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Bibliometric Analysis

Mapping environmental and agricultural health within One Health research: A bibliometric and science-mapping analysis

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Abstract

The position of environmental and agricultural health within One Health literature remains insufficiently characterized. The aim of this study was to examine publication patterns, collaboration networks, conceptual structures, thematic evolution, and research fronts connecting environmental and agricultural health within explicitly One Health-oriented literature. A total of 1,852 English-language articles were retrieved from Scopus. Bibliometric and science-mapping analyses were conducted using VOSviewer and Biblioshiny. Publication output increased markedly after 2020, while citations and collaboration connectivity remained concentrated among a limited group of countries and institutions. Antimicrobial resistance emerged as the most prominent cross-sectoral theme, whereas environment and livestock formed internally cohesive but comparatively specialized clusters. The literature evolved from relatively fragmented topics toward broader One Health, resistance, environmental, and zoonotic themes. Bibliographic coupling identified 15 research fronts involving genomic epidemiology, agricultural-soil resistomes, environmental surveillance, plant agriculture, microplastics, and governance. Overall, environmental and agricultural themes became increasingly visible within the selected corpus, but their representation and thematic connections remained uneven. Future research should strengthen connections with plant health, soil functions, integrated pest management, agricultural-worker health, biodiversity, and preventive agroecosystem management.

Keywords: One Health, environmental health, agricultural health, science mapping, antimicrobial resistance

Introduction

The modern One Health movement gained international momentum in 2004 through the *One World, One Health* symposium and the formulation of the Manhattan Principles. This milestone called for a more integrated response to infectious diseases, biodiversity loss, ecosystem degradation, land-use change, and threats to global food systems. It helped reposition health as an outcome of interactions among humans, animals, and their shared environments rather than as the exclusive responsibility of medical or veterinary sectors. Subsequent applications of One Health demonstrated that translating this integrative vision into practice requires alignment among health priorities, development agendas, institutional capacity, and cross-sectoral

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Received: August 6, 2026 - Accepted: October 26, 2026 - Published online: November 8, 2026

coordination, particularly in resource-constrained settings [1]. The *One World, One Health* agenda has also stimulated broader consideration of how global health collaboration intersects with food security, agricultural production, and local sociocultural contexts [2].

The scope of One Health has continued to expand since this formative period. The contemporary definition proposed by the One Health High-Level Expert Panel describes One Health as an integrated and unifying approach that aims to sustainably balance and optimize the health of humans, animals, plants, and ecosystems. It recognizes that the health of people, domestic and wild animals, plants, and the wider environment is closely linked and interdependent [3]. This definition extends One Health beyond its conventional association with zoonotic disease surveillance and control, providing a broader conceptual foundation for addressing antimicrobial resistance, food safety, environmental contamination, climate change, biodiversity loss, plant health, and the sustainability of food-production systems.

Agriculture occupies a central position within this expanded framework. Agricultural systems produce food, support livelihoods, modify landscapes, consume natural resources, and create points of interaction among humans, livestock, wildlife, plants, microorganisms, and environmental reservoirs. Farms, croplands, livestock-production systems, aquaculture facilities, slaughterhouses, food-processing environments, and agricultural watersheds are therefore not merely sites of production. They are interconnected ecological and occupational environments in which biological hazards, chemical contaminants, resistance determinants, and health risks may emerge and circulate. Agriculture consequently represents one of the clearest operational settings in which the interdependence proposed by One Health can be examined.

This interdependence is particularly evident in agroecosystems affected by antimicrobial use. Agricultural environments may receive antimicrobial residues, resistant microorganisms, and resistance genes through livestock production, manure application, irrigation water, wastewater, and other production-related pathways. These inputs can interact with soil and water microbial communities and facilitate the selection, persistence, and transmission of antimicrobial resistance among animals, humans, and environmental reservoirs. Antibiotic resistance in agroecosystems must therefore be understood as an ecological One Health problem rather than solely as a clinical or veterinary concern [4]. Recent genomic evidence from swine farms has further demonstrated that resistant bacterial lineages can be shared across animals, farm workers, and surrounding environmental niches, illustrating how agricultural production connects veterinary, occupational, environmental, and public health risks [5].

Environmental and agricultural health are also connected through the management of animal waste and agricultural inputs. Antibiotic residues in livestock manure can alter microbial processes and increase greenhouse gas emissions during storage, linking antimicrobial use and manure management with environmental quality and climate change [6]. Similarly, pesticides may move across soil, water, crops, food products, wildlife, and non-target organisms while creating exposure pathways for farmers and surrounding communities [7,8]. Assessing pesticides from a One Health perspective therefore requires simultaneous consideration of their environmental fate, effects on aquatic and terrestrial organisms, and risks to human health rather than separate evaluations of individual environmental compartments [9]. These examples demonstrate that agricultural practices generate environmental pathways through which hazards can be transported, transformed, accumulated, and transferred across health domains.

Agricultural health should consequently be interpreted more broadly than crop productivity or the absence of disease in farm animals. It encompasses plant and crop health, soil functions, pest and disease management, food-system safety, agricultural-worker health, agroecosystem resilience, and the environmental consequences of agricultural practices [7,10,11]. Soil is especially important because it supports crop production, regulates nutrient and water cycles, hosts diverse microbial communities, and mediates the movement of pathogens, pesticides, antimicrobial residues, and resistance genes. Integrated soil-health management can therefore connect plant protection with ecological processes and broader One Health outcomes. Experiences in soil-borne disease and arthropod-pest management indicate that preventive, diversified, and biologically informed strategies can support plant health while reducing unintended consequences for humans and ecosystems [12].

Integrated pest management is particularly relevant to this intersection. By combining ecological knowledge, crop management, biological control, monitoring, decision thresholds, and selective interventions, integrated pest management seeks to suppress damaging pest populations while reducing unnecessary reliance on chemical pesticides. However, it has traditionally been framed as a crop-protection strategy rather than as a wider intervention connecting plant health, occupational safety, food-system integrity, biodiversity, resistance management, and ecosystem health. Emerging research has begun to position pest management within climate-smart One Health by emphasizing the need to consider crop productivity, ecological stability, climate resilience, farmer health, animal exposure, and environmental consequences within a common decision framework [13,14]. The proposed mainstreaming of integrated pest management into climate-smart One Health further indicates that pest management can serve as an operational bridge among plant, human, animal, and ecosystem health [15].

Climate change adds another layer of interdependence to the agricultural–environmental interface [16]. Changes in temperature, precipitation, water availability, vegetation, and extreme weather can affect crop and livestock production, vector ecology, pathogen transmission, food security, occupational conditions, and rural livelihoods. These effects are particularly important for communities whose health and economic security depend directly on agriculture and natural resources. Evidence from pastoralist regions shows that climate-related health impacts are mediated through interacting environmental, livestock, food-security, mobility, and socioeconomic pathways, making them difficult to understand through a single disciplinary perspective [17]. One Health can therefore provide a framework for examining how environmental change is translated into agricultural, animal, and human-health consequences.

Despite its expanding conceptual scope, the integration of environmental and agricultural health into One Health remains scientifically and institutionally challenging. Effective implementation requires coordination among public-health agencies, veterinary services, environmental authorities, agricultural institutions, food-system actors, and local communities. Fragmented surveillance, incompatible information systems, uneven resource allocation, insufficient interdisciplinary capacity, and weak cross-sectoral governance may prevent these sectors from functioning as an integrated system. For example, an assessment of One Health governance in China identified continuing challenges related to real-time monitoring, data integration, resource allocation, workforce capacity, financial support, and coordination across human, animal, and environmental health sectors [18]. These challenges illustrate the continuing gap between recognizing interdependence conceptually and operationalizing it through research, policy, surveillance, and intervention.

The scientific literature reflects this complexity. Research relevant to environmental and agricultural One Health is distributed across public health, veterinary medicine, microbiology, environmental science, agriculture, soil science, plant protection, food safety, toxicology, occupational health, climate science, and sustainability governance [19]. Within this dispersed landscape, environmental and agricultural health may be represented through different interfaces, including antimicrobial resistance in agroecosystems, zoonotic transmission on farms, soil and water contamination, pesticide exposure, food safety, agricultural occupational health, biodiversity, climate adaptation, plant health, and integrated pest management. However, the existence of these research streams does not necessarily indicate that they form a coherent and well-integrated knowledge domain [14,20,21].

This distinction is critical. A publication may refer to agriculture only as the location of disease emergence, the environment only as a transmission reservoir, or One Health only as a general policy recommendation without placing environmental or agricultural health at the center of its analysis. Conversely, studies of soil health, pesticide exposure, plant disease, biological control, and agroecosystem resilience may correspond substantively with One Health principles while remaining weakly connected to the dominant concepts, publication outlets, and collaboration networks of the field. It is therefore necessary to determine not only whether environmental and agricultural concepts occur in One Health publications, but also how they are positioned within the intellectual, collaborative, and thematic structure of the literature.

The need for such an assessment is not based solely on the expansion of publication output. It arises from an unresolved structural question: whether the environmental and agricultural dimensions recognized by contemporary One Health have developed into an interconnected research domain or remain dispersed across partially connected bodies of literature. Existing studies provide important evidence on specific interfaces, including antimicrobial resistance in agroecosystems, soil and plant health, agricultural chemical exposure, climate-sensitive agricultural systems, and climate-smart pest management [4,9,12,13]. Nevertheless, their collective position within the broader architecture of One Health research has not been sufficiently clarified.

Previous bibliometric studies have provided valuable overviews of the growth, productivity, collaboration patterns, and major research priorities of One Health scholarship. However, these studies have generally examined One Health at a broad field level or have concentrated on established topics such as zoonotic diseases, antimicrobial resistance, food safety, and vector-borne infections. Although several studies have noted the comparatively limited representation of environmental health, they have not specifically examined how environmental and agricultural health are jointly positioned within the conceptual, collaborative, and intellectual structure of explicitly One Health-oriented literature. In particular, limited attention has been given to whether agricultural dimensions beyond livestock and food-animal production, including plant health, soil functions, agricultural-worker health, pest management, and agroecosystem resilience, are connected to the dominant themes and contemporary research fronts of the field [22-25].

The present study addresses this gap by focusing specifically on the intersection of One Health, environmental health, and agricultural health rather than mapping the entire One Health literature. It combines performance analysis, co-authorship and keyword networks, thematic mapping, thematic evolution, bibliographic coupling, and citation analysis to examine not only the visibility of environmental and agricultural concepts, but also their structural position, thematic development, temporal transformation, and relationship with contemporary research fronts. This focused approach provides a more differentiated understanding of how environmental and agricultural dimensions are represented within a selected corpus of explicitly One Health-oriented publications.

The multidisciplinary character of this literature cannot be fully understood through isolated case studies or conventional narrative synthesis alone. A systematic mapping approach is needed to distinguish scientific productivity from citation influence, identify the actors and institutions shaping the field, reveal patterns of national and international collaboration, examine relationships among concepts, and trace changes in thematic priorities. Such an approach can also clarify whether environmental and agricultural themes occupy central and well-developed positions or remain fragmented around more established subjects such as zoonotic diseases, food safety, and antimicrobial resistance.

Bibliometric analysis combined with science mapping and thematic analysis provides an appropriate framework for addressing this need. Publication and citation analyses can characterize the development and scientific influence of the literature. Analyses of authors, institutions, countries, and publication sources can identify the principal contributors and the geographical and institutional distribution of knowledge production. Co-authorship mapping can reveal the structure of scientific collaboration, while keyword co-occurrence analysis can identify relationships among major concepts. Thematic mapping can evaluate the relevance and development of research themes, whereas thematic evolution can trace their continuity, transformation, and emergence over time. Bibliographic coupling can further identify contemporary research frontiers based on shared intellectual foundations.

A bibliometric and thematic analysis is therefore needed to establish how research connecting environmental health, agricultural health, and One Health has developed since the 2004 milestone, how scientific influence and collaboration are distributed, how its conceptual themes are structured and transformed, and which research directions are emerging. Clarifying these patterns can strengthen the conceptual foundation for integrating environmental and agricultural perspectives into One Health research and implementation. It can also identify areas

in which formal recognition of interconnected health domains has not yet been matched by sustained scientific attention, collaboration, or thematic development.

Based on this research gap, the present study addresses the following research questions:

RQ1. How has research at the intersection of One Health, environmental health, and agricultural health developed in terms of publication output and accumulated citations since 2004?

RQ2. How are scientific contributions, influence, and collaboration distributed across authors, institutions, countries, and publication sources within this research domain?

RQ3. What conceptual themes characterize the intersection of environmental and agricultural health within One Health research, and how are these themes positioned in terms of relevance and development?

RQ4. How have the principal themes and conceptual relationships within this research domain evolved over time?

RQ5. What intellectual foundations and contemporary research frontiers characterize the intersection of environmental health, agricultural health, and One Health?

Accordingly, the aim of this study was to systematically examine the development, intellectual structure, collaborative landscape, thematic organization, and research frontiers of scientific publications connecting environmental and agricultural health within the One Health framework. By examining how these domains have been represented and organized in the scientific literature, the study sought to provide an evidence-based understanding of their position within the broader development of One Health research.

Methods

Study design and data collection

This study employed a bibliometric and science-mapping design to examine the development, scientific influence, collaborative structure, conceptual organization, thematic evolution, and research fronts of publications connecting One Health, environmental health, and agricultural health. The analytical framework combined bibliometric performance analysis, co-authorship mapping, author-keyword co-occurrence analysis, thematic mapping, thematic-evolution analysis, document-level bibliographic coupling, and citation analysis.

Bibliographic data were retrieved from the Scopus database on July 27, 2026. Scopus was selected because it provides structured metadata required for bibliometric analysis and science mapping, including documents, authors, affiliations, countries, publication sources, abstracts, keywords, citation counts, and cited references. All publication and citation indicators reflect the metadata indexed in Scopus as of the retrieval date. Records from 2026 represent a partial publication year and were not directly compared with complete annual totals when interpreting publication growth.

The search strategy was designed to identify publications containing terminology related to One Health and both environmental and agricultural concepts. The search expression entered into Scopus was "one health" AND (environment* OR ecosystem* OR biodivers* OR "environmental health" OR "ecosystem health" OR "ecological health" OR "soil health" OR "soil quality" OR "water quality" OR pollution OR contamin* OR "climate change") AND (agricultur* OR farming OR farm OR farms OR farmer* OR agrifood OR "agri-food" OR agroecosystem* OR agroecolog* OR "plant health" OR "crop health" OR "crop production" OR "crop protection" OR "plant protection" OR horticultur* OR "agricultural pest*" OR "crop pest*" OR "plant pest*" OR "pest management" OR pesticide* OR insecticide* OR fungicide* OR herbicide* OR "integrated pest management" OR "biological control" OR "food production" OR "food system*" OR "food safety" OR "food security" OR "agricultural worker*" OR "farm worker*" OR farmworker* OR "occupational pesticide exposure" OR "pesticide exposure" OR "agricultural exposure").

The mandatory inclusion of the phrase "One Health" restricted the corpus to publications explicitly using One Health terminology, while the environmental and agricultural term groups required the presence of terms relating to both dimensions. This intentionally focused search strategy was designed to identify a selected corpus in which One Health, environmental health, and agricultural health were explicitly connected. Consequently, the resulting dataset does not

represent the entire One Health field or all studies substantively addressing human–animal–plant–environment interactions. Relevant studies that did not use the specified terminology in their titles, abstracts, or keywords may not have been captured.

Eligibility and data extraction

Record identification and refinement were conducted exclusively through the search fields and filtering functions available in Scopus. The initial search across all Scopus fields identified 52,356 records. Restriction to the title, abstract, and keyword fields reduced the dataset to 3,470 records. Limiting the publication period to 2004–2026 produced 3,463 records. The records were subsequently restricted to articles at the final publication stage, yielding 1,911 records. Restricting the results to English-language publications produced the final corpus of 1,852 articles.

No independent title, abstract, or full-text screening was conducted after database filtering. The record identification, database filtering, and inclusion procedures are presented in **Figure 1**.

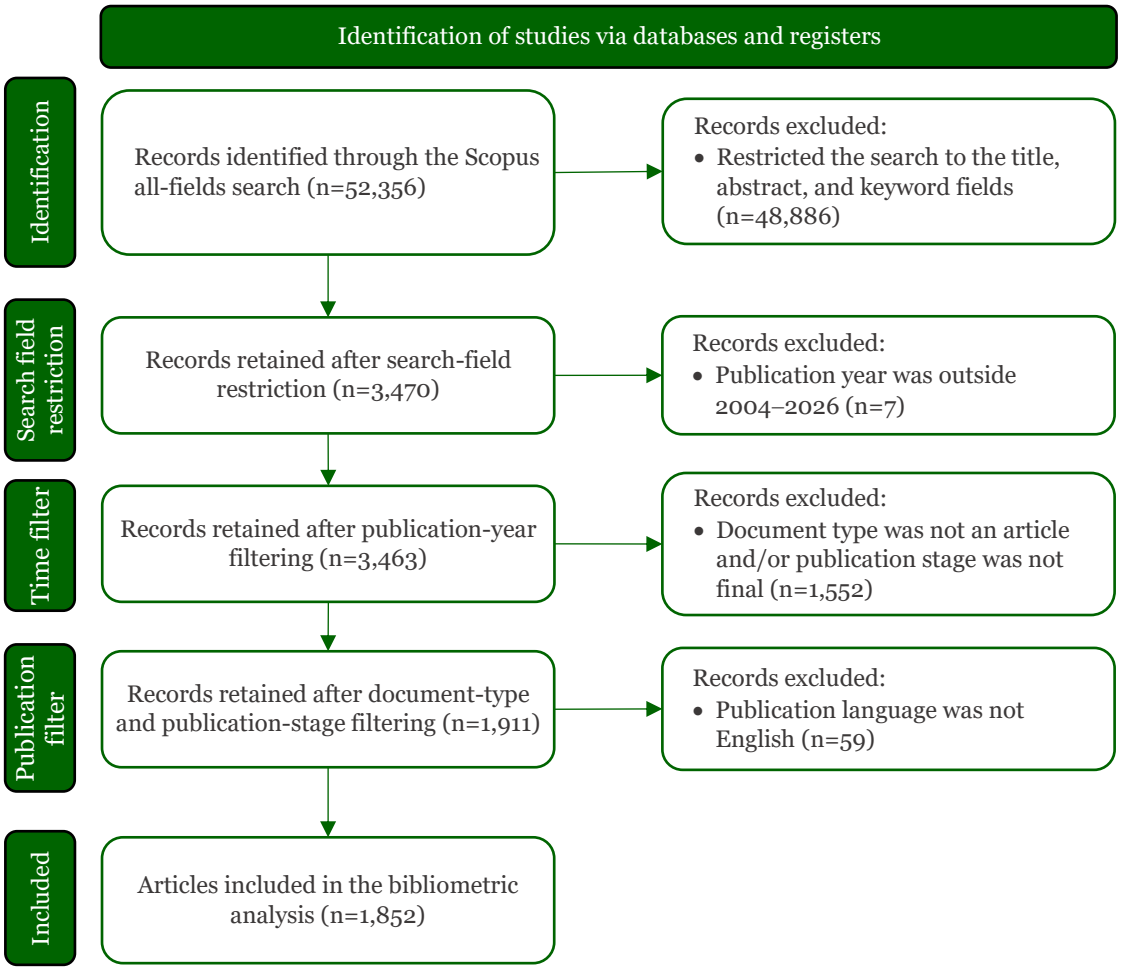


Figure 1. PRISMA flow diagram.

The complete bibliographic records were exported from Scopus in comma-separated values format. All metadata fields available through the Scopus export interface were retained, including document titles, authors, publication years, source titles, abstracts, author keywords, indexed keywords, affiliations, countries, document types, publication stages, languages, digital object identifiers, citation counts, and cited references.

No documents were manually removed after Scopus filtering. Data preprocessing focused on lexical standardization rather than altering the composition of the corpus. A thesaurus file was applied in VOSviewer to harmonize equivalent expressions and reduce variation arising from abbreviations, capitalization, hyphenation, singular and plural forms, alternative spellings, and abbreviated scientific names. For analyses conducted in R, synonym and stop-word files were

used to consolidate conceptually equivalent expressions and remove generic or analytically uninformative terms. Conceptually distinct expressions, including "antimicrobial resistance" and "antibiotic resistance," were retained separately when their consolidation could obscure differences in thematic organization. Author keywords were used as the primary textual field for keyword co-occurrence, thematic mapping, and thematic-evolution analyses.

Bibliometric performance analysis

Bibliometric performance analysis was conducted at the document, source, author, institution, and country levels. Annual scientific production was measured using the number of articles published in each year. Annual citation influence was calculated as the cumulative number of Scopus citations received by documents published in each year, as of July 27, 2026. These citation values represent accumulated citations received by each publication-year cohort rather than citations received during the corresponding calendar year.

Source performance was assessed using publication output and total citations. Author, institution, and country performance were evaluated using publication output, total citations, and total link strength (TLS). TLS represented the cumulative strength of an entity's relationships with other entities in the corresponding bibliometric network. Institutional information was obtained from Scopus affiliation metadata, while country information was derived from author-affiliation addresses. Because Scopus records affiliations at different organizational levels, institutional entries could represent universities, faculties, schools, research institutes, government agencies, or international organizations.

Publication output, accumulated citation counts, and total link strength (TLS) were evaluated as separate indicators representing research productivity, citation impact, and collaboration strength, respectively, following established bibliometric performance-analysis frameworks [26,27]. To enable comparison among indicators with different numerical scales, these indicators were transformed using maximum normalization: $N(X_i)=X_i/\max(X)$, where $N(X_i)$ represents the normalized value of indicator X for entity $_i$, Xi is the observed value for entity $_i$, and max(X) is the highest observed value of that indicator within the corresponding analytical category. In addition to these individual indicators, a composite overall score (OS) was developed to provide a supplementary summary of bibliometric performance. For scientific sources, the OS was calculated as the arithmetic mean of normalized publication output and normalized citation count: $OSi=(N(Pub_i)+N(Cit_i))/2$. For authors, institutions, and countries, the OS was calculated as the arithmetic mean of normalized publication output, normalized citation count, and normalized total link strength: $OS_i=(N(Pub_i)+N(Cit_i)+N(TLS_i))/3$, where $N(Pub_i)$, $N(Cit_i)$, and $N(TLS_i)$ represent the normalized values of publication output, citation count, and total link strength, respectively. This approach follows previously reported bibliometric composite-scoring frameworks [28], with equal weighting applied to all components to avoid introducing subjective differential weights in the absence of an established empirical basis. The OS was intended as a comparative measure within each analytical category rather than an absolute measure of research quality or scientific excellence. Normalized values and overall scores were rounded to three decimal places for presentation.

The most highly cited individual publications were identified using total Scopus citation counts recorded on July 27, 2026. Documents were ranked in descending order, and the 10 publications with the highest accumulated citation counts were retained. Citation counts were not normalized by publication year because this analysis was intended to identify accumulated citation influence rather than age-adjusted citation performance. Consequently, this ranking is subject to citation-window bias, as older publications have had more time to accumulate citations than more recent publications. The principal intellectual contribution of each publication was evaluated based on its title, abstract, author keywords, publication source, and available bibliographic metadata.

VOSviewer analysis

VOSviewer version 1.6.20 was used to construct and visualize the author co-authorship, country co-authorship, author-keyword co-occurrence, and document-level bibliographic-coupling networks. VOSviewer supports the construction and graphical representation of bibliometric networks based on co-authorship, co-occurrence, citation, co-citation, and bibliographic-

coupling relationships. Full counting was applied throughout the network analyses, and association-strength normalization was used to standardize relationships among nodes. Full counting was selected because the analyses aimed to map the presence and overall structure of relationships within the selected corpus rather than estimate the proportional contributions of individual authors, institutions, or countries. Because this approach may give greater influence to publications involving many contributing entities, TLS was interpreted as an indicator of network connectivity rather than proportional research contribution.

For the author co-authorship analysis, authors were used as the unit of analysis, and a minimum threshold of one publication per author was applied. Author-name variants were standardized using the thesaurus file when clear lexical or formatting differences referred to the same author. Nodes represented authors, links represented co-authorship relationships, and TLS represented the cumulative strength of each author's collaboration links.

For the country co-authorship analysis, countries identified from author-affiliation addresses were used as the unit of analysis. A minimum threshold of one publication per country was applied to retain the geographical breadth of the corpus. Nodes represented countries, links represented international co-authorship relationships, and TLS represented the cumulative strength of each country's collaborative relationships. Countries with no co-authorship links to other countries were excluded from the final network visualization. Country-level total link strength values were derived from the final connected network after excluding countries without collaboration links.

Author-keyword co-occurrence analysis was used to identify the conceptual structure of the literature. Author keywords were used as the unit of analysis, and terms occurring at least five times were considered for inclusion. Nodes represented standardized author keywords, node size reflected occurrence frequency, links represented co-occurrence relationships, and TLS represented the cumulative strength of each keyword's connections. Spatial proximity indicated conceptual relatedness, while node color represented cluster membership.

Document-level bibliographic coupling was used to identify research fronts based on shared cited references. Two documents are bibliographically coupled when they cite one or more references in common, with stronger coupling indicating a greater number of shared references. Documents were used as the unit of analysis, and a minimum threshold of 20 Scopus citations per document was applied to obtain an interpretable network focused on publications with sufficient citation visibility within the selected corpus. This threshold was intended to reduce network density and visual congestion while retaining documents suitable for identifying established research fronts. However, it may underrepresent recent publications that have had less time to accumulate citations. Documents not connected to the bibliographic-coupling network were excluded from the final visualization. Links represented shared cited references between documents, while TLS represented the cumulative strength of each document's bibliographic-coupling relationships.

Clusters generated by VOSviewer were interpreted inductively. Keyword clusters were labeled by examining their most frequent and strongly connected terms, whereas bibliographic-coupling clusters were labeled through examination of publication titles, abstracts, TLS, citation influence, and shared conceptual focus. Representative publications within each bibliographic-coupling cluster were selected primarily according to TLS and subsequently assessed for citation influence and thematic relevance.

R and biblioshiny analysis

The Scopus dataset was imported into R version 4.5.2 and analyzed through the Biblioshiny interface of the Bibliometrix package. Bibliometrix provides an integrated workflow for importing bibliographic records, conducting performance analysis, constructing bibliometric networks, and examining the conceptual, intellectual, and social structures of scientific literature [29]. Biblioshiny was used to generate the thematic map and thematic-evolution analysis from the standardized author-keyword field. Synonym and stop-word files were applied before analysis, while stemming was not used to avoid altering scientific names, technical terminology, and other domain-specific expressions.

The thematic map was constructed from the 250 most relevant standardized author keywords using the Louvain community-detection algorithm. Callon centrality measured the strength of a theme's relationships with other themes and was interpreted as an indicator of its relevance to the overall research domain. Callon density measured the internal strength of relationships among terms within the same theme and was interpreted as an indicator of thematic development.

Themes with high centrality and high density were classified as motor themes, whereas themes with low centrality and high density were classified as niche themes. Themes with high centrality and low density were classified as basic themes, while themes with low centrality and low density were classified as emerging or declining themes. Themes positioned on or close to the median centrality or density lines were interpreted as boundary themes. Cluster frequency represented the cumulative occurrence frequency of the author keywords assigned to each thematic cluster, while bubble size was proportional to this frequency. These categories describe the relative strategic positions of themes within the analyzed keyword network and should not be interpreted as absolute measures of scientific importance, quality, or maturity. Similarly, the label "emerging or declining" does not independently distinguish a newly developing theme from one receiving decreasing attention; temporal evidence is required for such an interpretation.

The thematic-evolution analysis traced the continuity, transformation, merging, and fragmentation of author-keyword clusters across four periods: 2006–2019, 2020–2022, 2023–2024, and 2025–2026. The period boundaries were set at 2019, 2022, and 2024 to distinguish the formative, expansion, differentiation, and most recent phases of the literature while retaining sufficient records for theme construction within each interval.

The thematic-evolution analysis used the 250 most relevant standardized author keywords and a minimum cluster frequency of five per thousand documents, meaning that a term cluster had to reach a frequency equivalent to at least five occurrences per 1,000 documents within the corresponding period to be retained. Themes were identified using the Louvain algorithm. Three labels were retained for each cluster, with a label-size parameter of 0.3. Relationships between themes in consecutive periods were measured using the inclusion index weighted by keyword occurrences. A minimum weighted inclusion index of 0.1 was applied to suppress weak relationships. The width of each evolutionary flow represented the strength of thematic continuity based on the frequency and overlap of shared keywords.

Interpretive and consistency procedures

Thematic and research-front labels were treated as interpretive classifications rather than automatically generated substantive findings. Labels were assigned by examining the most frequent and strongly connected keywords or documents and evaluating their shared conceptual content. The same interpretive principles were applied across the VOSviewer keyword clusters, Biblioshiny thematic clusters, thematic-evolution pathways, and bibliographic-coupling research fronts. Accordingly, thematic positions and labels were interpreted comparatively within the selected corpus and were not treated as universal measures of thematic importance or maturity.

Bibliographic indicators, network metrics, cluster memberships, representative publications, and citation counts were cross-checked against the original Scopus exports and the corresponding VOSviewer and Biblioshiny outputs before reporting. The standardized author-keyword vocabulary was applied consistently across keyword co-occurrence, thematic mapping, and thematic-evolution analyses to maintain comparability among the conceptual analyses.

Results

Publication and citation trends

Although the predefined search window began in 2004, the earliest eligible publication identified in the final corpus was published in 2006. Annual publication output and cumulative citations for research at the intersection of One Health, environmental health, and agricultural health are presented in **Figure 2**. Scientific output remained limited through 2012, with no more than five publications per year. Publication output increased to 24 articles in 2013 before declining to 11 in 2014, followed by a progressive increase to 71 articles in 2020.

A marked expansion occurred thereafter, with publication output rising to 136 articles in 2021, 169 in 2022, 190 in 2023, and 254 in 2024, reaching a peak of 429 publications in 2025. By the retrieval date of July 27, 2026, 409 publications had been indexed for 2026. However, this count represents a partial publication year and is therefore not directly comparable with the complete-year output for 2025.

Cumulative citations increased across publication-year cohorts from 2015 to 2022, rising from 1,073 citations for publications issued in 2015 to a peak of 3,930 for those published in 2022. Citation totals were lower for subsequent cohorts, with 2,514 citations in 2023, 2,263 in 2024, 1,335 in 2025, and 128 in 2026. The lower citation counts may partly reflect the shorter time available for recent publications to accumulate citations. Thus, although publication output increased substantially after 2020, the highest cumulative citation count was recorded for publications from 2022.

Leading scientific sources

The leading scientific sources in terms of publication output and citation impact are presented in **Table 1**. One Health recorded the highest publication output, with 111 articles and 1,278 accumulated citations. Science of the Total Environment published 46 articles and received the highest number of citations among the listed sources, with 1,636. Antibiotics contributed 68 publications and received 1,042 citations.

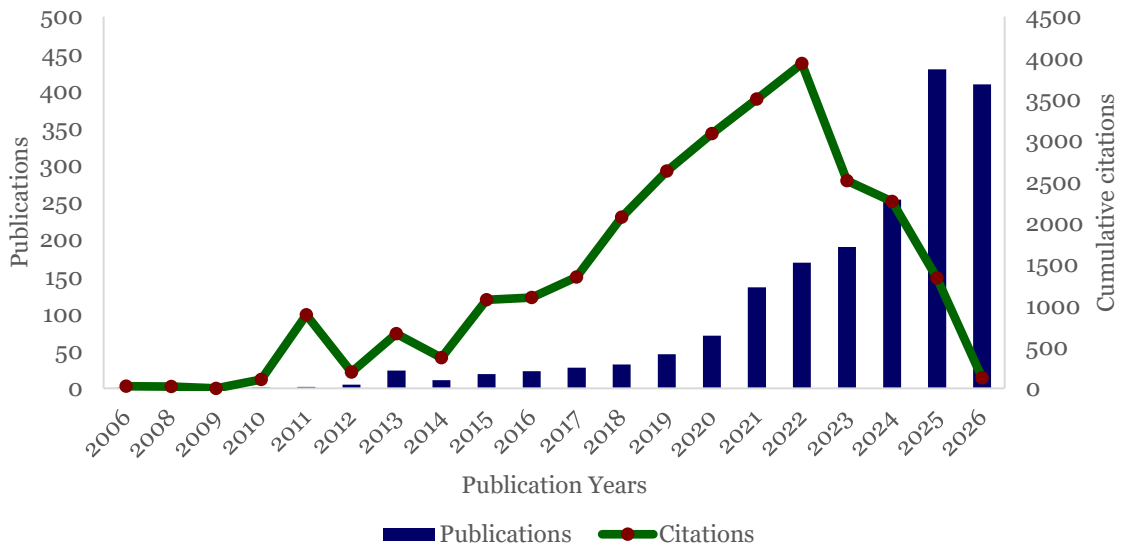


Figure 2. Annual publication output and cumulative citations of publications at the intersection of One Health, environmental health, and agricultural health, 2006–2026. The 2026 data cover the period up to July 27, 2026, and represent a partial publication year.

Several sources received substantial citation counts despite relatively modest publication output. Microbiology Spectrum published 19 articles and received 1,506 citations, while Preventive Veterinary Medicine contributed 15 publications and accumulated 1,107 citations. *Proceedings of the National Academy of Sciences of the United States of America* recorded only four publications but received 840 citations, indicating the highest average citation count per publication among the listed sources.

Other leading sources included Frontiers in Microbiology, Frontiers in Public Health, Microorganisms, and Frontiers in Veterinary Science. These findings reveal two distinct patterns among the leading sources: journals with high publication productivity and those with lower output but substantial citation impact.

Table 1. Leading scientific sources based on publication output and accumulated citations

Sources	Pub	Cit	N-Pub	N-Cit	OS
One Health	111	1278	1.000	0.781	0.891
Science of the Total Environment	46	1636	0.414	1.000	0.707

Sources	Pub	Cit	N-Pub	N-Cit	OS
Antibiotics	68	1042	0.613	0.637	0.625
Microbiology Spectrum	19	1506	0.171	0.921	0.546
Frontiers in Microbiology	48	802	0.432	0.490	0.461
Preventive Veterinary Medicine	15	1107	0.135	0.677	0.406
Frontiers in Public Health	33	482	0.297	0.295	0.296
Proceedings of the National Academy of Sciences of the United States of America	4	840	0.036	0.513	0.275
Microorganisms	35	367	0.315	0.224	0.270
Frontiers in Veterinary Science	36	317	0.324	0.194	0.259

Cit: citations; N-Pub/Cit: normalized values (max: 1.000); OS: overall score (composite index); pub: publications

Leading authors, institutions, and countries

The leading authors, institutions, and countries, ranked by overall score (OS), are presented in **Tables 2–4**. Nilton Lincopan achieved the highest overall score among the listed authors (OS=0.866), followed by Luísa Peixe (OS=0.704) and Barbara Häsler (OS=0.693). Although Lincopan had the highest collaboration strength (TLS=55), Häsler recorded the highest citation count, with 291 citations from five publications. Fernanda Esposito demonstrated the second-highest collaboration strength (TLS=48), despite having four publications and 104 citations. These findings illustrate the differences between overall bibliometric performance, citation impact, and collaboration strength.

Table 2. Leading authors based on publication output, accumulated citations, and collaboration strength

Author	Pub	Cit	TLS	N-Pub	N-Cit	N-TLS	OS
Lincopan, Nilton	8	174	55	1.000	0.598	1.000	0.866
Peixe, Luísa	8	165	30	1.000	0.567	0.545	0.704
Häsler, Barbara	5	291	25	0.625	1.000	0.455	0.693
Nguyen-Viet, Hung	7	146	36	0.875	0.502	0.655	0.677
Gray, Gregory C.	7	154	30	0.875	0.529	0.545	0.650
Li, Ruichao	8	73	35	1.000	0.251	0.636	0.629
Novais, Carla	7	150	27	0.875	0.515	0.491	0.627
Fontana, Herrison	5	152	40	0.625	0.522	0.727	0.625
Esposito, Fernanda	4	104	48	0.500	0.357	0.873	0.577
Shoaib, Muhammad	7	61	31	0.875	0.210	0.564	0.549

Cit: citations; N-Pub/Cit/TLS: normalized values (max: 1.000); OS: overall score (composite index); pub: publications; TLS: total link strength

The School of Global Health, Shanghai Jiao Tong University School of Medicine achieved the highest overall score among the listed institutions (OS=0.809), followed by the Centers for Disease Control and Prevention (OS=0.754) and the Food and Agriculture Organization of the United Nations (OS=0.647). The Centers for Disease Control and Prevention received the highest institutional citation count, with 285 citations from six publications, whereas the School of Global Health recorded the highest collaboration strength (TLS=47). The University of Chinese Academy of Sciences accumulated 261 citations from seven publications but had a relatively low collaboration strength (TLS=3). Utrecht University received 280 citations from only two publications, resulting in an overall score of 0.524.

Table 3. Leading institutions based on publication output, accumulated citations, and collaboration strength

Institutions	Pub	Cit	TLS	N-Pub	N-Cit	N-TLS	OS
School of Global Health, Shanghai Jiao Tong University School of Medicine	8	122	47	1.000	0.428	1.000	0.809
Centers for Disease Control and Prevention	6	285	24	0.750	1.000	0.511	0.754
Food and Agriculture Organization of the United Nations	5	114	43	0.625	0.400	0.915	0.647
University of Chinese Academy of Sciences	7	261	3	0.875	0.916	0.064	0.618
International Livestock Research Institute	6	184	17	0.750	0.646	0.362	0.586
EcoHealth Alliance	4	171	27	0.500	0.600	0.574	0.558
Utrecht University	2	280	16	0.250	0.982	0.340	0.524
University of Agriculture Faisalabad	6	83	24	0.750	0.291	0.511	0.517

Institutions	Pub	Cit	TLS	N-Pub	N-Cit	N-TLS	OS
French Agency for Food, Environmental and Occupational Health & Safety (ANSES)	2	151	33	0.250	0.530	0.702	0.494
Technical University of Denmark (DTU)	2	151	33	0.250	0.530	0.702	0.494

Cit: citations; N-Pub/Cit/TLS: normalized values (max: 1.000); OS: overall score (composite index); pub: publications; TLS: total link strength

The United States achieved the highest overall score (OS=1.000), followed by the United Kingdom (OS=0.788), China (OS=0.425), and Italy (OS=0.424). The United States also recorded the highest publication output, citation count, and collaboration strength, with 353 publications, 8,215 citations, and a TLS of 579. The United Kingdom ranked second in all three indicators, with 220 publications, 6,292 citations, and a TLS of 565. Although China ranked third in overall score, Italy had a higher collaboration strength (TLS=272 vs 220), while China had more publications (186 vs 165) and citations (3,019 vs 2,742). France recorded the third-highest collaboration strength (TLS=284), followed by Italy (TLS=272). Canada and Australia received 3,915 and 3,722 citations, respectively, from 92 and 111 publications. These results demonstrate that the countries' overall rankings reflect different combinations of research productivity, citation impact, and collaboration strength.

Table 4. Leading countries based on publication output, accumulated citations, and collaboration strength

Countries	Pub	Cit	TLS	N-Pub	N-Cit	N-TLS	OS
United States	353	8,215	579	1.000	1.000	1.000	1.000
United Kingdom	220	6,292	565	0.623	0.766	0.976	0.788
China	186	3,019	220	0.527	0.367	0.380	0.425
Italy	165	2,742	272	0.467	0.334	0.470	0.424
France	116	3,160	284	0.329	0.385	0.491	0.401
Australia	111	3,722	233	0.314	0.453	0.402	0.390
Canada	92	3,915	221	0.261	0.477	0.382	0.373
Germany	88	2,019	229	0.249	0.246	0.396	0.297
Brazil	138	2,073	140	0.391	0.252	0.242	0.295
Spain	107	1,617	206	0.303	0.197	0.356	0.285

Cit: citations; N-Pub/Cit/TLS: normalized values (max: 1.000); OS: overall score (composite index); pub: publications; TLS: total link strength

Collaboration network analysis

The author co-authorship analysis applied a minimum threshold of one publication. The resulting network was distributed across 21 clusters, representing multiple interconnected research groups (**Figure 3**). Nilton Lincopan occupied the most prominent position, with eight publications, 37 links, and the highest TLS of 55. Other strongly connected authors included Fernanda Esposito (TLS=48), Herrison Fontana (TLS=40), Hung Nguyen-Viet (TLS=36), Ruichao Li (TLS=35), Muhammad Shoaib (TLS=31), Luísa Peixe (TLS=30), and Carla Novais (TLS=27). The network contained several identifiable collaboration groups connected through intermediate authors, alongside smaller clusters positioned more peripherally.

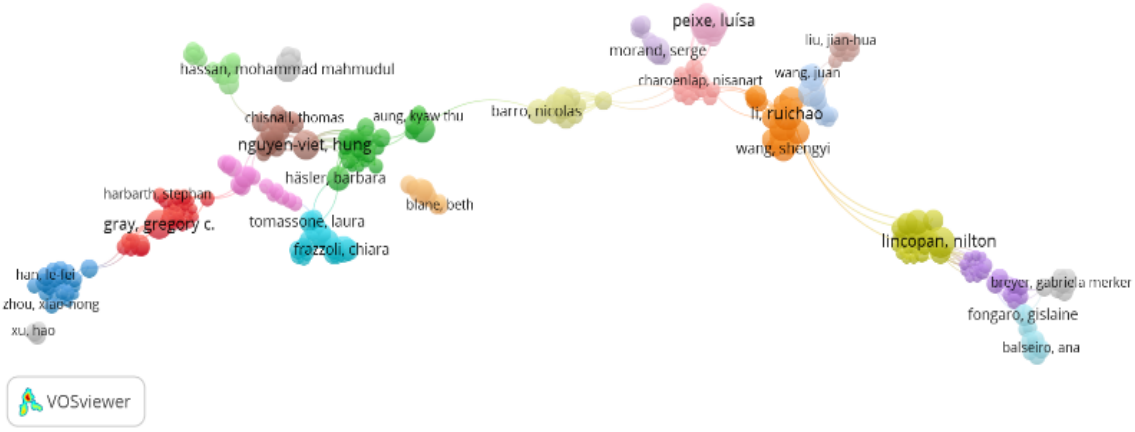


Figure 3. Author co-authorship network in research connecting One Health, environmental health, and agricultural health.

The country co-authorship analysis applied a minimum threshold of one publication and generated six collaboration clusters (**Figure 4**). The United States was the largest and most strongly connected node, with 353 publications, 77 links, and a TLS of 579. The United Kingdom recorded the highest number of links, with 82 connections, and ranked second in collaboration strength with a TLS of 565. Other countries with high TLS included France (TLS=284), Italy (TLS=272), Australia (TLS=233), Germany (TLS=229), Canada (TLS=221), China (TLS=220), Belgium (TLS=208), and Spain (TLS=206).

European countries formed a dense collaborative structure involving the United Kingdom, France, Italy, Germany, Spain, Portugal, Belgium, Denmark, and the Netherlands. The United States occupied a central position linking multiple regional groups, while China, Australia, Thailand, Japan, and other Asia-Pacific countries formed another closely connected segment. African countries, including Kenya, South Africa, Ethiopia, Nigeria, Uganda, Zambia, Ghana, and Burkina Faso, were also integrated into the broader international collaboration network.

Keyword co-occurrence and thematic clusters

The author-keyword co-occurrence analysis identified 10 thematic clusters representing the conceptual structure of research at the intersection of One Health, environmental health, and agricultural health (**Figure 5** and **Table 5**). One Health was the most frequently occurring and strongly connected keyword, with 942 occurrences and a TLS of 1,986. Other prominent keywords included antimicrobial resistance (373 occurrences; TLS=1,026), zoonoses (158; TLS=413), food safety (119; TLS=327), *Escherichia coli* (115; TLS=370), antibiotic resistance (82; TLS=195), and antimicrobial resistance genes (74; TLS=182).

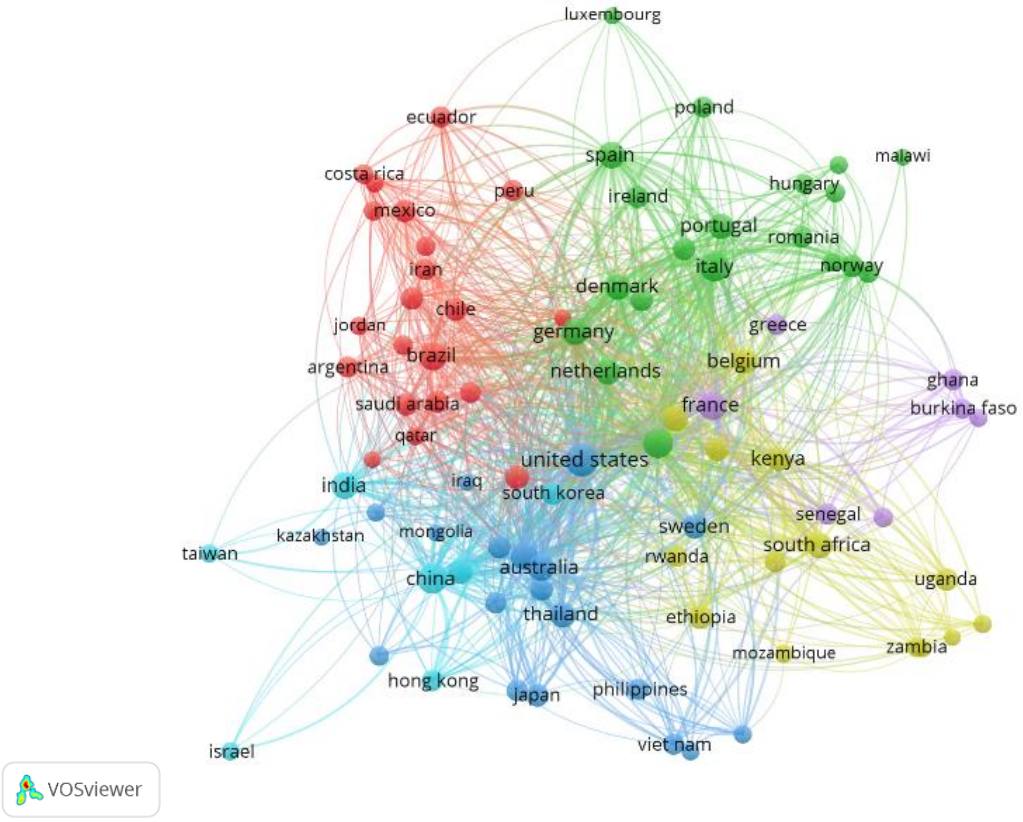


Figure 4. Country co-authorship network in research connecting One Health, environmental health, and agricultural health

The 10 clusters were grouped into three broad, interconnected domains. The first encompassed One Health governance, public health, zoonotic disease control, and zoonotic epidemiology (Clusters 1 and 3). The second covered sustainable agrifood systems, climate resilience, environmental exposure, ecological risk assessment, food safety, and environmental surveillance (Clusters 2, 5, and 6). The third focused on antimicrobial resistance and pathogen

transmission across food-animal production systems, including molecular epidemiology, genomic transmission, livestock management, and farm–environment interfaces (Clusters 4 and 7–9). Cluster 10 represented a smaller, specialized theme focused on disease surveillance and targeted control.

Antimicrobial resistance-related keywords were closely associated with antimicrobial resistance genes, antibiotic resistance, resistomes, metagenomics, whole-genome sequencing, mobile genetic elements, and *E. coli*. Zoonoses were linked to public health, animal health, governance, epidemiology, and prevention. Environmental and agricultural keywords—including environment, climate change, agriculture, food security, sustainability, aquaculture, pesticides, water quality, and soil health—formed overlapping connections across several clusters. The surveillance cluster occupied a comparatively peripheral position, with anthrax and phage therapy extending away from the denser central network.

Thematic map

The strategic positioning of the five thematic clusters is presented in **Figure 6**, whereas their constituent terms, Callon centrality, Callon density, cluster frequency, and thematic characteristics are presented in **Table 6**. The thematic map positions each cluster according to its relative centrality and internal density within the analyzed author-keyword network.

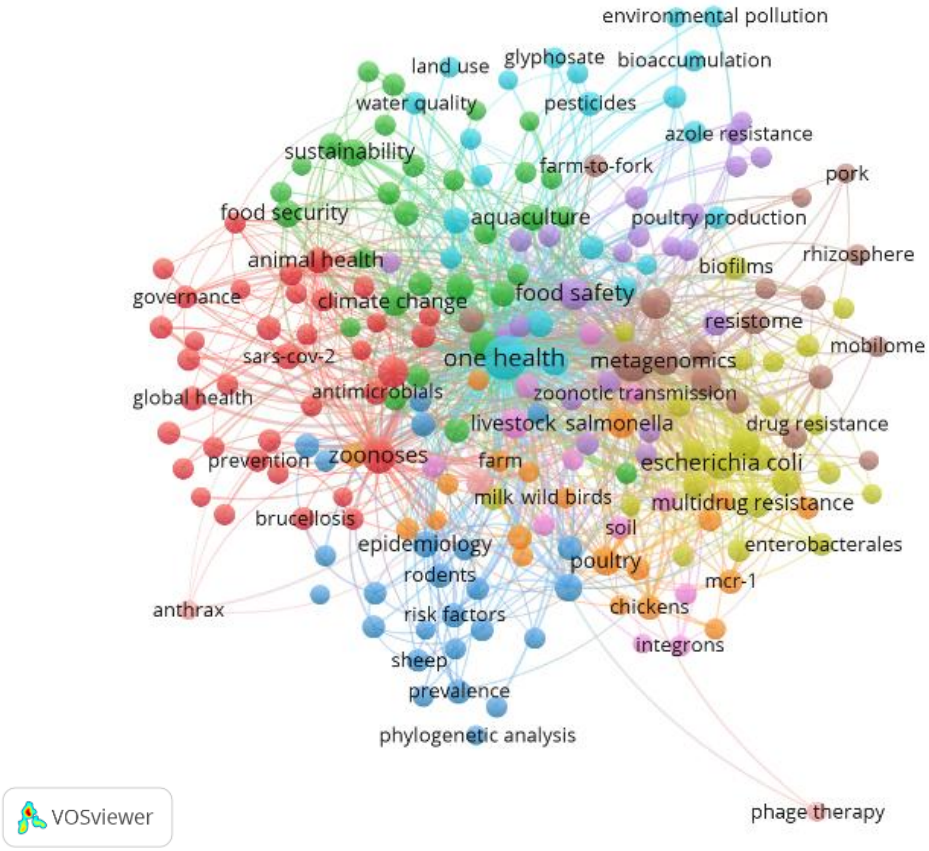


Figure 5. Author-keyword co-occurrence network in research connecting One Health, environmental health, and agricultural health.

The One Health cluster was the largest theme, with a cluster frequency of 1,820. It had the highest Callon centrality (0.402) and a Callon density of 8.566. The cluster was positioned near the boundary between the motor- and basic-theme quadrants, indicating comparatively strong connections with other themes and intermediate internal cohesion within the analyzed keyword network. Its constituent terms included zoonoses, food safety, public health, climate change, food security, surveillance, sustainability, animal health, and environmental health.

The antimicrobial resistance cluster was positioned within the basic-theme quadrant. It had a cluster frequency of 1,068, a Callon centrality of 0.378, and a Callon density of 8.009. The cluster was characterized by *E. coli*, whole-genome sequencing, multidrug resistance,

Salmonella, extended-spectrum beta-lactamase, poultry, antibiotics, virulence factors, and genomic surveillance. Its position reflected comparatively strong connections with other themes but lower internal cohesion than the themes located above the horizontal reference line.

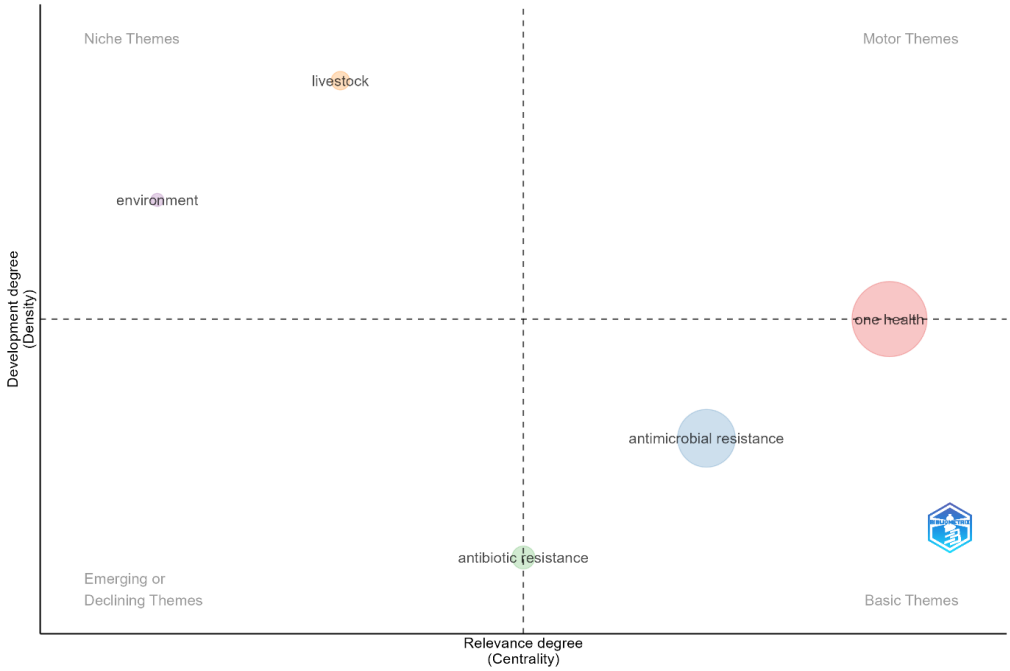


Figure 6. Thematic map of author keywords in research connecting One Health, environmental health, and agricultural health.

The antibiotic resistance cluster was located near the boundary between the emerging-or-declining and basic-theme quadrants. It had a cluster frequency of 365, a Callon centrality of 0.332, and the lowest Callon density among the five themes (5.789). Its constituent terms included antimicrobial resistance genes, aquaculture, metagenomics, wildlife, resistome, mobile genetic elements, microbiome, horizontal gene transfer, and farm-to-fork. This position indicated moderate connections with other themes and comparatively limited internal cohesion within the analyzed keyword network.

The environment and livestock clusters occupied the niche-theme quadrant. The environment cluster recorded a frequency of 269, a Callon centrality of 0.258, and a Callon density of 9.032. It connected agriculture, risk assessment, wastewater, food, antimicrobials, milk, pesticides, heavy metals, and surface water. The livestock cluster had a frequency of 318, a Callon centrality of 0.280, and the highest Callon density (9.554). It encompassed pigs, epidemiology, cattle, risk factors, prevalence, biosecurity, rodents, vector-borne diseases, soil, and farmers. The relatively high densities and lower centralities of these two clusters indicated strong internal cohesion but comparatively limited connections with other themes in the analyzed keyword network.

No cluster was located entirely within the motor-theme quadrant. These findings indicate that One Health occupied the most central strategic position, antimicrobial resistance represented a broad basic theme, antibiotic resistance occupied a low-density boundary position, and environment and livestock formed internally cohesive but comparatively specialized themes.

Thematic evolution analysis

The evolution of research themes across four periods: 2006–2019, 2020–2022, 2023–2024, and 2025–2026 is illustrated in **Figure 7**. During 2006–2019, the thematic structure was distributed across broad health domains and disease-specific topics, including food safety, animal health, One Health, vector-borne diseases, environment, livestock, Q fever, and *Salmonella*. Among these themes, One Health and livestock showed the clearest continuity into 2020–2022. The One Health theme retained 87 shared occurrences with its successor theme, with a weighted inclusion index of 0.66, whereas livestock maintained complete thematic continuity, with both weighted and unweighted inclusion indices of 1.00.

Table 5. Author-keyword co-occurrence clusters and thematic characterization

Cluster	Thematic label	Representative author keywords (occurrences)	Thematic characterization
1	One Health governance and zoonotic disease control	Zoonoses (158); public health (66); animal health (30); SARS-CoV-2 (23); antimicrobial use (17); global health (14)	Encompasses the governance and public-health dimensions of One Health, linking zoonotic disease prevention and control with animal health, antimicrobial use, veterinary public health, health systems, policy, and intersectoral collaboration.
2	Sustainable agrifood systems and climate resilience	Environment (62); climate change (49); food security (40); sustainability (32); agriculture (31); aquaculture (30)	Connects agriculture and aquaculture with climate change, food security, biodiversity, ecosystem health, animal welfare, food systems, and sustainable development, reflecting a broad socioecological orientation.
3	Zoonotic epidemiology and livestock-associated health risks	Pigs (34); epidemiology (25); risk factors (18); foodborne pathogens (17); rodents (15); leptospirosis (14)	Represents epidemiological investigation of zoonotic infections across livestock, wildlife, and production environments, with emphasis on prevalence, risk factors, serological surveillance, molecular detection, and outbreak investigation.
4	Molecular epidemiology of food-animal antimicrobial resistance	*Escherichia coli* (115); whole-genome sequencing (71); multidrug resistance (58); extended-spectrum beta-lactamase (55); virulence factors (22); *Staphylococcus aureus* (18)	Focuses on genomic and laboratory characterization of resistant and virulent bacteria associated with livestock, dairy farms, animal-derived foods, and food-production chains.
5	Food safety and environmental hazard surveillance	Food safety (119); wastewater (22); environmental surveillance (11); food-producing animals (9); mycotoxins (9); antifungal resistance (8)	Links food safety with wastewater and environmental surveillance, fungal and parasitic hazards, agricultural exposure, food-producing animals, fresh produce, irrigation water, and environmental contamination pathways.
6	One Health and environmental risk assessment	One Health (942); antibiotics (39); environmental health (28); risk assessment (26); microbiome (19); pesticides (17)	Connects One Health with environmental and chemical exposure, including antibiotics, pesticides, heavy metals, microplastics, pharmaceuticals, water quality, bioaccumulation, land use, and ecological risk assessment.
7	Poultry, livestock, and vector-associated pathogen transmission	Salmonella (57); poultry (47); cattle (20); chickens (19); vector-borne diseases (14); mcr-1 (14)	Covers pathogen transmission and antimicrobial resistance in poultry and livestock systems, including foodborne bacteria, colistin resistance, vectors, wildlife interfaces, and genomic surveillance.
8	Antimicrobial resistomes and genetic transmission	Antimicrobial resistance (373); antibiotic resistance (82); antimicrobial resistance genes (74); metagenomics (32); wildlife (29); resistome (25)	Represents the genomic and ecological organization of antimicrobial resistance through resistance genes, resistomes, metagenomics, plasmids, mobile genetic elements, horizontal gene transfer, wildlife, and environmental reservoirs.
9	Livestock management and farm–environment interfaces	Livestock (55); environmental contamination (16); soil (12); farmer (10); water (10); animal husbandry (8)	Links livestock management and farming practices with farmers, soil, water, environmental contamination, animal husbandry, microbial communities, and zoonotic transmission within farm environments.
10	Disease surveillance and targeted control	Surveillance (38); anthrax (5); phage therapy (5)	Constitutes a small, specialized cluster connecting infectious-disease surveillance with anthrax monitoring and bacteriophage-based control approaches.

Table 6. Strategic positioning and thematic composition of author-keyword clusters in research connecting One Health, environmental health, and agricultural health

Thematic cluster	Constituent terms	Callon centrality	Callon density	Cluster frequency	Strategic position	Thematic characterization
One Health	One Health; zoonoses; food safety; public health; climate change; food security; surveillance; sustainability; animal health; environmental health	0.402	8.566	1,820	Motor–basic boundary theme	The largest and most central theme, connecting zoonotic diseases and public health with food safety, climate change, sustainability, animal health, environmental health, governance, and intersectoral collaboration. Its boundary position indicates comparatively strong connections with other themes and intermediate internal cohesion within the analyzed keyword network.
Antimicrobial resistance	Antimicrobial resistance; *Escherichia coli*; whole-genome sequencing; multidrug resistance; Salmonella; extended-spectrum beta-lactamase; poultry; antibiotics; virulence factors; genomic surveillance	0.378	8.009	1,068	Basic theme	A broadly connected theme concerning antimicrobial resistance in food-animal and agricultural systems. It combines resistant bacterial pathogens with genomic characterization, poultry production, foodborne transmission, plasmids, and virulence. Its comparatively high centrality and lower density characterize it as a broadly connected basic theme with lower internal cohesion than the niche themes.
Antibiotic resistance	Antibiotic resistance; antimicrobial resistance genes; aquaculture; metagenomics; wildlife; resistome; mobile genetic elements; microbiome; horizontal gene transfer; farm-to-fork	0.332	5.789	365	Emerging/declining–basic boundary theme	A low-density theme linking antibiotic resistance with resistance genes, resistomes, metagenomics, aquaculture, wildlife, microbial communities, mobile genetic elements, and horizontal gene transfer. Its boundary position indicates moderate connections with other themes and comparatively limited internal cohesion.
Environment	Environment; agriculture; risk assessment; wastewater; food; antimicrobials; milk; pesticides; heavy metals; surface water	0.258	9.032	269	Niche theme	An internally cohesive theme addressing environmental pathways associated with agricultural production, wastewater, antimicrobials, pesticides, heavy metals, food, milk, and surface water. Its high density and lower centrality indicate strong internal relationships but comparatively limited connections with other themes in the analyzed keyword network.
Livestock	Livestock; pigs; epidemiology; cattle; risk factors; prevalence; biosecurity; rodents; vector-borne diseases; soil	0.280	9.554	318	Niche theme	The theme with the highest Callon density, focusing on livestock-associated epidemiology, disease prevalence, risk factors, biosecurity, vectors, rodents, soil, water, and farmers. Its high density and comparatively low centrality characterize it as an internally cohesive but relatively specialized theme within the analyzed keyword network.

During 2020–2022, the thematic structure became increasingly concentrated around One Health and livestock, accompanied by antimicrobial resistance, antibiotic resistance, antibiotics, antimicrobial stewardship, food systems, and polymerase chain reaction. The One Health theme maintained a strong evolutionary pathway into 2023–2024, retaining 188 shared occurrences and a weighted inclusion index of 0.65. Its continuity was supported by terms including zoonoses, public health, SARS-CoV-2, climate change, food security, sustainability, animal welfare, emerging infectious diseases, and intersectoral collaboration.

The 2023–2024 period exhibited greater thematic differentiation. Antimicrobial resistance, One Health, and *E. coli* formed the largest themes, while animal health, environment, wastewater, surveillance, water quality, and genotoxicity appeared as more specialized thematic structures. Antimicrobial resistance developed into organism-, environment-, and surveillance-related pathways, whereas the *E. coli* theme concentrated on antibiotic resistance genes, extended-spectrum beta-lactamase, multidrug resistance, whole-genome sequencing, plasmids, carbapenemases, and colistin resistance. Environmental research was also differentiated into environment, wastewater, water quality, and genotoxicity themes.

In 2025–2026, the thematic structure converged into six major themes: One Health, antimicrobial resistance, environment, zoonoses, antibiotic resistance, and antimicrobials. One Health remained the largest and most persistent theme, retaining 218 shared occurrences from the preceding period and a weighted inclusion index of 0.62.

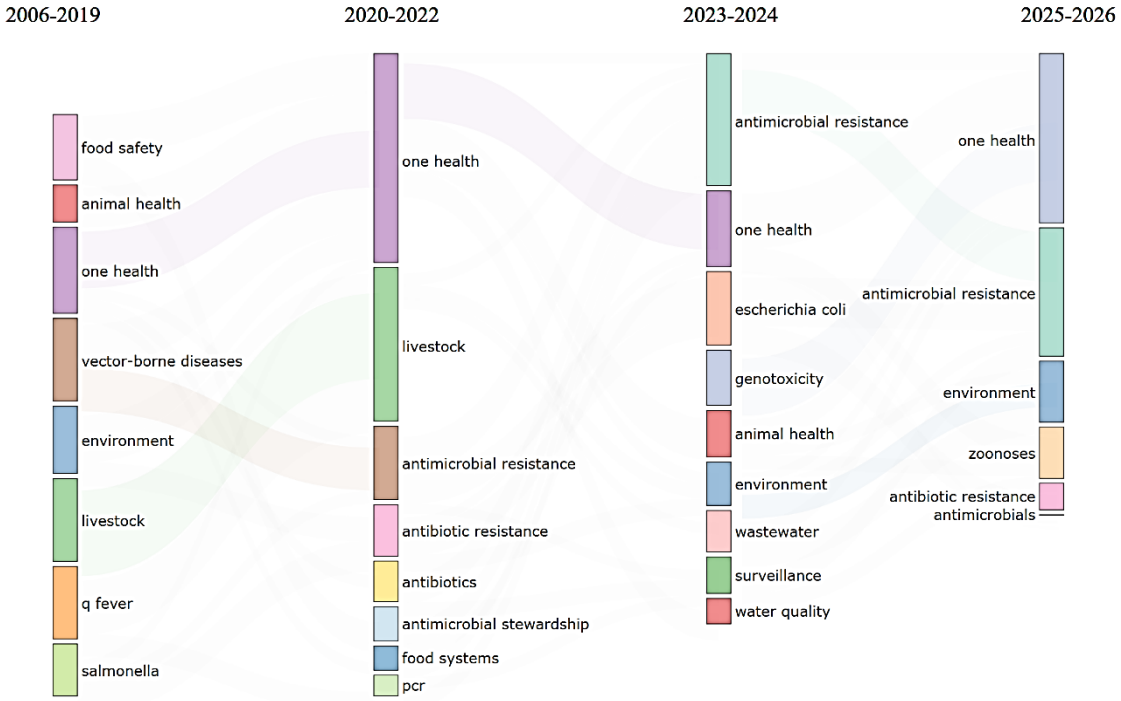


Figure 7. Thematic evolution of author keywords across four periods in research connecting One Health, environmental health, and agricultural health.

The pathway was sustained by One Health, climate change, sustainability, food security, microbiome, and SARS-CoV-2. Antimicrobial resistance also maintained substantial continuity, with 82 shared occurrences and a weighted inclusion index of 0.57, and received additional contributions from the preceding *E. coli* and surveillance themes.

The environment theme in 2025–2026 developed from several earlier themes, including environment, wastewater, animal health, antimicrobial resistance, and One Health. Its direct continuity from the 2023–2024 environment theme was represented by environment, surface water, and human health, while the wastewater pathway contributed wastewater, azole resistance, antifungal resistance, and *Aspergillus fumigatus*. Zoonoses re-emerged as a distinct theme through pathways originating from One Health, animal health, antimicrobial resistance, environment, and surveillance. Overall, the thematic evolution showed sustained continuity in One Health and antimicrobial resistance, increasing specialization during 2023–2024, and

subsequent convergence into broader One Health, resistance, environmental, and zoonotic themes during 2025–2026.

Bibliographic coupling and research frontiers

The document-level bibliographic-coupling analysis applied the predefined minimum threshold of 20 Scopus citations per document. Among the documents meeting this threshold, 276 were connected within the network and distributed across 15 clusters (**Figure 8**). The network exhibited a dense central structure accompanied by several smaller, more peripheral clusters. Koutsoumanis *et al.* (2021) [30] had the highest total link strength (TLS=149), followed by McEwen and Collignon (2018) [31] (TLS=137), Lopes *et al.* (2021) [32] (TLS=91), and Knight *et al.* (2017) [33] (TLS=68).

Clusters 1 and 2 represented broader conceptual and systems-oriented research fronts. Cluster 1 connected infectious-disease emergence, meat production, food systems, wildlife markets, and pandemic prevention. Cluster 2 addressed the ethical, social-ecological, and governance foundations of One Health, including disease-control interventions, ecosystem resilience, and prevention-oriented policy.

Clusters 3–9 formed the main antimicrobial resistance-related research fronts within the network. These clusters covered cross-sectoral antimicrobial resistance, resistant bacteria in agricultural soils, transmission through food and farm environments, aquatic resistomes, environmental surveillance, resistance governance, and antimicrobial use in plant agriculture. Cluster 3 was centered on One Health antimicrobial resistance across human, animal, food, wildlife, and environmental compartments. Cluster 4 focused more specifically on agricultural-soil resistomes, colistin resistance, livestock production, and farm-to-fork transmission. Clusters 5 and 6 addressed exposure pathways through food, water, livestock, aquaculture, wastewater, and agricultural effluents.

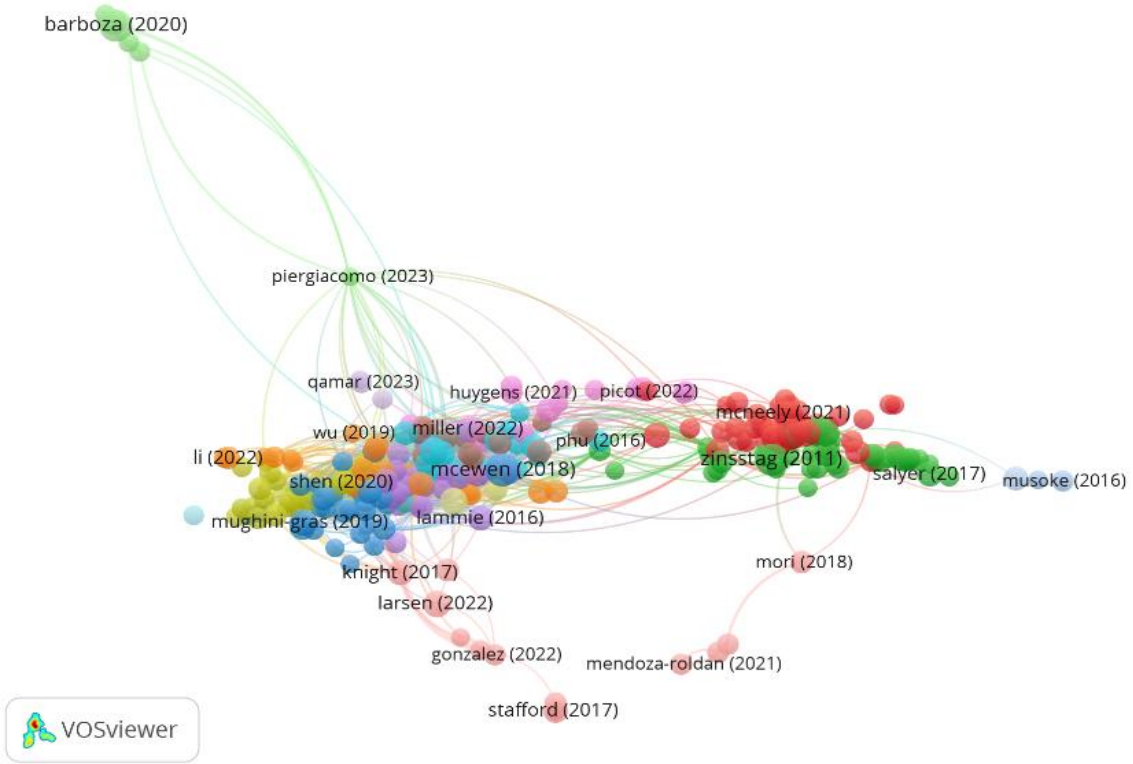


Figure 8. Document-level bibliographic-coupling network of publications with at least 20 Scopus citations. Node size represents accumulated citation counts, links represent shared cited references, and colors indicate bibliographic-coupling clusters.

Clusters 10–15 represented more specialized research fronts. Cluster 10 focused on cross-species pathogen evolution and transmission involving livestock, wildlife, soil, and wastewater. Cluster 11 addressed microplastics and xenobiotic contaminants across aquatic organisms, farm animals, food products, and human-exposure pathways. Cluster 12 connected environmental health, sentinel surveillance, and the operational application of One Health. Clusters 13–15 represented narrower research fronts concerning sociocultural drivers of antimicrobial use, resistance and food safety in livestock production, and resistant or zoonotic pathogens circulating across human, animal, and environmental compartments. The thematic characteristics and representative publications for each cluster are presented in **Table 7**.

Highly cited publications and intellectual contributions

The 10 most highly cited publications in the selected corpus are presented in **Table 8**, together with their principal intellectual contributions. Because the citation counts were not normalized by publication year, the ranking reflects cumulative citation influence and is affected by differences in citation windows. The most highly cited publication was McEwen and Collignon (2018) [31], with 968 citations. The article framed antimicrobial resistance as an interconnected One Health challenge involving antimicrobial use, resistant organisms, and resistance determinants across human, animal, agricultural, and environmental sectors. Zinsstag *et al.* (2011) [34] ranked second with 890 citations and established a systemic conceptual foundation by tracing the transition from One Medicine to One Health and linking human and animal health with social and ecological systems.

Discussion

The present study examined how environmental and agricultural health are represented and structurally positioned within a selected corpus of explicitly One Health-oriented publications. The combined evidence from publication performance, collaboration networks, keyword co-occurrence, thematic mapping, thematic evolution, bibliographic coupling, and highly cited publications reveals a rapidly expanding but structurally uneven body of literature within the analyzed corpus. Environmental and agricultural concerns are increasingly visible, yet their incorporation is concentrated around a limited set of established problems, most notably antimicrobial resistance (AMR), zoonotic diseases, food safety, and livestock-associated transmission. Within the selected corpus, AMR emerged as the most prominent intellectual bridge connecting research on humans, animals, food-production systems, wildlife, soil, water, and other environmental reservoirs. Conversely, plant health, soil ecological functions, integrated pest management (IPM), biological control, agricultural occupational health, and the preventive management of agroecosystems remain less central. These findings suggest that the growing recognition of human, animal, plant, and ecosystem health within One Health has not been accompanied by equally balanced thematic representation across these domains in the selected corpus [3,35,36].

The temporal pattern revealed a transition from a relatively small body of literature to rapidly expanding interdisciplinary research. Annual output remained limited during the formative period but increased markedly after 2020, reaching its highest complete-year level in 2025. This expansion coincided with increased attention to pandemic preparedness, AMR, environmental contamination, climate change, food-system vulnerability, biodiversity loss, and sustainability. The observed growth is consistent with the broader evolution of One Health from a framework primarily associated with comparative medicine and zoonotic-disease control toward a more comprehensive approach encompassing environmental sustainability, food-system resilience, climate-related risks, and multisectoral governance [3,34]. Nevertheless, the increase in publication output should not be interpreted as evidence of balanced thematic development, as research remained concentrated around established health threats rather than the full range of agricultural and ecological determinants of health. Alongside this expansion, collaboration patterns revealed a globally connected but geographically uneven research landscape.

Table 7. Bibliographic coupling clusters and associated research frontiers in One Health, environmental health, and agricultural health

Cluster	Research frontier	Representative documents	Main focus
1	Infectious-disease emergence, food systems, and animal production	Espinosa *et al.* (2020) [37]; Aiyar and Pingali (2020) [38]	Relationships among meat production, animal farming, wildlife contact, food-system vulnerability, pandemic risk, biodiversity loss, and proactive food-safety strategies.
2	One Health ethics, social-ecological systems, and preventive governance	Degeling *et al.* (2016) [39]; de Garine-Wichatitsky *et al.* (2021) [40]	Ethical evaluation of One Health interventions and management of health within resilient agricultural and natural social-ecological systems.
3	Cross-sectoral antimicrobial resistance and genomic epidemiology	McEwen and Collignon (2018) [31]; Aworh *et al.* (2021) [41]	Antimicrobial use and resistance across humans, livestock, poultry, wildlife, food, and environmental compartments, supported by molecular and genomic transmission evidence.
4	Agricultural-soil resistomes and livestock-associated resistance	Lopes *et al.* (2021) [32]; Furlan and Stehling (2021) [42]	Resistant *Escherichia coli*, resistance genes, virulence determinants, colistin resistance, and microbial-resistance circulation across agricultural and non-agricultural soils.
5	Food-to-human transmission and integrated exposure pathways	Antunes *et al.* (2020) [43]; Opatowski *et al.* (2021) [44]	Movement of resistant and pathogenic bacteria through food, water, livestock, humans, and household or community environments, including quantitative exposure modeling.
6	Environmental and aquatic dissemination of antimicrobial resistance	Koutsoumanis *et al.* (2021) [30]; Tian *et al.* (2024) [45]	Emergence and movement of antimicrobial-resistant bacteria, resistance genes, and resistomes through food chains, aquaculture, wastewater, surface water, and agricultural effluents.
7	Resistance management in food-animal production systems	Skandalis *et al.* (2021) [46]; Berman *et al.* (2023) [47]	Environmental spread of antimicrobial resistance and implementation of One Health-based policies, national action plans, biosecurity, and interventions in food-producing animals.
8	Environmental antimicrobial resistance surveillance and stewardship governance	Franklin *et al.* (2024) [48]; Li *et al.* (2024) [49]	Surveillance of antimicrobial resistance in freshwater and wildlife, environmental monitoring frameworks, water stewardship, and integration of environmental evidence into antimicrobial resistance governance.
9	Plant agriculture and nature-based environmental interventions	Miller *et al.* (2022) [50]; Borsetto *et al.* (2025) [51]	Antimicrobial use and resistance in plant agriculture, environmental pathways of resistance, and nature-based interventions for limiting pathogen and resistance-gene dispersal.
10	Cross-species pathogen evolution and environmental transmission	Knight *et al.* (2017) [33]; Larsen *et al.* (2022) [52]	Evolution and interspecies transmission of resistant pathogens across wildlife, livestock, humans, soils, animal-production materials, and wastewater environments.
11	Microplastics, xenobiotics, and food-chain exposure	Piergiacomo *et al.* (2023) [53]; Barboza *et al.* (2020) [54]	Interactions among microplastics, xenobiotic contaminants, antimicrobial resistance, aquatic-organism health, seafood safety, and human dietary exposure.
12	Environmental health and sentinel-based One Health surveillance	Rabinowitz *et al.* (2013) [55]; Musoke *et al.* (2016) [56]	Integration of environmental health into One Health and the use of human, animal, and environmental indicators for disease prediction, surveillance, and control.
13	Sociocultural drivers of antimicrobial use in livestock	Alhaji *et al.* (2019) [57]; Alhaji *et al.* (2018) [58]	Antimicrobial access, use, misuse, and associated public-health risks in dairy and pastoral livestock systems, with particular attention to social and behavioral drivers.
14	Livestock-associated resistance and food-safety risks	Lienen *et al.* (2021) [59]; Qamar *et al.* (2023) [60]	Livestock-associated resistant bacteria, antimicrobial-resistance genes, drug residues, farm exposure, animal-derived foods, and their implications for food safety.
15	Environmental reservoirs of resistant and zoonotic pathogens	Pot *et al.* (2021) [61]; Larsen *et al.* (2016) [62]	Resistant bacterial lineages and previously unrecognized zoonotic pathogens circulating across humans, wildlife, and environmental reservoirs.

Table 8. Publications with the highest accumulated citation counts and their principal intellectual contributions within the selected corpus

Author and year	Title	Source	Citations	Main contribution
McEwen and Collignon (2018) [31]	Antimicrobial resistance: A One Health perspective	Microbiology Spectrum	968	Framed antimicrobial resistance as an interconnected human–animal–environmental challenge. The article linked antimicrobial use in human medicine and animal agriculture with transmission of resistant organisms and environmental resistome expansion through industrial, residential, and farm waste, while emphasizing regulation, surveillance, stewardship, sanitation, biosecurity, and alternatives to antimicrobials.
Zinsstag *et al.* (2011) [34]	From “One Medicine” to “One Health” and systemic approaches to health and well-being	Preventive Veterinary Medicine	890	Traced the conceptual development from One Medicine to One Health and ecosystem-based approaches. The article advanced a systemic perspective integrating human and animal health with social, ecological, and institutional contexts and emphasized the need to overcome disciplinary silos through interdisciplinary and transdisciplinary approaches.
Barboza *et al.* (2020) [54]	Microplastics in wild fish from North East Atlantic Ocean and its potential for causing neurotoxic effects, lipid oxidative damage, and human health risks associated with ingestion exposure	Science of the Total Environment	827	Demonstrated the occurrence of microplastics in commercially important wild fish and associated their presence with neurotoxicity and oxidative damage. The study also estimated human exposure through fish consumption, connecting marine pollution, aquatic-animal health, food safety, and human health.
Adisasmito *et al.* (2022) [3]	One Health: A new definition for a sustainable and healthy future	PLOS Pathogens	769	Advanced a contemporary definition of One Health as an integrated and unifying approach for sustainably balancing and optimizing the health of humans, animals, plants, and ecosystems. The article broadened the framework beyond zoonotic diseases by explicitly incorporating ecological integrity, sustainability, and multisectoral action.
Clark *et al.* (2019) [63]	Multiple health and environmental impacts of foods	Proceedings of the National Academy of Sciences of the United States of America	710	Quantified associations between major food groups, human-health outcomes, and agriculturally driven environmental impacts. The study showed that foods associated with improved health generally had lower environmental burdens, whereas red and processed meats were associated with both greater disease risks and higher environmental impacts.

Author and year	Title	Source	Citations	Main contribution
Koutsoumanis *et al.* (2021) [30]	Role played by the environment in the emergence and spread of antimicrobial resistance (AMR) through the food chain	EFSA Journal	334	Assessed sources and transmission pathways of antimicrobial-resistant bacteria and resistance genes across plant production, terrestrial livestock, aquaculture, and post-harvest environments. The article identified manure, soil, irrigation water, surface water, feed, wildlife, and production environments as relevant pathways and emphasized hygiene, biosecurity, and food-safety management.
Mughini-Gras *et al.* (2019) [64]	Attributable sources of community-acquired carriage of *Escherichia coli* containing β-lactam antibiotic resistance genes: A population-based modeling study	The Lancet Planetary Health	256	Quantified the relative contributions of human transmission, food, companion animals, farm animals, freshwater, and wildlife to community carriage of ESBL- and AmpC-producing *Escherichia coli*. The study provided source-attribution evidence for resistance transmission across human, food, animal, and environmental compartments.
Larsen *et al.* (2022) [52]	Emergence of methicillin resistance predates the clinical use of antibiotics	Nature	248	Demonstrated that methicillin-resistant *Staphylococcus aureus* emerged in European hedgehogs before the clinical antibiotic era through co-evolution with antibiotic-producing dermatophytes. The findings linked wildlife, microbial ecology, livestock, and human health and showed that clinically relevant resistance can originate in natural ecosystems.
Espinosa *et al.* (2020) [37]	Infectious diseases and meat production	Environmental and Resource Economics	234	Examined how animal farming and meat consumption contribute to infectious-disease emergence and amplification through wildlife contact, intensive production, animal transport, biodiversity loss, water use, and climate change. The study also considered biosecurity, preparedness, economic incentives, and alternative food-production systems.
Miller *et al.* (2022) [50]	Antimicrobial use and resistance in plant agriculture: A One Health perspective	Agriculture	221	Extended One Health antimicrobial-resistance research into plant agriculture. The article connected bactericide, fungicide, and pesticide use with resistance among plant pathogens, environmental microorganisms, and zoonotic bacteria, while emphasizing horizontal gene transfer, cross-resistance, food security, sustainable crop production, and prudent antimicrobial use.

Note: Citation counts represent accumulated Scopus citations as of July 27, 2026, and were not normalized by publication year. The ranking is therefore affected by citation-window bias and should not be interpreted as an age-adjusted comparison of scientific influence.

The United States and the United Kingdom occupied leading positions in publication output, citation impact, and international collaboration, while European countries formed a particularly dense collaborative structure. China, Australia, Canada, Brazil, and several other countries also contributed substantially, although through different combinations of productivity, influence, and network connectivity. International organizations such as the Food and Agriculture Organization of the United Nations and the International Livestock Research Institute further demonstrate the importance of cross-border institutions in connecting public health, veterinary medicine, agricultural production, food systems, and environmental research. These patterns indicate that publication output, accumulated citations, and collaboration connectivity were concentrated among a relatively limited group of countries and institutions. However, these indicators represent different dimensions of bibliometric performance and should not be interpreted as direct measures of research quality, proportional contribution, or scientific leadership. The geographical distribution also reflects the structure of the selected, English-language, Scopus-indexed corpus and may underrepresent locally oriented or non-English scholarship.

Beyond publication and collaboration patterns, one of the most consistent patterns across the analytical components was the prominence of AMR within the selected corpus. AMR was among the most frequent and strongly connected author keywords, formed a broad basic theme in the thematic map, displayed continuity across the thematic-evolution periods, dominated several bibliographic-coupling clusters, and appeared prominently among the most highly cited publications. This convergence indicates that AMR served as a prominent cross-sectoral theme through which research on human health, animal health, agriculture, food systems, wildlife, and environmental health was connected within the analyzed literature.

The prominence of AMR reflects its capacity to connect antimicrobial use and resistance across human medicine, livestock production, food systems, wildlife, soil, water, wastewater, and other environmental compartments. Previous One Health research has similarly emphasized environmental transmission pathways, agricultural antimicrobial use, resistance genes, and cross-sectoral surveillance [4,30,31]. Within the selected corpus, these connections made AMR the clearest cross-sectoral research pathway. Nevertheless, its prominence should be interpreted in relation to the search strategy, which explicitly included antimicrobial, agricultural, and environmental terminology. The results therefore indicate thematic prominence within the analyzed literature rather than the universal dominance of AMR across the broader One Health field.

While AMR provided a prominent connection across sectors, the thematic map revealed differences in the relative positioning of environmental and livestock research. Both themes exhibited comparatively high Callon density but lower centrality, indicating strong internal cohesion alongside more limited connections with other themes in the analyzed keyword network. The environmental theme encompassed wastewater, antimicrobials, pesticides, heavy metals, food, milk, and surface water, whereas the livestock theme focused on epidemiology, disease prevalence, biosecurity, vectors, soil, water, and farmers. These positions characterize both themes as specialized bodies of research rather than demonstrating their absolute maturity or importance. Their comparatively limited centrality suggests that environmental and livestock research was not connected equally with all other thematic clusters in the selected corpus. This pattern supports greater attention to links among environmental exposures, livestock systems, plant health, soil functions, agricultural workers, and preventive agroecosystem management. However, thematic positioning should not be interpreted as direct evidence of integration or fragmentation in One Health practice.

Agricultural occupational health remained weakly represented within the selected corpus. Although farmers and agricultural settings appeared in the livestock and environmental themes, occupational exposure, pesticide-related risks, heat stress, injury, and worker-centered interventions did not form a prominent thematic cluster. This pattern suggests limited visibility within explicitly One Health-oriented publications rather than an absence of occupational-health research in the broader literature. Greater linkage between worker health, animal health, crop production, environmental exposure, and agroecosystem management could broaden the agricultural scope of future One Health research.

The thematic-evolution analysis provided further insight into how these research priorities changed over time. The literature shifted from relatively fragmented disease- and sector-specific topics during 2006–2019 toward broader One Health, resistance, environmental, and zoonotic themes. One Health and livestock demonstrated early thematic continuity, while AMR, antibiotic resistance, environmental surveillance, and genomic approaches became more differentiated during subsequent periods. In 2025–2026, several specialized streams converged into broader thematic clusters, although this most recent interval represents a partial publication period. These patterns indicate changes in keyword organization within the selected corpus and should not be interpreted as evidence that the wider field has achieved substantive cross-sectoral integration.

Consistent with these temporal changes, bibliographic-coupling analysis identified contemporary research fronts involving genomic epidemiology, agricultural-soil resistomes, food- and water-mediated transmission, environmental surveillance, plant agriculture, microplastics, and One Health governance. These fronts demonstrate increasing thematic breadth but remain largely organized around hazard detection, transmission, and control. Future research could strengthen connections with plant health, soil ecological functions, agricultural occupational health, biodiversity, integrated pest management, biological control, and preventive agroecosystem management.

Addressing these areas will require interdisciplinary studies that evaluate outcomes across multiple health and environmental domains rather than relying on One Health terminology alone. Potential interventions include antimicrobial-use reduction, manure and wastewater management, crop diversification, soil-health management, farm biosecurity, water stewardship, occupational protection, and ecologically based pest management. Evaluation frameworks could incorporate human and animal disease outcomes, crop health, worker exposure, soil and water quality, biodiversity, productivity, livelihood effects, and intervention costs. Such approaches would help establish whether cross-sectoral interventions produce measurable benefits across interconnected health and agricultural systems.

Achieving this level of integration will also require linked datasets, interoperable surveillance, cross-sectoral governance, and meaningful participation from agricultural, environmental, veterinary, public-health, and community stakeholders. These directions arise from the thematic gaps and network structures observed within the selected corpus and should be evaluated through empirical interdisciplinary research.

The present study combined bibliometric performance analysis, collaboration mapping, keyword co-occurrence, thematic mapping, thematic evolution, bibliographic coupling, and citation analysis. This multidimensional approach made it possible to distinguish publication growth from citation influence, assess the distribution of scientific contributions and collaboration patterns, evaluate the relevance and development of themes, trace temporal transformations, and identify contemporary research fronts.

Several limitations should be considered when interpreting the findings. First, the use of full counting may give greater influence to publications involving multiple authors, institutions, or countries because each participating entity receives full credit. Consequently, publication output and TLS should be interpreted as indicators of observed productivity and network connectivity within the selected corpus rather than as proportional measures of individual, institutional, or national research contribution. Second, the use of raw accumulated citation counts introduces a strong citation-window bias because older publications have had substantially more time to receive citations than recently published studies. Accordingly, the highly cited publication ranking represents accumulated citation influence as of July 27, 2026, rather than publication-year-normalized or age-adjusted scientific impact. The minimum threshold of 20 citations used for bibliographic coupling improved network interpretability but reduced the visibility of recent publications that had not yet accumulated sufficient citations. In addition, records from 2026 represent an incomplete publication year. Third, the intentionally restrictive search strategy represents an important source of selection bias. Requiring the simultaneous presence of explicit One Health, environmental, and agricultural terminology produced a focused corpus but may have excluded substantively relevant studies using different disciplinary language or not explicitly adopting the One Health label. This limitation is particularly important when interpreting the

relatively low visibility of plant health, integrated pest management, agricultural occupational health, agricultural economics, digital supply chains, and sustainability governance.

Research in these areas may align with One Health principles without explicitly identifying itself as One Health research. Consequently, the observed thematic gaps should be interpreted as characteristics of the retrieved literature and search terminology rather than evidence of the absence or limited importance of these subjects in broader interdisciplinary scholarship.

Conclusions

Within the selected corpus, publications explicitly connecting One Health, environmental health, and agricultural health increased substantially, particularly after 2020, although publication output, accumulated citations, and collaboration connectivity remained concentrated among a limited group of countries and institutions. AMR was the most prominent cross-sectoral theme, while environment and livestock formed internally cohesive but comparatively specialized thematic clusters. The analyzed literature evolved from relatively fragmented disease- and sector-specific topics toward broader One Health, resistance, environmental, and zoonotic themes. Bibliographic coupling further identified research fronts involving genomic epidemiology, agricultural-soil resistomes, food- and water-mediated transmission, environmental surveillance, plant agriculture, microplastics, and One Health governance. These findings indicate increasing visibility but uneven representation and connectivity of environmental and agricultural themes within the analyzed corpus. Future research should strengthen thematic and methodological connections with plant health, soil ecological functions, integrated pest management, agricultural-worker health, biodiversity, and preventive agroecosystem management through broader collaboration, interoperable surveillance, and multidomain outcome assessment.

Acknowledgment

None.

Competing interests

All the authors declare that there are no conflicts of interest.

Funding

This study received no external funding.

Underlying data

Derived data supporting the findings of this study are available from the corresponding author on request.

Declaration of artificial intelligence use

Microsoft Copilot was used during manuscript preparation to support language refinement, improve clarity and readability, and assist with the organization of selected sections. All AI-assisted suggestions were critically reviewed, revised, and verified by the authors. The AI tool was not used for data collection, bibliometric analysis, visualization, or final scientific decision-making. The final content and interpretations are solely the responsibility of the authors.

How to cite

Fazli QS, Idroes GM, Delya MI, *et al*. Mapping environmental and agricultural health within One Health research: A bibliometric and science-mapping analysis. Narra Rev 2026; 2 (3): e40 - http://doi.org/10.52225/narrarev.v2i3.40.

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