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SYSTEMATIC REVIEW **Open Access**

The use of WHONET for antimicrobial resistance surveillance: a systematic review

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Abstract

Antimicrobial Resistance (AMR) is a global public health threat. Several surveillance systems/networks were established to provide critical data to detect resistance patterns, guide treatments, and inform policies to mitigate AMR's public health impact. WHONET software was developed in 1989 as a free software that manages and analyses microbiology laboratory data, entirely dedicated to antimicrobial susceptibility test results. A systematic search was conducted in five electronic databases, PubMed, ScienceDirect, Web of Science, Scopus, and Embase, from their inception until December 31st, 2024. It included all articles that reported using WHONET. From the initial 4,636 articles retrieved, 511 were included. Most studies were cross-sectional or prevalence studies (72.4%), with the majority utilizing secondary data sources (83.2%). Articles included data from 110 countries, with the highest amount coming from China, and the number of publications increased over time. Additionally, most articles included data from 2 to 3 years before publication. Of the 2160 organisms examined across the studies, *Enterobacterales* (43.8%), *Staphylococcus spp*. (12.5%) and *Pseudomonas spp.* (9.3%) were the most covered microorganisms. In conclusion, the review highlights the growing interest in WHONET and AMR. WHONET's ability to leverage routine and secondary data for AMR monitoring is advantageous compared to other systems. However, expanding WHONET's application and integrating advanced analytics are essential for enhancing its role in a comprehensive One Health approach to combat AMR, particularly in LMICs.

Clinical trial number

Not applicable.

Keywords WHONET, Antimicrobial resistance, Data management, Data quality, Systematic review

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Introduction

Antimicrobial Resistance (AMR) is a critical global health concern characterized by the ability of microorganisms, such as bacteria, viruses, fungi, and parasites, to evolve to resist antimicrobial treatments, making standard therapies ineffective and leading to persistent infections and mortality. The World Health Organization (WHO) underscores that AMR significantly threatens public health, food security, and development, with projections indicating that, without effective interventions, AMR could cause up to 10 million deaths annually by 2050 without effective and sustainable action [1, 2].

Several surveillance systems/networks were established to provide critical data to detect resistance patterns, guide treatments, and inform policies to mitigate AMR's public health impact. The National Antimicrobial Resistance Monitoring System (NARMS) in the U.S., the European Antimicrobial Resistance Surveillance Network (EARS-Net), and the Central Asian and European Surveillance of Antimicrobial Resistance Network (CAESAR) in the WHO European region are key platforms for tracking AMR trends. NARMS monitors Resistance in humans, retail meats, and food animals [3]. EARS-Net and CAESAR collect data on bacterial pathogens, supporting targeted interventions in the WHO European region [4, 5]. Such regional networks help to identify trends, patterns, and outbreaks and promote cross-border collaboration [6].

In response to this threat, the WHONET software was developed by the World Health Organization Collaborating Centre for Surveillance of Antimicrobial Resistance at the Brigham and Women's Hospital and Harvard Medical School in Boston, Massachusetts [7, 8]. WHONET is a free, Windows-based software that manages and analyses microbiology laboratory data, particularly on antimicrobial susceptibility test results. Since its inception in 1989, WHONET has supported local, national, regional, and global surveillance efforts, facilitated data standardization and sharing across over 2,300 laboratories in more than 130 countries, and is available in 44 languages [7]. The WHONET software is freely available for download on the WHONET.org website, and it is widely used by public health professionals, microbiologists, epidemiologists, data managers, researchers, and laboratory scientists worldwide [9, 10], with national data available in the platform upon registration.

WHONET enables laboratories to manage and analyze their microbiological data efficiently to allow for the detection of emerging resistance patterns and inform empirical treatment guidelines. The software's versatility and continuous adaptations allow for its application across various sectors, including human, animal, and environmental health, embracing a One Health approach to AMR surveillance. Moreover, WHONET's integration capabilities with existing laboratory information systems streamline data capture and analysis processes, reducing redundancy and potential errors [11, 12].

The global adoption of WHONET reflects its effectiveness as a tool for facilitating data collection and analysis methodologies, enabling meaningful comparisons of antimicrobial resistance trends and patterns across different periods and geographies. At a higher level, since it provides a worldwide standardized platform for AMR data management, WHONET aids collaborative research and informs public health interventions to mitigate the impact of antimicrobial Resistance worldwide [13]. The software is updated annually to include the latest antimicrobial susceptibility testing (AST) guidelines, particularly the most used ones, such as the Clinical and Laboratory Standards Institute (CLSI) [14] and the European Committee on Antimicrobial Susceptibility Testing (EUCAST) [15].

Additionally, WHONET's accessory software enables merging data via BacLink [16, 17]. Its strong analytical capacity for AMR data and hospital-acquired infections has made it a model to newer systems [13], including the MSF Mini-Lab [18].

The software is now interoperable with SILAB for Africa (SILABFA), a laboratory information system in animal sectors [19]; District Health Information System 2 (DHIS2), a data management and monitoring platform widely implemented in low and middle-income countries [20, 21]; and the Quick Analysis of Antimicrobial Patterns and Trends (QAAPT) tool for data analysis and visualization [22]. Furthermore, SaTScan, a spatial, temporal, and space-time scan statistics software, has been integrated into WHONET to enable space-time monitoring for cluster and outbreak detection functionalities [23, 24]. WHO and FAO also use WHONET for country annual reporting to the Global Antimicrobial Resistance and Use Surveillance System (GLASS) [2, 25, 26] and the International FAO Antimicrobial Resistance Monitoring (InFARM) [27], the global AMR platforms on human, animal, environmental, and food resistance data.

To further understand the extent of its use in scientific literature, we conducted this systematic review of original studies utilizing WHONET, focusing on their methodologies, geographic distribution, and applications across One Health sectors. By examining these factors, we aim to comprehensively understand WHONET's role in antimicrobial resistance monitoring beyond routine data management and its contributions to public health decision-making.

Methods

Search strategy

This study analyzed papers that used WHONET software for AMR data management and/or analysis at any study stage and for any field of study, humans, animals, and/or environment.

We utilized PRISMA Guidelines (Fig. 1) to define the search strategy. We defined a general search query that allowed to capture the name of the software and other different variations, using Boolean operators: “WHONET” OR “WHO NET” OR “WHO-NET” OR “WHO Network”. Studies were identified by systematically searching five electronic databases: PubMed, ScienceDirect, Web of Science, Scopus, and Embase, from their inception until December 31st, 2024. The search was conducted in all databases in April 2023 and repeated in January 2025.

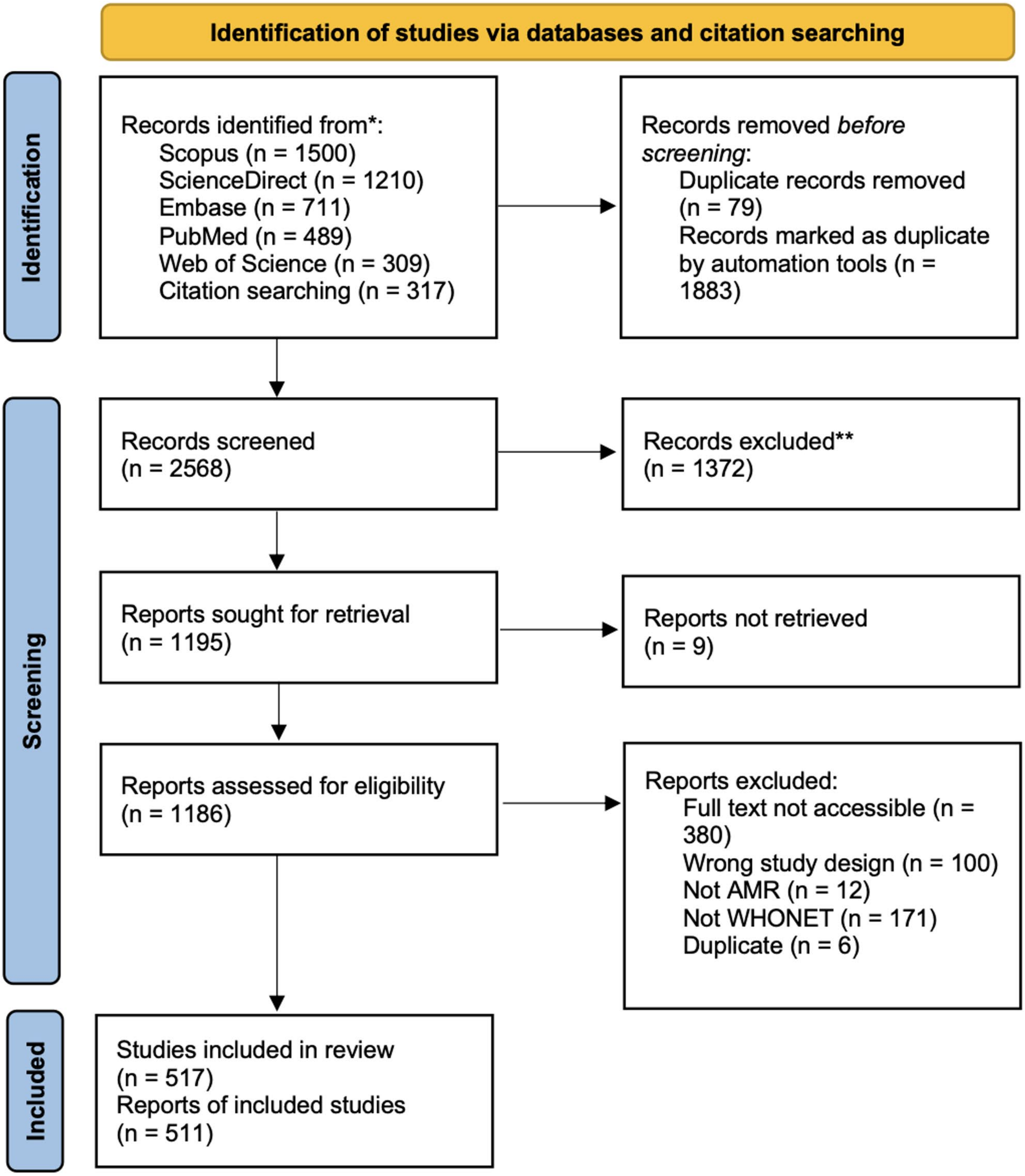

Fig. 1 PRISMA flowchart showing the screening process of the review

Regarding inclusion criteria, we included any article that conducted AMR analysis using WHONET, in human, animal, food or environment, from a One Health perspective. As exclusion criteria, we defined the following:

- Studies that do not use WHONET.
- Studies with no mention of WHONET.
- Wrong study design: reviews (including narrative, scoping and systematic reviews), viewpoints or perspectives, conference proceedings, abstracts only, and editorials.

Systematic reviews identified were excluded but used for snowballing to identify additional relevant original publications.

We did not exclude articles based on language and did not apply any other restriction.

Reviewers screened articles in two phases: title and abstract, and full-text, and data were extracted from each study. The protocol of this review was registered in PROSPERO (ID: CRD42023411376) [28].

Selection process, data extraction, and risk of bias

The authors independently reviewed the selected articles in pairs based on predefined eligibility criteria. The screening process in Covidence [29] involved assessing the title and abstract, and full text. Studies were classified as "Yes," "Unclear," or "No" for inclusion. Articles receiving a "No" from both reviewers were excluded, while those marked "Unclear" or "Yes" proceeded to the next phase. Discrepancies between reviewers' classifications were resolved through discussion, consensus, or consultation with a third researcher.

Two reviewers independently performed data extraction, with conflicts resolved through reconciliation. The extracted data included details such as the journal of publication, year, country of study, income classification (low, lower-middle, upper-middle income, based on the World Bank Group 2024 groups) [30], article title, study objectives, design, timeframe, use of secondary data sources, tested organisms, AST guidelines, sample size, purpose of WHONET use, and additional statistical software applied.

For the One Health sectors classifications, we included five distinct sources: humans, food, animals, aquaculture, and the environment. The animal category includes chicken/poultry and livestock such as cows, cattle, goats, pigs, and pets like cats and dogs. The food category covers fruits and vegetables, meat (e.g., pork, beef), and animal-derived products (e.g. meat and dairy), while the environmental samples include trees and water/wastewater. Aquaculture is treated as a separate category, primarily consisting of fish and shellfish. These groupings help distinguish between different sources and types of samples in the analysis.

We used the Joanna Briggs Institute Critical Appraisal Checklist for Prevalence Studies, as this tool was specifically designed to assess the methodological quality, validity, and reliability of prevalence data [31], ensuring a rigorous evaluation of AMR studies using WHONET. All reviewers conducted the risk of bias assessment independently, with a second reviewer providing a parallel evaluation. A third reviewer revised the extracted data when needed to solve any inconsistencies.

Data synthesis

The qualitative synthesis was conducted as a narrative review, summarizing the findings of studies that utilized WHONET, including their methodologies, key applications, and primary outcomes. This synthesis provides an overview of how WHONET has been used across different settings and its impact on AMR surveillance.

Data synthesis was performed using Microsoft Excel, with further analysis and visualization conducted using R version 4.3.2.

Results

From the 4,319 articles retrieved from the search and 317 from citation searching, we removed 1,960 duplicates, which resulted in 2,568 screened for title and abstract. After removing those that did not fulfill inclusion criteria, we ended up with 1,186 articles for full-text review. Of these, 380 did not have accessible full texts, whereas 100 had the wrong study design, and 2 were duplicates. Moreover, 171 articles did not use WHONET, and 12 did not focus on AMR. We finally included 511 reports from 517 studies.

Regarding the study design of included articles (Supplementary Table 1), most studies were cross-sectional or prevalence studies ($n = 370$, 72.4%), followed by cohort studies ($n = 129$, 25.2%). Most studies utilized secondary data sources ($n = 425$, 83.2%).

Most included articles were written in English ($n = 444$, 86.9%), followed by Spanish ($n = 36$, 7.0%) and Chinese ($n = 11$, 2.2%).

Among the 511 articles identified, 15 were multi-country studies, and to capture the full geographic representation, we extracted and counted each country involved separately. This approach resulted in a total of 641 country instances. Articles were then categorized based on the World Bank's income classifications and regional groupings. Of the 641 instances, 171 were from high-income countries, 292 from upper-middle-income countries, 156 from lower-middle-income countries, and 22 from low-income countries, as shown in Fig. 2. Regionally, the highest representation came from East Asia & Pacific (219), followed by Europe & Central Asia

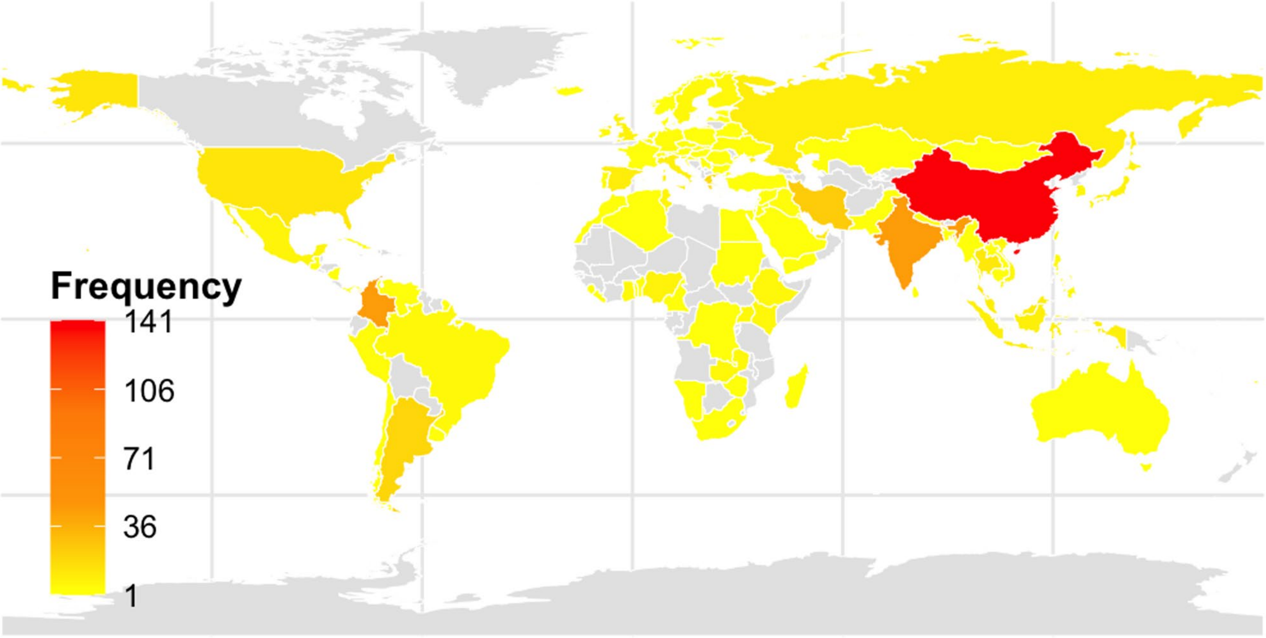

Fig. 2 Map of distribution of the data source of the WHONET articles

(133), Latin America & the Caribbean (94), Middle East & North Africa (73), Sub-Saharan Africa (55), South Asia (54), and North America (13).

Overall, our review encompassed articles that reported data from 110 countries, reflecting a broad global distribution. China was the most frequently represented country, appearing in 141 articles. India and Colombia followed this, with each country featured in 44 articles.

The number of articles included in the review has increased steadily over time. From just a few articles per year in the late 1990s and early 2000s (e.g., 2 articles in 1995 and 1998), there was a marked rise beginning around 2010. The most substantial growth occurred in the last five years, peaking at 71 articles in 2024, followed by 54 in 2023 and 47 in 2021. This trend highlights the growing interest and body of research that uses WHONET over the past three decades, with over half of all included articles (271 out of 511) published between 2020 and 2024.

The studies on AMR using WHONET took, on average, around 2.5 years to be published, ranging from 0 to 22 years. While 14 articles (2.7%) were published in the same year data collection was completed, most studies ($n = 397$, 77.7%) were published between 1 and 3 years after data collection. The distribution is shown in Fig. 3.

Furthermore, most articles (90%) included both the first and last author from the same country of the data, with only 8% of the articles having either the first or the last author and 2% having neither authors from the countries of the data. The full distribution based on the income group is presented in Fig. 4.

We analyzed the organisms covered in our review. Table 1 lists the most frequent organisms featured in the articles and those covered in the WHO Bacterial Priority Pathogens List 2024 [26]. Of the 2160 organisms examined across 511 studies, *Enterobacterales* was the most frequently covered group, constituting around 43.8% of all microorganisms studied (n = 946), followed by *Staphylococcus spp*. (n = 270, 12.5%) and *Pseudomonas spp.* (n = 201, 9.3%). Other relevant organisms from the WHO Priority List include *Staphylococcus aureus* (n = 209, 9.7%), *Pseudomonas aeruginosa* (n = 195, 9.0%), and *Streptococcus pneumoniae* (n = 59, 2.7%).

From the microorganisms included in the WHO Priority List, several have been studied across countries, with some being more extensively researched than others. For instance, *Staphylococcus aureus* was studied in 93 countries from all world regions, making it one of the most analyzed pathogens, followed closely by *Pseudomonas aeruginosa*, which was examined in 58 countries. *Streptococcus pneumoniae* and *Acinetobacter*, including its species Acinetobacter baumannii, were studied in 58 and 55 countries, respectively. Other notable pathogens like *Neisseria gonorrhoeae* and *Salmonella* were covered in 40 and 36 countries from all regions. In comparison, *Haemophilus influenzae* was studied in 10 countries from all regions except Latin America & the Caribbean and Middle East & North Africa. The full distribution is in Fig. 5.

On the other hand, some microorganisms were studied in far fewer countries. *Streptococcus Group A* was only researched in 3 countries in East Asia & Pacific, Europe & Central Asia, and North America. *Mycobacterium*

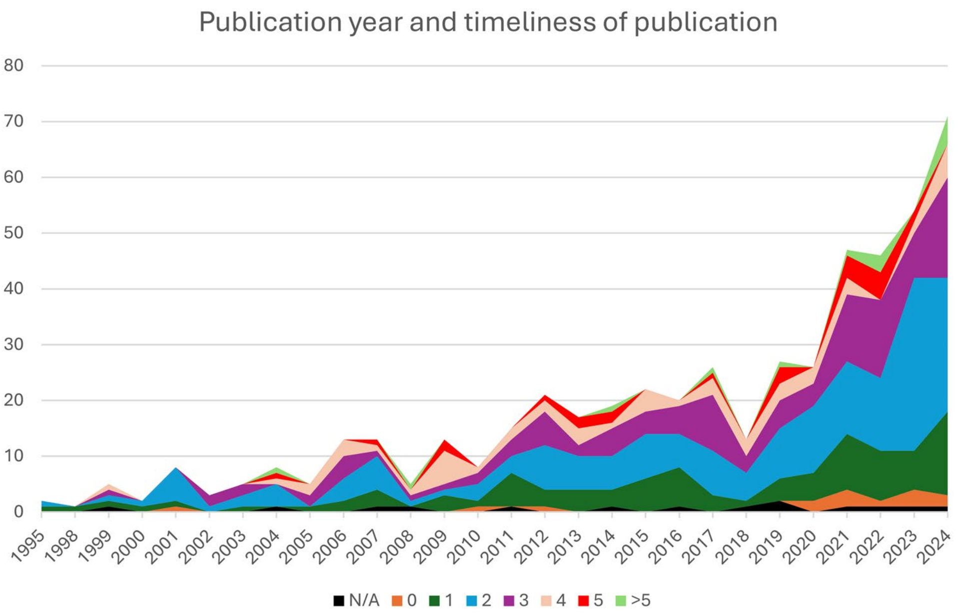

Fig. 3 Distribution of articles over time and the timeliness of the data reported

had the least geographic coverage, being studied in just 2 countries from the Middle East & North Africa region and North America. The analysis of *Enterobacterales* was notably widespread, covering 101 countries, while *Enterococcus faecium* was studied in 41 countries. Details can be found in the figure below and Supplementary Table 2.

Looking into the One Health sectors covered, we clarified the data into several categories. The full breakdown is in Fig. 6. Most articles covered human health (*n* = 480), followed by food (*n* = 25) and animal sectors (*n* = 24). The least studied sector using WHONET is environment (*n* = 9).

For the human sector, the most frequent pathogen was Escherichis coli, covered in 239 articles (%), followed by *Klebsiella pneumoniae (n* = 221, 46.0%), and Staphylococcus aureus (*n* = 201, 41.9%). Conversely, the main pathogens analysed in the food sector were *Salmonella spp*. (*n* = 5), *Escherichia coli* (*n* = 4), and *Staphylococcus aureus* (*n* = 3), whereas the remaining sectors presented *Escherichia coli* as the main pathogen analysed: 12 in the animal sector, four in aquaculture and seven articles in environment. More information can be found in the Supplementary Table S3.

Furthermore, only two articles covered the three sectors. The first is from South Africa, Kalule et al. [33], which used stool specimens from children with diarrhea, meat samples, and community canal water samples. The second is from Zambia by Kasanga et al. [34], which used human samples, including blood, cerebrospinal fluid, stool, and urine; food samples, including meat, fruits, and vegetables; and environmental samples from water and hospital equipment.

Discussion

This article presents a systematic literature review on using the WHONET software in scientific literature. This is the first review of its kind in this context, aimed at enhancing our understanding of the worldwide use and application of the free, open-access WHONET software for scientific purposes and confirming the untapped value of routine AMR data.

Our analysis shows that global interest in WHONET is evident with an increasing number of articles over time, which is also impacted by the worldwide interest in antimicrobial resistance [35]. Although WHONET started over 30 years ago, it remains a vital software used by countries of all income groups, particularly upper and lower-middle-income countries. The articles covered data from 110 countries, which is possible given that it was reported to be used in over 130 countries [7].

China was the leading producer of publications using WHONET. The software has been used in China for over 25 years, per the first report of a WHONET training [36], where they have a network of over 1,300 Laboratories [37] and developed their own WHONET website with guidance and resources. Thus, this leadership could be explained by this period and the vast network of laboratories using WHONET. Similar trends are observed in other countries with well-established surveillance and research infrastructures, such as India and the United States, where national AMR programs and international collaborations have supported continuous WHONET implementation and data reporting [38, 39]. Conversely, countries with fewer publications may still use WHONET but face challenges related to laboratory capacity,

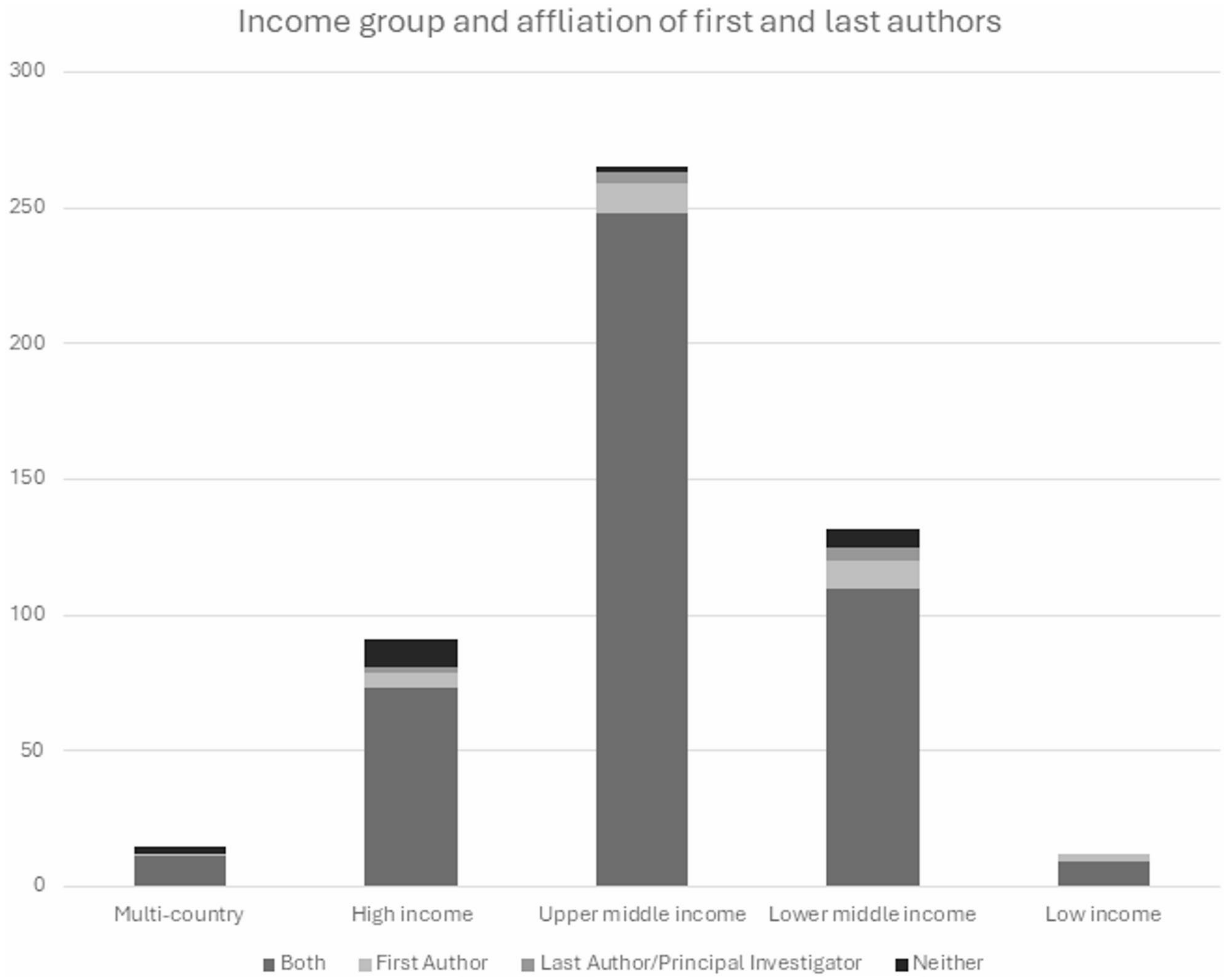

Fig. 4 Distribution of the articles based on the income groups of the country origin of the data and the first and last author's affiliations

data management, funding, or limited incentives for publishing surveillance findings.

That is a similar finding to other systematic reviews that investigate methodologies for infectious diseases [21] The recognized Chinese leadership in scientific research is evident in several scientific metrics, including being the nation with the most cited papers and participating in the top 1% of the most highly cited papers [40, 41]. Another possible influence is the population size and the volume of WHONET-related publications. Larger and more populous countries, such as China and India, tend to have more laboratories, research institutions, and surveillance activities, which may contribute to the higher number of reports observed. Yet, Colombia came as the third top country, which has a much smaller population than the abovementioned.

Furthermore, the timeliness of data reporting has been improving over the years. In recent years, we have found articles that report data from the same year or within one year, which is very good, considering the time it takes for research articles to be processed by scientific journals [42]. More than half (58%) of the articles were published within 2 to 3 years.

A recent study by Maharjan et al., highlighted the barriers to WHONET uptake, including limited interoperability with existing laboratory information systems, insufficient technical support, staff turnover, and lack of sustained training. Compared with other commercial systems, WHONET's strengths in AMR data analysis are challenged by workflow integration and reporting flexibility. To enhance adoption, targeted actions could include improving system interoperability, establishing continuous technical support and training-of-trainers programs, and embedding WHONET use within national AMR strategies and digital-health frameworks [43].

Our review also found that most studies relied on secondary data sources, such as laboratory records, surveillance databases, and routine health information systems [44]. The widespread use of these data beyond clinical purposes highlights their vital role and immense value

Table 1 – Organisms covered in the included articles

Organism	*N*	WHO bacterial priority pathogens list, 2024[a] [32]	Priority category
Acinetobacter spp.	190		
Acinetobacter baumannii	33	Yes[a]	Critical
Candida spp	63		
Citrobacter spp.	47		
Enterobacterales	946	Yes[b]	Critical
Escherichia coli	258		
Klebsiella spp.	283		
Klebsiella pneumoniae	239		
Proteus spp	80		
Salmonella spp.	102	Yes[c]	High
Serratia spp.	43		
Shigella spp.	24	Yes	High
Enterococcus spp.	149		
Enterococcus faecalis	50		
Enterococcus faecium	34	Yes	High
Haemophilus spp	22		
Haemophilus influenzae	18	Yes	Medium
Neisseria spp.	10		
Neisseria gonorrhoeae	7	Yes	High
Pseudomonas spp.	201		
Pseudomonas aeruginosa	195	Yes	High
Staphylococcus spp.	270		
Staphylococcus aureus	209	Yes	High
Streptococcus spp.	103		
Streptococcus pneumoniae	59	Yes	Medium
Group A Streptococci	5	Yes	Medium
Group B Streptococci	14	Yes	Medium
Mycobacterium spp.	3	Yes[b]	Critical
Other Gram-negative, bacillus	58		
Other Gram-positive, bacillus	27		
Other Gram-negative, coccus	10		
Other Gram-negative, spiral	13		
Gram-negative, curved bacillus	19		
Other Fungi	24		
Other Gram-negative, coccobacillus	3		
Other Gram-positive, coccus	3		

Notes: (a) The pathogens presented in this table are part of the WHO Priority List when resistance is present to a specific antibiotic; (b) the pathogen present in the list is *Mycobacterium tuberculosis* resistant to rifampicin; (c) Salmonella typhii and non-typhoidal Salmonella resistant to fluoroquinolones

for health research. It offers a cost-effective and scalable means to track and understand the resistance trends and patterns and inform policymaking and treatment guidelines [45]. Furthermore, with the strong push for the global digitalization of surveillance systems, leveraging routine and secondary data presents a valuable opportunity to strengthen AMR surveillance and evidence-based decision-making, particularly in resource-limited settings [46, 47]. This should be coupled with further analytics and artificial intelligence to enable real-time surveillance, outbreak detection, and response. However, this also requires strong health data protection measures in line with the General Data Protection Regulations [48] to protect the personal information in such databases for the appropriate use only [49–52].

We have observed significant variability in the geographic distribution of research on microorganisms included in the WHO Priority Pathogen List. Pathogens such as *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Acinetobacter spp.* (including *A. baumannii*) were among the most widely studied, indicating a high level of global concern and surveillance, given their roles in healthcare-associated infections and their increasing resistance to multiple antibiotics, as emphasized in global surveillance reports [53, 54]. Pathogens such as *Streptococcus Group A* and *Mycobacterium* were studied in only a few countries, suggesting gaps in geographic research

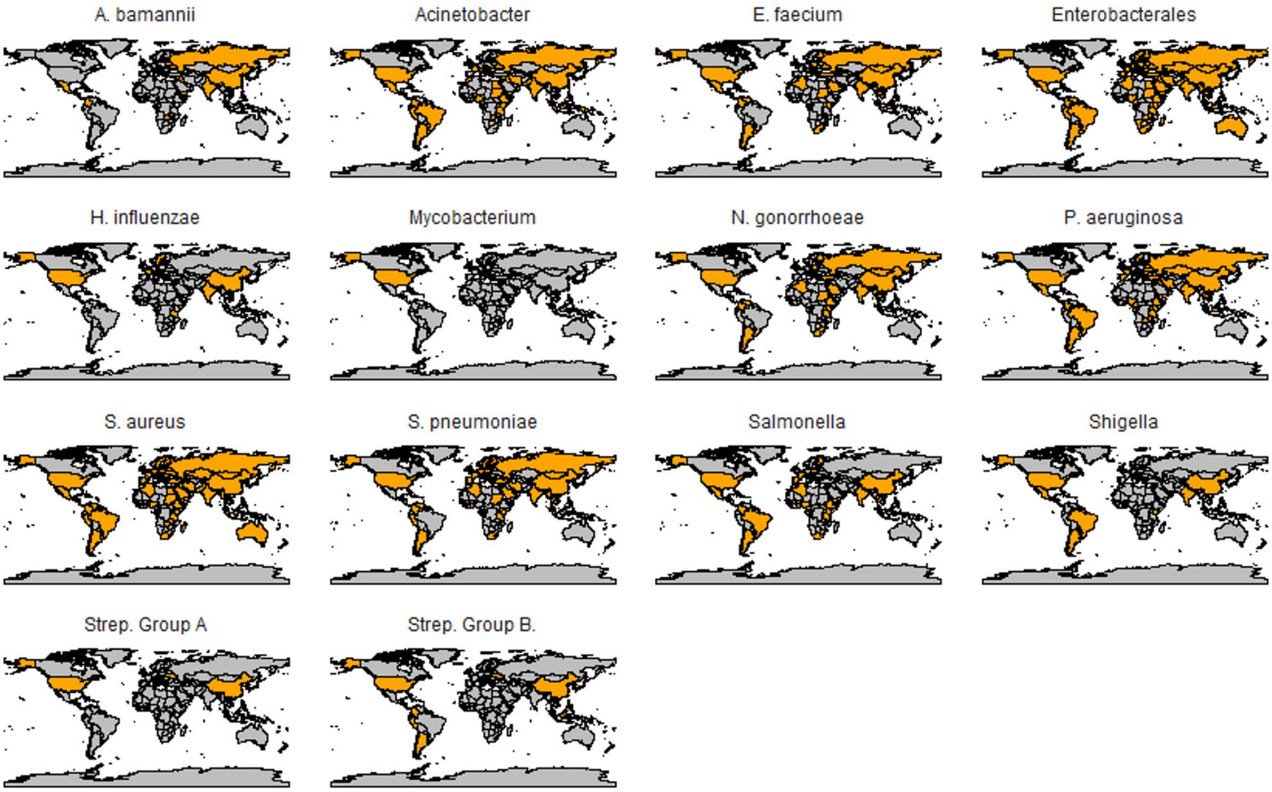

Fig. 5 Distribution of the studies for the WHO priority pathogens list

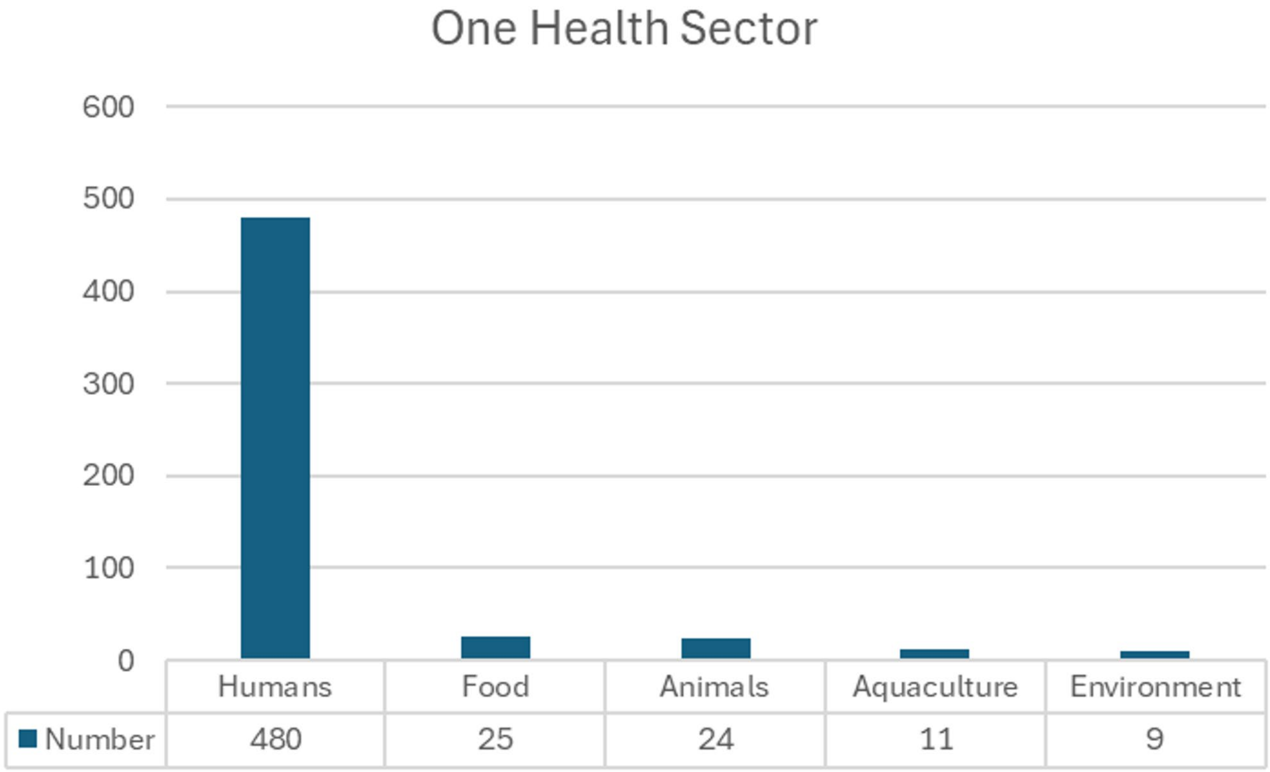

Fig. 6 Frequency of the data used from each of the one health sectors

coverage that may hinder global preparedness and response [55]. The extensive study of *Enterobacterales* across 101 countries also underscores the priority placed on this group due to its multidrug resistance, particularly among Gram-negative bacteria [56]. Moreover, the main pathogens studied in both humans and non-humans are part of the WHO Priority List, highlighting the alignment of global priorities with existing research. Nonetheless, these findings reiterate the need for more balanced global research efforts to ensure that less studied but clinically significant pathogens are not overlooked, particularly in lower resource settings where surveillance capacity may be limited [57].

Nevertheless, our review identified some limitations and challenges in the AMR publications. A significant challenge is that most research remains geographically and sectorally limited, with a strong focus on human health and the underrepresentation of veterinary and environmental health sectors, which are crucial for a One Health approach. Future studies should expand WHONET's application across diverse regions and sectors, particularly in low- and middle-income countries with the highest AMR burden [6, 16].

Another significant limitation is inconsistent data entry practices, particularly in low-resource settings like the WHO African Region, where WHONET is not fully used for primary data recording [58]. Many surveillance systems still rely on paper-based records or non-standardized laboratory systems, hindering data sharing, compromising data quality, and delaying surveillance efforts. The lack of standardization in data entry and quality can lead to duplication and reduced data quality, affecting the reliability of AMR surveillance and reporting. Addressing these challenges requires the adoption of WHONET for direct data entry, improved quality control mechanisms, and stronger regulatory frameworks to enhance data integrity and use of surveillance data for research [6, 16, 59]. Moreover, methodological transparency remains a concern, as many studies do not report data sources, analytical techniques, or AST guidelines' editions, which limit reproducibility.

In addition, integrating WHONET with spatial epidemiology, machine learning, or real-time outbreak detection tools could enhance its predictive capabilities. Further exploration into automated data processing, advanced statistical analyses, and AI-driven analytics would strengthen its role in global AMR surveillance. Future reviews should consider grey literature from public health institutions to capture a more comprehensive picture since numerous reports from various institutional levels have used WHONET.

Regarding process limitations in the systematic review, it is noted that while we did not apply any language restriction, many articles written in Chinese were excluded due to accessibility to the full text, which might originate selection bias. However, we aimed to lower this bias by utilizing translation tools in articles written in Persian, Russian, Ukrainian, or Japanese, which allowed us to increase the geographic completeness of this study.

In conclusion, this systematic literature review highlights the significant global interest and application of WHONET software in AMR research, with capacities confirmed in-country in over 110 countries. Despite its long history, WHONET remains a vital tool across diverse income groups, with notable contributions from China. The review confirms the importance of leveraging routine and secondary data for cost-effective AMR surveillance and the need for improved data reporting timeliness. However, challenges such as geographic and sectoral limitations, inconsistent data entry practices, and methodological transparency must be addressed to enhance the reliability and scope of AMR surveillance. Integrating WHONET with advanced analytics and ensuring strong health data protection measures are crucial for future improvements. Expanding WHONET's application across various regions and sectors will be essential for a comprehensive One Health approach to combat AMR.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12879-025-12420-1.

Supplementary Material 1

Supplementary Material 2

Acknowledgements

N/A.

Author contributions

ATA, JCX, and JS conceptualized the study. ATA, JCX, FM, and SW screened the articles. ATA, JCX, AE, FM, and ME extracted the articles. ATA and JCX conducted the analysis and drafted the manuscript. All authors reviewed the manuscript.

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Data availability

Data are included in the supplementary files, with more detailed datasets available upon request to the corresponding author.

Declarations

Ethical approval

Ethics approval was not required for this study, as it is based on published work and it did not collect primary data.

Competing interests

TFB and JS are the founders of the WHONET software. ATA has a prior professional affiliation with the WHONET group at Brigham and Women's Hospital, during which most of the research work was conducted, and JS has a current professional affiliation with the same group. All other authors declare no conflict of interest.

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