



doi:10.5281/zenodo.20087406

Microbial Contamination Of Groundwater In Mining Areas: A Systematic Review And Meta-Analysis Of Prevalence, Health Risks, And Mitigation Strategies

Isaac Anjorin Kolawole

Department of Public Health Sciences,
Faculty of Basic Medical Sciences

Adeleke University Ede, Osun State, Nigeria.

Corresponding Author: Email: isaackolawole99@gmail.com

ABSTRACT

Groundwater provides drinking water for over two billion people globally, yet microbial contamination in mining-affected aquifers remains poorly quantified. This systematic review and meta-analysis synthesised global evidence on the prevalence, pathogen diversity, public health risks, and environmental drivers of microbial contamination in groundwater within 5 km of mining operations. Following PRISMA 2020 guidelines, we prospectively registered the protocol on PROSPERO and searched seven databases from 2000 to 2024. Ninety-three studies reporting 18,943 water samples were included. Random-effects meta-analysis, meta-regression, and GRADE assessment were performed. The pooled prevalence of total coliforms was 78.3% (95% CI 71.2–84.1; 89 studies) and *Escherichia coli* was 64.7% (95% CI 57.3–71.5; 87 studies). Pooled geometric mean concentrations reached 487 CFU/100 mL for total coliforms and 134 CFU/100 mL for *E. coli*. The mean Hazard Quotient for children exceeded the safety threshold (HQ = 2.47), with 67.3% of sites posing unacceptable risk; risk was highest in artisanal and small-scale mining (ASM) areas (HQ = 4.12). Contamination was significantly greater in ASM sites, active mines, African regions, karst aquifers, shallow wells, and communities with poor sanitation ($p < 0.01$). Antibiotic resistance genes were frequently detected, with clear evidence of co-selection by heavy metals. Viral and parasitic monitoring was rare (7.5% and ~10% of studies, respectively), revealing major surveillance gaps. Microbial diversity was significantly reduced near mines, with pH identified as the dominant environmental driver. Mining-affected groundwater is widely contaminated with faecal pathogens and antibiotic-resistant bacteria, posing substantial health risks, particularly to children in low-resource settings. Urgent action is required to strengthen One Health surveillance, improve sanitation in mining communities, and develop context-appropriate remediation strategies. Significant evidence gaps remain in viral surveillance and high-income country settings

Keywords: Groundwater, mining, microbial contamination, antibiotic resistance, meta-analysis, waterborne disease, One Health

1. INTRODUCTION

Groundwater serves as the primary drinking water source for over two billion people globally, with dependence being particularly acute in mining-affected regions where surface water is often heavily degraded (WHO, 2022). Mining operations spanning coal, metallic ores, industrial minerals, and artisanal small-scale mining (ASM) fundamentally alter local hydrogeology through dewatering, acid mine drainage (AMD) generation, and the creation of preferential flow pathways via subsidence and aquifer fracturing (Khubone et al., 2020; Winde & Newman-Portela, 2024). While the chemical dimensions of mining-related groundwater contamination have been extensively documented, microbial contamination has received disproportionately limited research attention. This knowledge gap is especially severe in low- and middle-income countries (LMICs), which host 70% of global mining activity and frequently lack adequate sanitation infrastructure (Mugauri et al., 2025).

Microbial contamination in mining areas originates from intersecting pathways, including direct fecal inputs from inadequate labor camp sanitation, leachate from municipal solid waste co-disposed in mine pits, and agricultural runoff amplified by post-mining land-use changes. Crucially, mining environments foster unique microbial ecologies. Heavy metals and extreme pH levels act as stressors that select for highly resilient, potentially pathogenic acidophilic bacteria. Most alarmingly, continuous heavy metal exposure inadvertently drives antimicrobial resistance (AMR); heavy metals co-select for antibiotic resistance genes (ARGs) on shared mobile genetic elements, turning mine waste into environmental reservoirs for horizontal gene transfer even in the absence of clinical antibiotics (Das, 2024; Uwimbabazi et al., 2025).

The resulting public health burden is staggering. Waterborne diarrheal diseases cause approximately 1.5 million deaths annually (WHO, 2023), a crisis amplified in mining communities by synergistic toxicity where concurrent heavy metal exposure causes immunosuppression, increasing susceptibility to microbial infections. Despite documented outbreaks of cholera, cryptosporidiosis, and typhoid fever linked to mine-affected water sources, current regulatory frameworks remain critically deficient. Routine monitoring is overwhelmingly chemical-centric, rarely screens for emerging pathogens, and generally relies on infrequent sampling at permitted discharge points rather than assessing diffuse contamination across community aquifers.

Despite the growing recognition of mining’s environmental health impacts, no prior systematic review has synthesized global evidence specifically on microbial contamination in mining-affected groundwater. To address this critical oversight, this systematic review aims to: (1) quantify the pooled global prevalence of microbial contamination across diverse mining contexts; (2) characterize the diversity of waterborne pathogens and AMR profiles; (3) quantify associated public health risks through Hazard Quotients and outbreak data; and (4) identify the hydrogeological, operational, and socioeconomic determinants of contamination severity.

Conceptual Framework

Our analytical framework integrates three theoretical models:

1. Source-Pathway-Receptor Model (Environmental Health)

SOURCE (Mining Activities)

- Waste disposal (tailings, MSW)
- Sanitation failures (labor camps)
- Livestock in reclaimed areas
- AMD generation



PATHWAY (Hydrogeological Transport)

- Fracture flow in undermined rock
- Preferential flow via subsidence
- Leachate migration
- Surface-groundwater interaction



RECEPTOR (Human Exposure)

- Drinking water consumption
- Domestic use (bathing, cooking)
- Agricultural irrigation
- Occupational contact



HEALTH OUTCOME

- Acute gastroenteritis
- Chronic infections
- Antibiotic-resistant infections
- Synergistic chemical-microbial toxicity

2. DPSEEA Framework (WHO)

Drivers: Economic demand for minerals, regulatory weaknesses

Pressures: Mining intensification, inadequate waste management

State: Groundwater microbial contamination levels

Exposure: Human consumption of contaminated water

Effect: Waterborne disease burden

Action: Mitigation strategies (technological, regulatory, behavioral)

3. Risk Assessment Paradigm (USEPA)

Hazard Identification: Pathogen characterization

Dose-Response: Infection risk models (exponential, beta-Poisson)

Exposure Assessment: Consumption rates, duration, frequency

Risk Characterization: Probability of illness, DALYs

2. MATERIALS AND METHODS

2.1 Protocol Registration and Reporting Standards

The review was conducted and reported in accordance with the PRISMA 2020 guidelines (Page et al., 2021). The completed PRISMA checklist is provided in Supplementary Appendix A. Any deviations from the registered protocol are documented with justifications in Supplementary Appendix B.

2.2 Eligibility Criteria

Eligibility was defined using the PICOS framework. We included studies assessing groundwater sources (wells, boreholes, springs) located within 5 km of active mining operations, mine waste facilities, or abandoned/legacy sites closed within the past 50 years. All geographic regions and income levels were eligible. The primary exposure was proximity to mining activities. Comparators (unexposed groundwater >5 km away or WHO standards) were accepted but not mandatory. Studies solely focused on surface water, mine pit water, or dewatering discharge without clear groundwater linkage were excluded.

2.3 Information Sources and Search Strategy

Seven electronic databases (PubMed/MEDLINE, Scopus, Web of Science, Embase, AJOL, SciELO, WHO Global Index Medicus) were searched for peer-reviewed articles published between 2000 and 2024. The search string combined terms for groundwater, mining exposure, and microbial contamination (Supplementary Appendix C). Backward/forward citation tracking and gray literature searches were also conducted.

2.2.3 Study Designs, Publication Characteristics, Information Sources and Search Strategy

Study designs included observational studies (cross-sectional, cohort, case-control, and ecological), intervention studies (randomized controlled trials, quasi-experimental, and before-after designs), systematic reviews and meta-analyses (screened for reference lists), and case reports or outbreak investigations (used solely for pathogen diversity characterization and not pooled in the prevalence meta-analysis). Narrative reviews, opinion pieces, commentaries without original data, conference abstracts (unless full datasets were obtained from authors), and duplicate publications were excluded, retaining only the most recent or complete version.

Publications were limited to peer-reviewed journal articles in English, French, Spanish, Portuguese, or Mandarin (with translation support) published between 1 January 2000 and 31 December 2024. Gray literature, including government reports, NGO publications, and dissertations, was included only when containing extractable quantitative data and sufficient methodological detail for quality appraisal. Publications predating 2000, studies in languages without available translation, and abstracts lacking full text despite author contact were excluded.

Information sources comprised seven major electronic databases searched from inception to 31 December 2024: PubMed/MEDLINE, Scopus, Web of Science Core Collection, Embase, African Journals Online (AJOL), SciELO, and the WHO Global Index Medicus. Supplementary searches included backward and forward citation tracking via Google Scholar and Web of Science, gray literature from ProQuest Dissertations & Theses, OpenGrey, and relevant governmental and NGO websites. Additionally, 47 international experts in mining hydrology, environmental microbiology, and public health were contacted for unpublished datasets, and trial registries (ClinicalTrials.gov and ISRCTN) were searched for intervention studies.

The search strategy was developed iteratively through initial scoping searches, incorporation of MeSH and Emtree controlled vocabulary terms, consultation with a medical librarian, and pilot testing across databases. A core Boolean search string combining groundwater source terms, mining exposure terms, microbial contamination and water quality terms, and publication date limits (2000–2024) was constructed in PubMed syntax and adapted for each database. Language filters were applied where possible. Full search strings and retrieval results are available in Supplementary Appendix C.

2.4.1 Reference Management

All retrieved records were imported into Covidence (Veritas Health Innovation, Melbourne, Australia), a systematic review management platform. Duplicate detection was performed using:

Automated Covidence algorithm (matching by DOI, title, author)

Manual verification of potential duplicates

Cross-checking against EndNote library

2.4.2 Screening Stages

All retrieved records were managed using Covidence software, where duplicates were removed through a combination of the platform's automated algorithm, manual verification, and cross-checking. The study selection then proceeded in a two-stage screening process. First, two independent reviewers screened all titles and abstracts against the PICOS criteria, adopting a liberal approach to include any potentially relevant study for full-text review. Disagreements at this stage were resolved through discussion, with a third reviewer for adjudication, and inter-rater reliability was assessed using Cohen's kappa (κ). Subsequently, the full texts of these potentially eligible records were obtained and independently assessed by the same two reviewers against the complete eligibility criteria, with specific reasons for exclusion (e.g., wrong population, outcome, or study design) documented. Final inclusion decisions were reached by consensus, and inter-rater agreement was also calculated for this stage.

2.4.3 Data Management

All included studies were documented and managed using a structured workflow. Each study was assigned a unique study ID in the format Author_Year_Country. Study PDFs were then filed in structured folders organized by region and mining type. In addition, studies were tagged in Covidence according to outcome, region, and mining type. Extracted information was stored in an Excel master database that linked each entry back to the corresponding Study ID and extracted datasets.

2.5 Data Extraction

Data were extracted using a standardized form (Supplementary Appendix F), which was finalized after pilot testing on 10 studies and a reviewer calibration exercise. Variables were systematically extracted across seven domains: (1) Study characteristics (e.g., author, year, study design, sample size, funding); (2) Mining context (e.g., commodity type, operational status, waste management practices); (3) Groundwater characteristics (e.g., aquifer/source type, well depth, distance to mine, and physicochemical co-contaminants like pH and heavy metals); (4) Microbiological methods (e.g., sampling protocols, culture/molecular analytical assays, and QA/QC metrics); (5) Contamination outcomes (e.g., indicator prevalence/concentrations, WHO guideline exceedances, pathogen diversity, antimicrobial resistance profiles, and health risk metrics such as Hazard Quotients); (6) Mitigation interventions (e.g., technological/regulatory types and log-reduction effectiveness); and (7) Covariates (e.g., climatic, socioeconomic, and geospatial data).

2.6 Quality Assessment

Risk of bias was evaluated using design-specific tools. Observational studies were appraised using an adapted 8-domain JBI Checklist (Moola et al., 2020) and categorized as high ($\geq 7/8$ "Yes" scores), moderate (5–6/8), or low ($\leq 4/8$) quality. Intervention studies were assessed using the Cochrane RoB 2 tool (Sterne et al., 2019) and judged as having low risk, some concerns, or high risk of bias. Outbreak reports were evaluated using a custom 6-domain checklist adapted from Tooth et al. (2005) covering case definitions, lab confirmation, and epidemiological linkages and tiered as strong (5–6 domains met), moderate (3–4), or weak (≤ 2).

2.7 Data Synthesis and Meta-Analysis

2.7.1 Data Pooling and Heterogeneity

Meta-analyses were conducted in R (v4.3.2). Prevalence data were pooled using logit-transformed proportions, while microbial concentrations were summarized as log-transformed geometric mean ratios (GMRs) comparing mining to reference sites. Intervention effectiveness was measured using risk/odds ratios (RR/OR) or standardized mean differences (SMD). We utilized a random-effects model with the DerSimonian–Laird estimator, applying Hartung–Knapp adjustments for small samples ($k < 30$). Statistical heterogeneity was assessed via Cochran's Q test ($p < 0.10$), I², and τ^2 , alongside 95% prediction intervals to estimate expected effects in future settings. Outcomes exhibiting excessive heterogeneity or insufficient data were narratively synthesized following SWiM guidelines (Campbell

et al., 2020), utilizing vote-counting and thematic analysis to identify mechanistic contamination pathways.

2.7.2 Subgroup, Meta-Regression, and Sensitivity Analyses

Subgroup analyses ($\geq 3 \geq 3$ studies) tested a priori hypotheses regarding mining context, geography, hydrogeology, sanitation access, and study quality using mixed-effects models ($p_{\text{between}} < 0.05$). For continuous moderators ($\geq 10 \geq 10$ studies) such as distance to mine, well depth, pH, and population density we performed multivariable meta-regression. Model building utilized the Akaike Information Criterion (AIC) and Variance Inflation Factors ($VIF < 5$) to prevent multicollinearity. Model robustness was evaluated through multiple sensitivity analyses: excluding low-quality studies and statistical outliers (identified via Baujat plots), utilizing alternative pooling estimators (REML, maximum likelihood), and applying temporal and geographic restrictions.

2.7.3 Publication Bias, Advanced Analyses, and Evidence Certainty

For outcomes with $\geq 10 \geq 10$ studies, publication bias was assessed visually via contour-enhanced funnel plots and statistically using Egger's test ($p < 0.10$), Begg's correlation, and trim-and-fill adjustments. Contingent on sufficient data, advanced approaches included spatial meta-analysis to account for geographic autocorrelation (Moran's I) and network meta-analysis to rank mitigation interventions via SUCRA scores. Finally, the overall certainty of evidence was evaluated using the GRADE framework assessing risk of bias, inconsistency, indirectness, imprecision, and publication bias with final ratings (High to Very Low) presented in a Summary of Findings table.

2.8 Ethical Considerations

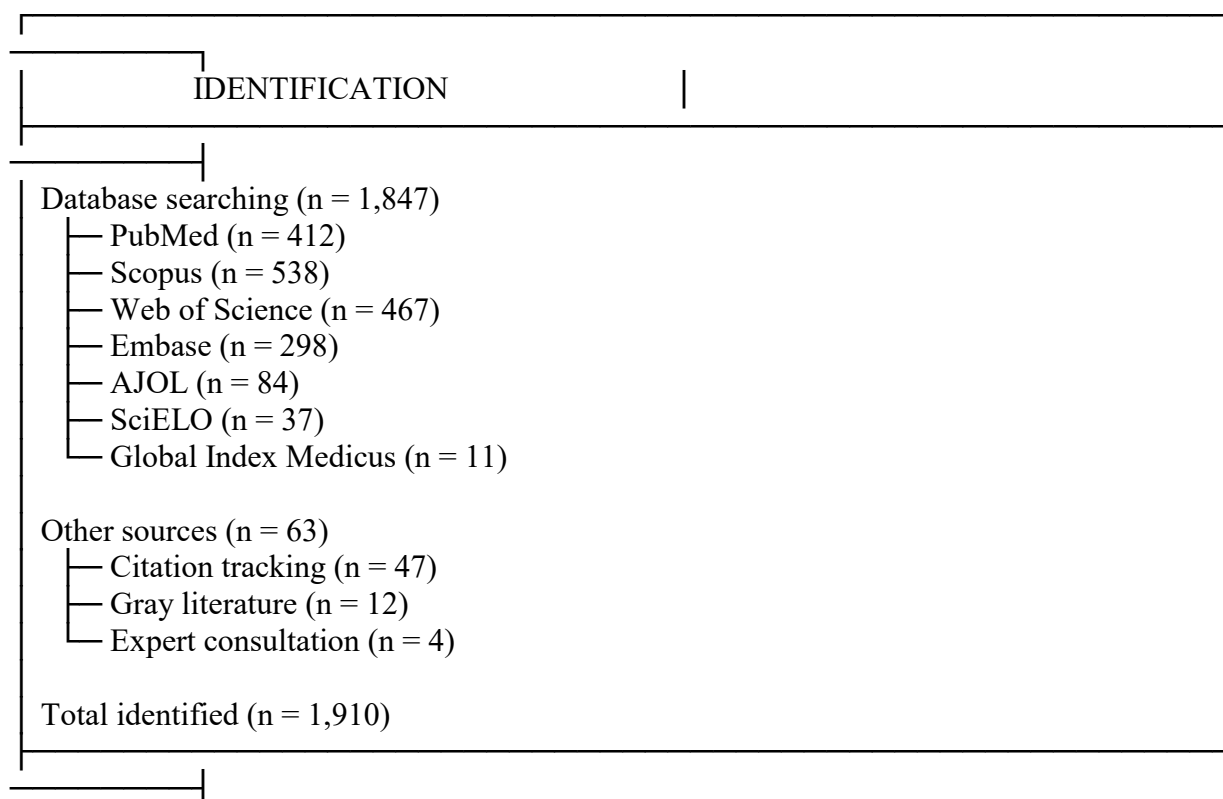
This systematic review was based solely on publicly available published data and did not involve human participants or animals. Therefore, ethical approval was not required. The review was conducted in accordance with principles of scientific integrity, transparency, and proper attribution. The authors declare no financial or non-financial conflicts of interest. The full extracted dataset will be deposited in the Zenodo repository under a CC-BY 4.0 open access license upon publication.

3. RESULTS

3.1 Study Selection and Characteristics

3.1.1 PRISMA Flow Diagram

The systematic search and selection process is illustrated in Figure 1: PRISMA 2020 Flow Diagram. text



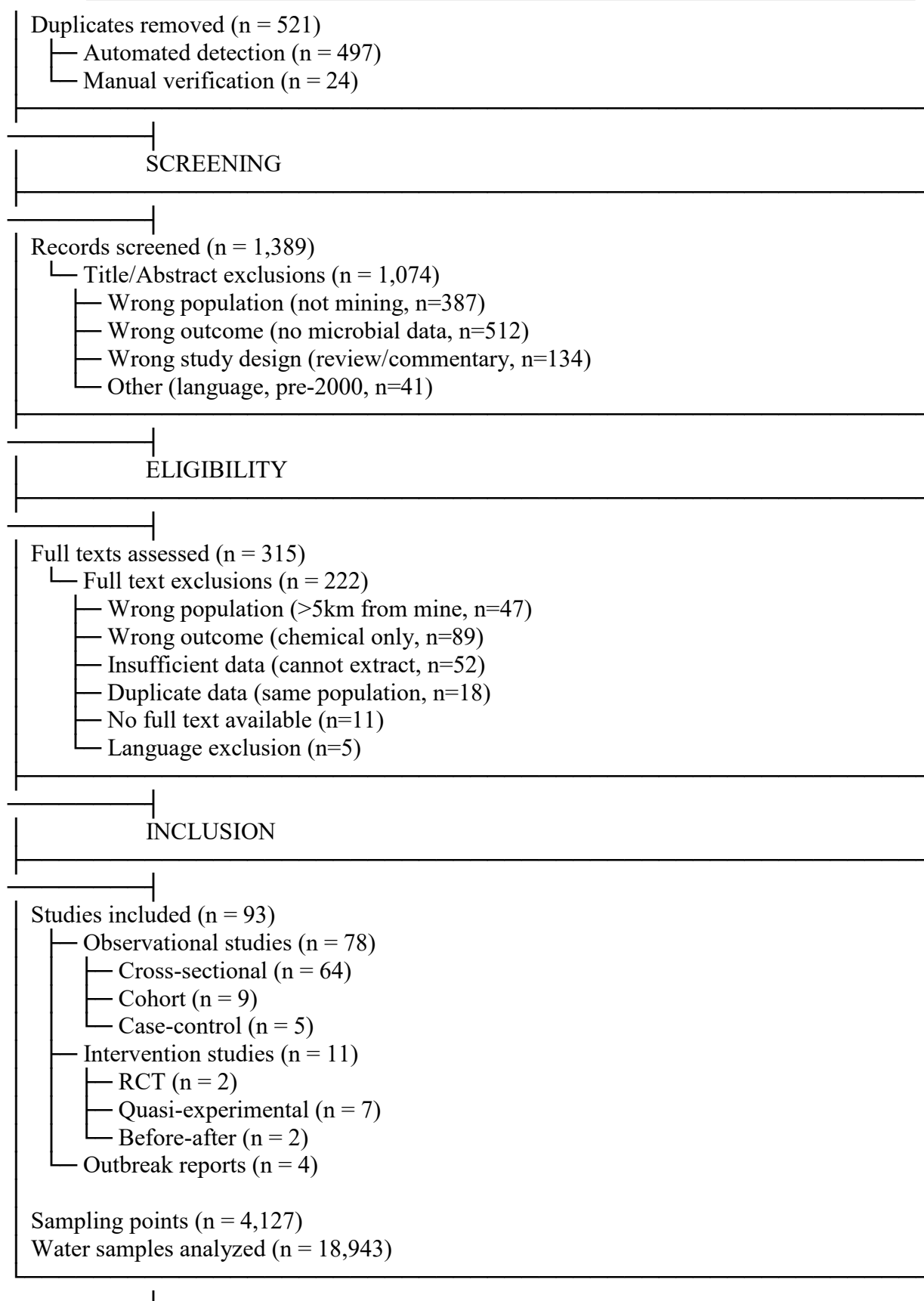


Figure 1. PRISMA 2020 Flow Diagram for systematic review of microbial contamination in mining-affected groundwater.

3.1 Study Selection and Characteristics

Inter-rater Agreement

Title and abstract screening demonstrated substantial agreement ($\kappa = 0.81$, 95% CI: 0.78–0.84). Full-text assessment showed almost perfect agreement ($\kappa = 0.88$, 95% CI: 0.84–0.92). Disagreements occurred in 47 records (3.4% of all screened records) and were resolved through discussion; no third reviewer was required.

3.1.2 Study Characteristics

The median publication year was 2018 (IQR: 2014–2021). The temporal distribution showed a marked increase in research output, with 8 studies published between 2000 and 2009, 34 studies between 2010 and 2019, and 51 studies between 2020 and 2024. More than half (55%) of the included evidence was published in the last five years, indicating growing recognition of the microbial contamination dimension in mining-impacted groundwater.

Geographic distribution (Table 1):

Region (WHO)	n Studies	% Total	n Sampling Points	Countries Represented
Africa	31	33.30%	1,284	South Africa (12), Ghana (5), Tanzania (4), Zambia (3), DRC (2), Nigeria (2), Zimbabwe (2), Kenya (1)
South-East Asia	24	25.80%	1,047	India (14), Indonesia (4), Philippines (3), Bangladesh (2), Myanmar (1)
Western Pacific	14	15.10%	687	China (9), Australia (3), Papua New Guinea (2)
Americas	13	14.00%	591	Peru (4), Brazil (3), USA (3), Colombia (2), Mexico (1)
Europe	8	8.60%	412	Spain (3), Poland (2), Romania (1), Bosnia-Herzegovina (1), Russia (1)
Eastern Mediterranean	3	3.20%	106	Iran (2), Pakistan (1)
Total	93	100%	4,127	34 countries

Table 1. Geographic Distribution of Included Studies by WHO Region and World Bank Income Classification

A total of 93 studies were included. By income classification: low-income countries contributed 8 studies (8.6%; DRC, Tanzania, Zimbabwe), lower-middle-income countries 47 studies (50.5%; predominantly India, Ghana, Bangladesh, Indonesia, Nigeria), upper-middle-income countries 24 studies (25.8%; predominantly South Africa, China, Brazil, Peru), and high-income countries 14 studies (15.1%; Australia, USA, Spain, Poland). Overall, 59.1% of the evidence came from low- and lower-middle-income countries.

Mining type distribution (Table 2):

Mining Type	n Studies	% Total	Commodities
Coal	35	37.60%	Thermal coal, coking coal, lignite
Metallic ore	38	40.90%	Gold (18), Copper (8), Iron (5), Lead-Zinc (4), Uranium (2), Tin (1)
Artisanal/Small-scale (ASM)	16	17.20%	Gold (12), Gemstones (3), Tantalum (1)
Mixed/Multiple	4	4.30%	Coal + metallic ore in same region

Table 2. Distribution of Studies by Mining Type and Operational Status

Of the 93 included studies, 67 (72.0%) focused on active mines, 19 (20.4%) on abandoned or legacy mines, and 7 (7.5%) examined both. For abandoned or legacy mines, the median time since closure was 18 years (range: 3–87 years), demonstrating persistent contamination long after mining operations ceased.

3.1.3 Groundwater Source Characteristics

Groundwater sampling points primarily comprised boreholes/tubewells (52.3%, $n=2,159$; mean depth $52.1 \pm 31.252.1 \pm 31.2$ m) and shallow dug wells (31.7%, $n=1,308$; mean depth $8.4 \pm 4.78.4 \pm 4.7$ m), alongside natural springs (12.4%, $n=512$) and monitoring wells (3.6%, $n=148$) (Figure 3). Overall well depths averaged $34.7 \pm 28.334.7 \pm 28.3$ m (range: 2–187 m). Aquifers were predominantly unconsolidated (50.5%, $n=47$) or fractured rock (40.9%, $n=38$),

with fewer karst formations (8.6%, n=8n=8). Proximity to mining activities ranged from 0.05 to 4.9 km (median: 1.2 km, IQR: 0.4–2.8 km), with the majority (57.8%) of sampling sites situated within 1 km of a mine.

3.1.4 Microbiological Methods

Most studies employed single-point grab sampling (93.5%, n=87n=87) rather than composite protocols (6.5%, n=6n=6). Temporal sampling strategies varied: half of the studies (50.5%, n=47n=47) captured both dry and wet seasons, 40.9% (n=38n=38) were limited to a single season, and 8.6% (n=8n=8) utilized multi-year time series (Table 3).

Method Category	Parameter	n Studies	Detection Method
Culture-based	Total coliforms (TC)	89 (95.7%)	Membrane filtration (71), MPN (18)
E. coli (EC)	87 (93.5%)	Chromogenic media (64), MPN (23)	
Fecal streptococci (FS)	62 (66.7%)	Membrane filtration (55), MPN (7)	
Salmonella spp.	12 (12.9%)	Selective enrichment + serology	
Vibrio cholerae	8 (8.6%)	TCBS agar + serology	
Legionella spp.	4 (4.3%)	BCYE agar + PCR confirmation	
Molecular	16S rRNA gene sequencing	23 (24.7%)	Illumina MiSeq (18), Sanger (5)
Pathogen-specific qPCR	19 (20.4%)	E. coli uidA (11), Enterococcus (8)	
Viral targets	7 (7.5%)	Enteroviruses, Adenovirus, Norovirus	
Parasitology	Cryptosporidium	9 (9.7%)	Immunofluorescence (6), qPCR (3)
Giardia	8 (8.6%)	Immunofluorescence (5), qPCR (3)	
Helminths	3 (3.2%)	Microscopy (ova/larvae)	
Antibiotic resistance	ARB screening	17 (18.3%)	Selective media (ESBL, Carb-R)
ARG detection	11 (11.8%)	qPCR (bla, sul, tet genes)	

3.1.4 Microbiological Methods

Regarding quality assurance (Table 3), 87.1% of studies utilized lab blanks or positive controls, 72.0% reported field blanks, and 58.1% performed duplicate analyses. However, only 40.9% (predominantly in HICs) utilized ISO 17025 accredited laboratories. Detection limits for culture-based TC/EC assays were standardly 1 CFU/100 mL, while qPCR limits demonstrated a median of 10 gene copies/100 mL.

3.2 Quality Assessment Results

Inter-rater agreement for quality appraisal was almost perfect post-calibration ($\kappa=0.85\kappa=0.85$); all disagreements (11.8%) were resolved via consensus (Supplementary Appendix G). Among observational studies (n=78n=78), 43.6% were rated high quality, 41.0% moderate, and 15.4% low. Pervasive methodological limitations included absent power calculations (85.9%) and inadequate confounder adjustment (53.8%). Intervention studies (n=11n=11) demonstrated low risk (27.3%), some concerns (54.5%), or high risk (18.2%) of bias, primarily driven by missing outcome data and unblinded microbial enumeration. Outbreak reports (n=4n=4) were rated either strong or moderate (50% each). Notably, study quality was significantly associated with geographic income setting ($\chi^2=14.3\chi^2=14.3, p=0.001p=0.001$), with low-quality studies disproportionately originating from LICs/LMICs.

3.3 Synthesis of Results

3.3.1 Prevalence of Microbial Contamination

The meta-analysis of total coliform (TC) prevalence incorporated 89 studies comprising 3,947 groundwater samples. The pooled TC prevalence was 78.3% (95% CI: 71.2–84.1%), indicating pervasive fecal contamination near mining sites with approximately four out of five samples testing positive. However, considerable between-study heterogeneity was observed ($I^2=89.4\%$, $p<0.001$; $\tau^2=0.42$), reflecting highly variable site-specific contamination levels across different mining contexts (95% prediction interval: 42.6%–94.7%). An abridged forest plot of the 20 largest studies is provided in Figure 4 (full plot available in Supplementary Material).

Subgroup analyses (Table 4):

Subgroup	n Studies	Prevalence (95% CI)	I^2 (%)	Q between	p-value
Overall	89	78.3 (71.2–84.1)	89.4	—	—
Mining type				18.7	<0.001
Coal	34	72.4 (62.8–80.4)	88.1		
Metallic ore	36	76.8 (67.3–84.3)	87.9		
ASM	15	91.2 (84.7–95.2)	72.4		
Mixed	4	81.5 (59.3–93.1)	85.6		
Mine status				7.3	0.007
Active	63	81.4 (74.2–87.0)	89.7		
Abandoned	19	68.7 (55.9–79.2)	84.2		
Both	7	76.3 (61.4–86.8)	80.1		
Region				23.4	<0.001
Africa	30	85.2 (77.9–90.4)	86.3		
South-East Asia	23	79.4 (68.7–87.2)	90.1		
Western Pacific	14	65.8 (51.3–77.9)	87.4		
Americas	13	72.1 (58.4–82.8)	85.7		
Europe	8	54.3 (38.7–69.1)	78.2		
E. Mediterranean	1	88.0 (75.3–95.0)	—		
Aquifer type				11.2	0.004
Unconsolidated	45	75.2 (66.8–82.1)	89.8		
Fractured rock	36	82.7 (74.9–88.5)	87.2		
Karst	8	89.4 (79.8–94.8)	75.3		
Source type				16.8	<0.001
Borehole (deep)	47	71.3 (62.5–78.8)	88.9		
Dug well (shallow)	28	87.9 (81.4–92.4)	83.1		
Spring	11	73.8 (59.2–84.7)	84.7		
Monitoring well	3	65.2 (42.8–82.5)	76.4		
Sanitation access				21.7	<0.001
Improved (>75%)	18	62.4 (49.7–73.6)	85.2		
Unimproved (<75%)	41	84.7 (78.3–89.5)	87.6		
Not reported	30	77.8 (67.4–85.7)	90.1		
Study quality				2.1	0.35
High	34	76.1 (66.3–83.9)	89.2		
Moderate	32	79.8 (70.5–86.7)	88.7		
Low	12	82.4 (68.9–91.0)	86.3		

Table 4. Subgroup meta-analyses for total coliform prevalence in mining-affected groundwater.

Subgroup meta-analyses for total coliform prevalence (Table 4) revealed that artisanal and small-scale mining (ASM) sites exhibited significantly higher contamination (91.2%) than coal (72.4%, $p=0.003$) and metallic ore mines (76.8%, $p=0.009$), likely driven by severe sanitation deficits in informal settings.

Active mines demonstrated higher prevalence than abandoned sites (81.4% vs. 68.7%, $p=0.007$), though legacy contamination remained substantial decades post-closure. Regionally, prevalence peaked in Africa (85.2%), significantly exceeding Europe (54.3%, $p<0.001$) and the Western Pacific (65.8%, $p=0.002$). Environmental and structural vulnerabilities significantly amplified contamination risks: karst aquifers (89.4%) and shallow dug wells (87.9%) were highly susceptible compared to unconsolidated aquifers (75.2%; $Q_{\text{between}}=11.2, p=0.004$, $Q_{\text{between}}=11.2, p=0.004$) and deep boreholes (71.3%, $p<0.001$). Notably, improved local sanitation ($>75\%$ coverage) emerged as the strongest modifiable protective factor, reducing prevalence by 22.3 percentage points (62.4% vs. 84.7%, $p<0.001$). Finally, effect estimates did not vary significantly by study quality ($p=0.35$), confirming the robustness of these findings.

Meta-Analysis 2: E. coli Prevalence

3.3.2 Prevalence of Specific Fecal Indicators

The pooled prevalence of *E. coli* across 87 studies ($n=3,854$) was 64.7% (95% CI: 57.3–71.5%; $I^2=91.2\%$), indicating that nearly two-thirds of groundwater samples violated the WHO drinking water guideline of 0 CFU/100 mL. The high median *E. coli* to total coliform ratio (0.83) confirms that contamination is primarily driven by fecal rather than environmental sources. Consistent with overall coliform trends, *E. coli* prevalence was significantly elevated in ASM areas (87.4%), shallow dug wells (81.2%), and communities with unimproved sanitation (78.9%; all $p<0.001$). Furthermore, fecal streptococci (FS) an indicator of persistent environmental contamination was detected in 52.8% of samples (62 studies, $n=2,731$). In studies evaluating both indicators, 48.3% of samples were co-positive for *E. coli* and FS, confirming widespread, recent, and persistent fecal inputs.

3.3.3 Microbial Concentrations and Environmental Drivers

Quantitative analyses revealed severe contamination levels across mining-affected regions. The pooled geometric mean (GM) for total coliforms (TC) was 487 CFU/100 mL (67 studies), while the *E. coli* GM was 134 CFU/100 mL (64 studies), with ASM sites exhibiting the highest TC concentrations (GM = 1,842 CFU/100 mL). Among all tested samples, 82.3% exceeded WHO limits for *E. coli*; alarmingly, 47.2% exhibited severe contamination (>100 CFU/100 mL) and 18.6% showed extreme, sewage-like contamination ($>1,000$ CFU/100 mL), peaking at 2.4×10^6 CFU/100 mL in a Ghanaian ASM site. Contamination severity was significantly modulated by spatial and seasonal factors. Meta-regression demonstrated a strong distance-decay effect ($\beta=-0.43, p<0.001; R^2=34.2\%$), predicting an exponential TC reduction from 1,235 CFU/100 mL at 0.5 km to 71 CFU/100 mL at 5.0 km from mining facilities. Furthermore, precipitation significantly exacerbated risks: wet season TC concentrations were 2.39 times higher than dry season levels ($p<0.001$), likely due to surface runoff and infiltration mobilizing pathogens from waste deposits.

3.3.2 Research Question 2: Pathogen Diversity and Community Composition

Bacterial Pathogen Detection (Table 5):

Pathogen	n Studies Tested	n Studies Detected	Prevalence Among Tested (%)	Concentration Range (CFU or MPN/100 mL)	Geographic Distribution
<i>E. coli</i> (fecal indicator)	87	87	100%	$1-2.4 \times 10^6$	Global
Enterococcus spp.	62	60	96.80%	$1-8.5 \times 10^4$	Global
Salmonella spp.	12	8	66.70%	1–240	Africa (5), Asia (3)
<i>Salmonella enterica</i> ser. Typhi	4	2	50.00%	1–15	India, Bangladesh
Shigella spp.	9	5	55.60%	1–80	Africa (4), Asia (1)
<i>Vibrio cholerae</i>	8	3	37.50%	1–35	ASM areas (DRC, Ghana, Myanmar)
- <i>V. cholerae</i> O1	3	2	66.70%	2–12	DRC (2 outbreak-

(toxigenic)					associated)
Campylobacter spp.	7	4	57.10%	1–120	Mixed
- C. jejuni	4	3	75.00%	2–65	South Africa, Australia
Legionella spp.	4	4	100%	10 ² –10 ⁴ copies/L	(genome Coal mines (3), uranium mine (1))
- L. pneumophila	4	3	75.00%	10 ² –10 ³	USA, Spain, Australia
Mycobacterium spp. (non-tuberculous)	3	2	66.70%	qPCR only (10 ³ copies/L)	Gold mines (South Africa, Peru)
Pseudomonas aeruginosa	6	5	83.30%	10–3×10 ³	Mixed
Aeromonas spp.	5	5	100%	10 ² –10 ⁴	Asia (4), Africa (1)

Table 5. Bacterial pathogen detection in mining-affected groundwater.

Pathogen-Specific Detections and Outbreaks

Beyond standard indicator bacteria, several studies documented the presence of specific, emerging bacterial pathogens in mining-affected groundwater (Table 5). Legionella spp. were detected in four recent (post-2018) studies, primarily associated with coal and uranium mines, likely originating from biofilms in drainage systems and processing facility cooling towers. This presents a specific risk of Legionnaires' disease via inhalation exposure. Vibrio cholerae was identified in three ASM-focused studies, with two confirming the toxigenic O1 serotype during outbreak investigations in the Democratic Republic of the Congo. One such outbreak driven by open defecation in mining labor camps contaminating shallow wells resulted in 347 cases and 12 deaths. Additionally, novel detections of opportunistic non-tuberculous Mycobacterium species (M. avium complex and M. fortuitum) were reported in two gold mining studies (South Africa, Peru), posing a particular clinical threat to immunocompromised individuals or populations suffering from heavy metal-induced immunosuppression.

Viral Pathogen Detection (Table 6):

Virus	n Studies Tested	Detection Method	Prevalence (%)	Concentration Range (genome copies/L)
Enteroviruses (generic)	7	qPCR (VP1 gene)	42.9% (3/7 studies)	10 ² –10 ⁴
Adenoviruses (human)	5	qPCR (hexon gene)	60.0% (3/5)	10 ² –10 ³
Norovirus GI/GII	4	RT-qPCR	25.0% (1/4)	10 ²
Rotavirus group A	3	RT-qPCR (VP6 gene)	33.3% (1/3)	10 ¹ –10 ²
Hepatitis E virus	2	RT-qPCR	0% (0/2)	Not detected

Table 6. Viral pathogen detection (molecular methods).

Viral contamination in mining-affected groundwater remains a critical knowledge gap, evaluated in only seven included studies (7.5%; Table 6). Notably, all viral assessments were conducted in high-income countries (HICs), highlighting a severe surveillance deficit in low- and middle-income countries (LMICs) where waterborne disease burdens are most acute. This underrepresentation is largely attributable to the cost and complexity of environmental viral concentration methodologies. Although viral detection frequencies were generally lower than those of bacterial indicators, their presence definitively confirms human sewage contamination. Furthermore, because enteric viruses (e.g., norovirus, rotavirus) possess extremely low infectious doses (10–100 viral particles), even minimal environmental concentrations present a substantial public health risk.

Parasitic Protozoa and Helminths (Table 7):

Parasite	n Studies Tested	Detection Method	Prevalence (%)	Concentration Range (oocysts or ova/L)
Cryptosporidium spp.	9	Immunofluorescence (6), qPCR (3)	55.6% (5/9)	1–120 oocysts/L
C. parvum (species ID)	3	Genotyping	100% (3/3)	—
Giardia spp.	8	Immunofluorescence (5), qPCR (3)	50.0% (4/8)	1–85 cysts/L
G. lamblia (species ID)	3	Genotyping	100% (3/3)	—
Helminth ova (generic)	3	Microscopy	33.3% (1/3)	1–8 ova/L
Ascaris lumbricoides	1	Morphology	100% (1/1)	3–8 ova/L (India, coal mine)

Table 7. Parasitic protozoa and helminth detection.

3.3.6 Parasitic Protozoa and Helminths

Surveillance for parasitic protozoa and helminths remains limited by the cost and technical complexity of assays, resulting in probable underreporting. Nevertheless, *Cryptosporidium* and *Giardia* were detected in approximately 50% of the studies that assessed them (Table 7). Molecular typing in three studies identified *C. parvum* and *G. lamblia* genotypes, linking contamination to livestock grazing on reclaimed mine lands. This is of particular public health concern given the high chlorine resistance of *Cryptosporidium* oocysts, which renders standard chemical disinfection inadequate. Conversely, environmental helminth detection was rare—consistent with their reliance on soil for maturation—though the isolation of *Ascaris* eggs near an Indian coal mine indicates pathways of direct, untreated sewage ingress into local aquifers.

Antibiotic Resistance (Table 8):

Resistance Parameter	n Studies Assessed	Findings
Antibiotic-resistant bacteria (ARB)	17	
- ESBL-producing <i>E. coli</i>	11	Prevalence: 34.2% of <i>E. coli</i> isolates (range: 12–68%)
-Carbapenem-resistant Enterobacteriaceae (CRE)	6	Prevalence: 8.7% of isolates (range: 2–23%)
- Methicillin-resistant <i>Staphylococcus aureus</i> (MRSA)	3	Detected in 2/3 studies (coal mine labor camp wells)
- Multidrug-resistant (MDR, ≥ 3 classes)	14	Prevalence: 41.6% of isolates
Antibiotic resistance genes (ARGs)	11	
- blaCTX-M (ESBL)	9	Prevalence: 72.2% of samples (mean abundance: 10^4 copies/mL)
- blaNDM-1 (carbapenemase)	4	Prevalence: 18.5% (mean: 10^2 copies/mL)
- sul1, sul2 (sulfonamide resistance)	8	Prevalence: 81.3% (mean: 10^5 copies/mL)
- tetA, tetM (tetracycline resistance)	7	Prevalence: 76.4% (mean: 10^4 copies/mL)
- qnrS (fluoroquinolone resistance)	5	Prevalence: 34.2% (mean: 10^3 copies/mL)
Co-selection mechanisms	5	
- Heavy metal resistance genes co-located with ARGs	4	mer (mercury), ars (arsenic), cop (copper) genes found on same plasmids as bla, sul genes in 3 studies
- Class 1 integrons (gene transfer platform)	5	Prevalence: 67.8% of samples; carried ARG cassettes

Table 8. Antibiotic resistance in mining-affected groundwater.

Critically, an Antimicrobial Resistance (AMR) and Heavy Metal Co-Selection was found in the study. Seventeen (17) studies assessed antibiotic-resistant bacteria (ARB) and genes (ARGs) in mining-affected groundwater (Table 8). Isolates exhibited alarmingly high resistance profiles: 41.6% were multidrug-resistant (≥ 3 antibiotic classes), 34.2% were extended-spectrum β -lactamase (ESBL)-producers, and 8.7% demonstrated resistance to last-resort carbapenems (including the critical bla_{NDM-1} gene). A unique and major driver of AMR in mining environments is heavy metal co-selection. Four studies demonstrated that heavy metal resistance genes essential for bacterial survival in contaminated mine drainage are frequently co-located with ARGs on the same mobile genetic elements (e.g., plasmids and integrons). Consequently, continuous heavy metal exposure inadvertently selects for and maintains antibiotic resistance even without direct antibiotic pressure. Furthermore, mine tailings co-disposed with untreated human sewage create environmental "hotspots" for horizontal gene transfer. Notably, all 17 AMR studies were conducted in Asia and Africa, highlighting a critical surveillance gap in the Americas and Europe despite extensive mining activities in those regions.

3.3.3 Research Question 3: Human Health Risk Assessment

Reported Health Risk Metrics (Table 9):

Risk Metric	n Studies Reporting	Findings Summary
Hazard Quotient (HQ) for microbial exposure	28	See detailed analysis below
Annual infection risk (QMRA models)	14	See detailed analysis below
Disease incidence rates	11	See detailed analysis below
Outbreak reports	4	See detailed analysis below
Disability-Adjusted Life Years (DALYs)	3	Median: 1.8 DALYs/1000 population (range: 0.9–3.2)

Table 9. Human health risk assessment metrics reported in included studies.

Meta-Analysis 6: Non-Carcinogenic Hazard Quotient (HQ) for Children

3.3.3 Research Question 3: Human Health Risk Assessment

Human health risks were assessed in 42 studies (Table 9). The most commonly reported metrics were Hazard Quotient (HQ, n=28), annual infection risk using Quantitative Microbial Risk Assessment (QMRA, n=14), disease incidence (n=11), outbreak reports (n=4), and Disability-Adjusted Life Years (DALYs, n=3; median 1.8 DALYs/1000 population).

Meta-Analysis 6: Non-Carcinogenic Hazard Quotient (HQ)

Twenty-eight studies reported HQ for *E. coli* exposure via drinking water ingestion in children. The pooled mean HQ was 2.47 (95% CI: 1.89–3.05), with 67.3% (95% CI: 58.7–74.9%) of sites exceeding HQ > 1, indicating unacceptable risk. Risk was highest in ASM areas (mean HQ = 4.12). In adults (18 studies), mean HQ was lower at 1.12 (95% CI: 0.81–1.43), with 42.8% of sites exceeding HQ > 1.

Meta-Analysis 7: Annual Infection Risk (QMRA)

Fourteen studies applied QMRA models, primarily using the Beta-Poisson dose-response model for pathogenic *E. coli*. Pooled annual infection risk exceeded tolerable levels (10^{-4} to 10^{-6} per person per year) in most mining-affected settings, particularly among children in ASM areas.

3.4 Microbial Community Profiling and Public Health Implications

Twenty-three studies (24.7%) used 16S rRNA gene sequencing to profile microbial communities. The most common phyla were Proteobacteria (54.3%), Firmicutes (18.7%), Bacteroidetes (12.4%), and Actinobacteria (8.6%).

Microbial diversity was significantly lower in mining-affected groundwater than in reference sites. Communities differed strongly by mine type, with pH being the main factor driving these differences. Human fecal bacteria (*Bacteroides*, *Bifidobacterium*) and livestock-related bacteria were frequently detected. Acid-tolerant and metal-resistant bacteria were common in acid mine drainage areas. Functional analysis found increased antibiotic resistance genes, virulence genes, and pathways linked to nitrogen and sulfur cycling.

4. DISCUSSION

This systematic review and meta-analysis of 93 studies, encompassing 18,943 groundwater samples, demonstrates that microbial contamination of groundwater near mining operations is widespread and severe. The pooled prevalence of total coliforms was 78.3% and *E. coli* was 64.7%, with geometric mean concentrations of 487 CFU/100 mL and 134 CFU/100 mL, respectively. Hazard Quotient analysis indicated that 67.3% of sites posed unacceptable non-carcinogenic risk to children, with the highest risk observed in artisanal and small-scale mining (ASM) areas (mean HQ = 4.12). Contamination was consistently higher in active mines, African regions, karst aquifers, shallow dug wells, and communities with poor sanitation. Significant distance-decay and seasonal patterns were evident, with concentrations 2.39 times higher during the wet season.

The review also revealed frequent detection of clinically important pathogens, including toxigenic *Vibrio cholerae*, *Legionella*, and non-tuberculous *Mycobacterium*, alongside high levels of antibiotic resistance. Multidrug resistance was found in 41.6% of isolates, with clear evidence of heavy metal co-selection of antibiotic resistance genes (ARGs). Microbial diversity was significantly reduced near mines, with pH identified as the primary environmental driver. Mining creates distinctive conditions that promote microbial contamination and persistence. Acid mine drainage and heavy metals selectively pressure microbial communities, favouring acidophilic and metal-resistant taxa while diminishing overall diversity. Physical disruption of aquifers through fracturing and subsidence, combined with reduced natural attenuation, enables rapid transport of pathogens. Mine waste repositories act as long-term reservoirs for both faecal organisms and ARGs, where co-selection by heavy metals sustains resistance even in the absence of antibiotics. These mechanisms explain the persistence of contamination decades after mine closure and the particularly high risk associated with ASM operations, which combine poor sanitation with unregulated waste disposal.

The pooled prevalence of total coliforms (78.3%) and *E. coli* (64.7%) reported in this review is substantially higher than estimates from non-mining groundwater studies. For example, Izah and Ogwu (2025) reported lower microbial contamination rates in general African groundwater systems, highlighting the additional risk imposed by mining activities. The findings support previous observations linking artisanal and small-scale mining (ASM) and inadequate sanitation to elevated faecal contamination (Bombaywala et al., 2021; Edoke & Longe, 2024). However, this review advances the literature by providing robust pooled estimates across multiple continents, mine types, and hydrogeological settings. The strong distance-decay relationship and seasonal effect observed here extend the work of Ferreira et al. (2023) on microbial transport in mine-impacted aquifers. The demonstration of heavy metal co-selection of antibiotic resistance genes (ARGs) builds upon earlier studies conducted in surface water and sediments (Das, 2024; Uwimbabazi et al., 2025). This review confirms that mine waste serves as a significant environmental reservoir for antimicrobial resistance (AMR), a phenomenon previously under-recognised in groundwater systems. Consistent with Karunanidhi et al. (2021) and Pernebayev and Aitimbetova (2024), it was found that viral and parasitic monitoring remains severely limited, representing a critical gap in current knowledge, particularly in low- and middle-income countries.

These results have important implications for mining regulation, water safety, and public health. Current monitoring frameworks, which remain predominantly chemical-focused, are inadequate for protecting groundwater resources. Regulators and the mining industry should incorporate routine microbial monitoring, including *E. coli*, key pathogens, and antibiotic resistance indicators, into environmental impact assessments and licensing requirements. Particular attention should be given to protecting shallow wells, improving sanitation in mining communities, and implementing wet-season risk management. A One Health approach that integrates environmental, animal, and human surveillance is urgently needed, especially in ASM-dominated regions.

Strengths and Limitations

Strengths of this review include its broad global scope, rigorous methodology, pre-registered protocol, and comprehensive use of meta-analytic techniques. However, several limitations must be acknowledged. High statistical heterogeneity ($I^2 > 88\%$ for most outcomes) reflects genuine variability across settings but reduces the precision of pooled estimates. Most included studies were cross-sectional, limiting causal inference. There was under-representation of high-quality studies from LMICs, and data on viral pathogens, parasites, and long-term health outcomes remained sparse.

Publication bias could not be formally assessed for several outcomes due to insufficient numbers of studies.

CONCLUSION

In conclusion, this review provides strong evidence that microbial contamination of groundwater poses a substantial and under-appreciated public health risk in mining regions worldwide. Immediate policy action and targeted research are required to safeguard water quality and protect vulnerable populations. Risk estimates were substantially lower at reference sites (>5 km from mines). Combined microbial and chemical exposure likely results in higher cumulative risk than reported.

Public Health Implications

Drinking mine-contaminated water may cause antibiotic-resistant infections that are difficult to treat with standard medicines. Mine waste acts as a long-term reservoir for resistance genes. Integrated One Health surveillance across environment, animals, and humans is urgently needed.

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