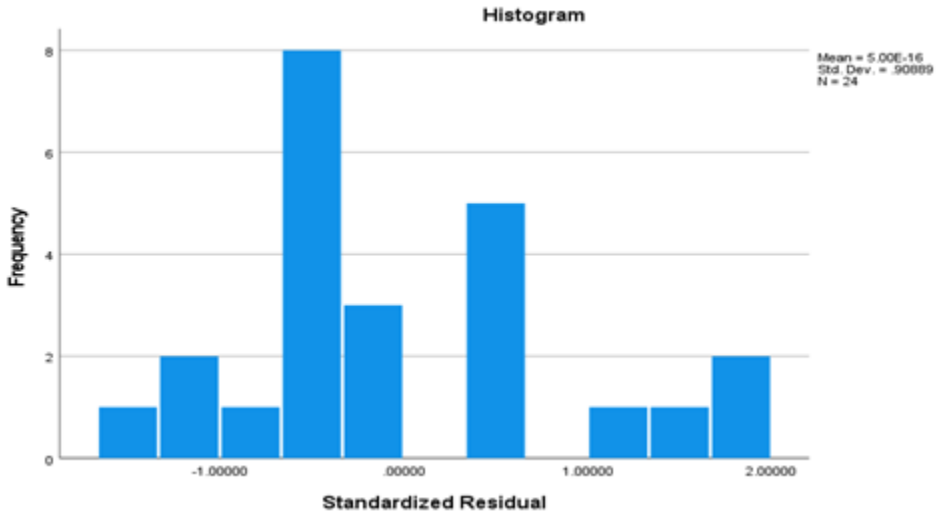
Evaluation of Assumption

Prior to interpreting the results for Research Question 1 from the multiple linear regression model, several key statistical assumptions were checked to ascertain the fit of

the model and the robustness of the conclusions. The assumptions assessed were linearity, normality of residuals, homoscedasticity, independence of residuals, and multicollinearity.

Figure 12

Histogram of Standardized Residuals

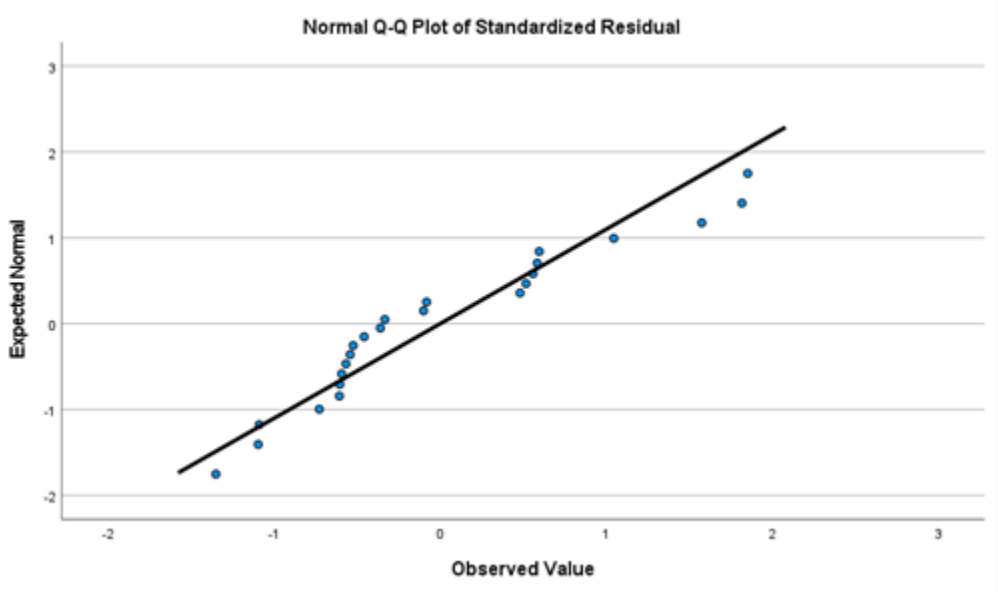


Linearity

This assumption was assessed through scatterplots of each independent variable plotted against the dependent variable (log_totalcases). Visual inspection suggested a mostly linear relationship between the outcome and continuous predictors (e.g., awareness_mean, village_safe_water_pct, pond_abate_pct and Tethering_dummy). Some plots showed variation, but no strong evidence was found for curvilinearity. Normality of residuals. The histogram (see Figure 12) and normal Q-Q plots (see Figure 13) were examining the distribution of standardized residuals. The histogram displayed an approximately symmetrical, bell-shaped distribution of standardized residuals.

Figure 13

Normal Q-Q Plot of Standardized Residuals for the Negative Binomial Regression Model Examining Predictors of Guinea Worm Case Counts



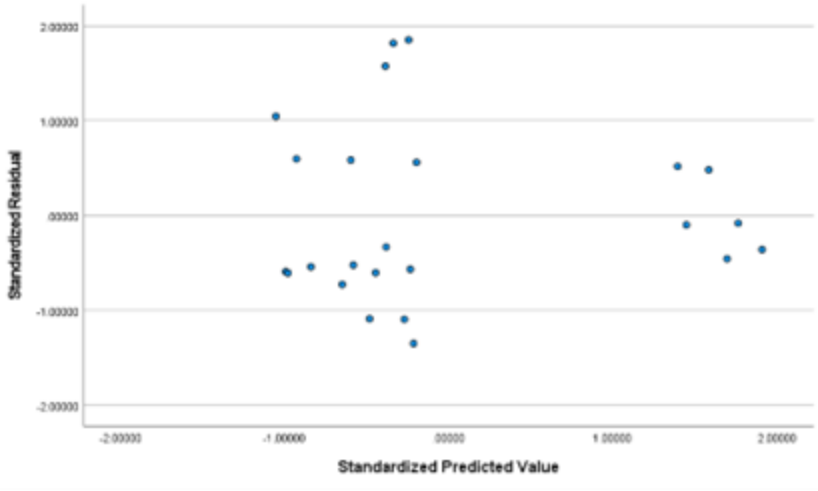
In addition, the normal Q-Q plot revealed that the plots strongly aligned with the diagonal reference line, confirming that the residuals approached a normal distribution. Accordingly, the normality assumption was deemed reasonably met.

Homoscedasticity

Homogeneity of variances was assessed by plotting standardized residuals versus standardized predicted values. The plot (see Figure 14) showed a more or less random spread, with no audience erupting into a shape or concerted effort to badger or flood an against. The constant variance assumption is promoted by the fact that there is no systematic structure of residual spread. Thus, the homoscedasticity assumption was deemed met.

Figure 14

Scatterplot of Standardized Residuals Versus Standardized Predicted Values



Multicollinearity

Variance inflation factor (VIF) and tolerance values were used to evaluate multicollinearity among predictors. All VIF values ranged from 1.18 to 1.47, which are well below the conventional cutoff of 10, indicating low collinearity. Tolerance values ranged from 0.68 to 0.85, exceeding the minimum threshold of 0.10. These diagnostics suggest that multicollinearity was not a concern in the model.

Independence of Residuals

The Durbin-Watson statistic was 2.22, which falls within the acceptable range (1.50–2.50), suggesting no evidence of autocorrelation among residuals. This supports the assumption that residuals are independent.

Bivariate Relationships (Pearson Correlation)

Pearson correlation coefficients were calculated to assess the strength and direction of linear relationships between study variables. Tethering practices were

significantly positively correlated with log-transformed Guinea worm case counts (r = .416, $p < .001$), indicating that more frequent reports of dog tethering were associated with higher case counts. Village access to safe water also showed a statistically significant positive correlation with log-transformed case counts ($r = .424$, $p = .015$), which may reflect programmatic targeting of interventions in high-incidence areas.

Neither pond treatment with Abate ($r = .189$, $p = .243$) nor mean awareness score ($r = –.277$, $p = .076$) showed statistically significant bivariate correlations with the dependent variable. Additionally, all correlations among predictors were below the conventional multicollinearity threshold of $r = .70$, further confirming that the independent variables were not highly intercorrelated.

Summary of Assumptions

All major assumptions for multiple linear regression—including linearity, normality of residuals, homoscedasticity, multicollinearity, and independence—were reasonably met. Therefore, the regression results for Research Question 1 can be considered valid and interpretable.

Multiple Linear Regression Analysis

A multiple linear regression analysis was conducted to examine whether the theory of change explains the association between programmatic indicators—dog tethering, pond treatment with Abate, awareness about Guinea worm disease and reward, and village access to safe water—and the log-transformed total number of Guinea worm disease cases (log_totalcases) reported at the country level. The predictors entered into

the model included dog tethering (Yes=1, No=0, pond treated with Abate (%), safe water access (%), and mean awareness score.

Sample and Descriptive Statistics

Descriptive statistics were first calculated using all available data for each variable (see Table 4). To characterize the analytical sample used in the multiple regression model, additional descriptive statistics were computed using only the 24 cases with complete data across all predictors and the dependent variable. The model was estimated using data from 24 country-year records (36.4% of total 66 records), as shown in the case processing summary. Forty-two cases (63.6%) were excluded due to missing values in one or more variables.

Table 4

Descriptive Statistics for Variables Included in the Multiple Linear Regression Model (N = 24)

Variable	Mean	SD	Minimum	Maximum	Skewness	Kurtosis
Log-transformed total cases	1.8344	0.97015	0.70	3.31	0.73	-0.41
Dog tethering	0.2500	0.44233	0.00	1.00	1.69	0.88
Ponds treated with Abate (%)	0.2779	0.37586	0.00	1.00	0.73	-1.29
Safe water access (%)	0.5978	0.21622	0.19	0.97	-0.17	-1.14
Mean awareness score	0.6418	0.20392	0.33	0.92	-0.43	-0.97

Note. N = 24. SD = Standard Deviation.

Model Fit

The overall model fit was evaluated using multiple indicators. The Omnibus Test of Model Coefficients was statistically significant, $\chi^2(4) = 18.306$, $p = .001$, indicating that the full model provided a significantly better fit to the data than the intercept-only model. The deviance-to-degrees of freedom ratio was 10.096/19 = 0.531, and the Pearson

chi-square/degrees of freedom ratio was also 0.531. Both values are well below 1, suggesting slight under dispersion but acceptable overall model fit (a ratio close to 1 typically indicates a good fit).

Model selection criteria were also assessed. The Akaike Information Criterion (AIC) was 59.327, Corrected AIC (AICC) was 64.268, Bayesian Information Criterion (BIC) was 66.395, and the Consistent AIC (CAIC) was 72.395. These information criteria support internal model comparisons, with lower values indicating better fit. These values can be used as benchmarks for evaluating alternative models in subsequent analyses.

Tests of Individual Predictors

The Wald chi-square tests for individual predictors (see Table 5) indicated that only dog tethering (Yes = 1, No = 0) was a statistically significant predictor of log-transformed total Guinea worm case counts, $\chi^2(1) = 13.739$, $p < .001$. The effects of ponds treated with Abate, safe water access, and mean average score were not statistically significant, with *p*-values greater than .05.

Parameter Estimates

The unstandardized regression coefficients (*B*), standard errors (*SE*), confidence intervals (95% CI), and significance levels (*p*) are summarized below:

Table 5

Parameter Estimates for the Multiple Linear Regression Model Predicting Log-Transformed Total Guinea Worm Cases

Predictor	*B*	*SE*	95% CI	Wald χ^2	*p*
Intercept	1.398	0.739	[-0.050, 2.846]	3.581	.058
Dog tethering (Yes = 1, No =0)	1.352	0.365	[0.637, 2.067]	13.739	<.001
Ponds treated with Abate (%)	-0.026	0.411	[-0.831, 0.780]	0.004	.950
Safe water access (%)	0.704	0.757	[-0.779, 2.188]	0.866	.352
Mean awareness score	-0.492	0.721	[-1.905, 0.922]	0.465	.495

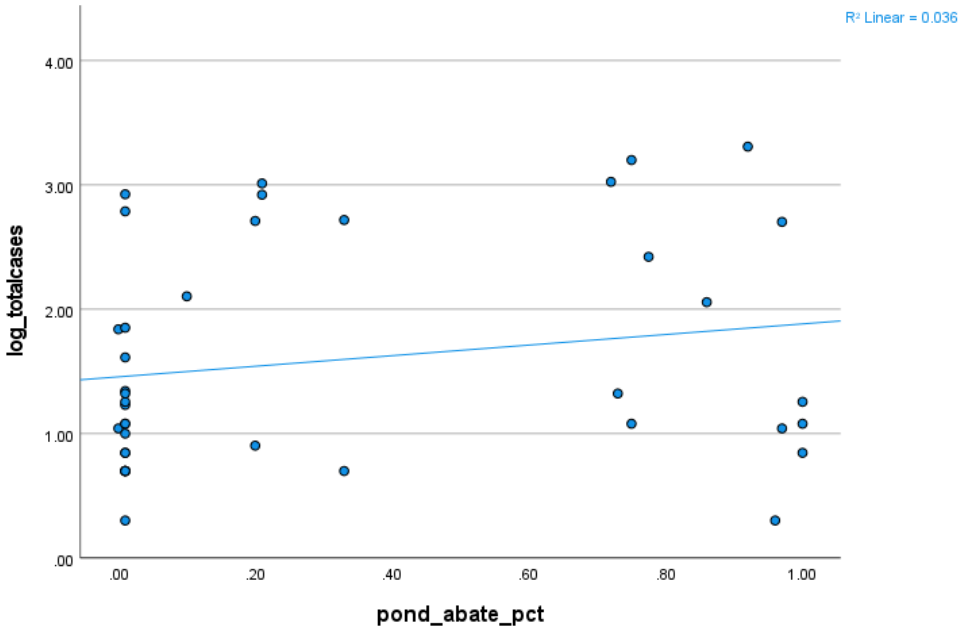
Note. *B* = unstandardized regression coefficient; *SE* = standard error; *CI* = confidence interval; Wald-χ^2 = Wald chi-square test statistic; *p* = significance level. Dependent variable: log-transformed total Guinea worm cases. Predictors: dog tethering, ponds treated with Abate, safe water sources, and mean awareness score.

The only statistically significant predictor was dog tethering ($B = 1.352$, $SE = 0.365$, $p < .001$), indicating that, after adjusting for other variables in the model, countries reporting dog tethering had significantly higher log-transformed Guinea worm case counts. The represents substantial effect, the presence of tethering (vs absence) was associated with 1.352-unit increase in the log-transformed total number of cases.

This counterintuitive finding may reflect the targeting of tethering intervention in areas with higher endemicity, rather than a causal effect of tethering on increased cases.

Figure 15

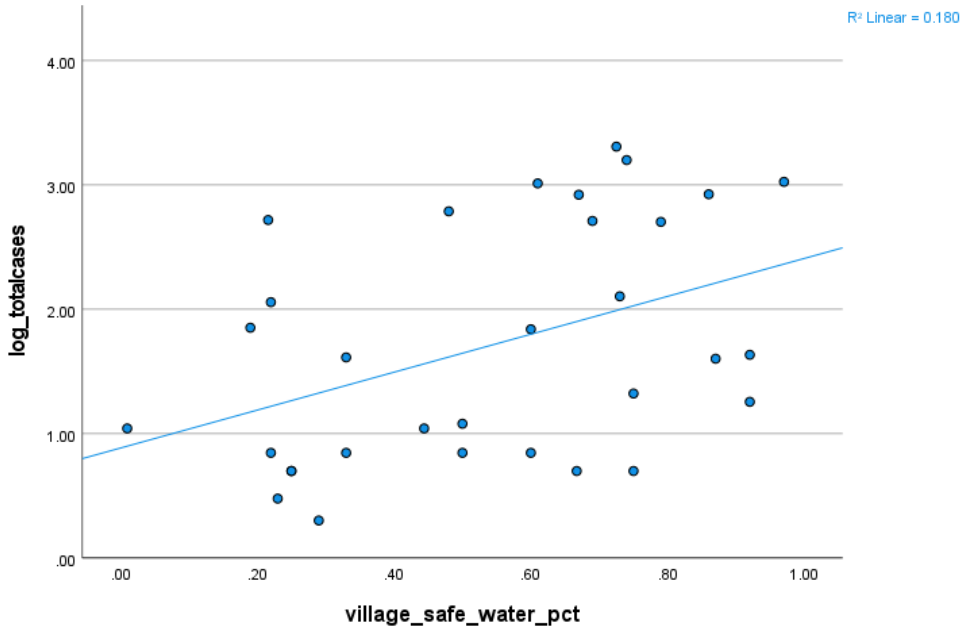
Scatter Plot Showing the Relationship Between Proportion of Ponds Treated with Abate and Log-transformed Total Guinea Worm Cases



A simple linear regression line is included, indicating a very weak positive relationship between pond treatment with Abate (%) (pond_abate_pct) and log-transformed Guinea worm case counts (log_totalcases) (R^2 = .036) (see Figure 15). This suggests that only 3.6% of the variance in reported case counts can be explained by the proportion of ponds treated. The scatter indicates substantial variability in case counts, across levels of treatment, with no apparent linear trend. The relationship is weak and not statistically significant, as confirmed by the regression analysis output.

Figure 16

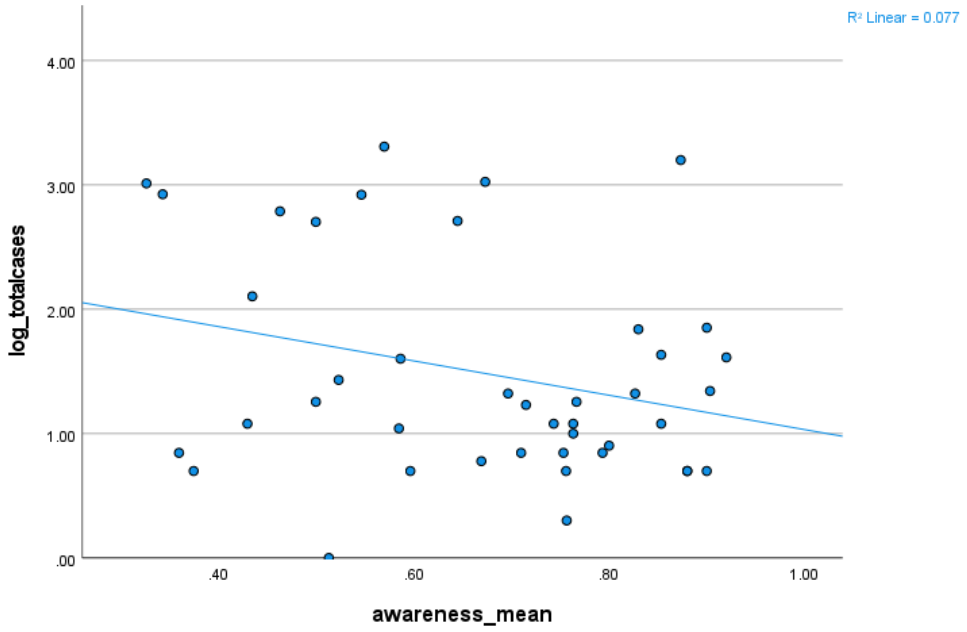
Scatter Plot Showing the Relationship Between Percentage of Villages With Access to Safe Water and Log-transformed Total Guinea Worm Cases



The scatter plot includes a fitted linear regression line and indicates a weak positive relationship between the percentage of villages with access to safe water (village_safe_water_pct) and log-transformed Guinea worm case counts (log_totalcases) (R^2 = .180) (see Figure 16). This suggests that approximately 18% of the variance in case counts can be explained by safe water access. Contrary to theoretical expectations, the positive upward trend implies that greater access to safe water may be associated with more reported cases—likely due to confounding factors such as enhanced surveillance or intervention targeting higher-risk or better-resourced villages or reverse causation where cases prompted increased provision of safe water than the reverse.

Figure 17

Scatter Plot Showing the Relationship Between Average Community Awareness and Log-transformed Total Guinea Worm Cases

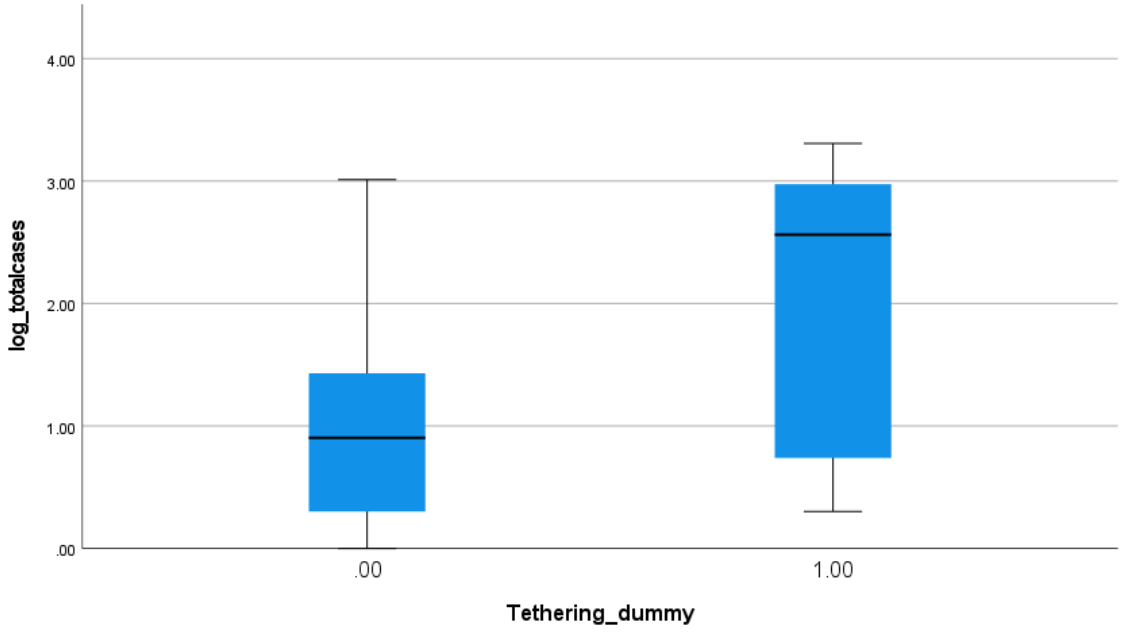


The scatter plot displays a weak negative relationship (R^2 = .077) between awareness_mean and log_totalcases (see Figure 17), indicating that about 7.7% of the variation in Guinea worm case counts may be explained by average awareness levels. The downward slope of regression line suggests that higher awareness is modestly associated with fewer reported cases. While the association is not strong, this trends aligns with the hypothesis that increasing community knowledge and reward system may contribute to reduced transmission, possibly through improved preventive behaviors or earlier detection and reporting.

All other predictors were non-significant, suggesting that, when controlling for other factors, pond treatment, awareness, and safe water access did not independently predict case counts in this model.

Figure 18

Boxplot Comparing Log-transformed Total Guinea Worm Cases by Reported Dog Tethering Practice



The boxplot (see Figure 18) displays a higher median of log-transformed total Guinea worm cases in countries reported dog tethering (Tethering_dummy = 1) compared to countries that did not (Tethering_dummy = 0). This pattern suggests that tethering was more commonly adopted in high incidence areas, potentially as a reactive intervention in response to observed outbreaks. While this does not imply causality, the result is consistent with regression analysis, showing a significant positive association

between tethering and case counts. This may reflect programmatic targeting efforts in high-burden areas.

The null hypothesis was partially rejected: among the four programmatic indicators tested, only dog tethering was significantly associated with Guinea worm case counts. Thus, the multiple regression analysis provided partial support for the theory of change. While tethering — the focal intervention in the theory of change — was significantly associated the higher log- transformed cases counts, other variables (i.e., awareness, access to safe water, and abate pond treatment) were not statistically significant.

These findings suggest that countries reporting tethering practices also had higher reported case counts, possibly reflecting increased surveillance or programmatic activity in high-burden settings rather than a direct causal effect. Unmeasured confounding variables, variation in implementation fidelity, or limitations in aggregated national-level data may obscure the true nature of the relationship. Additional analyses using disaggregated or longitudinal data are recommended to better understand the direction and magnitude of these effects.

Although dog tethering was a statistically significant and positive predictor of log-transformed Guinea worm case counts, this association should be interpreted cautiously. The observed relationship may indicate programmatic targeting of higher-burden areas rather than an effect of tethering on increased transmission. This interpretation is further explored in Chapter 5.

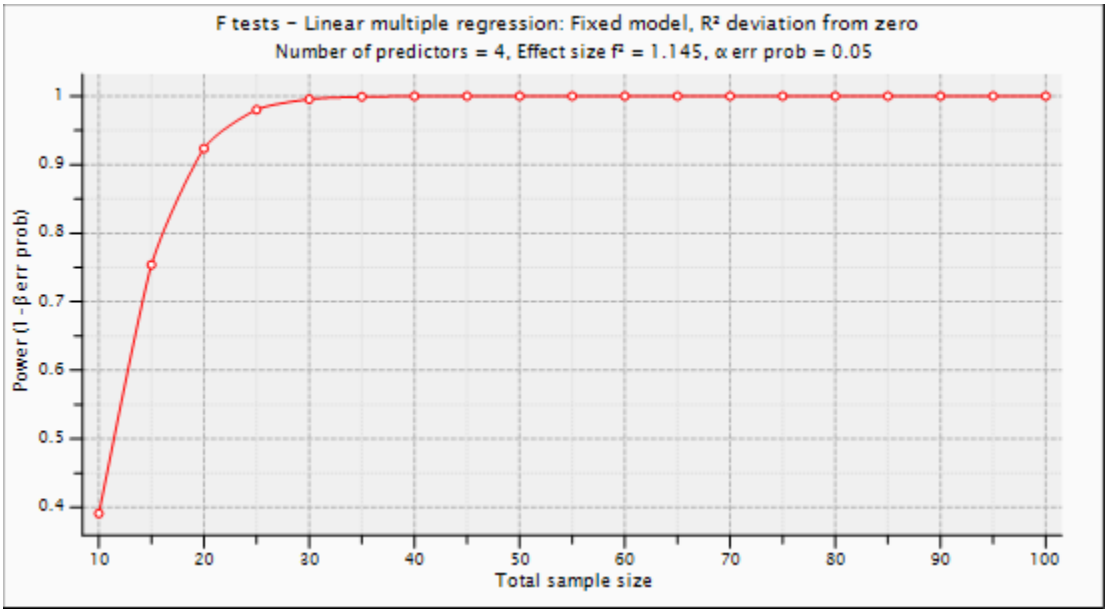
In summary, this model provided partial empirical support for the theory of change, dog tethering, the primary intervention, was significant predictor of Guinea worm disease burden at the country level, whereas other programmatic factors were not. However, the positive association likely reflects programmatic targeting in high-burden areas.

Post Hoc Power Analysis

To determine whether the multiple-regression model for Research Question 1 was adequately powered, a post-hoc analysis was performed in G*Power 3.1.9.7 (Faul et al., 2009). Entering the observed coefficient of determination ($R^2 = .511$), $\alpha = .05$, total sample size N = 24, and four predictors, the program produced an effect size $f^2 = 1.045$, non-centrality parameter $\lambda = 25.08$, critical $F(4, 19) = 2.90$, and achieved power $(1 – \beta) = .959$, indicating high sensitivity to detect effects of the observed magnitude. Power well above the conventional .80 threshold (Cohen, 1988) suggests that the nonsignificant coefficients for awareness, safe-water access, and pond-Abate coverage are unlikely to be due to insufficient sample size. Figure 18 displays the power curve demonstrating how power increases with sample size for the specified effect size and alpha level. Because post-hoc power is mathematically coupled to the observed effect size, however, this result should be regarded as descriptive rather than confirmatory (Hoenig & Heisey, 2001).

Figure 19

Post Hoc Power Analysis for Multiple Linear Regression with Four Predictors (Effect Size $f^2 = 1.145$, $\alpha = .05$)



Secondary Time Series Forecasting

In addition to the primary regression analyses, a secondary time series forecasting analysis was conducted to model future trends in Guinea worm disease cases and evaluate progress toward the 2030 eradication goal.

Angola

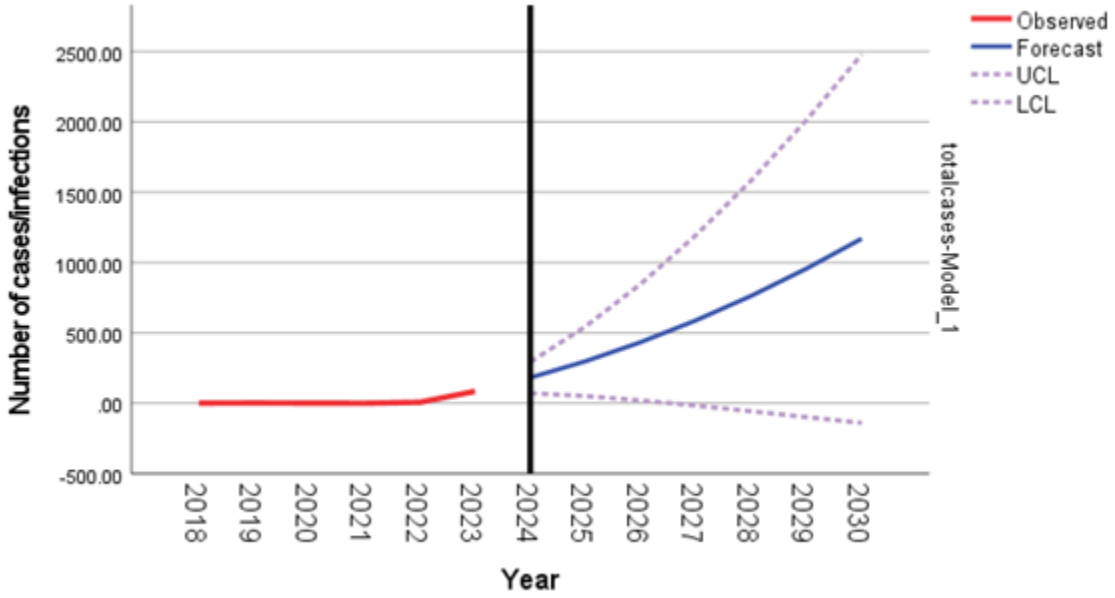
For Angola, time series forecasting was conducted using the SPSS Expert Modeler, which automatically selected an ARIMA(0,2,0) model to fit the observed data. The historical trend from 2018 to 2023 showed a relatively stable pattern with low case counts, followed by a noticeable increase in the most recent year. As shown in Figure 20, the ARIMA(0,2,0) model projected a substantial upward trend in case counts over the

forecast period from 2024 to 2030.

Specifically, the model forecasted an increase from 182.25 cases in 2024 to 1170.00 cases by 2030. The 95% confidence interval widened substantially over time, ranging from 71.60 to 292.90 cases in 2024 and from -139.25 to 2479.25 cases by 2030, indicating considerable uncertainty in long-term projections.

Figure 20

Forecasted Guinea Worm Disease Cases and Infections in Angola, 2024–2030



Model performance statistics revealed a root mean square error (RMSE) of 34.769 and a mean absolute percentage error (MAPE) of 782.199%, suggesting high forecast variability and limited precision. The R-squared value was .291, indicating that the model explained approximately 29% of the variation in the observed data. The model's results highlight a concerning forecasted increase in Guinea worm disease cases if current conditions persist without intensified eradication efforts. The findings underscore the

urgent need for immediate and aggressive interventions—including expanded surveillance, case containment, public health education, and community mobilization—to prevent a potential resurgence and align Angola's trajectory with the 2030 eradication target.

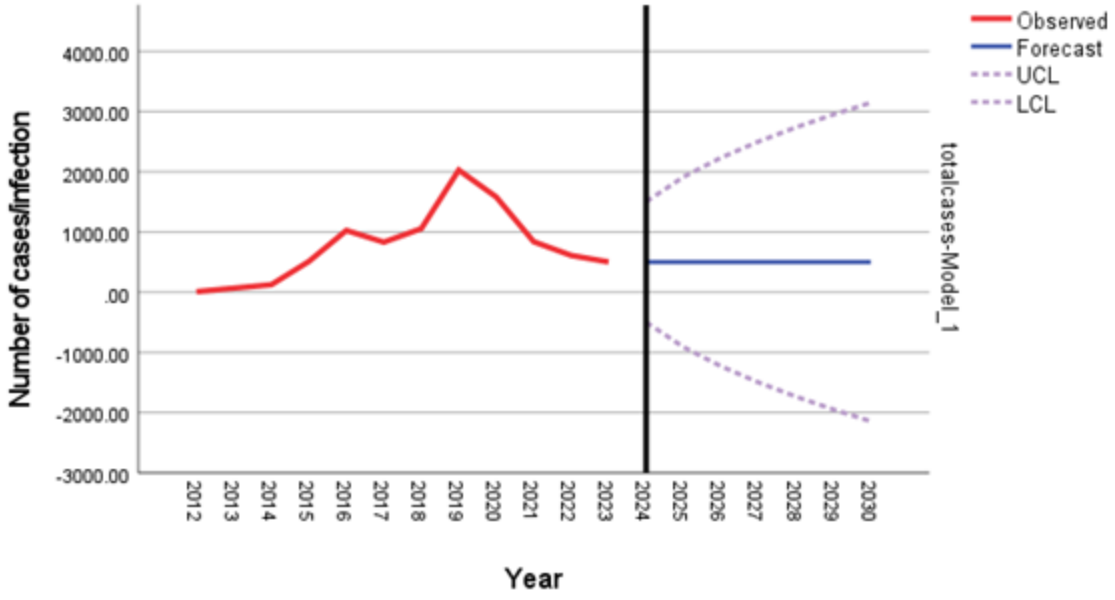
Chad

For Chad, the secondary time series forecasting analysis was conducted using the SPSS Expert Modeler. The Expert Modeler automatically selected a Simple model (constant model), suggesting no significant temporal trend or seasonality was detected in the historical data from 2012 to 2023 (Figure 21). The forecast projected a stable case count of approximately 503 cases annually from 2024 to 2030. The 95% confidence interval ranged widely, from –497.30 to 1503.10 cases in 2024 and expanding over time, reflecting considerable uncertainty. Model fit statistics indicated a moderate explanatory power (R^2 = .439) and a relatively high forecast error (RMSE = 454.478; MAPE = 43.761).

These findings suggest that if current trends continue without significant intervention acceleration, Guinea worm disease cases are unlikely to reach zero in Chad by 2030. Therefore, enhanced and targeted interventions—such as intensified dog tethering, broader pond treatment with Abate, improved access to safe water sources, and strengthened surveillance systems—remain critical to achieve eradication within the target timeline.

Figure 21

Forecasted Guinea Worm Disease Cases and Infections in Chad, 2024–2030



Ethiopia

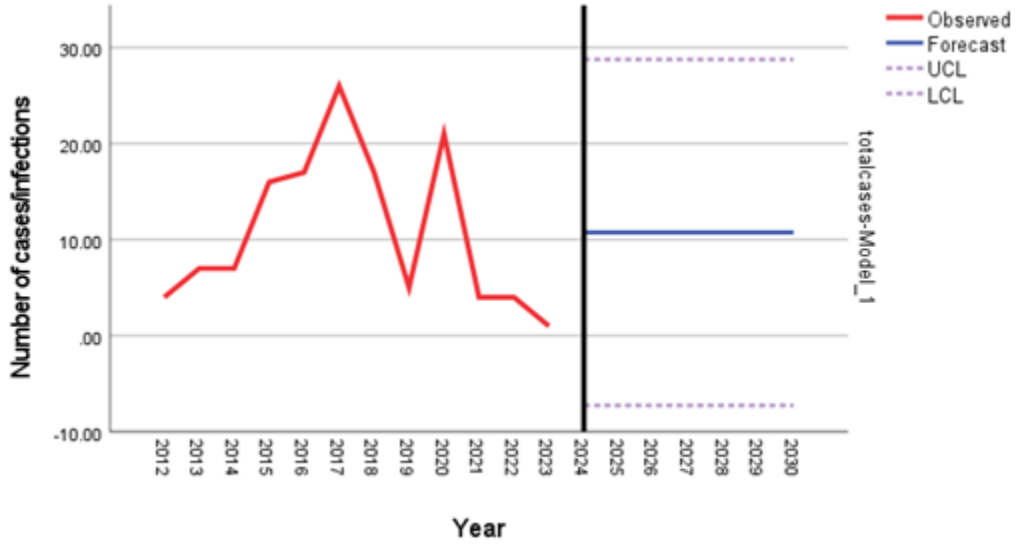
For Ethiopia, time series forecasting was conducted using the Expert Modeler function in SPSS, which automatically selected an ARIMA(0,0,0) model based on the historical case data. As shown in Figure 22, the observed trend between 2012 and 2023 reflected substantial fluctuations in the number of Guinea worm cases, although the overall pattern remained relatively low compared to other countries.

The ARIMA(0,0,0) model generated a constant forecast of approximately 10.75 cases per year for the period from 2024 to 2030 (see Table 6). The upper 95% confidence limit (UCL) was 28.76 cases, and the lower 95% confidence limit (LCL) was -7.26 cases across all forecasted years. Notably, the negative LCL values are not interpretable for case counts, suggesting that the lower bound of zero cases remains a plausible minimum.

Model performance statistics indicated a Root Mean Square Error (RMSE) of 8.18 and a Mean Absolute Percentage Error (MAPE) of 159.77%, reflecting a moderate degree of forecast uncertainty. The stationary R-squared value was essentially zero (1.11E-16), suggesting that the model explained minimal variation in the historical data. Overall, the forecast suggests that without intensified interventions, Ethiopia may continue to report an average of around 10–11 Guinea worm cases annually through 2030 (see Figure 22). Given the goal of achieving transmission interruption, the forecast highlights the necessity of maintaining and further strengthening surveillance, case containment, and public health response strategies to drive incidence toward zero.

Figure 22

Forecasted Guinea Worm Disease Cases and Infections in Ethiopia, 2024–2030



Mali

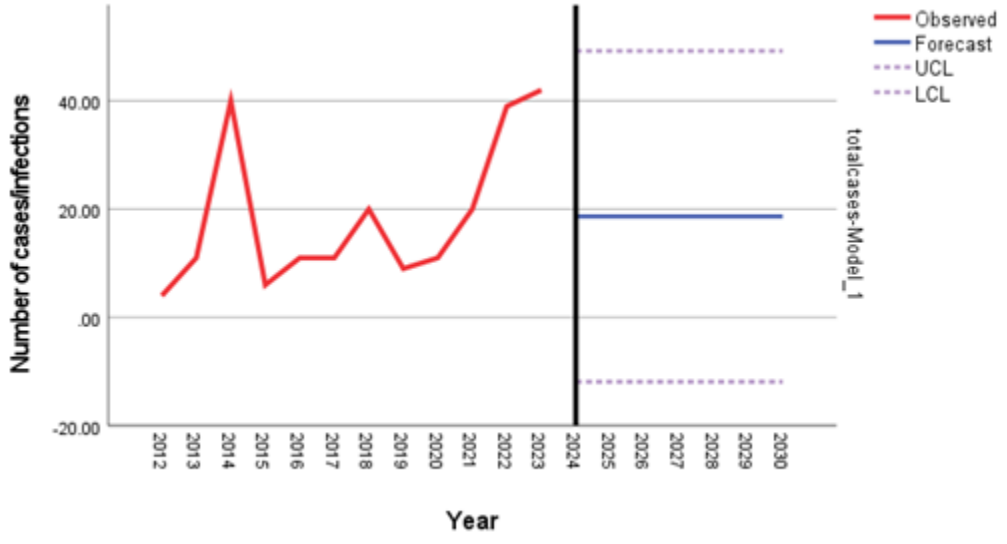
For Mali, time series forecasting was conducted using the SPSS Expert Modeler, which automatically selected an ARIMA(0,0,0) model based on the characteristics of the

available annual data (IBM Corp., 2021). The model indicated relatively stable but persistent low-level Guinea worm disease case counts through 2030 (see Figure 23) .

The forecasted number of total cases was approximately 18.67 per year from 2024 through 2030. The 95% confidence interval ranged from -11.89 to 49.23 cases annually, suggesting considerable uncertainty around the point forecasts. The model's performance statistics showed a root mean square error (RMSE) of 13.885 and a mean absolute percentage error (MAPE) of 94.861, reflecting moderate forecast error given the small number of observed cases and high year-to-year variability. The stationary R-squared and R-squared values were both 0.000, indicating that the model explained very little variance in the observed data.

Figure 23

Forecasted Guinea Worm Disease Cases and Infections in Mali, 2024–2030



Despite limitations in predictive power, the model suggests that without intensified interventions, Mali is unlikely to achieve complete interruption of

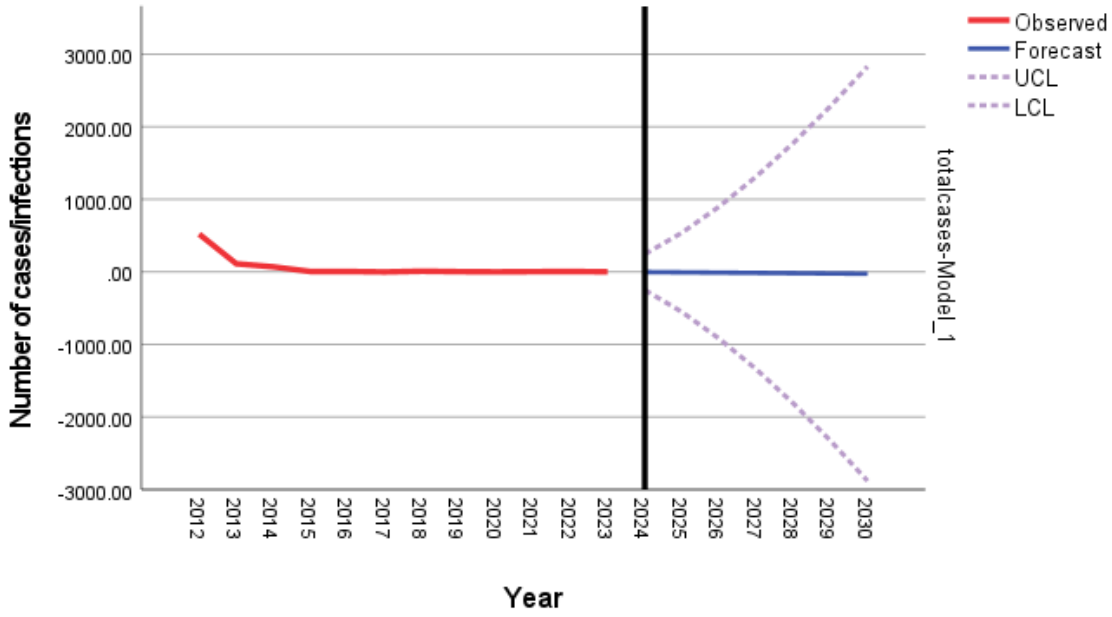
transmission by 2030. However, the relatively low predicted case numbers imply that intensified surveillance, community engagement, and targeted interventions could feasibly drive cases to zero within the remaining period.

South Sudan

The time series forecast for South Sudan employed the Expert Modeler in SPSS, which automatically selected a Brown exponential smoothing model. The model fit statistics indicated a stationary $R^2 = -0.127$ and a standard $R^2 = 0.432$, suggesting moderate predictive capacity with a root mean square error (RMSE) of 112.06 and a mean absolute percentage error (MAPE) of 278.25.

Figure 24

Forecasted Guinea Worm Disease Cases and Infections in South Sudan, 2024–2030



The forecasted number of Guinea worm cases was slightly negative beginning in 2024 (forecast = -1.84) and continued to decline to -24.87 by 2030. However, the wide

confidence intervals, spanning from -2880.68 to 2830.94 by 2030 (see Figure 24), indicated a high degree of uncertainty surrounding the forecasts. The widening upper and lower confidence limits over time suggested increasing variability and reduced precision in longer-term projections.

Despite the wide uncertainty bands, the central forecast trajectory suggested a continuing decline in case numbers, supporting the feasibility of achieving interruption of Guinea worm transmission in South Sudan by 2030 under current trends. However, the negative forecast values also highlighted model limitations and the need for cautious interpretation, emphasizing the importance of maintaining surveillance and rapid response capacity during the final stages of eradication efforts.

Summary of Time Series Forecasting Results Across Countries

The secondary time series forecasting analysis modeled future Guinea worm disease trends through 2030 for Angola, Chad, Ethiopia, Mali, and South Sudan. In Angola, the Expert Modeler selected an ARIMA(0,2,0) model, which projected a concerning upward trend in Guinea worm cases, increasing from 182.25 cases in 2024 to 1170.00 cases by 2030, highlighting the potential for resurgence if control efforts are not intensified. In Chad, the Expert Modeler selected a Simple model, forecasting approximately 503 cases annually through 2030, with wide confidence intervals and moderate model fit, indicating that intensified interventions are necessary to achieve eradication goals. For Ethiopia, the Expert Modeler selected an ARIMA(0,0,0) model,

Table 6

Statistical Analysis Summary for Time Series Forecasting by Country

Country	Model Type	Stationary R^2	R^2	RMSE	MAPE (%)	Forecasted Trend	2030 Target Feasibility
Angola	ARIMA(0,2,0)	-	0.291	34.769	782.199	Upward trend and growing risk	Unlikely without urgent intervention expansion
Chad	Simple (Constant)	0.439	0.439	454.478	43.761	Stable at high level	Unlikely without intensified intervention
Ethiopia	ARIMA(0,0,0)	1.11E-16	0.000	8.18	159.77	Stable at low level	Possible with strengthened efforts
Mali	ARIMA(0,0,0)	0.000	0.000	13.885	94.861	Persistent low-level transmission	Unlikely without accelerated efforts
South Sudan	Brown Exponential Smoothing	-0.127	0.432	112.06	278.25	Gradual decline with uncertainty	Possible, but surveillance must be maintained

Note. Statistical measures were derived from time series forecasting models selected by the SPSS Expert Modeler based on historical Guinea worm disease case data. RMSE = Root Mean Square Error; MAPE = Mean Absolute Percentage Error.

projecting approximately 10.75 cases per year with considerable forecast uncertainty, suggesting that strengthened surveillance and response activities remain critical to drive incidence toward zero. In Mali, an ARIMA(0,0,0) model forecasted about 18.67 cases per year, reflecting persistent low-level transmission and highlighting the need for enhanced community engagement and targeted interventions. In South Sudan, the Expert Modeler selected a Brown exponential smoothing model, forecasting a declining trend in case counts with wide uncertainty bands, supporting the feasibility of transmission interruption by 2030 under current efforts but emphasizing the importance of maintaining high-quality surveillance and rapid response systems.

Collectively, these forecasts suggest that while Ethiopia and South Sudan may be on a trajectory toward achieving the 2030 targets, Chad and Mali will require accelerated and intensified programmatic efforts to drive case counts to zero. In contrast, Angola demonstrated a concerning upward trend in projected case counts, indicating that without urgent and expanded interventions, eradication efforts may be further jeopardized.

Research Question 2

Research Question 2: What is the relationship between environmental factors (climate, temperature, water supply) and guinea worm cases or infection?

$H_0 2$: There is no relationship between environmental factors and the number of guinea worm cases or infections.

$H_a 2$: The environmental factors have a relationship with the number of guinea worm cases or infections.

Descriptive Statistics

The analytic dataset consisted of 814 monthly records from villages that reported at least one human case of Guinea worm disease (GWD) between 2012 and 2023. Following data integration with climate and environmental predictors, 718 records had complete information across all four variables used in the main analyses.

Table 7 summarizes the descriptive statistics for human GWD case counts and environmental predictors, including central tendency, dispersion, and measures of normality (skewness and kurtosis).

The number of human GWD cases per village-month ranged from 1 to 18 (M = 1.35, SD = 1.15), with high positive skewness (6.43) and excess kurtosis (64.74), indicating substantial right skew and overdispersion—an expected pattern for count data.

Monthly mean temperature values ranged from 20.33°C to 35.27°C (M = 27.73, SD = 1.73), with acceptable skewness (0.90) and kurtosis (2.55), suggesting approximately normal distribution. Monthly precipitation varied considerably (range = 0.00 mm to 337.09 mm, M = 99.08 mm, SD = 54.52), also showing moderate skewness (0.92) and kurtosis (2.23).

The water occurrence variable, measured as the percentage of surface water presence within a 10-meter buffer around each village, showed a strong positive skew (15.95) and leptokurtic distribution (kurtosis = 276.52), indicating that most villages had very low or no persistent surface water, while a few had substantial water presence.

These distributional patterns informed the decision to use generalized linear models for the regression analyses, particularly those suited for count outcomes with skewed distributions.

Table 7

Descriptive Statistics and Distribution Properties for GWD Cases and Environmental Predictors (N = 814)

Variable	N	Min	Max	Mean	Std. Dev.	Skewness	Kurtosis
Human GWD Cases (num_cases)	814	1	18	1.35	1.15	6.43	64.74
Temperature (°C, temp_imp)	805	20.33	35.27	27.73	1.73	0.90	2.55
Precipitation (mm, precip_imp)	805	0.00	337.09	99.08	54.52	0.92	2.23
Surface Water Occurrence (% area, water_val)	722	0.16	84.18	2.52	4.55	15.95	276.52

Note. Surface water occurrence calculated based on 10-meter buffer around village location. Valid N (listwise) = 718.

Correlation Among Environmental Predictors and Guinea Worm Cases

A Pearson correlation analysis was conducted to examine the linear relationships among monthly Guinea worm case counts and environmental predictors (temperature, precipitation, and surface water occurrence). Results indicated that the number of cases was not significantly correlated with any of the environmental variables: temperature (r = .013, p = .719), precipitation (r = –.036, p = .304), or surface water occurrence (r = −.009, p = .811). These results suggest no meaningful linear association between environmental predictors and the number of reported cases.

Table 8

Pearson Correlation Matrix of Monthly Guinea Worm Cases and Environmental Predictors (N = 718–814)

	Cases	Temperature	Precipitation	Surface Water Occurrence
Cases	1.000 (p = —)	0.013 (p = .719)	-0.036 (p = .304)	-0.009 (p = .811)
Temperature	0.013 (p = .719)	1.000 (p = —)	-0.436 (p < .001)	-0.226 (p < .001)
Precipitation	-0.036 (p = .304)	-0.436 (p < .001)	1.000 (p = —)	-0.005 (p = .898)
Surface Water Occurrence	-0.009 (p = .811)	-0.226 (p < .001)	-0.005 (p = .898)	1.000 (p = —)

Note. Pearson correlation coefficients are presented corresponding p values in parentheses. Statistically significant correlations at $p < .001$ are bolded. Shading is used sparingly to assist with readability but does not indicate statistical significance or effect size.

However, significant negative correlations were found between environmental predictors. Temperature was moderately negatively correlated with precipitation ($r = -.436$, $p < .001$), indicating that higher temperatures were associated with lower precipitation levels. Temperature also had a weak but statistically significant negative correlation with surface water occurrence ($r = -.226$, $p < .001$), suggesting that increased temperatures were associated with reduced surface water presence. No significant correlation was observed between precipitation and surface water occurrence ($r = -.005$, $p = .898$). These findings suggest interdependence between some environmental variables but no direct linear association between these predictors and monthly Guinea worm disease incidence.

Evaluation of Assumptions for Negative Binomial Regression

Count outcome variable: Negative Binomial Regression requires a dependent variable that is count-based—specifically, non-negative integers representing the number of times an event occurs. The dependent variable for this analysis, num_cases, represents the number of human Guinea worm disease (GWD) cases reported in a given village during a specific month. Values range from 1 to 18, with no negative or fractional values present. Since this variable reflects a count of discrete events (cases) and is based on surveillance data collected monthly per village, it meets the fundamental requirement of being a count outcome. Therefore, this assumption is satisfied, and a count model such as Negative Binomial Regression is appropriate for modeling this outcome.

Non normality and distributional skew. The dependent variable does not need to be normally distributed in Negative Binomial Regression. In fact, count variables are typically positively skewed and often display overdispersion, which the model is designed to accommodate. Descriptive statistics revealed that num_cases had a strong positive skew (Skewness = 6.43) and extreme kurtosis (Kurtosis = 64.74), indicating a highly non-normal and over dispersed distribution. This distributional pattern is typical of rare event data, where the majority of village-month observations have only one or a few reported cases, and a small number have disproportionately high counts. These results confirm that the assumption of non-normality is met and further justify the use of Negative Binomial Regression, which is robust to such distributional features. Use of a linear model would be inappropriate given the observed violation of the normality assumption for residuals and outcome values.

Overdispersion. Negative Binomial Regression (NBR) assumes that the variance of the count outcome exceeds its mean, a condition known as overdispersion. This assumption distinguishes it from the Poisson model, which requires the mean and variance of the dependent variable to be equal. When overdispersion is present, the Poisson model underestimates standard errors and inflates significance tests, whereas NBR accounts for the extra-Poisson variation, providing more reliable parameter estimates (Winkelmann, 2020; Waller & Gotway, 2021). Assessment of overdispersion helps justify the use of NBR over Poisson regression.

The Pearson Chi-Square/df ratio was 0.95, and the Deviance/df ratio was 0.50, both of which suggest that the model fits reasonably well and there is no evidence of

extreme overdispersion. Ratios close to 1 indicate that the variance is appropriately modeled, while values well above 1 would have indicated overdispersion (Zhou et al., 2020). Moreover, descriptive statistics revealed substantial skewness (6.43) and kurtosis (64.74) in the dependent variable (num_cases), suggesting a non-normal and skewed count distribution, further supporting the use of a count regression model that allows for variance inflation such as NBR (Kutner et al., 2022). Although the dispersion indicators are not extremely high, the use of NBR remains justified due to the nature of the count data and the distributional properties observed. The Akaike Information Criterion (AIC = 1898.96) and Bayesian Information Criterion (BIC = 1917.27) values serve as model fit diagnostics, and in future model comparisons, smaller AIC/BIC values would indicate better-fitting models. In summary, even though dispersion statistics do not show extreme overdispersion, the distributional properties of the count outcome and the appropriateness of NBR for such contexts provide justification for the chosen model.

Multicollinearity occurs when two or more independent variables in a regression model are highly correlated, potentially leading to unreliable and unstable estimates of regression coefficients. This can inflate the standard errors of the coefficients, making it difficult to assess the individual effect of each predictor (Kim, 2019). To detect multicollinearity, the Variance Inflation Factor (VIF) and Tolerance values are commonly used. A VIF value exceeding 10 or a Tolerance value below 0.1 typically indicates significant multicollinearity (Shrestha, 2020).

In this analysis, the VIF and Tolerance values for the predictors were as follows:

- temp_imp: VIF = 1.323, Tolerance = 0.756

- precip_imp: VIF = 1.255, Tolerance = 0.797
- water_val: VIF = 1.069, Tolerance = 0.936

All VIF values are well below the commonly accepted threshold of 10, and Tolerance values are well above 0.1, indicating that multicollinearity is not a concern in this model. These results suggest that the predictors are sufficiently independent of one another, satisfying the assumption of no multicollinearity.

To assess the assumption of linearity between the continuous predictors and the log-transformed expected count of the outcome (number of human Guinea worm disease cases), scatterplots were visually inspected. Each plot displayed the relationship between the dependent variable and the predictors: monthly average temperature (temp_imp), precipitation (precip_imp), and surface water occurrence (water_val). Although there was some dispersion, the plots revealed no clear non-linear patterns, suggesting an approximately linear relationship on the log scale.

The relatively even spread of points, particularly at the lower end of the outcome scale, is expected in count data models such as the negative binomial regression, which accommodate overdispersion and skewness in the outcome distribution. Based on these visual inspections, the assumption of linearity of the log link was considered to be sufficiently met for the included predictors. This approach is consistent with recommendations for evaluating generalized linear model assumptions using visual diagnostics (Coxe et al., 2019; Hilbe, 2021).

Negative Binomial Regression Results for Environmental Predictors of Guinea Worm Disease Cases: Initial Model with Three Environmental Predictors

A Negative Binomial Regression (NBR) analysis was conducted to assess whether environmental conditions were associated with the number of monthly reported human Guinea worm disease (GWD) cases at the village level. The outcome variable was the count of human GWD cases (num_cases). The predictors included average monthly temperature (temp_imp), monthly precipitation (precip_imp), and average surface water occurrence within a 10-meter buffer (water_val).

Sample and Model Setup. Of 814 total observations, 718 records (88.2%) had complete data and were included in the model. The analysis was based on a log link function and assumed a negative binomial distribution (see).

Model Fit and Goodness-of-Fit Statistics: The model demonstrated good fit as indicated by deviance per degrees of freedom (Deviance/df = 115.609 / 714 = 0.162), suggesting no evidence of overdispersion. However, the omnibus test was not statistically significant: $\chi^2(3) = 0.133$, $p = .988$, indicating that the overall model was not an improvement over the intercept-only model.

Parameter Estimates and Significance Tests: None of the environmental predictors were statistically significant:

Table 9

Negative Binomial Regression Parameter Estimates for Environmental Predictors of Human Guinea Worm Disease Cases (N = 718)

Predictor	*B*	*SE*	Wald χ^2	*df*	*p*	95% CI for Exp(*B*)
Intercept	0.596	0.978	0.371	1	.542	[0.267, 12.33]
Temperature	-0.010	0.033	0.093	1	.760	[0.928, 1.056]
Precipitation	0.000	0.0011	0.059	1	.808	[0.998, 1.002]
Surface Water	-0.003	0.012	0.056	1	.813	[0.974, 1.021]

Note. B = unstandardized regression coefficient; SE = standard error; Exp(B) = exponentiated coefficient; CI = confidence interval; df = degrees of freedom.

The coefficients for average temperature, precipitation, and water presence were small and nonsignificant, with wide confidence intervals crossing 1 for all predictors. This suggests that, when modeled simultaneously, none of the environmental predictors were significantly associated with human Guinea worm case counts in this model. The overall lack of statistical significance in both the omnibus and individual tests suggests limited explanatory power from these three variables.

Model With Two-Way Interaction Terms

To examine possible synergistic environmental effects, a second Negative-Binomial Regression (NBR) model was estimated that added the three two-way interactions among the monthly covariates: temperature × precipitation (temp_precip) temperature × surface-water occurrence (temp_water), and precipitation × surface-water occurrence (precip_water).

The model retained the original main effects: temperature (*temp_imp*), precipitation (*precip_imp*), and surface water occurrence (*water_val*). The model was estimated using 718 village-month observations. Dispersion characteristics remained

satisfactory (Deviance = 114.89; *df* = 711; Deviance/*df* = 0.162), indicating no overdispersion. Information criteria values were comparable to the main-effects-only model (AIC = 2,296.49; BIC = 2,328.52). The omnibus likelihood ratio test for model improvement was not statistically significant, $\chi^2(6) = 0.852$, $p = .991$, suggesting that the addition of interaction terms did not significantly improve fit relative to the intercept-only model. None of the interaction terms nor the main effects reached statistical significance at the $\alpha = .05$ level:

Table 10

Negative Binomial Regression of Monthly Guinea-Worm Cases on Environmental Predictors (N = 718)

Predictor	B	SE	Wald χ^2
Temperature × Precipitation	0.000	0.0006	0.55
Temperature × Surface water	0.001	0.0090	0.03
Precipitation × Surface water	0.000	0.0004	0.03
Temperature (°C)	–0.038	0.047	0.65
Precipitation (mm)	–0.012	0.016	0.57
Surface-water occurrence (%)	–0.044	0.196	0.05

Note. Unstandardized coefficients (*B*) are log-count estimates from a Negative Binomial Regression model with a log link function. SE = standard error. All tests are two-tailed. No predictor was statistically significant ($p > .42$).

The pseudo R^2 (Nagelkerke R^2) remained essentially zero, suggesting that the model explained negligible variance in the outcome. Given the large analytic sample (N = 718), this model had sufficient power to detect modest effect sizes. The absence of statistically significant main or interaction effects suggests that, at the village-month resolution, these environmental conditions and their interactions do not meaningfully

explain the variation in reported human Guinea worm cases. Further research may need to consider alternative environmental indicators, finer spatiotemporal granularity, or lagged ecological effects to better capture possible influences on transmission.

Model with Seasonality (Month of Emergence)

A third negative binomial regression model was specified to examine the potential seasonal variation in Guinea worm disease (GWD) transmission by incorporating the month of emergence (MonthEmerged) as a categorical predictor, along with the continuous environmental variables—monthly average temperature (temp_imp), total precipitation (precip_imp), and mean surface water occurrence (water_val).

The sample included 718 valid village-month records. Model fit remained satisfactory, as indicated by the deviance-to-degrees-of-freedom ratio (Deviance/*df* = 108.668 / 703 = 0.155), suggesting no overdispersion. The omnibus likelihood-ratio test was not statistically significant, $\chi^2(14) = 7.074$, $p = .932$, indicating that the inclusion of Month of emergence did not significantly improve the model over the intercept-only model.

Table 11

Parameter Estimates for Negative Binomial Regression Predicting Guinea Worm Cases by Month of Emergence and Environmental Factors

Parameters	*B*	*SE*	Wald	*p*
Intercept	1.262	1.1774	1.148	0.284
January (Month Emerged 1)	-0.009	0.6733	0	0.99
February (Month Emerged 2)	0.073	0.5932	0.015	0.901
March (Month Emerged 3)	0.439	0.5134	0.73	0.393
April (Month Emerged 4)	0.36	0.5129	0.493	0.483
May (Month Emerged 5)	0.525	0.4975	1.115	0.291
June (Month Emerged 6)	0.41	0.4844	0.717	0.397
July (Month Emerged 7)	0.333	0.5036	0.436	0.509
August (Month Emerged 8)	0.121	0.5212	0.054	0.817
September (Month Emerged 9)	0.215	0.5148	0.174	0.677
October (Month Emerged 10)	0.157	0.5266	0.089	0.766
November (Month Emerged 11)	0.128	0.5666	0.051	0.821
December (Month Emerged 12)	0	0		
Monthly Avg. Temperature (°C)	-0.045	0.0427	1.132	0.287
Total Precipitation (mm)	0	0.0015	0.106	0.745
Surface Water Occurrence (%)	-0.005	0.0126	0.159	0.69

Note. B = unstandardized regression coefficient; SE = standard error; Wald χ^2 = Wald chi-square statistic; p = significance level. The reference category for the Month of Emergence variable is December.

None of the predictors reached statistical significance:

- Monthly Avg. Temperature (°C): $B = –0.045$, $SE = 0.0427$, $p = .287$
- Total Precipitation (mm): $B = 0.000$, $SE = 0.0015$, $p = .745$
- Surface Water Occurrence (%): $B = –0.005$, $SE = 0.0126$, $p = .690$

Likewise, the overall effect of the categorical month variable was not significant (Wald $\chi^2 = 6.923$, $df = 11$, $p = .805$). All individual months compared to the reference month (December) showed non-significant associations with case counts (all $p > .28$).

Figure 25

Monthly Trends in Guinea Worm Case Counts and Environmental Variables by Country (2012–2023)

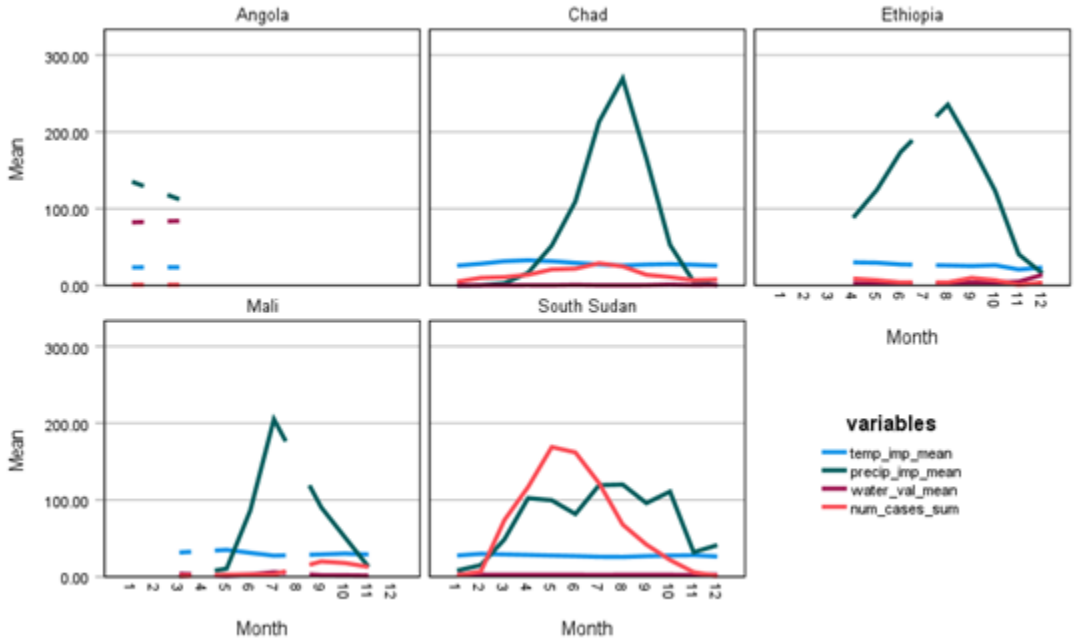


Figure 25 displays monthly trends in reported Guinea worm case counts and environmental conditions across five endemic countries. Line graphs show the average monthly values of temperature, precipitation, surface water occurrence, and total human Guinea worm cases for Angola, Chad, Ethiopia, Mali, and South Sudan. Data represent aggregated monthly village-level means and totals. Peak case counts were observed in South Sudan from April to August and in Chad between May and August, coinciding with the rise in surface water occurrence and precipitation. Ethiopia, Mali, and Angola reported fewer cases but showed similar environmental seasonality. Despite these visual patterns, regression models including seasonality (month of emergence) did not yield

statistically significant associations, suggesting that observed trends may be influenced by unmeasured behavioral or programmatic factors.

These findings suggest no statistically significant seasonal pattern in monthly GWD case counts when controlling for environmental variables. Therefore, seasonality—as measured by the month of emergence—does not explain additional variation in case incidence at the village-month level beyond what is captured by temperature, precipitation, and water occurrence.

Across all models, there was no significant relationship between the environmental predictors—temperature, precipitation, surface water presence—and the number of monthly human Guinea worm disease cases at the village level. Additionally, models exploring interaction effects and seasonality did not significantly improve model performance or explain variation in the outcome.

These results suggest that, in the current dataset, climatic and environmental variables alone may not sufficiently predict monthly GWD case incidence, highlighting the potential importance of behavioral, programmatic, or ecological covariates not included in the model.

Evaluation of Assumptions for Spatial Analysis

Before the spatial analysis could be carried out, significant assumptions were assessed to verify that the spatial analyses were suitable and appropriate for the methods used. These assumptions are valid for exploratory spatial data analysis (e.g. Global Moran's I and Local Indicators of Spatial Association [LISA]) as well as for subsequent analyses such as spatial regression modeling.

Valid Spatial Weights Matrix

A valid spatial weights matrix is the background of spatial analysis. In this study, spatial weights were generated in GeoDa using first-order queen contiguity and distance-based methods. Null geometries were excluded as well, so that there were valid geographic coordinates for all spatial units, which was a necessary condition to construct the spatial weights matrix (Anselin et al., 2022).

Assumptions for Global Moran's I and LISA

While Global Moran's I is a global test of spatial autocorrelation assuming stationarity, LISA (Local Moran's I) accommodates local spatial heterogeneity and helps identify significant spatial clusters or outliers (Ord & Getis, 2021).

Both methods rely on permutation-based significance testing, rather than assuming normality or homoscedasticity. In this study, p-values were calculated using 999 Monte Carlo permutations, a widely accepted approach for robust inference (Lee et al., 2023). Assumptions met include:

- Complete and valid spatial data (no missing coordinates or NULL geometries).
- Spatial weights matrix correctly defined and applied.
- Non-parametric permutation testing ensuring robustness in p-value estimation.

Stationarity: While Global Moran's I assumes global stationarity, LISA allows for local heterogeneity, making it appropriate to detect spatial clusters or outliers even when spatial processes are not uniform.

Assumptions for Spatial Regression

Spatial regression models, such as the Spatial Lag Model (SLM) or Spatial Error Model (SEM), require additional diagnostics beyond traditional regression:

Multicollinearity: Variance Inflation Factors (VIFs) were assessed previously and found to be well below the conventional threshold of 5, confirming the absence of multicollinearity (Kutner et al., 2019).

Residual spatial autocorrelation: The residuals from a non-spatial negative binomial model were evaluated using Global Moran's I, revealing spatial dependence that justifies the need for spatial regression models (Chi & Zhu, 2022).

Model selection: Further diagnostics, including Lagrange Multiplier (LM) tests, will be conducted to determine whether SLM or SEM is most appropriate based on the structure of residual spatial dependence.

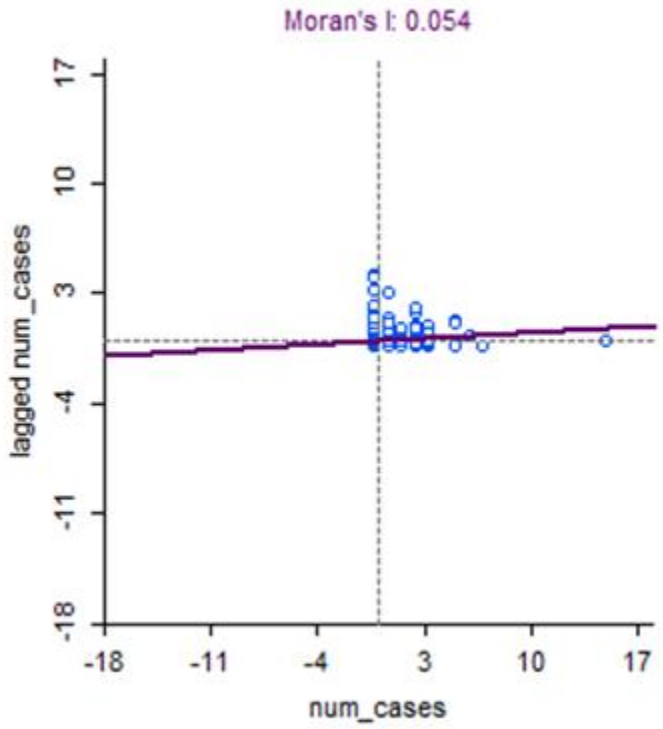
Spatial Analysis

Spatial Autocorrelation Analysis of Guinea Worm Cases (2012–2023): Global Moran's I: Global spatial autocorrelation was assessed using Moran's I to determine whether Guinea worm cases exhibited a clustered, dispersed, or random pattern across 722 villages from 2012 to 2023. A Global Moran's I analysis was performed to evaluate the presence of spatial autocorrelation in monthly Guinea worm human case counts across villages. The analysis produced a Moran's I value of 0.0543, with an expected value (E[I]) of -0.0014, standard deviation (SD) of 0.0208, a z-score of 2.7445, and a pseudo p-value of 0.011 based on 999 permutations. These results indicate a statistically significant and positive spatial autocorrelation, suggesting that villages with high or low

case counts tend to be located near other villages with similar counts rather than being randomly distributed.

Figure 26

Moran Scatterplot of Monthly Guinea-worm Case Counts (x-axis) Against their Spatially Lagged Values (y-axis) for 2019-2023 Village Data (N = 66).



Note. The slope of the fitted purple line equals the global Moran's I (0.054), indicating very weak—and statistic

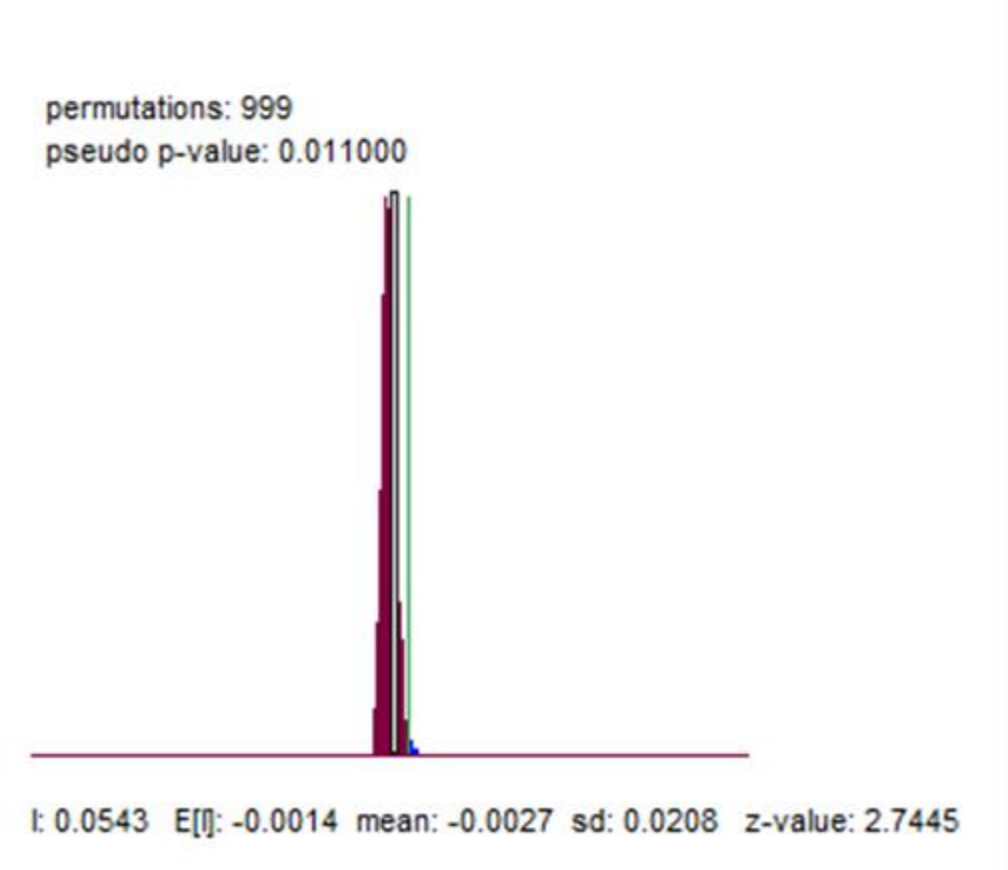
Table 12

Global Moran's I Results for Guinea Worm Cases, 2012–2023 (n = 722)

Statistic	Value
Moran's I	-0.0543
Expected I	-0.0014
z-value	2.7445
p-value	.011
Permutations	999

Figure 27

Histogram of the Global Moran's I Statistics Based on 999 Random Permutations for Guinea Worm Cases Across 722 Villages (2012-2023)



Local Spatial Clustering

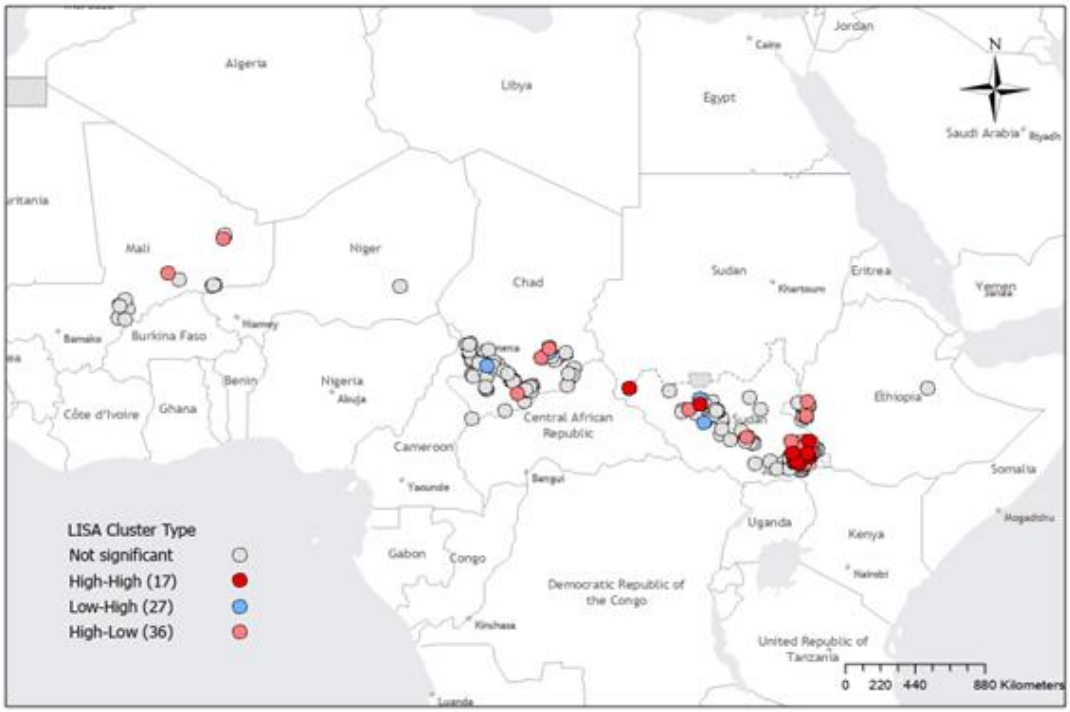
A LISA cluster analysis was conducted to detect local spatial clusters of monthly Guinea worm human case counts across villages. The results indicated statistically significant spatial clustering at the $p \leq .05$ level in 80 out of 722 villages (11.1%). Specifically:

- High-High clusters (n = 17) represent villages with high case counts surrounded by neighbors also exhibiting high case counts, signifying potential persistent hotspots of transmission.
- Low-High clusters (n = 27) reflect villages with low case counts but located near villages with high case counts, potentially representing buffer or transitional zones.
- High-Low clusters (n = 36) indicate villages with high case counts that are spatially proximate to villages with low case counts—suggesting potential outliers or spillover locations.
- Low-Low clusters were not observed in this dataset.

Figure 28 presents the LISA cluster map visualizing these clusters and outliers overlaid on a basemap in ArcGIS Pro. This spatial heterogeneity supports the need for geographically targeted interventions to interrupt Guinea worm transmission more efficiently.

Figure 28

LISA Cluster Map of Guinea Worm Case Counts by Village (2012–2023).



Note. Local Moran's I was calculated using 999 permutations. High-High clusters (in red) represent statistically significant hotspots of human Guinea worm cases.

The remaining 642 villages (88.9%) showed no statistically significant local spatial autocorrelation ($p > .05$). These findings are further supported by the LISA significance map, which shows clusters with varying levels of statistical significance, including 33 clusters at $p \leq .05$, 8 at $p \leq .01$, and 39 at $p \leq .001$ (see Figure 29).

Case counts and temperature

A Bivariate Moran's I analysis was conducted to assess the spatial association between reported Guinea worm case counts and temperature values in neighboring

villages. The analysis yielded a Moran's I value of 0.0118, with a z-score of 0.7133 and a pseudo p-value of 0.246 (based on 999 permutations).

Figure 29

LISA Significance Map of Guinea Worm Cases Across 722 Villages from 2012 to 2023, Illustrating Clusters with Varying Levels of Significance *($p \leq .05$, $p \leq .01$, and $p \leq .001$)*

Although the positive Moran's I suggests a slight tendency for villages with higher case counts to be surrounded by those with higher temperatures, this association was not statistically significant ($p > .05$). The observed spatial relationship does not differ meaningfully from a random spatial distribution, indicating no significant spatial co-dependence between Guinea worm cases and temperature in adjacent locations.

A Bivariate Local Moran's I (BiLISA) analysis was conducted to assess the spatial co-variation between Guinea worm case counts (num_cases) and temperature

(temp_imp) across 722 villages. While the global Bivariate Moran's I was low and not statistically significant (I = 0.012, z = 0.7133, p = 0.246), the local analysis revealed spatial heterogeneity in the relationship between these variables.

Out of the total villages, 245 exhibited statistically significant local spatial association between temperature and case counts ($p \leq .05$), broken down as follows:

- High-High clusters (n = 11): Villages with high case counts surrounded by high temperatures.
- Low-High outliers (n = 107): Villages with low case counts near areas of high temperature.
- High-Low outliers (n = 17): Villages with high case counts near areas of low temperature.
- Low-Low clusters (n = 110): Villages with low case counts surrounded by low temperatures.

Non-significant (n = 477): Villages without statistically significant spatial association between temperature and case counts.

The significance map revealed that 49 villages were significant at $p \leq .001$, 23 at $p \leq .01$, and 173 at $p \leq .05$, indicating that localized spatial clustering between temperature and Guinea worm cases exists despite the absence of a strong global association.

These patterns point to localized interactions between temperature and disease presence that might be masked in global statistics. High-high and low-low clusters, particularly in parts of South Sudan and central Chad, may reflect micro-environmental

factors influencing disease transmission dynamics and warrant further ecological or epidemiological investigation.

Case Counts vs. Precipitation Levels

To evaluate the spatial association between Guinea worm case counts and precipitation levels, a Bivariate Moran's I analysis was performed. The resulting Moran's I value was 0.0019, with a z-score of 0.1328 and a pseudo p-value of 0.449 (999 permutations). The results indicate no statistically significant spatial relationship ($p > .05$) between precipitation and case counts in neighboring villages suggesting that precipitation values do not systematically co-vary with Guinea worm incidence at the village level. The minimal Moran's I value and near-zero z-score suggest that precipitation levels do not spatially co-vary with case incidence and that the pattern observed is consistent with spatial randomness.

A Bivariate Local Moran's I (BiLISA) analysis was conducted to assess the spatial association between reported Guinea worm case counts and precipitation values in neighboring villages. The cluster map identified significant spatial clusters of co-variation between case counts and precipitation . Out of 722 villages analyzed, 223 locations exhibited statistically significant local spatial associations at $p \leq .05$, including:

- 6 High-High clusters, where villages with high case counts are surrounded by neighbors with high precipitation,
- 130 Low-Low clusters, where low case counts co-occur with low precipitation in neighboring areas,

- 73 Low-High spatial outliers, indicating villages with low case counts but surrounded by high precipitation values,
- 14 High-Low spatial outliers, where high case counts are surrounded by neighbors with low precipitation.

The corresponding significance map confirms the robustness of these clusters, with 116 locations significant at $p \leq .001$, 54 at $p \leq .01$, and 53 at $p \leq .05$ based on 999 permutations.

These findings suggest that while the global spatial association between case counts and precipitation was not statistically significant (Moran's I = 0.0019, $p = .449$), local spatial clusters reveal nuanced patterns of co-variation that would otherwise be obscured. Specifically, the presence of High-Low and Low-High spatial outliers may indicate transitional zones or potential mismatches between environmental risk and actual case reporting, meriting further investigation.

Case Counts vs. Surface Water Occurrence

A third Bivariate Moran's I analysis was conducted to assess the spatial relationship between reported Guinea worm cases and surface water occurrence. The analysis returned a Moran's I value of –0.0023, with a z-score of –0.1015 and a pseudo p-value of 0.438 (based on 999 permutations).

The negative Moran's I indicates an extremely weak and statistically non-significant spatial association ($p > .05$). This suggests that surface water presence does not exhibit spatial clustering patterns aligned with Guinea worm case distributions, and any apparent association is likely attributable to random spatial variation.

A Bivariate Local Moran's I (BiLISA) analysis was conducted to explore the spatial co-variation between reported Guinea worm case counts and surface water occurrence values in neighboring villages. The analysis identified significant local spatial associations in 146 out of 722 villages ($p \leq .05$) (see Table 13 and Figure 30), including:

- 4 High-High clusters, where high case counts coincide spatially with high surface water occurrence in neighboring villages,
- 106 Low-Low clusters, where both case counts and water presence were low in adjacent areas,
- 28 Low-High spatial outliers, representing villages with low case counts surrounded by high water occurrence,
- 8 High-Low spatial outliers, indicating high case counts among villages with surrounding low water presence.

The BiLISA significance map further validated these clusters, showing 71 locations significant at $p \leq .001$, 27 at $p \leq .01$, and 48 at $p \leq .05$. Despite the global Bivariate Moran's I being non-significant ($I = –0.0023$, $p = .438$), these local patterns reveal important micro-spatial dynamics that could be critical in understanding water-related transmission risks or the spatial targeting of surveillance and interventions.

Table 13

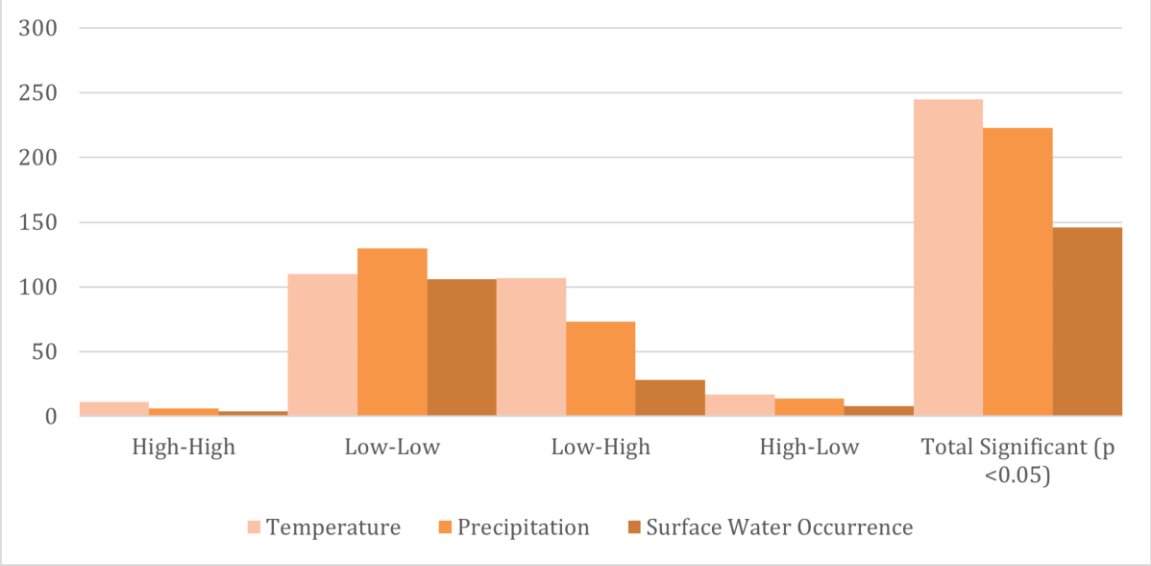
Bivariate Local Moran's I (BiLISA) Cluster Types by Environmental Predictor

Cluster Type	Temperature	Precipitation	Surface Water
High-High	11	6	4
Low-Low	110	130	106
Low-High (Outlier)	107	73	28
High-Low (Outlier)	17	14	8
Total Significant	245	223	146
Non-significant	477	499	576

Note. This table summarizes the number of villages exhibiting significant local spatial associations between Guinea worm case counts and three environmental predictors using Bivariate Local Moran's I (BiLISA). "High-High" and "Low-Low" represent spatial clusters, while "Low-High" and "High-Low" represent spatial outliers. Total N = 722 villages.

Figure 30

Significant Bivariate LISA Cluster Types by Environmental Predictor ($p \leq .05$)



Spatial Regression Results

To further examine the spatial dependency of Guinea worm human case counts and account for spatial autocorrelation in the residuals, spatial regression models were conducted using GeoDa. Specifically, the Spatial Lag Model (SLM) and Spatial Error Model (SEM) were applied using village-level data with three predictors: temperature, precipitation, and mean surface water occurrence.

Spatial Lag Model (SLM)

The Spatial Lag Model assumes that the number of cases in one village is influenced by the number of cases in neighboring villages (spatial spillover effect). The model includes a spatially lagged dependent variable (num_cases) as an additional predictor.

The SLM showed a significant spatial lag coefficient:

$\rho = 0.1304$, $z = 2.32$, $p = .0205$

This indicates that case counts in one village are positively associated with those in neighboring villages, confirming spatial dependency. However, none of the environmental predictors were statistically significant (Table 14).

Table 14

Spatial Regression Model Summary: SLM vs. SEM

Model	Spatial Coefficient	Temperature (B, p)	Precipitation (B, p)	Water Occurrence (B, p)	Log Likelihood	AIC	R^2	S.E. of Regression
SLM	ρ = 0.1304 (p = .0205)	0.0034 (p = .8309)	–0.00006 (p = .9442)	–0.0017 (p = .8574)	–1102.19	2214.39	0.0112	1.11
SEM	λ = 0.1304 (p = .0205)	0.0031 (p = .8488)	–0.000095 (p = .9149)	–0.0015 (p = .8675)	–1102.20	2212.4	0.0111	1.11

Spatial Error Model (SEM)

The SEM assumes that spatial autocorrelation arises from omitted variables that are spatially structured, and adjusts for it in the error term.

The spatial error coefficient was statistically significant, $\lambda = 0.1304$, $z = 2.32$, $p = .021$, indicating the presence of spatial autocorrelation in the residuals. As in the SLM, environmental predictors were not statistically significant (Table 14).

Model Comparison

Both spatial models revealed significant spatial autocorrelation—whether accounted for via the lagged dependent variable (SLM) or through the error term (SEM). However, neither temperature, precipitation, nor water occurrence were significant predictors of monthly human case counts in the spatial models. These findings differ from the earlier non-spatial negative binomial model, which showed significant positive effects for all three predictors.

The similarity in log likelihood and standard errors between SLM and SEM suggests both models perform comparably. Yet, SEM yielded a slightly lower AIC (2212.4 vs. 2214.39), suggesting marginally better model fit. These results imply that after adjusting for spatial effects, the environmental variables may not be as strong predictors as previously suggested, and that spatial clustering alone plays a meaningful role in explaining Guinea worm disease patterns.

There is no strong statistical evidence that temperature, precipitation, or surface water occurrence are associated with Guinea worm case counts across villages. However, spatial cluster analysis identified meaningful patterns (e.g., Low-High, High-Low

outliers) that inform potential areas for further investigation and public health intervention.

Summary of Spatial Regression Findings

The spatial regression analyses reinforce the presence of spatial autocorrelation in Guinea worm disease distribution, as evidenced by the statistically significant spatial coefficients in both the SLM ($\rho = 0.1304$, $p = .0205$) and SEM ($\lambda = 0.1304$, $p = .0205$) models. These findings suggest that transmission patterns are not randomly distributed but influenced by spatial proximity—that is, case counts in one village are affected by those in nearby villages.

However, after accounting for spatial dependence, none of the environmental predictors—temperature, precipitation, or surface water occurrence—were statistically significant in either model. This contrasts with earlier non-spatial analyses (e.g., Negative Binomial Regression), where environmental variables appeared more predictive. The discrepancy highlights the importance of spatial modeling in avoiding overestimation of predictor effects due to spatial clustering.

While the SEM had a slightly better fit (AIC = 2212.4) than the SLM (AIC = 2214.39), both models had low explanatory power ($R^2 \approx .011$), indicating that environmental factors alone are insufficient to explain the spatial distribution of cases. This underscores the need to explore additional socio-behavioral or programmatic variables in future modeling.

Research Question 3

Research Question 3: What is the relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about reporting guinea worm disease/infection?

$H_0$3: There is no relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about Guinea worm disease/infection.

H_a3: There is a relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about Guinea worm disease/infection.

Descriptive Statistics

Table 15 presents descriptive statistics for the variables used in the analysis of Research Question 3. The number of reported rumors (*Rumors*) ranged from 0 to 181,039, with a mean of 19,343.41 (*SD* = 38,303.84), indicating a wide dispersion and substantial variation across observations. The distribution of *Rumors* was positively skewed (Skewness = 2.79) and exhibited high kurtosis (7.79), suggesting the presence of extreme values or outliers.

Awareness about the Guinea worm reward system was assessed across three levels of endemicity. In endemic areas (*awareness_1*), the average awareness was 82.51% (*SD* = 11.23%). In at-risk areas (*awareness_2*), the mean awareness was 64.79% (*SD* = 28.47%), while in areas that were never endemic (*awareness_3*), the mean awareness was 47.57% (*SD* = 28.02%). The combined average awareness across all strata

(*awareness_mean*) was 67.33% (*SD* = 17.61%). The awareness variables displayed mild to moderate skewness, with the exception of *awareness_3*, which was approximately symmetric (Skewness = 0.07) (see Table 15).

In addition, the total number of confirmed Guinea worm cases also exhibited high variability, ranging from 0 to 2,030, with a mean of 161.92 (SD = 387.33), and a skewness value of 3.11 and kurtosis of 10.34, further confirming a heavy-tailed distribution. These patterns support the need for careful modeling approaches that accommodate non-normality and heteroscedasticity.

Table 15

Descriptive Statistics for Rumors and Awareness Variables

Variable	N	Min	Max	M	SD	Skewness	Kurtosis
Rumors	66	0	181039	19343.41	38303.84	2.79	7.79
Awareness (Endemic Areas)	40	.53	.99	.8251	.1123	-0.69	0.33
Awareness (At-Risk Areas)	38	.01	.98	.6479	.2847	-0.92	-0.25
Awareness (Never endemic)	30	.03	.98	.4757	.2802	0.07	-1.23
Mean Awareness Score	42	.33	.92	.6733	.1761	-0.43	-0.97
Total Cases	66	0	2030	161.92	387.33	3.11	10.34

Note. Awareness refers to knowledge about the reward. “Awareness (Endemic Areas)” = originally coded as awareness_1; “At-Risk Areas” = awareness_2; “Never Endemic Areas” = awareness_3. SD = standard deviation.

Correlation Among Rumors, Awareness levels and Total Reported

A Pearson product-moment correlation analysis was conducted to examine the associations among rumors, total confirmed Guinea worm cases, and awareness indicators across countries. Results indicated a significant positive correlation between the number of rumors and the total number of confirmed cases, $r(66) = .459$, $p < .001$, suggesting that countries with higher volumes of rumor reports also tended to report more confirmed Guinea worm cases. In terms of awareness, awareness_2 (at-risk areas) was significantly positively correlated with both awareness_1 (endemic areas), $r(37) = .355$, $p = .033$, and awareness_3 (never endemic areas), $r(30) = .395$, $p = .034$ (see Table 16). These associations suggest some consistency in community awareness patterns across different levels of endemicity. Interestingly, a significant negative correlation was observed between awareness_1 and total case counts, $r(40) = –.364$, $p = .021$, potentially indicating a protective influence of awareness in areas with historically higher disease burden.

Table 16

Pearson Correlation Matrix of Guinea Worm Rumors, Awareness Levels, and Total Reported Cases

	Rumors	Awareness (endemic)	Awareness (at risk)	Awareness (never endemic)	Mean Awareness	Total Cases
Rumors	1. —	-0.306 (*p* = 0.055)	0.006 (*p* = 0.973)	-0.154 (*p* = 0.417)	-0.173 (*p* = 0.275)	0.459 (p < .001)**
Awareness (endemic)	-0.306 (*p* = 0.055)	1—.000	0.355 (*p* = 0.033)	0.214 (*p* = 0.256)	0.552 (*p* = 0.001)**	-0.364 (*p* = 0.021)*
Awareness(at risk)	0.006 (*p* = 0.973)	0.355 (*p* = 0.033)*	—1.000	0.395 (*p* = 0.026)*	0.828 (p < .001)**	-0.077 (*p* = 0.645)
Awareness (never endemic)	-0.154 (*p* = 0.417)	0.214 (*p* = 0.256)	0.395 (*p* = 0.026)	1.0—00	0.810 (p < .001)**	-0.281 (*p* = 0.038)*
Mean awareness	-0.173 (*p* = 0.275)	0.552 (*p* = 0.001)	0.828 (p < .001)	0.810 (p < .001)	1.000)	-0.251 (*p* = 0.109)

Total cases	0.459 (p < .001)	-0.364 (*p* = 0.021)	-0.077 (*p* = 0.645)	-0.281 (*p* = 0.038)	-0.251 (*p* = 0.109)	1.000

Note. Values represent Pearson correlation coefficients with associated *p*-values in parentheses. $p < .05$ is indicated by *; $p < .01$ is indicated by **. Positive coefficients reflect direct relationships, and negative coefficients reflect inverse relationships between variables.

Multiple Linear Regression

To examine whether the percentage of people's awareness about the reward and knowledge about Guinea worm disease predicted the number of rumors reported, a multiple linear regression analysis was conducted. The dependent variable was the number of rumors (RUMORS), and the predictors included the awareness percentages from three levels of endemicity: endemic areas (*awareness_1*), at-risk areas (*awareness_2*), and never-endemic areas (*awareness_3*), as well as the composite awareness mean (*awareness_mean*).

Stepwise Model (Sequential Entry)

In the stepwise model, predictors were entered in stages to identify the most parsimonious model. The first step included only awareness (endemic areas), which significantly predicted RUMORS ($\beta = -.382$, $p = .041$), with an adjusted R^2 of .114, $F(1, 27) = 4.616$, $p = .041$.

Table 17

Regression Summary

Model	*R*	R^2	Adjusted R^2	*SE* of the Estimate	R^2 Change	*F* Change	*p*
1	.382	.146	.114	43732.793	.146	4.616	.041

Note. R^2 = coefficient of determination; *SE* = standard error; *p* = significance level.

Table 17 presents the stepwise regression model summary where only awareness (endemic areas) was retained as a predictor. R^2=0.146 means the model accounts for approximately 14.6% of the variance in the number of rumors, with an adjusted R^2 of .114, indicating moderate explanatory power and this model explained approximately 11.4% of the variance in rumors. The change in R^2 was statistically significant, F(1, 27) = 4.616, *p* = .041, demonstrating that awareness (endemic areas) alone significantly improves prediction of the outcome variable.

Table 18

ANOVA

Model	Sum of Squares	*df*	Mean Square	*F*	*p*
Regression	8828036838.8	1	8828036838.8	4.616	.041
Residual	51639044161	27	1912557191.1		
Total	60467080999	28			

Note. df = degrees of freedom; *F* = F statistic; *p* = significance level.

Table 18 displays the ANOVA results for the stepwise model. The regression sum of squares was 8.83×10^9 with one degree of freedom. The residual sum of squares was 5.16×10^{10} with 27 degrees of freedom. The model was statistically significant overall, $F(1, 27) = 4.62$, $p = .041$, indicating that awareness (endemic areas) significantly predicts the number of rumors.

Table 19

Regression Coefficient

Predictor	*B*	SE *B*	*β*	*t*	*p*	95% CI
(Constant)	157996.041	59052.675	–	2.676	0.013	[36829.961, 279162.122]
Awareness (Endemic Areas)	-152776.661	71110.243	-0.382	-2.148	0.041	[-298682.827, -6870.495]

Note. B = unstandardized coefficient; *SE B* = standard error; *β* = standardized coefficient; *t* = t-test statistic; *p* = significance level; CI = confidence interval.

Table 19 reports the unstandardized and standardized coefficients from the stepwise model. The constant term was statistically significant, $B = 157996.04$, $p = .013$. The awareness (endemic areas) coefficient was also significant, $B = –152776.66$, $\beta = –.382$, $t = –2.148$, $p = .041$. This suggests that for each one-unit increase in awareness in endemic areas, the number of rumors decreases by approximately 152,777. The 95% confidence interval for this effect ranges from. The regression equation follows the

standard linear form $\hat{Y} = B_0 + B_1X_1$ where $\hat{Y}$ is the predicted value of the dependent variable, B_0 is the intercept, and B_1 is the slope coefficient (Field, 2018). Where:

$\hat{Y}$ is the predicted number of RUMORS

B_0 =157996.04 is the constant (intercept)

B_1 =−152776.66 is the unstandardized coefficient for awareness (endemic areas)

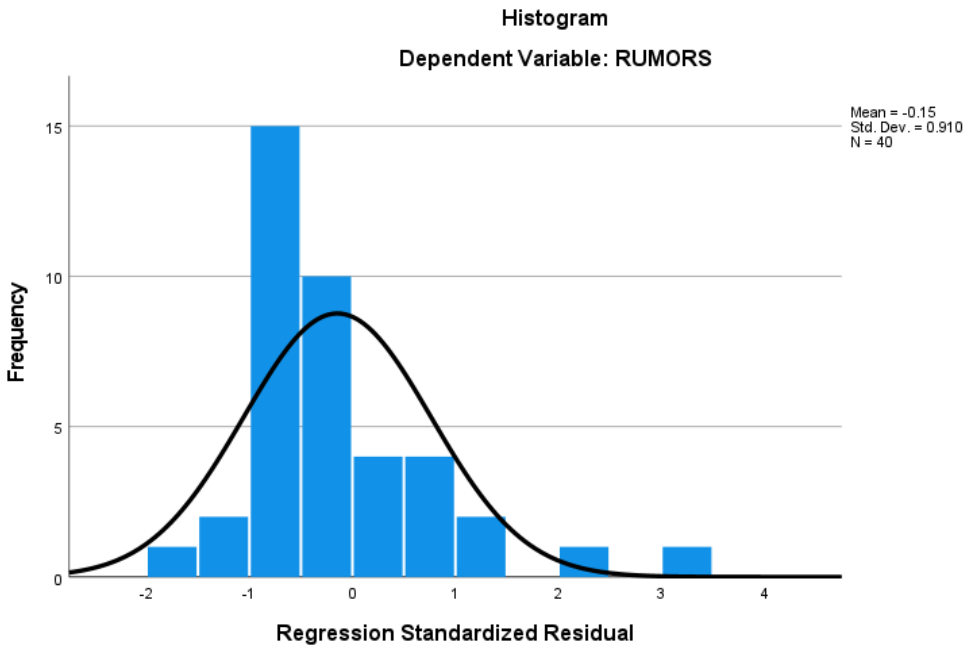
X_1 = awareness_1 (awareness level in endemic villages – level 1)

Thus, the model is: Predicted RUMORS=157996.04−152776.66 × awareness_1

Adding awareness_2 in Step 2 did not significantly improve the model (ΔR^2 = .001, p = .848). Including awareness_3 in Step 3 likewise did not contribute significantly (ΔR^2 = .008, p = .620). None of the additional predictors reached statistical significance beyond awareness (endemic areas), and multicollinearity remained within acceptable thresholds (VIF < 2).

Figure 31

Histogram of Standardized Residuals from the Multiple Linear Regression Model



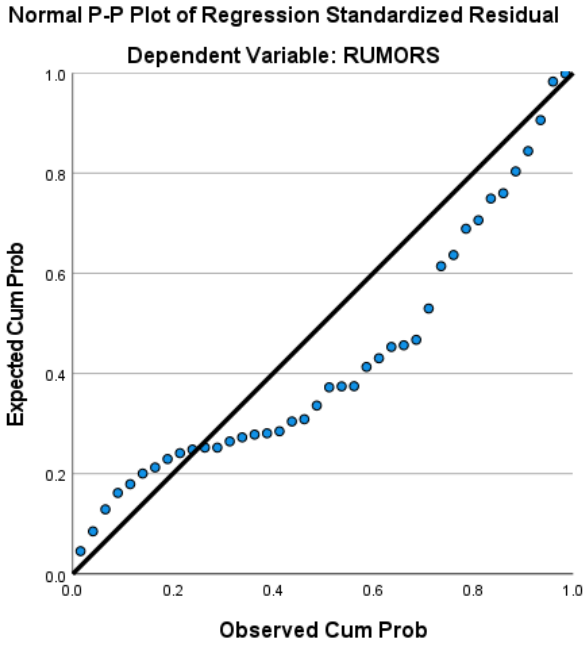
The distribution of standardized residuals was evaluated using both a histogram (see Figure 31) and a normal probability–probability (P–P) plot (see Figure 32). The histogram displayed an approximately symmetrical, bell-shaped curve centered around zero, with most residuals falling between –2 and +2. Although the distribution exhibited a slight negative skew (Mean = –0.15), the pattern closely resembled a normal distribution, suggesting acceptable normality.

Complementing this, the P–P plot showed that the observed cumulative probabilities closely followed the diagonal reference line, indicating alignment with the expected normal distribution. While minor deviations were observed at the extreme ends, the overall conformity of points supported the assumption of normally distributed

residuals. Taken together, these visual diagnostics suggest that the normality assumption for linear regression residuals was reasonably met.

Figure 32

Normal P–P plot of Standardized Residuals from the Multiple Linear Regression Model.

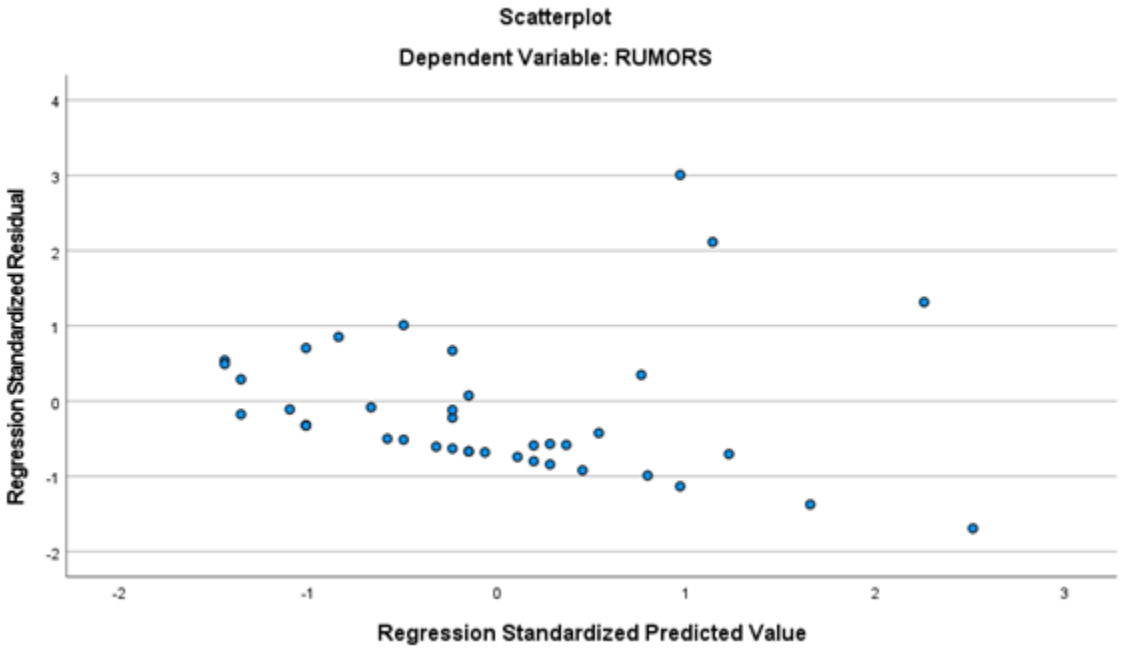


The scatter plot (see Figure 33) of standardized residuals against standardized predicted values is a visual diagnostic for checking the assumptions of linearity and homoscedasticity of the regression model. The dots are scattering for a smooth curve or pattern, so that would be a sign of linearity. Nevertheless, there is an indication of funneling—residuals show some conglomeration at low predicted values and greater dispersion at high predicted values—suggesting potential heteroskedasticity. However, the displacement is not much (and most residuals concentrate around to the horizontal line ($Y = 0$) means there is no extreme violation appeared. As such, although the model

seems to satisfy linearity assumption, some caution should be exercised with respect to constant variance across the entire spectrum of predicted values.

Figure 33

Standardized Residuals vs. Predicted Values for the Rumor Awareness Regression Model



Combined Model (Simultaneous Entry)

A multiple linear regression analysis was conducted using the simultaneous entry method to evaluate whether awareness about Guinea worm disease and reward—across multiple endemicity levels—significantly predicted the number of rumors reported. The independent variables were awareness_1 (endemic), awareness_2 (at-risk), and awareness_mean (overall awareness). The dependent variable was the total number of reported rumors.

The overall model was not statistically significant, $F(3, 25) = 1.537$, $p = .230$, and accounted for approximately 15.6% of the variance in rumor counts ($R^2 = .156$,

adjusted R^2 = .054) (see Table 20). This suggests that collectively, the awareness indicators did not provide a reliable prediction of rumor reporting across the sample.

Table 20

Model Summary

Model	*R*	R^2	Adjusted R^2	*SE* of the Estimate	R^2 Change	*F* Change	*p*
1	.395	.156	.054	45,189.272	.156	1.537	.230

Despite an R of .395 indicating a moderate correlation between predictors and the outcome variable, the lack of statistical significance (p = .230) implies that observed relationships may be due to chance. Additionally, the relatively small adjusted R^2 (5.4%) highlights the limited explanatory power of the full model.

Diagnostics such as the Durbin-Watson statistic (1.337) indicated acceptable independence of residuals. However, the lack of significance across all predictors suggests potential multicollinearity or overlapping variance. These findings suggest that when all awareness indicators are entered together, they do not significantly explain variations in rumor reporting—likely due to intercorrelation between the predictors. This reinforces the finding from the stepwise model where only awareness in endemic areas or awareness in level 1 (awareness_1) emerged as a significant predictor on its own.

Table 21

ANOVA Summary

Model	Sum of Squares	*df*	Mean Square	*F*	*p*
Regression	941,532,409.4	3	313,844,136.4	1.537	0.23
Residual	5,105,175,690.5	25	204,207,027.6		
Total	6,046,708,099.9	28			

Table 21 summarizes the ANOVA results for the regression model. The F-test tests whether the overall regression model provides a better fit to the data than a model with no predictors. The $F(3, 25) = 1.537$, $p = .230$ result suggests that the model is not statistically significant, indicating that the predictors collectively do not explain a significant amount of variance in rumors.

Table 22

Regression Coefficients

Predictor	*B*	*SE B*	*β*	*t*	*P*
(Constant)	159308.321	61073.670		2.608	0.015
Awareness (Endemic Area)	-139570.132	88607.964	-0.349	-1.575	0.128
Awareness in (At-Risk Areas)	29660.690	57813.446	0.168	0.513	0.612
Mean Awareness Score	-49165.974	98055.758	-0.180	-0.501	0.620

Table 22 presents the unstandardized and standardized regression coefficients for each awareness variable. None of the predictors are statistically significant at $\alpha = .05$. awareness in level 1 has a negative relationship with rumor count, while awareness in level 1 and mean awareness show weaker, non-significant effects. The confidence intervals include zero, reinforcing the conclusion that none of the predictors significantly contribute to the model.

Table 23

Residuals Statistics from the Multiple Linear Regression Model Predicting Rumors

Statistic	Minimum	Maximum	Mean	Std. Deviation	N
Predicted Value	-596.97	75207.41	30917.4	18906.632	36
Residual	-72120.406	129688.297	-2672.487	40620.942	36
Std. Predicted Value	-1.796	2.338	-0.077	1.031	36
Std. Residual	-1.596	2.87	-0.059	0.899	36

The residual statistics table provides a diagnostic assessment of the model's predictive accuracy and the distribution of errors. The predicted values for the dependent variable (RUMORS) ranged from –596.97 to 75,207.41, with a mean of 30,917.40, which is consistent with the overall distribution of observed values (see Table 23). This suggests that the model's predictions are reasonably centered, although there is variability in the individual estimates.

The unstandardized residuals (i.e., the differences between observed and predicted values) ranged from –72,120.41 to 129,688.30, with a mean of –2,672.49. This negative mean indicates a slight tendency for the model to underestimate the number of rumors, though this underestimation is not severe when considered relative to the overall scale and variability of the data.

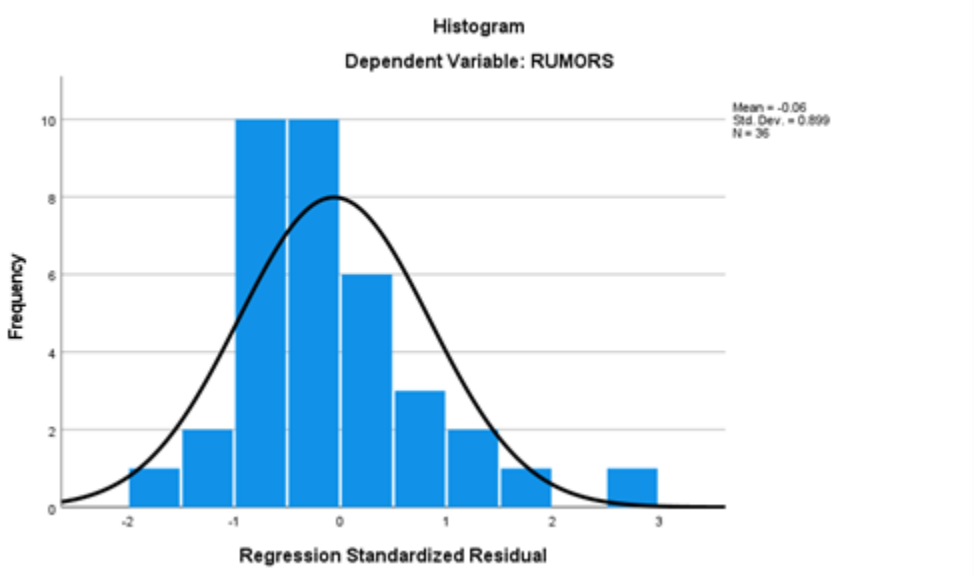
Standardized predicted values, which normalize predictions relative to the model's standard error, ranged from –1.80 to 2.34. This distribution is well within the expected range for normally distributed values and suggests that most predicted scores are within two standard deviations from the mean.

Similarly, standardized residuals ranged from –1.60 to 2.87. As values beyond ±3.00 are typically considered potential outliers, these results suggest there were no

extreme or influential outliers affecting the regression model. Overall, the residual distribution supports the assumption that the model's residuals are approximately normally distributed and do not contain undue leverage points.

Figure 34

Histogram of Standardized Residuals for the Regression Model Predicting Rumors

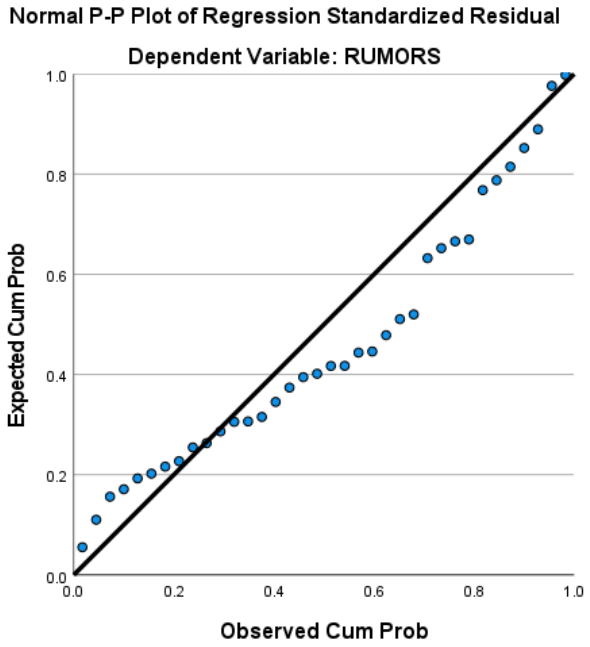


Regression assumptions were evaluated and appeared reasonably met. The standardized residuals were normally distributed (skewness = –0.06; histogram approximated normal curve; see Figure 34), and the P–P plot (see Figure 35) and scatterplot showed no major deviations from linearity or homoscedasticity. Collinearity diagnostics indicated no severe multicollinearity (VIFs < 4, condition indices < 30).

The residual plots (histogram and P-P plot) suggested acceptable normality of errors, and the scatterplot indicated no major heteroscedasticity or non-linearity. While multicollinearity was slightly elevated for awareness_mean (VIF = 3.828), it did not exceed critical thresholds that would suggest serious concern (VIF > 5).

Figure 35

Normal P–P Plot of Standardized Residuals for the Regression Model Predicting Rumors



These findings only partially support the alternative hypothesis (H_a) that awareness predicts the number of rumors, and the null hypothesis (H_0) cannot be fully rejected in the full model.

Exploratory Finding: Relationship Between Rumors and Total Cases

An exploratory simple linear regression was conducted to assess whether the number of reported Guinea worm rumors predicted the number of confirmed Guinea worm disease (GWD) cases. This analysis aimed to evaluate the potential role of rumors as a proxy for transmission awareness and case detection, with total reported GWD cases as the dependent variable and the number of rumors as the sole predictor.

Table 24

Model Summary for Rumors Predicting Total Cases

Model	R	R^2	Adjusted R^2	Std. Error of Estimate	*F*	*df1*	*df2*	p-value	Durbin-Watson
1	0.459	0.21	0.198	346.884	17.04	1	64	< .001	2.161

The model was statistically significant, $F(1, 64) = 17.04$, $p < .001$, and explained approximately 21.0% of the variance in total reported GWD cases ($R^2 = .210$, Adjusted $R^2 = .198$), with a standard error of the estimate of 346.88. The standardized beta coefficient indicated a moderate positive association between rumors and total cases ($\beta = .459$, $t = 4.13$, $p < .001$).

The unstandardized regression equation derived from the model where:

$\hat{Y}$ is the predicted number of cases

B_0 =72.23 is the constant (intercept)

B_1 =0.005 is the unstandardized coefficient for rumors

X_1 = Rumors

Thus, the model is: $\hat{Y} = B_0 + B_1 X_1$

$$\hat{Y} = 72.23 + 0.005 \text{ X Rumors}$$

This equation suggests that for every additional rumor, the number of confirmed cases is predicted to increase by 0.005, holding all else constant. If a country reported 10,000 rumors:

$$\hat{Y} = 72.23 + 0.005 \text{ X } 10000$$

Thus, the model predicts approximately 122 reported Guinea worm cases.

The Durbin–Watson value of 2.161 indicates no major concerns regarding autocorrelation in the residuals.

Table 25

ANOVA Summary

Model	*SS*	*df*	*MS*	*F*	*p*
Regression	2050388.811	1	2050388.811	17.04	< .001
Residual	7701031.811	64	120328.622		
Total	9751420.621	65			

Note. *SS* = sum of squares; *df* = degrees of freedom; *MS* = mean square; *F* = F-ratio; *p* = significance level.

The ANOVA table (see Table 25) supports the statistical significance of the overall regression model, $F(1, 64) = 17.040$, $p < .001$, confirming that the inclusion of the rumors variable significantly improved the model fit compared to a null model without predictors. The model explained 21.0% of the variance in total reported cases ($R^2 = .210$), suggesting that rumors play a meaningful role in identifying actual infections. The Durbin-Watson statistic (2.16) indicated no autocorrelation in the residuals, and collinearity diagnostics confirmed no multicollinearity (VIF = 1.00). Residual analysis showed a roughly normal distribution with no significant outliers.

Table 26

Regression Coefficient

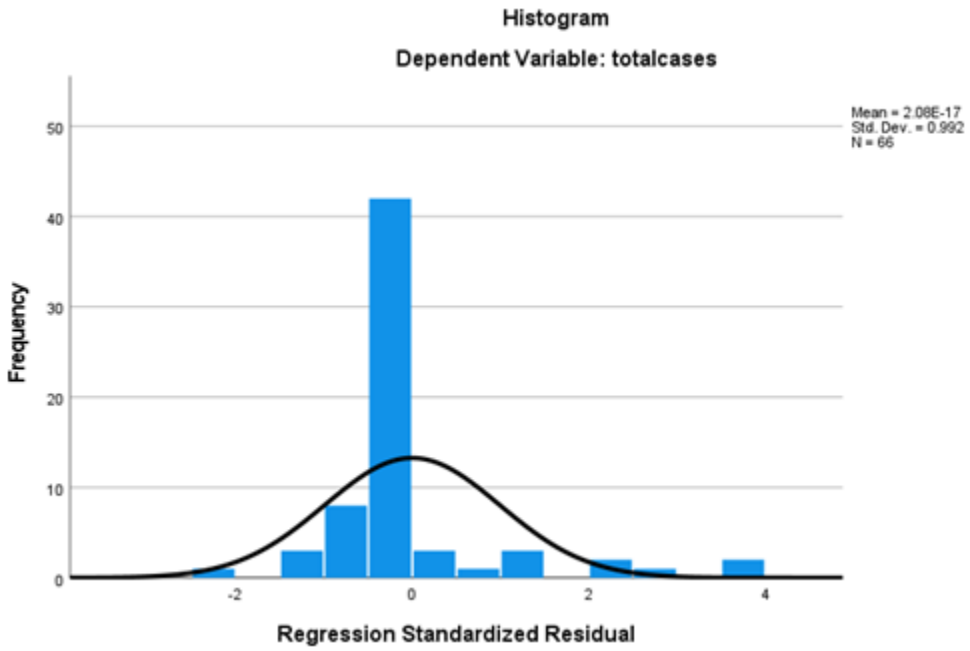
Predictor	*B*	*SE B*	*β*	*t*	*p*	95% CI
(Constant)	72.233	47.909		1.508	.137	-[23.476, 167.942]
Rumors	0.005	0.001	0.459	4.128	< .001	[0.002, 0.007]

Note. *B* = unstandardized regression coefficient; *SE B* = standard error of *B*; *β* = standardized beta; *CI* = confidence interval.

Table 26 displays the unstandardized and standardized coefficients. The regression coefficient for rumors was statistically significant ($B = 0.005$, $SE = 0.001$, $\beta = .459$, $t = 4.128$, $p < .001$), indicating that each additional rumor reported was associated with an increase of approximately 0.005 in confirmed Guinea worm cases, holding other factors constant. The 95% confidence interval for the slope ranged from 0.002 to 0.007, suggesting a small but consistent positive association. This finding supports the practical relevance of rumor tracking as a potential indicator of Guinea worm activity.

Figure 36

Histogram of Standardized Residuals for the Regression Model Predicting Total Guinea Worm Cases From Reported Rumors

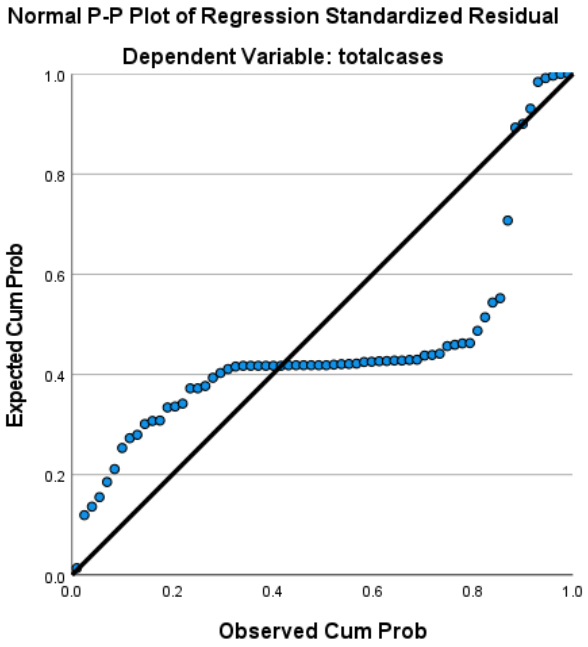


This histogram displays the distribution of standardized residuals. A bell-shaped curve is overlaid to help assess normality. The residuals appear approximately normally

distributed with a mean close to zero (Mean = 2.08E–17; SD = 0.992). Most residuals fall within ±2 standard deviations, indicating that the assumption of normality of errors is reasonably met. Residual analysis indicated no severe violations of regression assumptions. The standardized residuals were approximately normally distributed (Skewness = 0.00, Kurtosis ≈ 0), and fell mostly within the ±3 range. The Durbin–Watson statistic was 2.16, indicating no significant autocorrelation. Although the residual histogram (see Figure 36) showed a slight right skew and the P–P plot suggested some deviation from normality at the tails, the scatterplot of standardized predicted values and residuals did not display heteroscedasticity or non-linearity. Thus, the assumption of homoscedasticity was reasonably met.

Figure 37

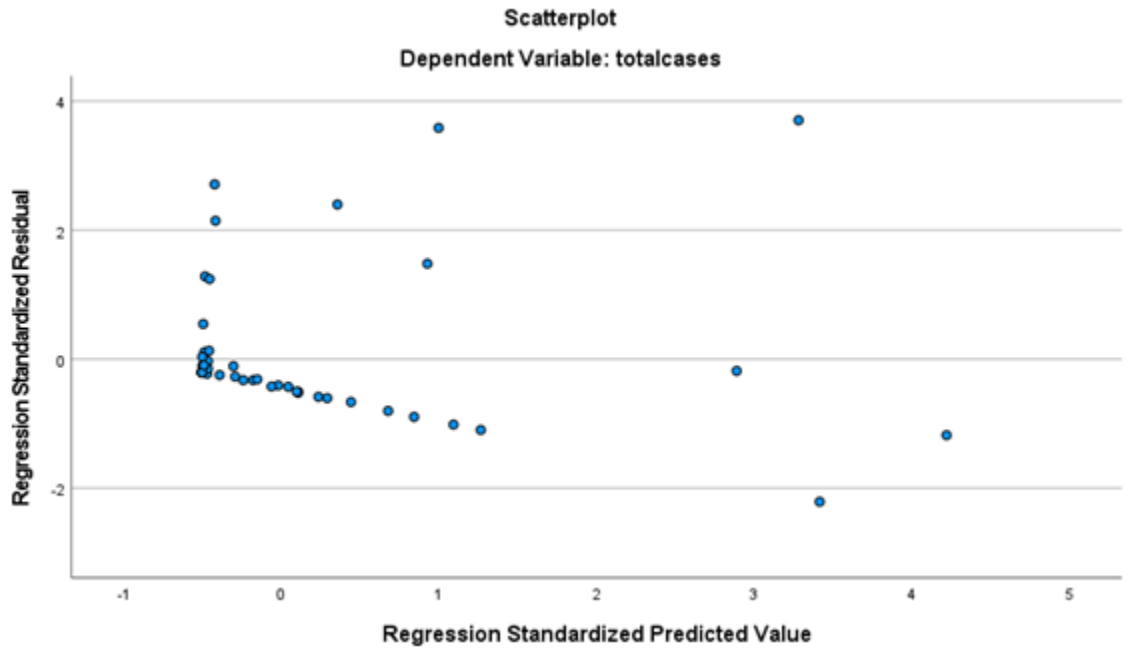
Normal Probability Plot of Standardized Residuals for the Regression Model Predicting Total Guinea Worm Cases



The P–P plot of standardized residuals (see Figure 37) also supported the assumption of normality. Most data points aligned closely with the diagonal reference line, indicating that the observed cumulative probability closely matched the expected normal distribution. Minor deviations were observed at the lower and upper ends, but no extreme departure from normality was evident.

Figure 38

Scatterplot of Standardized Residuals Versus Predicted Values for the Regression Model Predicting Total Guinea Worm Cases



The scatterplot of standardized residuals against standardized predicted values (see Figure 37) was used to assess both linearity and homoscedasticity. The points appeared randomly dispersed around zero, though some clustering and slight funneling at higher predicted values suggest mild heteroscedasticity. However, no clear pattern or systematic curvature was present, which supports the assumption of a linear relationship between the predictor (rumors) and the outcome (total cases). Additionally, no outliers exceeded ±3 standard deviations, suggesting that no individual case unduly influenced the regression model.

Summary

The purpose of this study was to examine the relationships between behavioral, programmatic, and environmental factors and Guinea worm disease incidence across endemic countries from 2012 to 2023. The study addressed three research questions, each with corresponding hypotheses, using a combination of regression analyses, spatial analyses, and secondary time series forecasting.

Research Question 1: Does the theory of change explain the association between dog tethering, ponds treated with Abate, people's awareness about the disease and reward, village access to safe water sources, and Guinea worm disease (in humans and animals)?

$H_0$1: The theory of change does not explain the association between the specified factors and Guinea worm disease incidence.

H_a1: The theory of change explains the association between the specified factors and Guinea worm disease incidence.

The null hypothesis ($H_0$1) was partially rejected.

Research Question 1 examined whether control and prevention activities—such as dog tethering, pond treatment with Abate, awareness of the reward, access to safe water, and knowledge of Guinea worm disease—were associated with the occurrence of reported Guinea worm infections in humans and animals at the country level. Descriptive statistics and comparative analyses showed variation in both case counts and reported prevention efforts across countries. Poisson and Negative Binomial models revealed that dog tethering was significantly associated with case counts (positive association), suggesting that this practice may be more prevalent in higher-transmission

settings as a reactive intervention. However, other prevention indicators—such as pond treatment with Abate, awareness about the reward, access to safe water sources, and knowledge about the disease—were not significantly associated with reported case counts at the aggregated country-year level.

Thus, the results provided only partial support for the theory of change, as only one component (dog tethering) showed a significant association, while other prevention strategies did not. While one component of the theory (dog tethering) was statistically significant, the absence of significance for other intervention measures indicates that the overall set of programmatic strategies was not uniformly predictive of Guinea worm disease occurrence when analyzed at the national aggregation level.

These findings suggest that the effectiveness of the theory of change may vary depending on localized implementation conditions, the quality of intervention delivery, and the scale at which relationships are assessed.

Research Question 2: What is the relationship between environmental factors (climate, temperature, water supply) and Guinea worm cases or infections?

$H_0$2: There is no relationship between environmental factors and the number of Guinea worm cases or infections.

H_a2: Environmental factors have a relationship with the number of Guinea worm cases or infections.

The null hypothesis ($H_0$2) was retained based on regression analysis, but spatial analyses revealed significant clustering.

Research Question 2 examined whether environmental factors—including monthly temperature, precipitation, and surface water occurrence—were associated with the number of Guinea worm cases or infections at the village level.

Negative Binomial Regression models indicated that none of the individual environmental predictors (temperature, precipitation, or surface water occurrence) were statistically significant predictors of monthly case counts (all p-values > .05).
Spatial regression models similarly showed no significant direct association between environmental variables and case incidence after adjusting for spatial autocorrelation.

While spatial analyses, including Global Moran's I and Local Indicators of Spatial Association (LISA), revealed significant spatial clustering of cases ($p < .001$), this clustering appeared independent of the measured environmental variables.
The presence of spatial dependence suggests that other factors—such as behavioral or programmatic interventions—may better explain transmission patterns.

Because no environmental factor was found to have a statistically significant relationship with Guinea worm case counts, the null hypothesis ($H_0 2$) was accepted.
These results indicate that environmental conditions alone, when analyzed independently at the monthly village scale, do not adequately predict Guinea worm disease incidence without integrating behavioral and programmatic context.

Research Question 3: What is the relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about reporting Guinea worm disease/infection?

$H_0$3: There is no relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about Guinea worm disease/infection reporting.

H_a3: There is relationship between the percentage of people's awareness about the reward, knowledge about the disease, and the number of rumors about Guinea worm disease/infection reporting.

The null hypothesis ($H_0$3) was partially rejected.

Research Question 3 investigated whether awareness indicators—specifically the percentage of people aware of the reward, knowledgeable about Guinea worm disease, or exposed to health education—were associated with the number of rumors reported about suspected cases or infections.

Descriptive statistics revealed variability in rumor reporting across countries and levels of endemicity. A stepwise multiple linear regression was conducted to examine whether awareness about Guinea worm disease and associated rewards predicted the number of rumors reported. The dependent variable was the number of rumors (RUMORS), and the independent variables entered into the model included awareness_1 (endemic areas), awareness_2 (at-risk areas), awareness_3 (never-endemic areas), and the composite mean awareness (awareness mean). Correlation analysis demonstrated that awareness in Level 1 endemic areas (awareness_1) was significantly associated with rumor reporting ($\beta = -.382$, $p = .041$) in the stepwise regression model, suggesting that higher community awareness was related to lower rumor counts in these settings. The stepwise method identified awareness (endemic areas) as the sole significant predictor

retained in the final model. The overall regression model was statistically significant, $F(1, 27) = 4.616$, $p = .041$, and explained approximately 14.6% of the variance in rumor counts ($R^2 = .146$, adjusted $R^2 = .114$). The regression equation was:

$$\hat{Y} = 157{,}996.04 - 152{,}776.66 \times \text{awareness (endemic areas)}$$

However, when awareness indicators for Level 2 (at-risk) and Level 3 (never endemic) areas were included in the multivariate model, the overall model did not remain statistically significant.

Assumption checks showed no major violations: residuals were approximately normally distributed, no severe multicollinearity was detected, and plots of residuals against predicted values showed an acceptable pattern. Furthermore, an exploratory regression revealed that the number of rumors significantly predicted total case counts ($\beta = .459$, $p < .001$), suggesting the operational importance of rumors in early case detection. Thus, the null hypothesis for RQ3 was partially rejected: while specific awareness indicators showed a significant relationship with rumor reporting, the combined multivariable models yielded inconsistent results across all awareness levels. These findings highlight the critical role of community engagement and rumor surveillance in maintaining high sensitivity of detection, particularly in areas with low or interrupted transmission.

Chapter 4 provided a comprehensive quantitative assessment of the drivers of Guinea worm occurrence, using country-level prevention indicators, environmental factors at the village level, and indicators of community awareness. The findings revealed

several statistically significant relationships that have direct implications for programmatic decision-making and surveillance enhancement.

In addition to the primary regression and spatial analyses, a secondary time series forecasting analysis was conducted to project future trends in Guinea worm disease incidence through 2030. Using the SPSS Expert Modeler, country-specific models were developed for Chad, Ethiopia, Mali, South Sudan, and Angola. The forecasts revealed that while South Sudan and Ethiopia may be on a trajectory toward achieving transmission interruption, Chad, Mali, and Angola are unlikely to reach zero cases without accelerated interventions. These forecasting results complement the cross-sectional analyses by highlighting the urgent need for intensified programmatic action in countries exhibiting persistent or rising transmission trends.

Chapter 5 will now interpret these results within the broader context of Guinea worm eradication efforts. The interpretation will consider the practical implications of the findings, identify study limitations, and provide evidence-based recommendations for surveillance, policy development, and integrated intervention strategies. The goal is to translate the empirical results into actionable insights that can inform neglected tropical disease (NTD) control programs, strengthen community engagement, and support the final stages of Guinea worm eradication efforts globally.

Chapter 5. Discussion, Conclusions, and Recommendations

Introduction

The purpose of this study was to examine the relationships between environmental, behavioral, and programmatic factors and the occurrence of Guinea worm disease in endemic and formerly endemic regions of Africa. Specifically, the study addressed three research questions focused on (1) evaluating the theory of change as it relates to key programmatic indicators and reported disease incidence, (2) identifying the relationship between environmental factors (temperature, precipitation, surface water presence) and reported human Guinea worm cases, and (3) assessing the role of community awareness and knowledge in relation to rumors and informal reporting of suspected cases/infections.

A quantitative research design was employed, utilizing secondary programmatic data from the Guinea Worm Eradication Program (GWEP), environmental data (climate and surface water occurrence), and survey-based awareness indicators. Data were collected across five countries and aggregated at either the village or national level, depending on the research question. The analyses included multiple linear regression, generalized linear models (negative binomial regression), and spatial analysis techniques such as Moran's I, Local Indicators of Spatial Association (LISA), and Spatial Lag/Error regression models.

Key findings indicated partial support for the theory of change, with dog tethering significantly associated with case counts, but other intervention indicators not reaching significance. Environmental factors such as temperature, precipitation, and surface water

occurrence were not significant predictors of monthly Guinea worm cases, although spatial clustering of cases was evident. Awareness levels in at-risk areas were positively associated with rumor reporting, underscoring the importance of community engagement for early case detection.

Chapter 4 presented the results of these analyses, organized by research question and hypothesis. Chapter 5 now interprets those findings, highlights implications for NTD surveillance and elimination programming, and discusses study limitations and recommendations for future research. The interpretation is structured around each research question and aligned with the overall objective of understanding how programmatic and environmental factors relate to Guinea worm transmission and reporting patterns.

Interpretation of Findings

Research Question 1

The analysis provided partial support for the program's theory of change. Multiple linear regression results showed that among the four predictors assessed—dog tethering, pond treatment with Abate, community awareness, and village access to safe water—only dog tethering showed a statistically significantly associated with log-transformed Guinea worm case counts. Notably, the association was positive, indicating that countries reporting tethering activities also reported higher numbers of infections.

This finding is consistent with prior field observations, which suggest that dog tethering is often a reactive measure employed in areas experiencing active transmission, rather than a preventive intervention applied uniformly (Molyneux et al., 2020; World

Health Organization [WHO], 2023a). Thus, the observed positive association likely reflects targeted program implementation in response to high disease burden, rather than tethering itself causing increased transmission. This interpretation aligns with WHO guidelines recommending tethering as a core containment strategy where canine infections persist (WHO, 2023b).

In contrast, pond treatment with Abate, community awareness, and access to safe water were not statistically significantly associated with case counts at the country-year level. This finding diverges from expectations established in prior literature, where Abate application has been shown to effectively disrupt transmission by killing copepods (Cairncross et al., 2002; Watts, 1987), and community awareness campaigns have been linked to enhanced rumor reporting and early detection (Hopkins et al., 2022). The discrepancy may partly reflect limitations of data aggregation: by collapsing programmatic indicators across entire countries and years, localized variations in intervention intensity, quality, and uptake were likely obscured (Weiss et al., 2023). Furthermore, issues such as self-reported coverage estimates, incomplete awareness surveys, and potential underreporting may have attenuated detectable effects.

Importantly, these findings do not contradict the existing body of evidence, but rather illustrate the limitations of using aggregated surveillance data to assess interventions that operate at the village or district level.

Previous studies, such as Eberhard et al. (2014), demonstrated stronger local-level associations between water access and reduced case incidence, suggesting that critical relationships may be masked at broader spatial and temporal scales. Theoretically, the

results provide partial empirical validation of the PRECEDE-PROCEED model applied in this study. The theory posits that both behavioral factors (e.g., tethering, awareness) and environmental interventions (e.g., Abate treatment, safe water provision) contribute to disease reduction. However, in this analysis, only one behavioral factor (tethering) demonstrated a significant relationship with case counts, suggesting that intervention presence alone may be insufficient without considering implementation intensity, timing, and local context (Green et al., 2022).

In sum, the findings extend existing knowledge by emphasizing the critical need for high-resolution monitoring frameworks and more granular evaluation of eradication activities. They reinforce the importance of disaggregated data collection, targeted surveillance, and contextual interpretation in understanding programmatic impact during the final stages of Guinea worm eradication (WHO, 2023a, 2023b)

While dog tethering showed a statistically significant association, the positive direction suggests surveillance bias or reactive program intensity rather than a causal effect of tethering on transmission reduction. Interpretations must remain bounded within the study's ecological and observational design constraints.

Research Question 2

This examined the relationship between environmental factors—monthly average temperature, total precipitation, and surface water occurrence—and the number of reported Guinea worm disease (GWD) cases at the village-month level across endemic regions from 2012 to 2023. The study employed Negative Binomial Regression and spatial regression models to assess both statistical associations and spatial dependencies.

The results indicated that none of the environmental predictors (temperature, precipitation, or surface water occurrence) were statistically significant predictors of monthly case counts (all $p > .42$). Additionally, two-way interaction terms between environmental were not statistically significant, and the inclusion of seasonality (i.e., month of emergence) did not improve model fit. Accordingly, the null hypothesis (H_o2) for RQ2 was retained.

Spatial diagnostic tests revealed modest but statistically significant global clustering of case counts (Global Moran's I = 0.0543, $p = .011$). However, spatial regression models (Spatial Lag and Spatial Error) indicated that spatial dependence contributed more to explaining case distribution than the environmental predictors themselves. This suggests that unmeasured spatial factors—such as variations in surveillance intensity, human and animal mobility patterns, and localized intervention efforts—may better account for the observed spatial heterogeneity.

These findings partially disconfirm earlier ecological studies that suggested strong seasonal or environmental drivers of Guinea worm transmission (Molyneux et al., 2020; Hopkins et al., 2023a; Perini et al., 2020). Prior research found associations between rainfall patterns, surface water availability, and disease risk at regional or seasonal scales. However, the present study demonstrates that at finer spatial and temporal resolutions—specifically, monthly village-level data—contemporaneous environmental conditions . alone do not explain variations in GWD cases.

Specifically, the environmental predictors assessed did not demonstrate statistically significant relationships with Guinea worm disease incidence at the monthly

village level. Monthly temperature was not significantly associated with case counts, disconfirming previous coarse-scale studies that had suggested warmer months correlated with elevated transmission risk (Molyneux et al., 2017; Hopkins et al., 2023b). Likewise, monthly precipitation showed no significant effect, contrary to modeling studies that predicted greater transmission during wet seasons through the formation of temporary ponds (Thiele et al., 2020). Surface-water occurrence values, derived from high-resolution remote sensing data, were also not significant predictors, challenging assumptions that proximity to static water bodies reliably forecasts infection risk (Guagliardo et al., 2020). Moreover, two-way interaction terms among temperature, precipitation, and surface water occurrence did not reveal any significant synergistic effects, extending the literature by demonstrating that combined climatic influences do not meaningfully explain case variations at this fine spatial-temporal resolution. Finally, adding seasonality through the month of emergence variable did not significantly enhance model fit, suggesting that observed peaks in national surveillance data may reflect programmatic factors, such as intensified case searches or reward campaigns, rather than intrinsic climatic seasonality.

Taken together, these findings underscore that while environmental conditions create a necessary background for transmission, they are not sufficient on their own to predict incident cases at the operational scale relevant for eradication efforts. Behavioral, programmatic, and ecological factors appear to play a more proximate and decisive role in determining residual transmission patterns at the village-month level.

Thus, while environmental conditions undoubtedly influence the basic ecology of transmission, behavioral, programmatic, and operational factors likely dominate as proximate drivers at micro-scales relevant for eradication planning.

Within the PRECEDE-PROCEED theoretical framework, these findings reinforce the notion that environmental factors alone are necessary but not sufficient determinants of health outcomes (Green et al., 2022). Behavioral interventions (e.g., dog tethering), public awareness, and health system responsiveness remain critical mediators between environmental conditions and disease risk. The observed residual spatial clustering even after adjusting for environmental variables underscores the relevance of behavioral surveillance, community engagement, and operational factors in interrupting transmission.

These results extend prior work by incorporating high-resolution environmental data into village-level modeling and reveal critical limitations in relying solely on static environmental proxies. Future predictive models and intervention strategies must integrate behavioral, ecological, and programmatic data to accurately target and monitor residual transmission foci.

Acceptance of the null hypothesis for environmental predictors does not imply that climate and hydrology are irrelevant. Rather, it reflects that at this fine analytical scale, environmental factors alone were insufficient to predict case incidence without accounting for the complex behavioral and operational dynamics of Guinea worm transmission.

Table 27

Summary of Environmental Predictor Findings: Direction of Effect, Consistency with Prior Research, and Contribution to the Field

Environmental factor	Direction & size of effect in this study	Consistency with prior work	Contribution to the field
Monthly temperature	Non-significant (B ≈ 0; p > .42 in all models)	Disconfirms coarse-scale studies that reported higher GWD risk in warmer months Molyneux et al., 2017; Hopkins et al., 2023b).	Shows that the temperature–risk relationship documented at regional or seasonal scales may not hold at the finer village-month resolution.
Monthly precipitation	Non-significant (p > .80).	Disconfirms modelling work that linked wet seasons to elevated transmission through pond formation (Thiele et al., 2020).	Extends knowledge by demonstrating that contemporaneous rainfall, absent behavioral data, does not independently predict incident cases.
Surface-water occurrence	Non-significant (p ≈ .81).	Disconfirms remote-sensing studies that used static water bodies as ecological risk proxies (Guagliardo et al., 2020)	Highlights that static "percent water" metrics alone are insufficient; dynamic, micro-level water contact or canine infection data may be required.
Two-way interactions	All non-significant	No prior GWD study tested these interactions.	Extends the literature by showing that synergistic effects of climate and hydrology are *not* evident at monthly scale.
Seasonality (month of emergence)	Non-significant overall effect	Disconfirms descriptive reports of strong seasonality when finer temporal and spatial controls are applied. (Molyneux et al., 2017; Hopkins et al., 2023b; Thiele et al., 2020; Guagliardo et al., 2020)	Indicates that reported peaks may be driven by programmatic factors (e.g., enhanced search campaigns) rather than climate alone.

Research Question 3

This aimed to investigate the relationship between community awareness variables—specifically, awareness about the reward for reporting Guinea worm disease, knowledge about the disease—and the number of rumors reported about suspected cases or infections. The analysis aimed to assess whether increased awareness at the

community level was associated with heightened informal surveillance sensitivity through rumor reporting.

Descriptive statistics and correlation analysis revealed that in Level 2 (at-risk) areas, awareness levels were positively and significantly associated with the volume of rumors reported. This finding supports the hypothesis that enhanced awareness leads to more active community reporting. Furthermore, the number of rumors showed a positive correlation with confirmed Guinea worm cases, suggesting that rumors may serve as an effective proxy indicator for early detection. Higher reward awareness has previously been linked to increased rumor reporting, which is considered a cornerstone of syndromic surveillance in low-incidence settings (Hopkins et al., 2022). Additionally, the positive correlation between rumors and confirmed case counts supports previous assertions that rumor reporting remains a valuable surveillance tool even as overall disease incidence declines. The findings reinforce the importance of maintaining community engagement and reward visibility, particularly in areas categorized as at-risk or formerly endemic.

However, when awareness variables were included together in a multiple regression model, the direction of association reversed: greater awareness was associated with fewer rumors, and the relationship reached statistical significance (B = –152,776.66, p = .041). This counterintuitive finding suggests potential collinearity or measurement overlap among awareness indicators across settings. Increased awareness may not operate uniformly across contexts, especially when behavioral reinforcement or contextual facilitators are lacking. When modeled individually, awareness measures aligned with expected patterns, but combined models were unstable. It is when multiple awareness

variables were entered simultaneously into regression models, the predictive relationships weakened, and the combined models were no longer statistically significant. Thus, the null hypothesis ($H_0 3$) for Research Question 3 was partially rejected: some awareness measures were significantly associated with rumors in bivariate analyses, but the overall multivariable model did not consistently retain statistical significance.

These findings are consistent with previous literature underscoring the role of awareness and reward sensitization in promoting early case detection (Breman, 2021; Guagliardo et al., 2020; WHO, 2023b). However, the present study advances this knowledge by showing that awareness–rumor relationships are more robust in bivariate models and may attenuate or reverse in multivariable frameworks. This underscores the importance of ensuring precise and non-redundant operationalization of community-level constructs in surveillance research.

Within the PRECEDE-PROCEED framework, the findings highlight that predisposing factors, such as community knowledge, attitudes, awareness and substantially influence health surveillance outcomes. Awareness campaigns can strengthen community participation in disease reporting, thereby enhancing passive and active surveillance systems and promoting earlier case containment. Increased awareness may not operate uniformly across settings, especially when behavioral reinforcement or contextual facilitators are lacking.

This study advances the understanding of Guinea worm eradication strategies in several important ways. First, it demonstrates the critical importance of maintaining high levels of community awareness about rewards, particularly in at-risk areas, to sustain

rumor reporting and facilitate early case detection. Second, the findings validate rumor reporting as a valuable proxy surveillance indicator, closely linked to actual transmission risks. This underscores the operational utility of rumors not merely as noise in surveillance systems but as meaningful signals that can enhance the sensitivity of detection efforts. Third, the study highlights the complexity inherent in modeling the effects of community awareness, especially when overlapping indicators of knowledge, perceptions, and behaviors are involved. These insights collectively extend previous literature and suggest that future interventions should not only aim to increase knowledge but also monitor and adapt to evolving patterns of risk perception within communities. While the findings support the operational utility of rumor surveillance, limitations related to self-reported awareness measures, survey variability, and potential ecological bias should be acknowledged. Furthermore, rumors were not verified individually as confirmed cases in this study, so the use of rumor counts as a surveillance metric requires cautious interpretation.

Overall, the findings of this study provide important insights into the multi-dimensional drivers of Guinea worm disease transmission in the pre-certification era. Across the three research questions, behavioral and programmatic factors emerged as more influential predictors of Guinea worm incidence and surveillance sensitivity than environmental variables alone. Research Question 1 demonstrated that while dog tethering was significantly associated with case patterns—likely reflecting reactive interventions—the broader theory of change requires more localized evaluation to fully capture its effects. Research Question 2 revealed that static environmental exposures such

as temperature, precipitation, and surface water occurrence did not independently predict monthly case incidence at the village level, challenging earlier ecological models and emphasizing the importance of integrating behavioral and spatial data. Research Question 3 highlighted that community awareness, particularly in at-risk areas, remained a vital driver of rumor reporting and early case detection, although multivariable modeling of awareness factors revealed complexities. Together, these findings confirm and extend prior literature by emphasizing that Guinea worm disease eradication is not solely a function of environmental risk but is profoundly shaped by human behavior, surveillance intensity, and programmatic responses. This synthesis underscores the need for dynamic, context-sensitive, and community-centered strategies to achieve final eradication goals.

Secondary Time Series Forecasting

The secondary time series forecasting analyses provided important insights into the projected trajectory of Guinea worm disease cases through 2030 across five endemic countries. While South Sudan and Ethiopia demonstrated potential for achieving interruption of transmission under current or slightly strengthened efforts, the forecasts for Chad, Mali, and Angola indicated persistent challenges.

In Chad, the projected persistence of approximately 503 cases annually suggest that intensified interventions, including enhanced dog tethering, pond treatment with Abate, and expanded access to safe drinking water, will be critical to disrupt ongoing transmission. Similarly, Mali’s forecast, indicating continued low-level transmission (~18.67 cases annually), underscores the need for accelerated efforts focused on surveillance, community engagement and containment.

In Ethiopia, the model forecasted stable case load of approximately 10.75 cases per year, emphasizing the importance of maintaining high-quality surveillance, rapid response mechanism, and case containment strategies to eliminate residual transmission. For South Sudan, the downward trend predicted by the Brown exponential smoothing model aligned with national eradication targets. However, the wide confidence intervals associated with the projection highlight the importance of long-term surveillance and ensuring capacity to prevent resurgence.

Angola's forecast, was particularly concerning, projecting a dramatic increase in case counts, from approximately 182 cases in 2024 to over 1100 cases by 2030, reflecting a deteriorating trend that, if undressed, could significantly derail global eradication timelines. The forecast underscores the urgency of scaling up eradication efforts in Angola, including improvements in case detection, response and prevention strategies.

Collectively, these projections reinforce the conclusion that achieving global Guinea worm eradication by 2030 remains feasible but contingent on immediate, intensified, and sustained intervention efforts, particularly in Chad, Mali, and Angola. Strengthening surveillance systems, targeting animal reservoirs, enhanced community awareness, and securing continuous long-term political commitment will be essential components of a successful eradication strategy across all remaining endemic settings.

While the findings of this study contribute valuable insights into the behavioral, programmatic, and environmental factors associated with Guinea worm disease transmission, they must be interpreted cautiously in light of several methodological limitations. The following section discusses potential data quality constraints, modeling

assumptions, and ecological biases that may have influenced the accuracy and generalizability of the projections. These limitations also inform recommendations for improving the utility and applicability of forecasting analyses in support of ongoing eradication efforts. .

Limitations of the Study

There were several limitations in this study that should be taken into account with explaining the results. First, although the RQ1 dataset included 66 country-level records, these were aggregated annually, which could mask more detailed temporal patterns in program implementation and case detection dynamics. Aggregation to the country level may also have obscured subnational variation in program coverage, community awareness, and environmental drivers that may mediate transmission outcomes. These limitations could be addressed using disaggregated subnational data (e.g., district- or village-level data) for a more fine-grained understanding of the contextual factors.

Second, our findings are from observational and retrospective data that were not sufficient for a causal inference. Despite the fact that there were strong associations identified through the regression models between programmatic and environmental indicators and Guinea-worm disease incidence, it would be inappropriate to imply that these relationships were causal. More specifically, the positive relationship between dog chaining and number of cases should be interpreted with caution because the practice of chaining could have been a response used more frequently in high-transmission areas.

Third, environmental exposure data (temperature, precipitation and surface water presence) were not observed directly, but were obtained from gridded fields by extracting

them at the village level using the zonal statistics function (value from the cells within a buffer of 10 m around each village). While this method facilitated spatial linkage, the environmental values were modeled estimates and might not have fully accounted for micro-ecological effects important for disease transmission. Moreover, fixed spatial buffers could cause spatial scale mismatches, which is termed the modifiable areal unit problem (MAUP), and can bias inference if exposure and outcome processes worked at different spatial scale.

Fourth, although spatial autocorrelation was explicitly assessed using Global Moran's I and Local Indicators of Spatial Association (LISA), spatial regression models (e.g., spatial lag and spatial error) assumed stationarity in relationships across space. Spatial heterogeneity—such as regional variation in program implementation or ecological conditions—may still have influenced outcomes in ways not fully accounted for by these models.

Fifth, self-reported awareness indicators may have been subject to social desirability bias or recall bias. These indicators, including awareness of rewards and knowledge about Guinea worm disease, were derived from survey-based data, and differences in question framing or implementation across countries may have affected comparability. Furthermore, stratification of awareness variables by endemicity level (endemic, at-risk, never endemic), while analytically useful, may have introduced ecological bias if within-group variability was not fully captured.

Sixth, although rumor reporting was examined in relation to awareness indicators and case detection, the study did not verify whether reported rumors ultimately led to

confirmed Guinea worm cases. As a result, interpreting rumors as a proxy for surveillance sensitivity should be approached with caution.

Seventh, the presence of missing data in certain years or variables necessitated imputation or the restriction of analyses to subsets of data, which may have introduced bias. For example, not all villages had complete monthly climate data from 2021 to 2023, and some regression models were estimated with reduced sample sizes. Although robust statistical techniques were used to address missingness and model assumptions were evaluated, these limitations may have affected the generalizability of the findings.

Finally, the internal validity of the study may have been constrained by inconsistencies in case and rumor definitions across countries, despite the existence of standard WHO definitions and reporting tools. External validity was also potentially affected by underreporting to national surveillance systems, undercoverage in low-endemic areas, and sampling biases. Additional limitations associated with the use of secondary surveillance data, including non-response bias, incomplete data, and lack of access to full case investigation forms, further constrained the comprehensiveness and generalizability of the results.

Despite these limitations, the integration of spatial, environmental, programmatic, and behavioral data provided novel insights into the multidimensional drivers of Guinea worm disease. This study offers a valuable foundation for programmatic decision-making and future research in Guinea worm surveillance, control, and elimination efforts.

Recommendations for Future Research and Practice

Recommendation for Future Research

Grounded in the strengths and limitations of this study, as well as the literature reviewed in Chapter 2, several recommendations for future research are proposed.

First, subnational and longitudinal analyses should be prioritized. Future studies should utilize finer-scale data (e.g., district or village-level) to examine temporal and spatial variations in Guinea worm transmission. Such analyses may reveal localized differences in risk patterns and intervention effectiveness that are not detectable through national-level aggregation.

Second, improved behavioral measurement is needed. Standardized, validated measures of community awareness, knowledge of Guinea worm disease, and reward incentives should be developed. Stratifying these measures by relevant population groups (e.g., pastoralists, children) could enhance the ability to tailor interventions and allow meaningful cross-country comparisons.

Third, future research should focus on the integration of disparate types of behavioral and environmental data. Studies that combine data on dog infection status, evidence of pond treatment, household-level water access, and behavioral practices would offer a more holistic understanding of the multifactorial determinants of transmission.

Fourth, predictive modeling and risk forecasting approaches could build upon the results of this study. Techniques such as time series modeling, logistic regression, or space-time simulations could be developed to predict areas at risk for transmission

persistence or reintroduction. These models could also support the design of optimized surveillance and intervention strategies during the eradication endgame.

Fifth, mixed-methods research designs are recommended. Incorporating qualitative approaches can deepen understanding of the social, ecological, and behavioral determinants influencing rumor reporting, dog tethering practices, water source use, and other relevant community behaviors.

Sixth, prospective ecological studies should be undertaken. By prospectively linking incidence with dynamic environmental changes—such as rainfall variation and surface water fluctuations—causal inference regarding environmental drivers could be improved.

These recommendations align with the study's conceptual framework, which emphasized the integration of environmental, behavioral, and programmatic factors, and reflect broader calls in the literature to adopt multifaceted approaches to Guinea worm surveillance and eradication (Hopkins et al., 2022; Eberhard et al., 2020).

Recommendations for Practice

Based on the findings of this study, several recommendations for practical action are proposed to strengthen Guinea worm disease eradication efforts.

First, surveillance and eradication programs should continue to prioritize active case detection, containment of human cases, and tethering of infected animals as core strategies to reduce transmission risk. Active surveillance remains critical given the low incidence levels and potential for missed cases.

Second, resources should be strategically allocated to geographic areas identified as persistent or emerging hotspots through spatial clustering analyses. The spatial clusters identified via Local Indicators of Spatial Association (LISA) offer opportunities to target interventions and optimize field deployment. Integrating hotspot mapping and environmental risk layers into programmatic planning can enhance operational efficiency and maximize impact.

Third, environmental surveillance efforts should monitor not only the presence of surface water but also the behavioral use patterns of water bodies by humans and animals. Recognizing that stagnant water presence alone may not fully predict transmission risk, surveillance teams should document behaviors related to water access and usage to refine risk assessments.

Fourth, strengthening behavioral surveillance is essential. Given that rumors serve as critical early warning signals for potential transmission, efforts to improve community awareness—particularly in Level 2 (at-risk) and Level 3 (never endemic) areas—should be prioritized. Achieving near-universal awareness (>95%) could bolster rumor reporting and early case detection.

Fifth, environmental risk factors such as rainfall and surface water presence should be systematically incorporated into monthly and seasonal planning for case follow-up and Abate application. National GIS teams should facilitate the automated integration of environmental datasets into program dashboards or hotspot detection tools to support real-time risk-based decision-making.

Sixth, for post-certification surveillance, passive case detection alone may be insufficient. Given the weak spatial association between environmental variables and case clustering observed in this study, continued rumor tracking, spatial modeling, and periodic environmental and ecological assessments will be necessary to mitigate the risk of Guinea worm reintroduction after certification.

Seventh, based on the secondary forecasting analysis, achieving zero Guinea worm disease cases by 2030 will require country-specific strategies informed by projected trends. In Chad and Mali, where forecasts indicated persistent or stable transmission, accelerated and intensified interventions are urgently required. Specifically, animal infection control efforts, particularly dog tethering and proactive pond treatment with Abate, must be scaled up to ensure coverage exceeds 90% of at-risk villages. Improving access to safe drinking water, enhancing reward awareness campaigns to achieve near-universal community saturation (>95%), and strengthening surveillance systems for rapid detection and response are critical in these settings.

Eighth, in Angola, where forecasted case counts were projected to increase substantially, urgent scaling-up of eradication efforts is needed. Expansion of programmatic reach, intensification of case search activities, and targeted deployment of interventions in newly affected areas should be prioritized to reverse the upward trend.

Ninth, in Ethiopia and South Sudan, where forecasts indicated relatively low and declining trends, eradication efforts must be sustained and reinforced to avoid resurgence. Maintenance of active surveillance, reward systems, environmental monitoring, and

continued operational research will be essential to achieving and certifying transmission interruption.

Finally, across all countries, continuous political commitment, community engagement, and sustained funding support from international and national partners will be essential. Investment in operational research and innovative approaches, including predictive analytics, mobile surveillance tools, and rapid response mechanisms, should be prioritized to address emerging challenges and to accelerate the path toward eradication by the 2030 target.

These recommendations are firmly grounded in the study's findings and scope and are consistent with the conceptual framework and literature base reviewed in Chapter 2. They aim to ensure that Guinea worm eradication efforts remain adaptive, evidence-based, and sustainable.

Implications

The findings of this study partially support the theory of change for Guinea worm eradication. Dog tethering practices were significantly associated with case patterns, whereas other components of the theory—such as awareness levels and Abate coverage—were not statistically significant at the aggregated country-year level. This suggests that while the theory remains conceptually valid, its application and evaluation may require finer geographic resolution (e.g., village or district level) to fully capture local programmatic and behavioral dynamics.

Methodologically, this study demonstrates the utility of combining traditional regression models (e.g., Negative Binomial Regression) with spatial analyses (e.g.,

Global Moran's I, Local Indicators of Spatial Association [LISA], and Spatial Lag models) to investigate complex public health challenges. The integration of environmental, behavioral, and spatial data offers a replicable framework that can be applied to strengthen surveillance and intervention strategies for other neglected tropical diseases (NTDs), advancing broader global health equity and social justice goals.

In addition, the secondary time series forecasting analysis contributed novel insights by modeling future case trajectories. Forecasts suggested that while some countries (Ethiopia, South Sudan) may be on a declining path toward eradication, others (Chad, Mali, Angola) face considerable risk of ongoing transmission without intensified, targeted interventions. These projections highlight the critical need for proactive, country-specific planning and underscore the importance of not relying on passive trends to achieve the 2030 eradication target.

At the policy level, the findings have important implications for the global Guinea worm eradication initiative and related neglected tropical disease programs. In particular, the results may inform integrated strategies aligned with the Sustainable Development Goals (SDGs) and the WHO NTD Roadmap 2021–2030 by emphasizing the importance of context-specific, spatially targeted, and behaviorally sensitive approaches.

At the community level, the use of rumor reporting and awareness campaigns as surveillance tools empowers individuals to participate actively in disease elimination efforts, increasing local ownership, responsiveness, and trust in health systems. Promoting community engagement through targeted reward programs and educational initiatives can thus further enhance surveillance sensitivity and accelerate case detection.

Finally, more precise spatial targeting of interventions, based on identification of high-risk clusters and environmental risk profiles, could improve program efficiency, reduce operational costs, and contribute to faster Guinea worm eradication. Ultimately, reducing Guinea worm transmission improves health, economic productivity, and quality of life in vulnerable and marginalized rural communities, delivering sustained positive social change.

Conclusion

This study investigated the relationships between environmental, behavioral, and programmatic factors and Guinea worm disease transmission across endemic and formerly endemic countries from 2012 to 2023. Guided by a theory of change framework and grounded in an integrated dataset of monthly and annual program indicators, awareness surveys, and environmental exposures, three research questions were examined using multivariate regression, spatial analysis, and time series forecasting techniques.

The results of the analysis provided partial support for the theory of change. For Research Question 1, only dog tethering was found to be significantly associated with increased case counts, suggesting that this practice may be more prevalent in high-burden settings as a reactive strategy rather than a direct driver of transmission. Other interventions such as Abate application and improved water access did not show significant associations at the country level, highlighting the potential limitations of using aggregated data to evaluate localized intervention effects.

For Research Question 2, Negative Binomial Regression and spatial models revealed that temperature, precipitation, and surface water occurrence were not statistically significant predictors of monthly Guinea worm case counts at the village level. However, spatial diagnostics, including Global Moran's I and Local Indicators of Spatial Association (LISA), identified significant spatial clustering of cases, reinforcing the importance of spatial heterogeneity in transmission dynamics. These findings suggest that while environmental conditions may contribute to risk, they alone are insufficient to explain patterns of transmission without accounting for behavioral and programmatic factors.

For Research Question 3, awareness about Guinea worm disease and the reward program—particularly in areas categorized as Level 2 (at risk)—was positively associated with the number of rumors reported. This underscores the importance of maintaining awareness even in areas with no recent transmission to support early detection. Additional analyses also revealed a positive correlation between rumor volume and actual case counts, suggesting that rumor surveillance remains a valuable tool for identifying potential outbreaks.

Complementing the cross-sectional analyses, a secondary time series forecasting analysis was conducted to model future case trends in the five endemic countries. The forecasts indicated that while Ethiopia and South Sudan may be on track to achieve zero transmission by 2030 if current efforts are maintained, Chad, Mali, and Angola will require accelerated, intensified, and geographically targeted interventions to meet

eradication targets. These findings reinforce the urgency of strategic planning based on both spatial risk profiles and projected case trajectories.

This study represents more than an academic exercise—it offers a blueprint for integrated, evidence-based action. By combining statistical modeling, spatial diagnostics, and time series forecasting, the study demonstrated how diverse analytic method can work in concert to generate complementary insights. This multi-lens approach emphasizes that addressing Guinea worm transmission requires a coordinated response that considers behavioral, environmental, and programmatic factors collectively.

The study also contributes to a data-informed public health legacy. The validation of rumor surveillance, LISA cluster mapping, and predictive forecasting enhances the practical toolbox available to eradication programs. These methods are not simply academic—they are operationally relevant and capable of guiding real-time decision-making, risk anticipation, and resource prioritization.

Grounded in principles of social justice and systems thinking, the research underscores the importance of equity, particularly in reaching underserved and high-risk communities. It elevates the value of village-level and community-informed approaches while acknowledging the limitations of national aggregate indicators. This aligns with broader goals such as Sustainable Development Goal 3.3 on ending neglected tropical diseases (NTDs) and SDG 6.1 on access to safe and affordable drinking water.

While the study did not aim to predict eradication timelines with precision, the methods and findings offer practical tools for monitoring residual transmission and improving program performance. By integrating statistical, spatial, and temporal data,

this research contributes to a growing literature advocating for dynamic, context-sensitive, and community-centered approaches to NTD surveillance and control.

In sum, this dissertation provides new understandings into the spatial, statistical, and temporal drivers of Guinea worm transmission in the pre-certification era and offers methodological and programmatic recommendations to support the final mile toward global eradication by 2030.

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Appendix: Data Use Agreement

DATA USE AGREEMENT

This Data Use Agreement ("Agreement"), effective as of (4 March 2024.) ("Effective Date"), is entered into by and between (Junerlyn Agua.)("Data Recipient") and (World Health Organization.) ("Data Provider"). The purpose of this Agreement is to provide Data Recipient with access to a Limited Data Set ("LDS") for use in research in accord with the HIPAA and FERPA Regulations.

1. Definitions. Unless otherwise specified in this Agreement, all capitalized terms used in this Agreement not otherwise defined have the meaning established for purposes of the "HIPAA Regulations" codified at Title 45 parts 160 through 164 of the United States Code of Federal Regulations, as amended from time to time.

2. Preparation of the LDS. Data Provider shall prepare and furnish to Data Recipient a LDS in accord with any applicable HIPAA or FERPA Regulations.

3. Data to be included in the LDS. **No direct identifiers such as names may be included in the Limited Data Set (LDS).** The researcher will not name the Data Provider in the doctoral study that is published in Proquest unless the Data Provider makes a written request for the researcher to do so. In preparing the LDS, Data Provider or designee shall include the **data fields specified as follows**, which are the minimum necessary to accomplish the research:

- Line list of villages reporting cases and animal infection with geocoordinates,
- Aggregated data on cases and animal infection,
- Surveillance data and
- Awareness surveys

4. Responsibilities of Data Recipient. Data Recipient agrees to:

a. Use or disclose the LDS only as permitted by this Agreement or as required by law;

b. Use appropriate safeguards to prevent use or disclosure of the LDS other than as permitted by this Agreement or required by law;

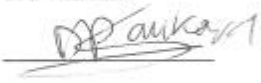
c. Report to Data Provider any use or disclosure of the LDS of which it becomes aware that is not permitted by this Agreement or required by law;

d. Require any of its subcontractors or agents that receive or have access to the LDS to agree to the same restrictions and conditions on the use and/or disclosure of the LDS that apply to Data Recipient under this Agreement; and

e. Not use the information in the LDS to identify or contact the individuals who are data subjects.

5. Permitted Uses and Disclosures of the LDS. Data Recipient may use and/or disclose the LDS for its research activities only.

DATA PROVIDER

Signed: 

Print Name: DR DIEUDONNE SANKARA

Print Title: Team Lead

Eradication and Elimination

Global NTD Programme

World Health Organization

DATA RECIPIENT

Signed: 

Print Name: JUNERLYN AGUA

Print Title: PhD Candidate

Walden University