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RESEARCH ARTICLE

Zoonoses research in veterinary epidemiology from 1956 to 2024: A bibliometric and network analysis of global trends, research collaboration, and the shift toward molecular and genomic approaches

Imron Rosyadi[1], Ahmad Kusumaatmaja[2], Wahyu Aristyaning Putri[3], Woro Anindito Sri Tunjung[3], Hanif Khoirudin[4], Annisa Salma Rosy Audina[1] and Muhammad Salman Al Farisi[5]

1. Department of Veterinary Clinical Pathology, Faculty of Veterinary Medicine, Universitas Gadjah Mada, Yogyakarta, Indonesia.
2. Department of Physics, Faculty of Mathematics and Natural Sciences, Universitas Gadjah Mada, Sekip Utara, BLS 21, Yogyakarta 55281, Indonesia.
3. Department of Tropical Biology, Faculty of Biology, Universitas Gadjah Mada, Yogyakarta 55281, Indonesia.
4. Fumalife, Sendowo, Sinduadi, Mlati, Sleman, Special Region of Yogyakarta 55281, Indonesia.
5. Graduate School of Life Science and Systems Engineering, Kyushu Institute of Technology, Kitakyushu 808-0196, Japan.

ABSTRACT

Background and Aim: Zoonotic diseases pose substantial threats to global public health, emphasizing the importance of veterinary epidemiology in surveillance and prevention. However, the growth, geographic distribution, collaborative networks, and thematic evolution of zoonoses research remain insufficiently characterized. This study aimed to map the bibliometric landscape of zoonoses research in veterinary epidemiology from 1956 to 2024, with particular emphasis on the transition toward molecular and genomic approaches.

Materials and Methods: A bibliometric analysis was conducted using 1,867 Scopus-indexed documents published between 1956 and 2024 and retrieved on February 14, 2026. Publication trends, citation performance, geographic contributions, institutional productivity, and international collaboration were evaluated. Co-authorship and keyword co-occurrence networks were constructed using VOSviewer with association-strength normalization. Temporal overlay visualization and comparative keyword-frequency analysis were used to identify emerging research themes and quantify changes in molecular, genomic, and serological research emphasis.

Results: Annual publication output increased at a compound annual growth rate of 14.4% during 2000–2024 (R^2 = 0.88), reaching 329 documents in 2024. Research articles accounted for 77.8% of publications, while English-language documents represented 94.2%. The United States contributed the most publications (400; 21.4%), followed by Brazil (196; 10.5%) and the United Kingdom (193; 10.3%). Internationally co-authored publications represented 38.2% of records with usable affiliation data. The corpus accumulated 54,734 citations, with an h-index of 109. Keyword network analysis identified five thematic clusters spanning epidemiology, public health, serological surveillance, molecular genetics, and companion-animal research. The proportion of publications containing molecular or genomic keywords increased significantly from 50.5% in 2005–2014 to 70.2% in 2015–2024 ($p < 0.001$), indicating a measurable shift in research emphasis.

Conclusion: Zoonoses research in veterinary epidemiology has expanded substantially, accompanied by increasing molecular and genomic emphasis and growing international collaboration. Nevertheless, geographic disparities persist. Strengthening genomic surveillance capacity, interdisciplinary One Health research, and equitable partnerships with endemic regions may improve future zoonotic disease surveillance and control. These findings reflect bibliometric trends rather than verified changes in laboratory practices.

Keywords: bibliometric analysis, genomic surveillance, international research collaboration, molecular epidemiology, One Health, research trends, veterinary epidemiology, zoonotic diseases.

INTRODUCTION

Zoonotic diseases, defined as infections naturally transmissible between vertebrate animals and humans, remain among the most persistent and consequential challenges to global public health. Current estimates

Corresponding Author: Imron Rosyadi
E-mail: imron.rosyadi@ugm.ac.id

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Co-authors: AK: ahmad_k@ugm.ac.id; WAP: wahyuaristyaningputri@ugm.ac.id; WAST: wanindito@ugm.ac.id; HK: hanif_k@ugm.ac.id; ASRA: annisa.salma.r@mail.ugm.ac.id; MSAF: alfarisi-m788@m.kyutech.ac.jp

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indicate that approximately 60% of recognized human infectious diseases and up to 75% of emerging infectious diseases are zoonotic in origin, collectively accounting for an estimated 2.5 billion human illnesses and 2.7 million deaths annually [1, 2]. This burden is disproportionately distributed, with endemic zoonoses, including bovine tuberculosis, brucellosis, leptospirosis, and cysticercosis, contributing substantially to morbidity and mortality in low- and middle-income countries, where livestock dependence and close human–animal interactions are common. Comparative investigations of mammalian host–pathogen relationships have identified ecological determinants influencing zoonotic emergence [3], while domestic animals serve as important reservoirs for several viral zoonoses of veterinary and public health significance [4]. The interconnected medical, veterinary, ecological, and economic consequences of zoonotic diseases necessitate multidisciplinary approaches, positioning veterinary epidemiology as a fundamental component of surveillance, prevention, and control strategies.

The 21st century has demonstrated the capacity of zoonotic pathogens to trigger major public health emergencies. Outbreaks involving severe acute respiratory syndrome coronavirus (SARS-CoV) in 2003, highly pathogenic avian influenza A(H5N1), Middle East respiratory syndrome coronavirus (MERS-CoV), Ebola virus disease in West Africa, and coronavirus disease 2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), have highlighted the importance of the human–animal interface in infectious disease emergence [5, 6]. These events illustrate how pathogens maintained in wildlife or livestock reservoirs may cross species barriers through spillover events, subsequently spreading under favorable ecological, socioeconomic, and environmental conditions. Globalization, international trade, population mobility, and urbanization can further facilitate pathogen dissemination. Understanding the mechanisms underlying pathogen maintenance, interspecies transmission, and disease emergence is therefore essential for effective zoonotic disease prevention. Veterinary epidemiology plays a particularly important role because surveillance and interventions targeting animal reservoirs can provide opportunities for early detection and disease control.

Veterinary epidemiology contributes to zoonotic disease prevention through several complementary approaches. Cross-sectional and longitudinal serological surveys quantify infection frequency and distribution in animal populations, while epidemiological investigations identify risk factors associated with pathogen maintenance and transmission, including husbandry practices, host demographics, environmental exposure, and vector ecology. Furthermore, veterinary epidemiological studies evaluate the effectiveness of preventive interventions, such as vaccination, animal movement restrictions, and test-and-slaughter programs. Surveillance of animal populations can facilitate the identification of emerging pathogens before or shortly after transmission to humans. The importance of animal-based surveillance was demonstrated during the COVID-19 pandemic, when genomic investigations of farmed mink identified bidirectional SARS-CoV-2 transmission between humans and animals and the establishment of an additional animal reservoir [7]. These observations emphasize that effective zoonotic disease control requires coordinated surveillance of both human and animal populations.

The One Health framework provides a conceptual foundation for integrating human, animal, and environmental health into coordinated disease prevention and control strategies [8, 9]. This approach recognizes that zoonotic disease emergence is influenced by interconnected ecological, biological, and socioeconomic factors. Land-use changes, deforestation, agricultural intensification, wildlife trade, climate change, and antimicrobial use can modify interactions among humans, animals, and their environments, potentially increasing opportunities for pathogen transmission. Consequently, interventions targeting individual sectors may be insufficient to address the complex determinants of zoonotic disease emergence. Previous investigations have demonstrated the value of integrated surveillance systems that combine human, animal, and environmental health information to improve outbreak detection and epidemiological risk assessment [10, 11]. The increasing adoption of One Health principles has also encouraged veterinary epidemiological research to incorporate molecular, ecological, and socioeconomic information into multidisciplinary investigations.

Alongside these conceptual developments, advances in molecular technologies have substantially expanded the analytical capabilities of veterinary epidemiology. Traditionally, zoonotic disease investigations relied primarily on serological surveys and phenotypic characterization of pathogens to estimate infection prevalence, assess exposure, and identify potential reservoirs. Although these approaches remain essential, they provide limited resolution for investigating genetic diversity and complex transmission relationships. Molecular techniques, including polymerase chain reaction (PCR), multilocus sequence typing, whole-genome sequencing, and metagenomics, have improved pathogen identification, genetic characterization, and the investigation of transmission pathways. For example, Feng and Xiao [12] demonstrated the importance of molecular genotyping

in distinguishing host-associated assemblages of *Giardia* species and evaluating their zoonotic potential. Similarly, molecular investigations have advanced the understanding of *Cryptosporidium* species [13], *Coxiella burnetii* [14], and *Anaplasma phagocytophilum* [15]. These developments illustrate the increasing contribution of molecular and genomic approaches to veterinary epidemiology, complementing conventional serological and descriptive methods and supporting more detailed investigations of pathogen diversity and transmission.

Despite increasing scientific attention to zoonotic diseases and the growing adoption of One Health approaches, the overall structure and evolution of zoonoses research within veterinary epidemiology remain insufficiently characterized. The expanding volume of publications, increasing methodological diversity, and development of international research collaborations have made it difficult to evaluate the field comprehensively through conventional narrative reviews. Although bibliometric investigations have examined broader One Health research [11] and individual zoonotic pathogens, a focused quantitative assessment of the intersection between zoonoses and veterinary epidemiology remains limited. Consequently, the historical development, geographic distribution, institutional contributions, collaborative relationships, and thematic organization of this specific research domain have not been systematically characterized within a unified analytical framework.

An important unresolved question concerns whether the increasing application of molecular and genomic technologies has produced a measurable change in the thematic emphasis of published veterinary epidemiological research. Although molecular diagnostics, genetic characterization, and genomic surveillance have become increasingly prominent, the extent to which molecular and genomic terminology has gained importance relative to conventional serological approaches requires quantitative assessment. Similarly, the development of international co-authorship networks and the participation of institutions from regions with substantial endemic zoonotic disease burdens remain incompletely understood. Identifying geographic disparities and changes in research collaboration is particularly important because the distribution of scientific output may not correspond to the geographic distribution of zoonotic disease burdens.

A further limitation of existing research mapping is the tendency to examine either the broader One Health literature, which includes extensive human clinical and policy-oriented research, or individual zoonotic diseases, which cannot adequately represent the thematic diversity of veterinary epidemiology. A focused bibliometric investigation is therefore needed to characterize publication growth, research productivity, citation influence, international collaboration, and emerging scientific themes within the veterinary epidemiological literature. Such an investigation can provide evidence for identifying underrepresented research areas, evaluating changes in scientific priorities, and informing future research investment and collaborative initiatives.

However, bibliometric findings must be interpreted within the boundaries of the selected database and search strategy. The use of Scopus-indexed records containing the specified zoonoses, veterinary, and epidemiology search terms may exclude relevant studies employing alternative terminology or indexed exclusively in other databases. Accordingly, the resulting patterns represent the literature retrieved through the defined search strategy rather than the entirety of worldwide zoonoses research.

This study aimed to comprehensively characterize the historical development, research productivity, geographic distribution, collaborative networks, citation impact, and thematic evolution of zoonoses research within veterinary epidemiology through a bibliometric and network analysis of 1,867 Scopus-indexed documents published between 1956 and 2024.

Specifically, the study sought to quantify annual publication trends, identify periods of accelerated research growth, and characterize the distribution of publications by document type, source, language, and subject area. It further aimed to identify the leading contributing countries, institutions, journals, and authors; evaluate citation performance; and examine the structure of international research collaboration through co-authorship network analysis. Keyword co-occurrence mapping and temporal overlay visualization were used to identify major thematic clusters, characterize their relationships, and investigate changes in research emphasis over time.

Particular attention was given to quantifying the relative prevalence of molecular and genomic terminology compared with conventional serological terminology across two periods, 2005–2014 and 2015–2024. This comparison was intended to determine whether the increasing prominence of molecular and genomic approaches could be demonstrated quantitatively within the retrieved literature. The study also examined the geographic concentration and diversification of research contributions to identify potential disparities in scientific participation and opportunities for international collaboration.

The study hypothesized that zoonoses research within veterinary epidemiology had experienced sustained publication growth, increasing emphasis on molecular and genomic research, and gradual geographic diversify-

cation beyond established North American and European research centers. By integrating descriptive bibliometric indicators with collaboration and thematic network analyses, the study sought to provide a reproducible assessment of the field's development and identify research priorities relevant to zoonotic disease surveillance, One Health integration, and international capacity building. The findings are intended to support evidence-informed research planning while recognizing that changes in bibliometric terminology do not necessarily demonstrate corresponding changes in laboratory practices or the operational implementation of surveillance systems.

MATERIALS AND METHODS

Ethical approval

This study was based exclusively on the analysis of previously published bibliographic records retrieved from the Scopus database. It did not involve experimental animals, human participants, biological samples, clinical interventions, or the collection of identifiable personal data. Therefore, ethical approval from an institutional ethics committee and informed consent were not required. The study used bibliographic metadata for quantitative assessment of scientific publications, research productivity, citation patterns, collaboration networks, and thematic development. The research procedures were designed to support transparency, methodological consistency, and reproducibility in bibliometric analysis.

Study period and location

The bibliometric analysis covered scientific publications indexed in Scopus from 1956 through December 31, 2024. Bibliographic records were retrieved and exported on February 14, 2026. The analysis was conducted using electronic bibliographic data, without geographical restrictions on the countries or institutions represented in the retrieved publications. To assess the reproducibility of the search strategy, the identical search was repeated on September 16, 2026, with the publication period restricted to years before 2025. The original dataset, retrieved on February 14, 2026, was retained for all analyses to ensure consistency in publication counts, citation indicators, and network construction.

Study design

This study employed a retrospective, descriptive, and quantitative bibliometric design to characterize the development of zoonoses research within veterinary epidemiology. Bibliometric methods were used to examine publication growth, research productivity, citation performance, geographic contributions, institutional participation, international collaboration, and thematic evolution. The analytical framework combined descriptive statistics, co-authorship network analysis, keyword co-occurrence mapping, temporal overlay visualization, and comparative keyword-frequency analysis.

The sampling frame comprised publications indexed in Scopus between 1956 and 2024 that satisfied the predefined search criteria. All eligible records were included without random sampling. The final analytical dataset consisted of 1,867 publications. No experimental allocation, intervention groups, or blinding procedures were applicable because the study analyzed existing bibliographic records. The primary units of analysis were publications, authors, institutions, countries, citations, and keywords. Comparative analyses were conducted to evaluate changes in molecular/genomic and serological research terminology between 2005–2014 and 2015–2024. Descriptive and network-based analytical methods were applied to identify publication trends, collaboration patterns, and emerging research themes.

Data source and search strategy

Scopus (Elsevier) was selected as the sole bibliographic database because of its broad coverage of peer-reviewed publications across biomedical, veterinary, and life sciences and its structured bibliographic metadata, which support quantitative analysis and network construction. Scopus provides standardized information on authors, institutional affiliations, publication sources, citation counts, and keywords. Using a single database also minimized potential inconsistencies associated with merging records from multiple bibliographic sources, although publications indexed exclusively in other databases were not captured.

The search strategy combined three terms, "zoonoses," "veterinary," and "epidemiology," using the Boolean operator AND to identify publications relevant to zoonotic diseases and veterinary epidemiology. The search covered publications from 1956 through 2024. No restrictions were applied to document type, source type, publication stage, or language during retrieval, allowing the composition of the retrieved literature to be assessed comprehensively.

The search was performed using the Scopus Advanced Search interface with the following field-tagged query:

TITLE-ABS-KEY(zoonoses AND veterinary AND epidemiology)

This query searched the title, abstract, and keyword fields for the three specified terms. The complete dataset was exported on February 14, 2026, yielding 1,867 documents, all of which were retained for analysis. The search terms were combined as separate Boolean conditions rather than as the exact phrase "veterinary epidemiology."

When the identical search was repeated on September 16, 2026, with publication years restricted to before 2025, Scopus returned 1,914 records. The difference between the original and repeated searches was consistent with the continuous updating of Scopus records and indexing coverage. Consequently, the original dataset of 1,867 documents was maintained as the fixed analytical corpus, while the repeated search result was recorded to facilitate independent verification of the retrieval strategy.

Inclusion and exclusion criteria

Publications were eligible for inclusion if they were indexed in Scopus between 1956 and 2024, satisfied the specified Boolean search criteria, and contained the bibliographic metadata necessary for analysis, including authorship, institutional affiliations, publication year, source information, and keywords. The simultaneous occurrence of the terms "zoonoses," "veterinary," and "epidemiology" within the searched fields was used to operationally define relevance to the intersection of zoonotic disease research and veterinary epidemiology.

Publications were excluded only when essential bibliographic metadata were unavailable. No records met this exclusion criterion, and no duplicate records were identified in the retrieved dataset. Therefore, all 1,867 records were included in the final analysis. The publication selection process is illustrated in Figure 1.

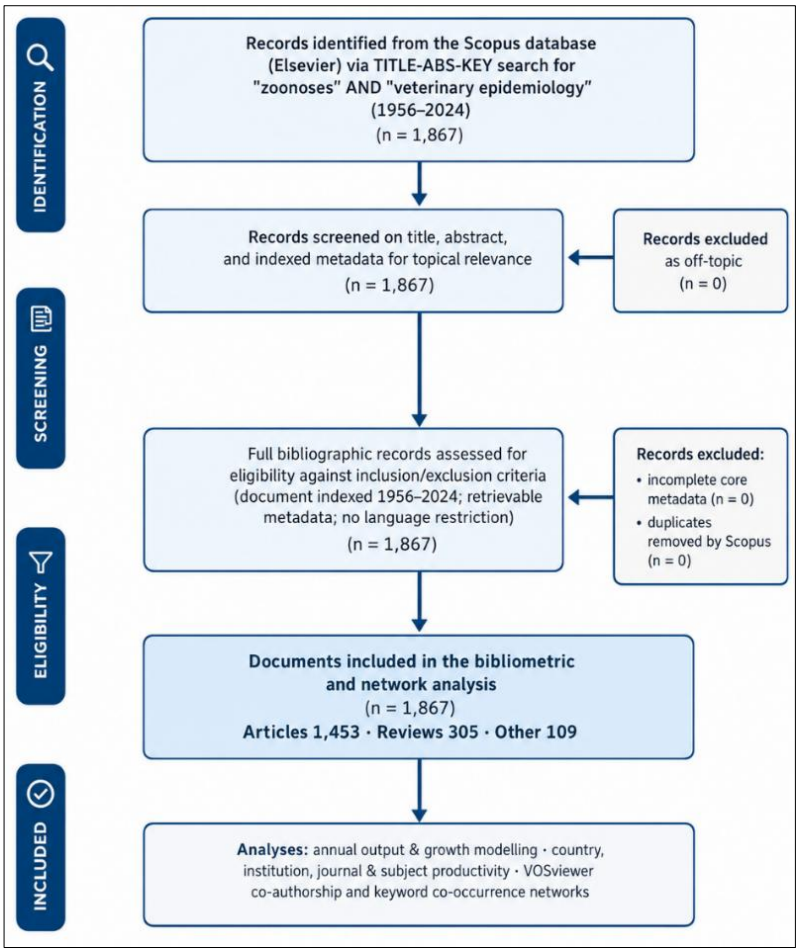


Figure 1: Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA)-style flow diagram illustrating document identification, screening, eligibility assessment, and inclusion in the bibliometric analysis. A single Scopus search using the field-tagged query TITLE-ABS-KEY(zoonoses AND veterinary AND epidemiology) retrieved 1,867 records. The Boolean search criteria established the operational definition of topical relevance. No duplicate records or records with missing essential bibliographic metadata were identified. Consequently, all 1,867 retrieved documents were included in the final analysis.

Data extraction and management

Complete bibliographic records were exported from Scopus in comma-separated values (CSV) format. Extracted variables included author names and identifiers, publication titles, publication years, journal or source titles, volumes, issues, citation counts, institutional affiliations, author keywords, indexed keywords, publication languages, and document types.

The exported records were examined for completeness and internal consistency before analysis. Descriptive indicators, including annual publication output, document type, source type, language distribution, and the productivity of countries, institutions, journals, and subject areas, were calculated directly from the extracted metadata.

Country-level publication counts were calculated using the total analytical corpus of 1,867 documents as the denominator. Because publications could include authors affiliated with institutions in multiple countries, individual publications could contribute to more than one country's output. Consequently, country-level counts represented research participation rather than mutually exclusive publication categories, and the sum of country contributions could exceed the total number of unique publications.

Author and institutional names were standardized using Scopus author and affiliation identifiers to reduce inconsistencies caused by alternative spellings, name variants, and homonymous authors. Remaining discrepancies were harmonized manually. For keyword analysis, a VOSviewer thesaurus file was used to standardize synonymous expressions and spelling variations, including American and British spelling differences, singular and plural forms, and alternative hyphenation. These procedures reduced fragmentation of equivalent terms across keyword co-occurrence networks. All descriptive analyses were performed using the harmonized bibliographic metadata.

Classification of molecular/genomic and serological keywords

Keywords were assigned to predefined molecular/genomic and serological categories to evaluate changes in research emphasis over time. The molecular/genomic category included genetics, molecular epidemiology, phylogeny, sequence analysis, genotype, PCR, deoxyribonucleic acid (DNA), whole-genome sequencing, genome, and sequencing.

The serological category included seroprevalence, seroepidemiology, serology, antibody, antibodies, and enzyme-linked immunosorbent assay. Terms considered ambiguous or insufficiently specific to either methodological category, including "isolation and purification," "classification," and "microbiology," were excluded from the comparative classification to avoid artificially increasing the estimated prevalence of molecular/genomic terminology. However, these terms were retained in the descriptive keyword co-occurrence analysis.

The two categories were not mutually exclusive. Publications containing both molecular/genomic and serological keywords contributed to both categories. Keyword classification involved researcher judgment; therefore, the complete keyword lists, excluded ambiguous terms, and VOSviewer thesaurus file were made available as Supplementary Material (DOI: 10.5281/zenodo.22885549) to facilitate independent evaluation and reproducibility.

Bibliometric indicators

Research productivity was assessed using annual publication counts, which were examined to characterize long-term growth patterns and identify periods of accelerated publication activity. Citation performance was evaluated using total citation counts, mean and median citations per publication, and the h-index of the retrieved corpus. The ten most-cited publications were identified to characterize influential contributions to the field.

Geographic and institutional research productivity was evaluated using publication counts associated with individual countries and institutions. Journal productivity and disciplinary distribution were assessed using publication source information and subject area classifications assigned by Scopus.

Citation indicators were calculated using citation counts recorded at the time of the original data export. Because citation accumulation depends partly on publication age, older documents generally have greater opportunities to receive citations. Accordingly, citation-based rankings were interpreted with consideration of this temporal bias.

Network construction and visualization

Co-authorship and keyword co-occurrence networks were constructed and visualized using VOSviewer version 1.6.20 (Center for Science and Technology Studies, Leiden University, Leiden, the Netherlands). VOSviewer

generates network maps in which the spatial proximity of nodes represents the strength of their relationships. Association-strength normalization was applied to quantify relationships between network items, and the software's clustering algorithm was used to identify groups of closely connected items.

For the country co-authorship network, a minimum threshold of five publications per country was applied, yielding 80 eligible countries. For the author co-authorship network, a minimum of five publications per author identified 60 eligible authors, of whom 29 were connected under the reported network criteria. For the keyword co-occurrence network, a minimum threshold of 100 occurrences per term yielded 94 eligible keywords.

In the network visualizations, node size represented the number of publications or keyword occurrences, depending on the analysis. Link thickness represented relationship strength, while node color indicated cluster membership. These visual characteristics were used to examine research collaboration patterns and thematic relationships.

Temporal overlay visualizations were generated to characterize changes in collaboration and keyword emphasis over time. In these maps, node color represented the average publication year associated with each item rather than its cluster membership. Cooler colors indicated earlier average publication years, whereas warmer colors represented more recent research activity. Comparing cluster and temporal overlay maps enabled the structural and chronological characteristics of the networks to be examined jointly.

Network normalization and clustering

Network relatedness was calculated using association-strength normalization:

$$s_{ij} = c_{ij}/(w_i w_j)$$

where s_{ij} represents the normalized association-strength between items i and j, c_{ij} denotes the number of co-occurrences or co-authored publications involving the two items, and w_i and w_j represent their respective total occurrence weights.

Clusters were identified using VOSviewer's smart-local-moving modularity algorithm, with the resolution parameter set to 1.00 and the minimum cluster size set to 1. Node weights represented publication counts in co-authorship networks and occurrence frequencies in keyword networks. Link strength represented the number of co-occurrences or co-authored documents, while total link strength was calculated as the sum of the link strengths associated with each node.

The reported modularity values (Q) were 0.115 for the keyword co-occurrence network (94 nodes and five clusters), 0.409 for the country co-authorship network (83 nodes and five clusters), and 0.766 for the author co-authorship network (50 connected nodes and 12 clusters).

The relatively low modularity of the keyword network was associated with its high edge density (99.6%), indicating extensive connectivity among frequently occurring terms. In contrast, the country and author networks exhibited greater modularity, indicating more distinct collaborative groupings. These findings were interpreted in relation to the structural characteristics of each network.

The modularity calculations were independently replicated using Python NetworkX with association-strength normalization and Louvain community detection at a resolution parameter of 1.0. The replication script (modularity_computation.py) is provided as Supplementary Material (DOI: 10.5281/zenodo.22885549).

Threshold justification

Network inclusion thresholds were selected to balance analytical coverage and visual interpretability. For the country co-authorship network, a minimum of five publications was used to exclude countries with limited representation while retaining the principal contributors to the retrieved literature. For the keyword co-occurrence network, a minimum of 100 occurrences was applied to emphasize frequently used terms and reduce visual complexity associated with less common keywords. For the author co-authorship network, a minimum of five publications was used to identify authors with repeated contributions to the field.

These thresholds yielded 80 eligible countries, 94 keywords, and 60 eligible authors, respectively, providing a basis for evaluating major collaboration structures and thematic patterns.

Robustness checks

Sensitivity analyses were conducted to evaluate the stability of network structures under alternative inclusion thresholds. The keyword co-occurrence network was reconstructed using minimum occurrence thresholds of 75 and 150, while the country co-authorship network was evaluated using minimum publication thresholds of 3 and 10. The number of clusters and the assignment of prominent keywords and countries

remained stable across these settings, supporting the robustness of the principal network patterns.

The temporal shift in research emphasis was evaluated independently of the network visualization by comparing the proportions of publications containing molecular/genomic and serological keywords across two equal periods: 2005–2014 and 2015–2024. This approach enabled the thematic trends observed in the overlay maps to be examined quantitatively.

Data analysis and reproducibility

Descriptive statistical analyses were performed using Python 3, with pandas and NumPy for data processing and Matplotlib for figure generation. Publication counts, percentages, citation indicators, and research productivity measures were calculated from the harmonized Scopus metadata. Annual publication trends were assessed using descriptive analysis and growth modeling, while keyword frequencies were compared between predefined periods.

The corpus h-index was defined as the largest integer h for which at least h publications had each received h or more citations. International collaboration was evaluated using the multiple-country publication (MCP) ratio, calculated as the number of publications involving affiliations from at least two countries divided by the total number of publications with usable affiliation data. The remaining publications were classified as single-country publications (SCP).

Network analyses were performed using VOSviewer, with independent modularity verification conducted using Python NetworkX. No additional dedicated bibliometric software package was used. All analytical indicators were derived from the exported Scopus records or the specified network analysis procedures.

The original Scopus export date, search strategy, inclusion criteria, software versions, network thresholds, and analytical procedures were documented to facilitate reproducibility. Because Scopus is continuously updated, repeated searches may return different record counts. Therefore, all reported analyses were based on the fixed dataset of 1,867 publications retrieved on February 14, 2026.

The complete exported CSV dataset, molecular/genomic and serological keyword classification lists, excluded ambiguous terms, VOSviewer thesaurus file, analytical scripts (modularity_computation.py and keyword_growth_analysis.py), and derived tables covering keyword-period comparisons, Lotka's law fitting, country participation counts, and author productivity are provided as Supplementary Material (DOI: 10.5281/zenodo.22885549). These materials support independent reproduction and evaluation of the reported bibliometric analyses.

RESULTS

Growth and composition of the literature

The bibliometric dataset comprised 1,867 documents published between 1956 and 2024. Journal articles accounted for the largest proportion (1,453; 77.8%), followed by review articles (305; 16.3%), conference papers (26; 1.4%), book chapters (18; 1.0%), notes (18; 1.0%), books (14; 0.7%), and letters (12; 0.6%). The remaining documents included short surveys, editorials, and corrections. The predominance of journal articles and reviews indicated that the retrieved literature consisted primarily of peer-reviewed publications. However, because reviews represent secondary research, this distribution should not be interpreted as evidence that all publications reported original investigations.

English was the predominant publication language (1,759; 94.2%), followed by German (32), French (25), Spanish (14), and Italian (10). Russian, Dutch, and Portuguese each accounted for fewer than ten publications. This distribution demonstrated the substantial predominance of English-language publications within the retrieved Scopus-indexed literature, alongside contributions in several other languages.

The annual publication trend (Figure 2) revealed relatively limited research output during the first four decades, followed by substantial expansion after 2000. Annual output remained below ten documents in most years before 2000 but increased progressively thereafter, exceeding 100 publications in 2014 and reaching 329 publications in 2024. Two pronounced increases were identified. The first occurred in 2014, when publication output increased from 39 documents in 2013 to 104 in 2014. The second occurred in 2024, when output increased from 112 documents in 2023 to 329 in 2024. An earlier local peak of 35 documents was recorded in 1974, although this increase was not followed by sustained growth comparable to that observed after 2000.

Quantified publication growth

Log-linear modeling of annual publication output during 2000–2024 indicated an average annual growth rate of approximately 15% ($R^2 = 0.88$). The compound annual growth rate was 14.4%, corresponding to an increase

from 13 documents in 2000 to 329 in 2024.

The two major annual increases represented 2.67-fold growth in 2014 (39–104 documents) and 2.94-fold growth in 2024 (112–329 documents). Publications from 2015 to 2024 accounted for 73.5% of the entire corpus, while those published during 2020–2024 represented 45.0%. In contrast, publications before 2000 contributed only 6.0% of the total. These findings demonstrated that research output was strongly concentrated in the most recent decades of the study period.

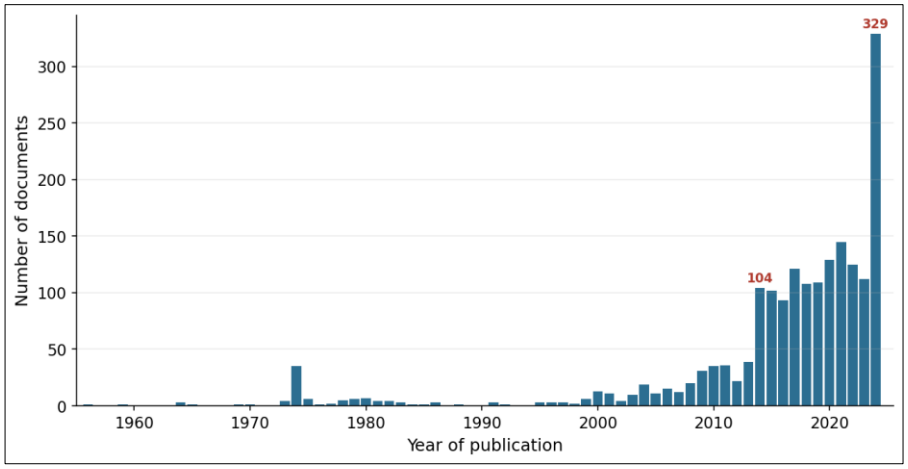


Figure 2: Annual publication output of zoonoses research within veterinary epidemiology indexed in Scopus from 1956 to 2024 (n = 1,867). Two pronounced increases in annual publication output were observed in 2014 (104 documents) and 2024 (329 documents).

Most-cited publications

The ten most-cited publications (Table 1) covered molecular parasitology, emerging viral diseases, antimicrobial resistance, and dairy cattle health, reflecting the thematic diversity of influential research within the retrieved literature [5–7, 12–18].

The most-cited publication was the review of emerging coronaviruses by Chen *et al.* [5], which received 2,361 citations. This was followed by the review of *Giardia* species and giardiasis by Feng and Xiao [12], with 974 citations, and the investigation of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission on mink farms [7], with 753 citations.

To account partially for differences in publication age, citation performance was also evaluated using citations per year (Table 1). Chen *et al.* [5] ranked first, with 337.3 citations/year, followed by Oude Munnink *et al.* [7] (125.5 citations/year) and Feng and Xiao [12] (60.9 citations/year). These findings indicated particularly high citation rates for coronavirus-related publications within the analyzed corpus.

Complete bibliographic information, including DOIs and document types, is presented in Table 1 and the reference list. Additional relevant sources are provided in references [19, 20]. Because older publications have had more time to accumulate citations, total citation rankings should be interpreted alongside citation rates. The high citation rankings of publications from 2020 to 2021 were particularly notable given their comparatively recent publication dates.

Leading countries and international collaboration

Research output was concentrated among a relatively small group of countries, predominantly those with established scientific research infrastructure (Table 2). The United States contributed the largest number of publications (400; 21.4%), followed by Brazil (196; 10.5%), the United Kingdom (193; 10.3%), Germany (156; 8.4%), and Italy (147; 7.9%). The remaining countries among the ten leading contributors were France (133), Spain (108), China (105), Australia (93), and the Netherlands (66).

Brazil was the only middle-income country among the five leading contributors, indicating its substantial participation in veterinary epidemiological research on zoonoses. Additional verification of country-level participation counts confirmed 66 publications from the Netherlands and 60 each from Japan and India.

Within the retrieved corpus, rabies was represented in 108 documents, compared with 105 documents mentioning cattle. These findings indicated that rabies-related and companion-animal research contributed substantially to the literature alongside investigations involving livestock.

To assess the consistency of country-level rankings, the original Scopus search was repeated on September

16, 2026. The ten leading countries retained the same rank order as in the original dataset, although their publication counts increased by 4–7 documents. China remained eighth, with 110 publications in the repeated search compared with 105 in the original dataset. These differences were consistent with subsequent additions and updates to Scopus records.

Table 1: The ten most-cited publications on zoonoses in veterinary epidemiology, ranked by total citations recorded in Scopus as of February 14, 2026.

Reference	Year	Source title	Citations	Citations/year	Document type	DOI
Chen *et al.* [5]	2020	J. Med. Virol.	2361	337.3	Review	10.1002/jmv.25681
Feng and Xiao [12]	2011	Clin. Microbiol. Rev.	974	60.9	Article	10.1128/CMR.00033-10
Oude Munnink *et al.* [7]	2021	Science	753	125.5	Article	10.1126/science.abe5901
Eldin *et al.* [14]	2017	Clin. Microbiol. Rev.	696	69.6	Review	10.1128/CMR.00045-16
Ferri *et al.* [16]	2017	Crit. Rev. Food Sci. Nutr.	675	67.5	Article	10.1080/10408398.2015.1077192
Ryan *et al.* [13]	2014	Parasitology	541	41.6	Review	10.1017/S0031182014001085
Stuen *et al.* [15]	2013	Front. Cell. Infect. Microbiol.	470	33.6	Review	10.3389/fcimb.2013.00031
Fan *et al.* [6]	2019	Viruses	451	56.4	Review	10.3390/v11030210
LeBlanc *et al.* [17]	2006	J. Dairy Sci.	410	19.5	Article	10.3168/jds.S0022-0302(06)72195-6
Mas-Coma *et al.* [18]	1999	Bull. World Health Organ.	395	14.1	Article	Not assigned

DOI = Digital object identifier. Citation counts represent a cross-sectional snapshot retrieved from Scopus on February 14, 2026. Citations/year represents an age-normalized citation measure that partially accounts for differences in publication age. Total citation counts may favor older publications because they have had longer to accumulate citations. The 1999 article published in the *Bulletin of the World Health Organization* has no DOI reported in the supplied bibliographic data. Source titles are presented using journal abbreviations.

Table 2: The ten most productive countries in zoonoses research within veterinary epidemiology. Percentages are calculated relative to the full corpus (n = 1,867); because documents may carry affiliations from multiple countries, values reflect participation and do not sum to 100%.

Rank	Country	Documents (%)
1	United States	400 (21.4)
2	Brazil	196 (10.5)
3	United Kingdom	193 (10.3)
4	Germany	156 (8.4)
5	Italy	147 (7.9)
6	France	133 (7.1)
7	Spain	108 (5.8)
8	China	105 (5.6)
9	Australia	93 (5.0)
10	Netherlands	66 (3.5)

Percentages were calculated relative to the complete bibliometric corpus (n = 1,867). Publications involving affiliations from multiple countries were counted once for each participating country. Consequently, country-level counts represent research participation rather than mutually exclusive publication categories, and the percentages do not sum to 100%.

International collaboration and normalization

The country co-authorship network demonstrated that the United States had the highest total link strength, indicating its central position in international research collaboration. The United States–United Kingdom, United States–Brazil, and United States–Germany collaborations were among the strongest bilateral relationships.

Of the 1,824 publications with usable affiliation information, 1,127 (61.8%) were classified as SCP, while 697 (38.2%) were MCP. The resulting MCP ratio was 0.38, indicating that slightly more than one-third of publications with usable affiliation data involved international collaboration.

Country-level productivity was evaluated using absolute publication counts rather than indicators normalized for population size, gross domestic product, or national research capacity. Consequently, the reported country rankings represent absolute contributions to the retrieved literature rather than relative research productivity. Countries with smaller populations or research systems, including the Netherlands and Switzerland, may exhibit different relative positions when normalized indicators are considered.

Impact, open access, and author productivity

The 1,867 publications accumulated 54,734 citations, corresponding to a mean of 29.3 citations and a

median of 11 citations per document. The difference between the mean and median indicated a right-skewed citation distribution, with a relatively small number of highly cited publications contributing substantially to the total citation count.

The corpus had an h-index of 109, indicating that at least 109 publications had each received 109 or more citations. At the time of data extraction, 294 publications (15.7%) had received no citations.

Regarding publication accessibility, 1,010 documents (54.1%) were classified as open access in Scopus, including gold, green, hybrid, and bronze categories. The remaining 857 documents (45.9%) were not designated as open access. These classifications reflected the accessibility information recorded in Scopus and did not independently establish whether individual publications were freely accessible under all licensing or geographic conditions.

Author-level analysis identified 11,142 unique contributors, of whom 88.7% were associated with only one publication. Only 62 authors had contributed to five or more publications, indicating a highly uneven distribution of research productivity.

The author productivity distribution was evaluated using Lotka's law. Log–log regression produced an exponent of 3.65 (R^2 = 0.97), exceeding the classical theoretical exponent of approximately 2. This finding indicated a steeper decline in the number of authors with increasing publication counts than predicted by the conventional Lotka distribution.

The most productive author was I. García-Bocanegra, with 15 publications, followed by D. Cano-Terriza and D. Otranto, with 13 publications each, and D. Carmena, with 12 publications (Table 3). These authors also occupied prominent positions in the author co-authorship network, demonstrating consistency between the productivity rankings and network visualization.

Table 3: The ten most prolific authors in zoonoses research within veterinary epidemiology, ranked by publication count and primary country affiliation.

Rank	Author	Country	Documents
1	García-Bocanegra, I.	Spain	15
2	Cano-Terriza, D.	Spain	13
3	Otranto, D.	Italy	13
4	Carmena, D.	Spain	12
5	Mesquita, João R.	Portugal	10
6	Caballero-Gómez, J.	Spain	9
7	Yabsley, Michael J.	United States	8
8	González-Barrio, D.	Spain	8
9	Ulrich, Rainer G.	Germany	8
10	Dorny, P.	Belgium	8

Author productivity represents the number of publications attributed to each author within the bibliometric corpus of 1,867 Scopus-indexed documents published between 1956 and 2024. Country refers to the author's primary institutional affiliation as recorded in the analyzed bibliographic dataset. The listed authors correspond to prominent nodes in the author co-authorship network. Author names and publication counts are reproduced from the supplied data.

Institutional productivity showed a similar concentration among established research organizations (Table 4). The United States Centers for Disease Control and Prevention contributed the most publications (57; 3.1%), followed by the Friedrich-Loeffler-Institut, Germany (46; 2.5%), and Fundação Oswaldo Cruz, Brazil (40; 2.1%).

Brazil was represented by three institutions among the ten most productive organizations: Fundação Oswaldo Cruz, Universidade de São Paulo, and Universidade Estadual Paulista. The University of Pretoria, South Africa, was also represented among the leading institutions, indicating contributions from research organizations in the Global South.

The country co-authorship network (Figure 3) demonstrated the central position of the United States, with extensive collaborative connections involving European and Asian countries. European countries also formed a densely interconnected research network.

Temporal overlay visualization revealed differences in the average publication years associated with participating countries. Established contributors from North America and Europe generally displayed earlier average publication years, whereas several Latin American countries, including Colombia, Argentina, Chile, and Peru, together with selected African and Asian countries, displayed more recent average publication years. These patterns indicated increasing participation by countries outside the traditional research centers, although the overall collaboration structure remained concentrated around established contributors.

Table 4: The ten most productive institutions in zoonoses research within veterinary epidemiology, ranked by publication count.

Rank	Institution	Country	Documents (%)
1	Centers for Disease Control and Prevention	United States	57 (3.1)
2	Friedrich-Loeffler-Institut	Germany	46 (2.5)
3	Fundação Oswaldo Cruz	Brazil	40 (2.1)
4	Universidade de São Paulo	Brazil	34 (1.8)
5	Instituto de Salud Carlos III	Spain	29 (1.6)
6	Universidade Estadual Paulista	Brazil	28 (1.5)
7	Universität Zürich	Switzerland	28 (1.5)
8	University of Liverpool	United Kingdom	28 (1.5)
9	University of Pretoria	South Africa	28 (1.5)
10	University of California, Davis	United States	27 (1.4)

Percentages were calculated relative to the complete bibliometric corpus (n = 1,867). Institutional publication counts represent the number of documents associated with each institution in the Scopus affiliation metadata. Publications involving multiple institutions may contribute to the counts of more than one institution. Therefore, institutional contributions are not mutually exclusive, and their percentages do not sum to 100%.

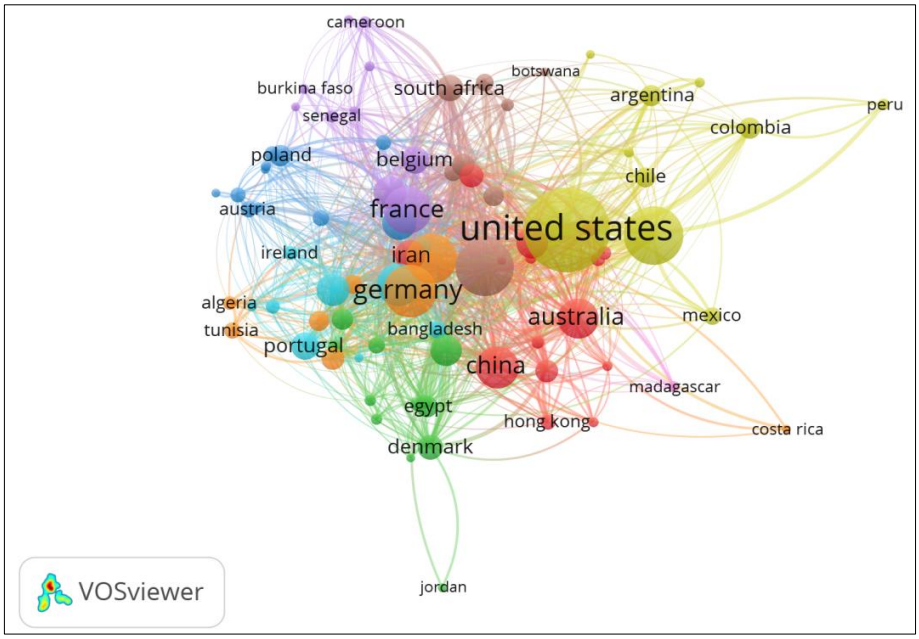


Figure 3: Temporal overlay visualization of the country co-authorship network in zoonoses research within veterinary epidemiology. Countries with at least five publications were included, yielding 80 eligible countries. Full counting and association-strength normalization were applied. Node size represents the number of publications, link thickness indicates co-authorship link strength, and node color represents the average publication year. Established contributors, including the United States and Germany, are represented by cooler colors, whereas several Latin American and other countries with more recent average publication years appear in warmer colors. The reported network modularity was Q = 0.409, with five clusters, independently evaluated using the Louvain community detection algorithm implemented in NetworkX.

Thematic structure and its evolution

Keyword co-occurrence analysis identified several interconnected thematic groups within the retrieved literature (Figure 4). The central epidemiology and public health cluster included epidemiology, zoonoses, public health, One Health, and risk factor, reflecting the relationship between epidemiological investigations and public health applications.

A serological cluster included seroprevalence, seroepidemiology, blood sampling, brucellosis, cattle, and goat, representing research focused on livestock-associated infections and exposure assessment. A molecular and genetic cluster contained genetics, isolation and purification, classification, DNA extraction, genetic variability, and phylogeny, reflecting research involving pathogen characterization and genetic investigations.

A companion-animal cluster included dog, cat, and associated diseases, indicating the representation of companion animals within zoonotic disease research.

The frequent occurrence and central network position of One Health indicated its bibliometric connectivity with multiple research themes. However, keyword co-occurrence and network centrality demonstrate

relationships among terms in the literature rather than directly confirming operational integration among human, animal, and environmental health sectors.

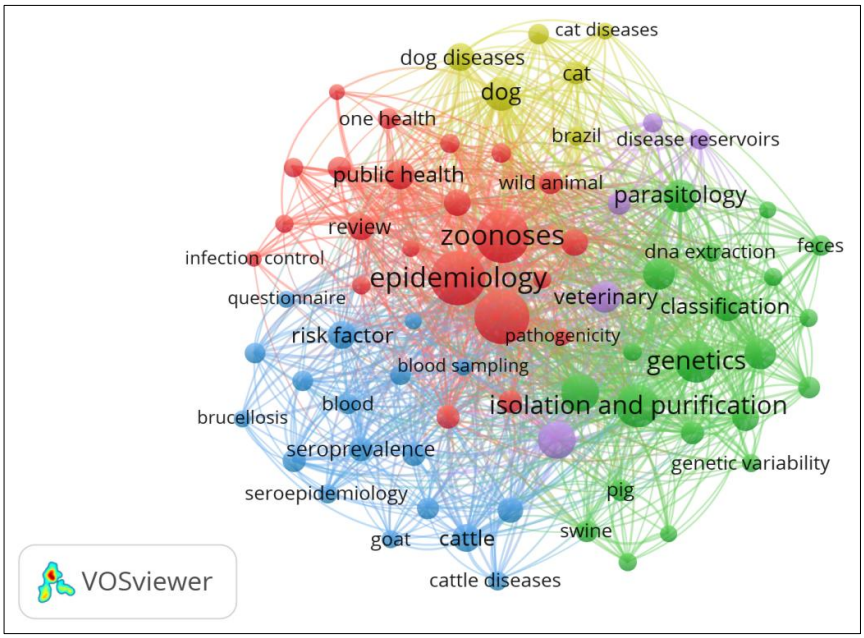


Figure 4: Keyword co-occurrence network illustrating the thematic structure of zoonoses research within veterinary epidemiology. A minimum threshold of 100 keyword occurrences yielded 94 terms distributed across five clusters. The network was constructed using full counting, association-strength normalization, and a clustering resolution parameter of 1.00. Node size represents keyword occurrence frequency, link thickness indicates co-occurrence strength, and node color denotes cluster membership. The principal thematic groups include epidemiology and public health (red), serological and risk factor investigations (blue), molecular and genetic characterization (green), and companion-animal diseases (yellow). The reported network modularity was Q = 0.115, independently evaluated using the Louvain community detection algorithm implemented in NetworkX.

Keyword network characteristics

The keyword co-occurrence network comprised 94 terms meeting the minimum threshold of 100 occurrences and was divided into five clusters. The epidemiology/public health and molecular/genetic clusters were the largest.

The terms epidemiology, zoonoses, genetics, and isolation and purification exhibited the highest total link strengths, identifying them as prominent structural components of the keyword network.

Sensitivity analyses using minimum occurrence thresholds of 75 and 150 demonstrated stable cluster membership and rankings among the most prominent terms. These findings indicated that the principal thematic organization was not substantially affected by the evaluated threshold changes.

Temporal evolution of research themes

Temporal overlay visualization (Figure 5) revealed differences in the average publication years associated with major research themes. Keywords related to conventional serological and descriptive epidemiology generally corresponded to earlier publication periods, whereas terms associated with molecular and genomic research, including genetics, isolation and purification, classification, and genetic variability, were more prominent in publications with later average publication years.

One Health was also associated with more recent publications, consistent with its increasing representation in the retrieved literature after the mid-2010s.

Collectively, the keyword co-occurrence and temporal overlay analyses (Figures 4 and 5) indicated increasing emphasis on molecular and genomic terminology relative to traditional serological terminology. These findings reflected changes in publication themes and keyword usage rather than direct evidence of changes in the laboratory methods employed in individual studies.

Quantitative assessment of thematic changes

The temporal changes observed in the keyword overlay were further evaluated by comparing keyword frequencies between 2005–2014 and 2015–2024.

The proportion of publications containing molecular or genomic keywords increased from 50.5% in 2005–2014 to 70.2% in 2015–2024, representing an absolute increase of 19.7 percentage points. The increase was statistically significant ($\chi^2 = 45.5$, $p < 0.001$), with reported 95% confidence intervals of 45.0%–55.9% and 67.9%–72.7%, respectively.

In comparison, the proportion of publications containing serological keywords increased from 24.0% to 26.9% between the corresponding periods. This difference was not statistically significant ($\chi^2 = 1.0$, $p = 0.31$).

The molecular/genomic and serological categories were not mutually exclusive because individual publications could contain keywords from both categories. Therefore, these findings indicated an increasing prevalence of molecular/genomic terminology without demonstrating the replacement or abandonment of conventional serological approaches.

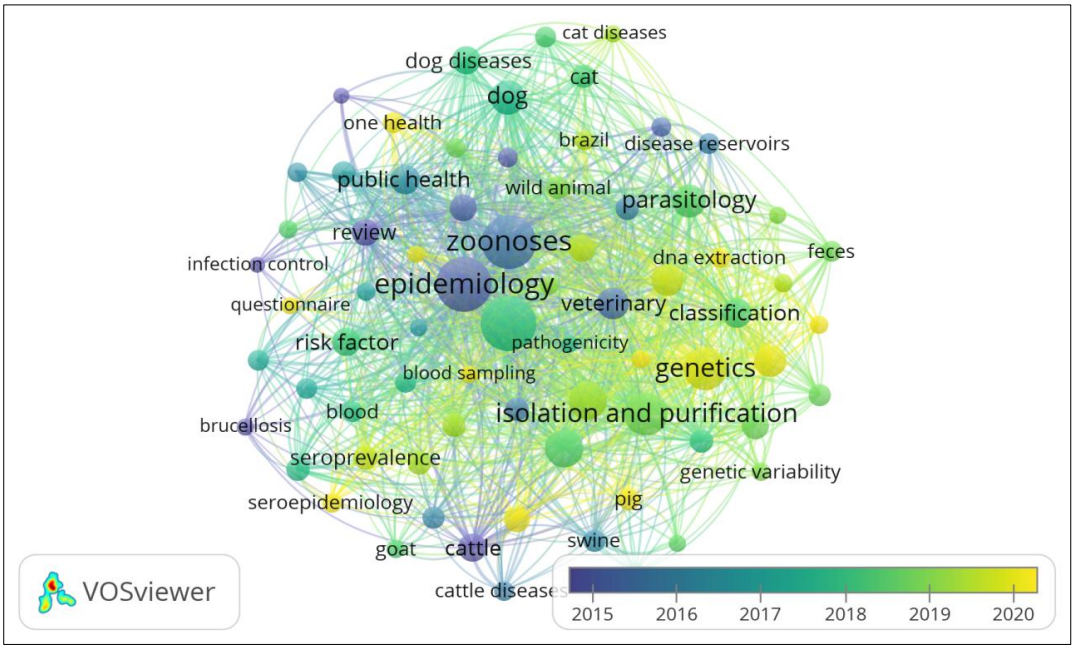


Figure 5: Temporal overlay visualization of the keyword co-occurrence network illustrating changes in research themes over time. The network includes 94 terms meeting the minimum threshold of 100 occurrences and was constructed using full counting and association-strength normalization, consistent with Figure 4. Node size represents keyword occurrence frequency, link thickness indicates co-occurrence strength, and node color represents the average publication year of documents containing each keyword rather than cluster membership. Molecular and genomic research terms, including genetics, isolation and purification, and classification, were associated with more recent average publication years than conventional serological terms. These patterns indicate changes in keyword prevalence and research emphasis rather than verified changes in laboratory methods.

Frequency distribution of research keywords

The most frequently occurring author and indexed keywords were zoonosis/zoonoses (n = 1,637/1,180), epidemiology (1,166), veterinary medicine (1,125), prevalence (921), phylogeny (682), genetics (667), isolation and purification (651), microbiology (517), dog (514), PCR (502), public health (472), genotype (456), parasitology (417), cattle (393), livestock (352), risk factor (341), and molecular epidemiology (335).

The keyword dog occurred more frequently (514 occurrences) than cattle (393 occurrences), indicating substantial representation of companion-animal research within the retrieved literature. This pattern was consistent with the presence of publications addressing rabies and canine vector-borne and parasitic zoonoses.

The simultaneous prominence of molecular terms, including phylogeny, genetics, PCR, and genotype, and conventional epidemiological terms, including prevalence, risk factor, and seroprevalence, demonstrated the coexistence of different research approaches within the field.

The overall frequency ranking of prominent keywords remained consistent when author-supplied and Scopus-indexed keywords were evaluated separately, supporting the stability of the observed thematic patterns.

DISCUSSION

This bibliometric analysis of 1,867 Scopus-indexed documents published between 1956 and 2024 provides a quantitative assessment of the development of zoonoses research within veterinary epidemiology. Three

principal findings emerged. First, research output increased substantially, with pronounced annual increases in 2014 and 2024. Second, scientific productivity remained concentrated in established research centers, particularly the United States and European countries, although contributions from Latin America, Asia, and Africa indicated increasing geographic diversification. Third, keyword analyses demonstrated a measurable increase in molecular and genomic research terminology relative to conventional serological terminology, alongside the growing prominence of the One Health framework. These findings provide insights into the development of research priorities, international collaboration, and thematic relationships within the retrieved literature. However, the observed patterns represent bibliometric associations rather than direct evidence of changes in laboratory practices or the effectiveness of zoonotic disease control interventions.

Comparison with previous bibliometric studies

The present findings extend previous bibliometric investigations by focusing specifically on zoonoses research within veterinary epidemiology. Raphael *et al.* [11] examined the broader One Health research landscape and similarly identified increasing publication output and the importance of interdisciplinary collaboration. However, the broader scope of that analysis did not specifically characterize the veterinary epidemiological component or quantify changes in the relative prevalence of molecular/genomic and serological research terminology.

In contrast to bibliometric investigations focusing on individual zoonotic pathogens, the present study examined research trends across multiple diseases and methodological approaches. This broader veterinary epidemiological perspective enabled the identification of common patterns in publication growth, geographic participation, international collaboration, and thematic evolution. The findings also demonstrated the prominence of the United States and European countries, consistent with established patterns of biomedical research productivity, while highlighting Brazil as a major contributor to zoonoses research.

The increasing representation of molecular and genomic terminology, together with the growing prominence of One Health, suggests that the retrieved literature has become more thematically diverse and interdisciplinary. Nevertheless, keyword-based relationships cannot independently establish the extent to which these approaches have been implemented in individual investigations or integrated into operational surveillance systems.

Growth dynamics and potential contributing factors

The pronounced increases in annual publication output during 2014 and 2024 (Figure 2) indicate periods of accelerated growth within the retrieved literature. However, bibliometric data alone cannot establish the underlying causes of these increases. Potential explanations should therefore be considered hypotheses rather than demonstrated causal relationships.

The increase observed in 2014 coincided with the growing institutional recognition of One Health as an interdisciplinary framework for addressing infectious diseases at the human–animal–environment interface. International initiatives introduced during 2013 emphasized the integration of human, animal, and environmental health into research and practice, accompanied by the development of dedicated research funding opportunities [21]. These developments may have contributed to increased scientific activity and collaboration across disciplines. The West African Ebola epidemic, which began in late 2013, may also have stimulated interest in zoonotic disease emergence and transmission. However, the present analysis did not directly evaluate the effects of these events on publication output.

The larger increase observed in 2024 initially suggested a possible association with the continuing scientific response to the coronavirus disease 2019 (COVID-19) pandemic. Nevertheless, only 28 of the 329 documents published in 2024 (8.5%) were related to coronaviruses or COVID-19, while 85.1% were journal articles distributed across multiple research themes. These findings do not support the interpretation that the increase was predominantly driven by coronavirus-related publications.

Instead, the 2024 increase may reflect broader expansion of research activity, changes in Scopus indexing coverage, and sustained scientific interest in zoonotic diseases following the pandemic. Advances in computational approaches, including machine-learning, large-scale data analysis, and digital surveillance technologies, may also have facilitated research in this field [19]. However, these potential explanations were not evaluated directly and should not be interpreted as established determinants of publication growth.

Furthermore, the exceptionally high-output recorded in a single year does not necessarily indicate a sustained change in long-term publication trends. Additional publication data from subsequent years will be

required to determine whether the 2024 increase represents continued expansion or a temporary fluctuation.

Geographic concentration and diversification of research

The predominance of the United States and European countries in publication output reflects the concentration of research activity among countries with established scientific institutions, funding systems, and research infrastructure. The leading contributions of the United States Centers for Disease Control and Prevention and the Friedrich-Loeffler-Institut in Germany further demonstrate the importance of national research and reference institutions in zoonotic disease investigations.

Brazil's position as the second-largest contributor was particularly notable. The country also accounted for three of the ten most productive institutions, indicating substantial institutional participation in veterinary epidemiological research. This pattern may be associated with Brazil's burden of endemic zoonoses, including leishmaniasis, leptospirosis, and Chagas disease, together with its established scientific and public health infrastructure. Research on diagnostic innovations for canine visceral leishmaniasis illustrates the contribution of locally relevant investigations to methodological development [22]. Nevertheless, the present bibliometric analysis did not directly assess the relationship between disease burden, research investment, and publication productivity.

The temporal overlay of international collaboration networks (Figure 3) revealed more recent average publication years among several Latin American, African, and Asian countries. These patterns suggest increasing participation by countries outside the traditional North American and European research centers. However, the network remained organized around established high-output countries, indicating that geographic diversification has not eliminated existing differences in scientific participation.

This observation is particularly relevant because endemic zoonotic diseases disproportionately affect low- and middle-income countries, where diagnostic infrastructure, surveillance resources, and outbreak-response capacity may be constrained [2, 20]. Strengthening research participation in these settings could support investigations addressing locally relevant disease priorities and facilitate the development of sustainable surveillance capacity.

Integrated surveillance initiatives, including the human–animal–environmental surveillance system described in Gujarat, India, demonstrate potential approaches for improving cross-sectoral information sharing and pathogen detection [23]. Such initiatives provide examples of locally implemented One Health activities, although their effectiveness cannot be inferred from the present bibliometric results.

The increasing participation of countries outside established research centers also highlights the importance of equitable international collaboration. Research partnerships should promote local scientific leadership, institutional development, technical capacity, and shared access to research resources. However, co-authorship networks alone cannot determine whether collaborations are equitable or whether participating institutions have comparable roles in research design, funding, and decision-making.

China's contribution requires similarly cautious interpretation. Although the country demonstrated recent research activity in the temporal network overlays, it ranked eighth in cumulative publication output, contributing 105 documents (5.6%). The repeated Scopus search conducted on September 16, 2026, confirmed that China remained eighth. Therefore, the available evidence supports increasing geographic diversification rather than a definitive shift in global research leadership toward any single emerging contributor.

Increasing emphasis on molecular and genomic research

One of the principal findings was the increasing prevalence of molecular and genomic terminology within the retrieved literature. The proportion of publications containing molecular/genomic keywords increased from 50.5% during 2005–2014 to 70.2% during 2015–2024 ($p < 0.001$). In contrast, the proportion containing serological keywords increased only slightly, from 24.0% to 26.9%, without a statistically significant difference ($p = 0.31$).

These findings indicate a change in the relative representation of research themes rather than the replacement of conventional serological approaches. Because individual publications could contain both molecular/genomic and serological keywords, the two categories were not mutually exclusive. Furthermore, keyword classification was based on bibliographic metadata rather than full-text verification of laboratory methods.

Serological investigations remain essential for estimating pathogen exposure, evaluating population-level immunity, and conducting epidemiological surveillance. However, serological methods alone may provide limited resolution for distinguishing closely related pathogen strains, reconstructing transmission pathways, or identifying

genetic variation. Molecular and genomic techniques complement these approaches by enabling more detailed pathogen characterization and investigation of epidemiological relationships.

For example, Feng and Xiao [12] demonstrated the importance of molecular genotyping in distinguishing host-associated assemblages of *Giardia* species and evaluating their zoonotic potential. Comparable molecular approaches have advanced the understanding of *Cryptosporidium* species [13], *Coxiella burnetii* [14], and *Anaplasma phagocytophilum* [15]. These investigations illustrate the scientific value of molecular characterization in zoonotic disease research.

The keyword co-occurrence network (Figure 4) contained prominent terms associated with genetics, phylogeny, genetic variability, and pathogen characterization. Temporal overlay analysis (Figure 5) indicated that several of these terms were associated with more recent average publication years than conventional serological terminology.

However, terms such as "isolation and purification" and "classification" were excluded from the predefined molecular/genomic comparison because they were not considered sufficiently specific to molecular methods. Their presence in the descriptive keyword network should therefore be distinguished from the quantitative evidence supporting increased molecular/genomic keyword prevalence.

Collectively, these findings support an increasing bibliometric emphasis on molecular and genomic research while recognizing the continued importance of conventional epidemiological and serological approaches.

Integration of molecular approaches and One Health

The increasing prominence of molecular and genomic terminology occurred alongside the growing representation of One Health within the keyword networks. One Health appeared as a central term in the keyword co-occurrence analysis (Figure 4) and was associated with more recent publication years in the temporal overlay (Figure 5).

These observations suggest increasing attention to research approaches that consider interactions among human, animal, and environmental health. Molecular and genomic technologies can support this framework by facilitating pathogen characterization across host species and environmental compartments, while interdisciplinary surveillance can provide the epidemiological context needed to interpret molecular findings.

Previous investigations have emphasized the potential benefits of integrating human, animal, and environmental surveillance information for outbreak detection and epidemiological risk assessment [10, 11]. However, the centrality of One Health within a bibliometric network does not demonstrate that the underlying studies implemented fully integrated surveillance systems.

The investigation of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission on mink farms provides an example of how genomic epidemiology can contribute to understanding transmission between humans and animals [7]. Such approaches may support more targeted surveillance and disease control strategies when combined with appropriate epidemiological and clinical information.

For veterinary practice, molecular diagnostics may improve pathogen identification and support the selection of appropriate surveillance and control measures. Nevertheless, their effectiveness depends on diagnostic validation, sampling quality, laboratory infrastructure, interpretation, and integration with conventional epidemiological methods.

Methodological innovations may also improve animal handling and diagnostic procedures. For example, the development of a semi-automatic needle for standardized lymph node sampling in canine visceral leishmaniasis illustrates the potential contribution of diagnostic innovation to veterinary investigations [22]. However, improvements in diagnostic accuracy or animal welfare should be evaluated directly rather than assumed from technological development alone.

Emerging and re-emerging zoonoses and ecological drivers

The representation of emerging and re-emerging zoonoses within the literature reflects the continuing importance of ecological and anthropogenic factors in infectious disease transmission.

Land-use changes, deforestation, and agricultural intensification can alter interactions among humans, livestock, wildlife, and their environments, potentially increasing opportunities for pathogen transmission. Intensive livestock production may also create conditions that facilitate pathogen maintenance and transmission within animal populations [24].

Climate change can influence the geographic distribution of vectors and reservoir hosts, modify suitable habitats, and alter patterns of exposure to infectious agents. International trade, wildlife movement, and human

mobility may further contribute to the geographic dissemination of pathogens following spillover events [25].

These factors frequently interact, emphasizing the importance of multidisciplinary approaches to zoonotic disease surveillance and prevention. The One Health framework provides a basis for examining relationships among ecological, veterinary, environmental, and human health determinants [9].

The increasing representation of interdisciplinary terminology within the analyzed literature is consistent with growing scientific attention to these interconnected processes. However, the present bibliometric analysis did not directly measure ecological changes, pathogen spillover rates, or the causal relationships between environmental drivers and disease emergence.

Surveillance, veterinary education, and risk-based prioritization

Effective zoonotic disease control requires the translation of scientific findings into surveillance systems, diagnostic services, workforce development, and evidence-informed prioritization.

Established national surveillance programs provide longitudinal information that can support the detection and investigation of infectious disease trends. For example, surveillance of *Salmonella* species, *Campylobacter* species, verotoxigenic *Escherichia coli*, and *Listeria* species contributes to monitoring zoonotic and foodborne pathogens.

Integrated surveillance approaches, such as the system described in Gujarat, India, demonstrate potential opportunities for improving information sharing among human, animal, and environmental health sectors [23]. Such systems may be particularly relevant in settings where coordinated surveillance could strengthen early detection and outbreak-response capacity.

Veterinary and medical education also plays an important role in preparing professionals to address zoonotic disease threats. Training in infection prevention, biosecurity, molecular diagnostics, epidemiological investigation, and interdisciplinary collaboration can support the development of a workforce capable of implementing One Health principles.

Professional and scientific exchanges, including multidisciplinary meetings such as the International Congress on Pathogens at the Human–Animal Interface, may further facilitate knowledge sharing and collaboration among veterinary, medical, and environmental health professionals.

Because surveillance and control resources are limited, risk-based prioritization is essential for identifying zoonotic diseases requiring immediate attention. Structured approaches, including conjoint analysis, can support the ranking of disease priorities according to epidemiological burden, feasibility of intervention, and other relevant criteria [2].

The coexistence of applied surveillance themes and molecular research topics within the retrieved literature suggests that veterinary epidemiological research continues to address both fundamental scientific questions and practical disease control needs.

Limitations

Several methodological limitations should be considered when interpreting the findings.

First, the study relied exclusively on Scopus, excluding relevant publications indexed only in other databases, including Web of Science, PubMed, and regional bibliographic resources. The search strategy required the simultaneous occurrence of the terms "zoonoses," "veterinary," and "epidemiology" within the specified bibliographic fields. Consequently, relevant investigations using alternative terminology, such as "zoonotic disease," "molecular epidemiology," "surveillance," "reservoir," "One Health," or individual pathogen names, may not have been retrieved. The dataset therefore represents a reproducible, search-defined subset of the literature rather than an exhaustive global census.

Second, the predominance of English-language publications (94.2%) may reflect both the international use of English in scientific communication and differences in database coverage. Research published in other languages or regional journals may consequently be underrepresented.

Third, historical publication trends may be influenced by changes in Scopus indexing coverage. The expansion of database coverage over time, particularly for older publications, may contribute to apparent increases in publication output. Therefore, long-term growth patterns cannot be attributed exclusively to increases in research activity.

Fourth, citation indicators were derived from a single data extraction date and are subject to publication-age effects. Older documents have had more time to accumulate citations, whereas recent publications may not yet have reached their full citation potential. Citation rankings therefore reflect accumulated influence at the time of

retrieval rather than a definitive measure of scientific importance.

Fifth, the inclusion of review articles may influence citation distributions and keyword frequencies because reviews often summarize multiple research themes and may receive more citations than individual primary investigations.

Sixth, country and institutional publication counts reflected participation in publications with potentially multiple affiliations. These indicators were not normalized for population size, national research expenditure, livestock populations, or zoonotic disease burden. Consequently, the reported rankings describe absolute publication contributions rather than relative research capacity or output adjusted for epidemiological need.

Seventh, co-authorship networks identify bibliographic collaboration but cannot determine the quality, equity, leadership distribution, funding arrangements, or practical outcomes of research partnerships.

Eighth, keyword co-occurrence networks depend on the selected occurrence thresholds, normalization procedures, and clustering parameters. Although sensitivity analyses supported the stability of prominent thematic patterns, alternative analytical settings could produce different network structures.

Ninth, the classification of molecular/genomic and serological keywords involved researcher judgment. Although predefined classification rules and thesaurus-based harmonization were applied, potential classification inconsistencies could not be eliminated. Scopus-indexed keywords may also reflect indexing conventions rather than the terminology or methods used by the original authors.

Tenth, the molecular/genomic and serological categories were not mutually exclusive. Publications containing terms from both categories contributed to both groups, limiting interpretation of their relative frequencies as competing methodological approaches.

Eleventh, the study did not systematically verify the laboratory methods reported in the full texts of individual publications. Consequently, the observed increase in molecular/genomic terminology should not be interpreted as direct evidence that molecular methods replaced conventional serological techniques.

Finally, bibliometric indicators cannot independently establish the methodological quality, validity, clinical relevance, or practical effectiveness of the underlying research. These limitations define the scope of the conclusions and emphasize the need for complementary methodological and epidemiological investigations.

Future research directions

Future bibliometric investigations should consider integrating multiple bibliographic databases to improve literature coverage and reduce database-specific indexing bias. Including regional and non-English-language publications would provide a more comprehensive representation of research contributions, particularly from countries with substantial endemic zoonotic disease burdens.

The application of citation indicators normalized for publication age, document type, and research field could improve comparisons of scientific influence. Similarly, country-level productivity assessments incorporating population size, research expenditure, livestock populations, and zoonotic disease burden could provide a more informative evaluation of research capacity relative to epidemiological needs.

Future studies should also investigate the relationship between bibliometric keyword trends and the actual laboratory methods used in published investigations. Full-text methodological assessments could determine whether the increasing prevalence of molecular/genomic terminology corresponds to greater use of molecular diagnostics, genomic sequencing, and integrated surveillance approaches.

Further research should examine the structure and equity of international scientific collaboration. Beyond co-authorship counts, indicators of institutional leadership, funding participation, authorship position, and research capacity development could help evaluate whether international partnerships contribute to sustainable scientific development in endemic regions.

Strengthening molecular and genomic surveillance capacity in low- and middle-income countries represents another important priority. Investments in diagnostic infrastructure, laboratory training, bioinformatics expertise, and interoperable surveillance systems may support more effective integration of molecular and conventional epidemiological approaches.

The continued development of integrated human–animal–environmental data systems and computational methods, including machine-learning approaches for zoonotic disease risk assessment, may also support future surveillance and prevention strategies [19]. However, their effectiveness should be evaluated through appropriately designed implementation and epidemiological studies.

Policy and practical implications for veterinary services in low- and middle-income countries

The concentration of endemic zoonotic disease burdens in many low- and middle-income countries, together with their comparatively limited representation in the retrieved literature, highlights the importance of strengthening locally relevant veterinary research and surveillance capacity.

For veterinary services, an important priority is improving diagnostic capacity for endemic zoonoses, including brucellosis, bovine tuberculosis, leptospirosis, rabies, and cysticercosis. Where appropriate and feasible, validated field-deployable molecular assays, including portable real-time PCR systems and targeted sequencing, could complement existing serological and conventional diagnostic methods.

At the surveillance system level, integrated platforms linking human, animal, and environmental health information may improve coordination and support timely identification of zoonotic threats. The integrated surveillance approach described in Gujarat, India, provides an example of cross-sectoral collaboration that may inform the development of similar systems in other settings [23]. However, implementation should be adapted to local epidemiological priorities, institutional capacity, available resources, and diagnostic infrastructure.

International funding agencies, research institutions, and public health organizations should consider supporting laboratory infrastructure, technical training, data-sharing systems, and sustainable research partnerships in endemic regions. Such initiatives should emphasize local leadership, equitable access to research resources, and long-term institutional capacity development.

Together, these priorities could help translate the expanding scientific literature and increasing molecular/genomic research emphasis into more accessible and context-appropriate approaches to zoonotic disease surveillance and prevention. Their practical effectiveness, however, requires direct evaluation rather than inference from bibliometric trends alone.

CONCLUSION

This bibliometric analysis of 1,867 Scopus-indexed publications from 1956 to 2024 demonstrated substantial growth in zoonoses research within veterinary epidemiology, particularly during the past two decades. Publication output increased at a compound annual growth rate of 14.4% during 2000–2024, with pronounced increases in 2014 and 2024. Research productivity remained concentrated in the United States and European countries, although Brazil emerged as a major contributor and increasing participation from Latin American, Asian, and African countries indicated geographic diversification. International collaboration accounted for 38.2% of publications with usable affiliation data. Keyword analyses revealed five thematic clusters and a significant increase in molecular/genomic keyword prevalence from 50.5% in 2005–2014 to 70.2% in 2015–2024 ($p < 0.001$), whereas the corresponding increase in serological keyword prevalence was not statistically significant. These findings indicate an evolving research emphasis rather than a verified replacement of conventional laboratory methods.

A principal strength of this study is its comprehensive bibliometric assessment of a large, historically extensive dataset covering nearly seven decades of research. The integration of publication trends, citation indicators, geographic productivity, international co-authorship networks, keyword co-occurrence analysis, and temporal overlay visualization provided a multidimensional assessment of the field. The use of a predefined search strategy, documented analytical thresholds, keyword classification criteria, sensitivity analyses, and supplementary computational materials strengthened methodological transparency and reproducibility. Quantitative comparison of molecular/genomic and serological keyword prevalence also provided evidence of changes in research emphasis beyond visual network interpretation alone.

Zoonoses research within veterinary epidemiology has expanded substantially, accompanied by increasing international participation and a measurable shift toward molecular and genomic research themes. Nevertheless, geographic disparities and differences in research capacity remain important challenges. Continued integration of conventional epidemiological approaches with molecular technologies, interdisciplinary One Health collaboration, and equitable research capacity development may strengthen the scientific foundation for zoonotic disease surveillance and control. Translating these bibliometric trends into demonstrable improvements in animal and public health will require sustained investment and direct evaluation of practical outcomes.

DATA AVAILABILITY

The bibliographic dataset was retrieved from Scopus using the field-tagged search query described in the Materials and Methods section. The exported comma-separated values (CSV) dataset and the scripts used to

generate the figures and perform the analyses are available in the Zenodo repository at https://doi.org/10.5281/zenodo.22885549.

GENERATIVE AI DECLARATION

Generative AI tools were used solely to support language refinement and formatting. All scientific content, data analysis and interpretation, conclusions, and reference verification were independently conducted by the authors. The authors remain fully responsible for the accuracy, integrity, and overall content of the work.

AUTHORS' CONTRIBUTIONS

IR: Conceptualization, data curation, formal analysis, and writing of the original draft. AK and WAP: Methodology, bibliometric network analysis, and visualization. WAST and HK: Data extraction, validation, and interpretation. ASRA: Literature curation and reference management. MSAF: Study design, data interpretation, and critical revision and editing of the manuscript for important intellectual content. All authors have read, revised, and approved the final manuscript.

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COMPETING INTERESTS

The authors declare that they have no competing interests.

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