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Bibliometric analysis of the One Health approach and antimicrobial resistance in agro-environmental systems

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Abstract: Antimicrobial resistance has become a cross-sectoral challenge in agri-food and environmental systems, creating demand for evidence that is comparable across human, animal, and environmental health. This study quantitatively examined the evolution of research on the One Health approach and antimicrobial resistance in agro-environmental settings through bibliometric mapping of Scopus records retrieved on 5 February 2026. After thematic screening, metadata cleaning, and standardisation, the final dataset was processed in Bibliometrix and VOSviewer using productivity indicators, collaboration networks, Lotka's law, Bradford's law, and RPYS. The corpus comprised 2,515 documents published between 1981 and 2026 in 818 sources by 12,943 authors. Annual growth reached 9.87%, mean co-authorship was 6.7 authors per document, international collaboration accounted for 36.22%, and the average citation rate was 27.78 citations per document. Scientific output rose sharply after 2018 and reached 612 documents in 2025. Seventeen core journals accounted for 833 articles, and 117 countries contributed to the field, with China and the United States leading production. The resulting profile shows a domain that combines environmental transmission, genomic surveillance, and risk-oriented management across value chains, reinforcing the need for harmonised metrics and coordinated action on biosecurity, effluent control, and antimicrobial stewardship.

Keywords: Genomic surveillance, antibiotic use, food safety, resistance genes.

Resumo: A resistência aos antimicrobianos tornou-se um desafio transversal nos sistemas agroalimentares e ambientais, gerando demanda por evidências comparáveis entre a saúde humana, animal e ambiental. Este estudo examinou quantitativamente a evolução da pesquisa sobre a abordagem One Health e a resistência aos antimicrobianos em contextos agroambientais por meio do mapeamento bibliométrico de registros da Scopus recuperados em 5 de fevereiro de 2026. Após a triagem temática, a limpeza dos metadados e sua padronização, o conjunto final de dados foi processado no Bibliometrix e no VOSviewer com uso de indicadores de produtividade, redes de colaboração, lei de Lotka, lei de Bradford e RPYS. O corpus compreendeu 2.515 documentos publicados entre 1981 e 2026, em 818 fontes, por 12.943 autores. O crescimento anual atingiu 9,87%, a média de coautoria foi de 6,7 autores por documento, a colaboração internacional representou 36,22% e a taxa média de citação foi de 27,78 citações por documento. A produção científica cresceu de forma acentuada após 2018 e alcançou 612 documentos em 2025. Dezessete periódicos centrais concentraram 833 artigos, e 117 países contribuíram para o campo, com China e Estados Unidos na liderança da produção. O perfil resultante mostra um domínio que integra transmissão ambiental, vigilância genômica e gestão orientada ao risco ao longo das cadeias de valor, reforçando a necessidade de métricas harmonizadas e de ação coordenada em biossegurança, controle de efluentes e uso responsável de antimicrobianos.

Keywords: Vigilância genômica, uso de antibióticos, segurança dos alimentos, genes de resistência.

Introduction

Antimicrobial resistance (AMR) has moved beyond a restricted clinical concern and now represents a major source of mortality and health loss worldwide [1]. Global burden estimates indicate that resistant bacterial infections were associated with 4.95 million deaths and directly attributable to 1.27 million deaths in 2019, with substantial burden concentrated in invasive infections and in priority pathogens such as *Escherichia coli* and *Klebsiella pneumoniae* [2].

A central driver of resistance selection is the sustained expansion of antimicrobial consumption [3]. Global antibiotic use in humans increased markedly during the first fifteen years of this century and reached 34.8 billion defined daily doses (DDDs), while consumption patterns across regions became increasingly similar [4,5]. More recent WHO surveillance has also shown the scale of the problem by compiling data from more than 23 million bacteriologically confirmed cases reported by 104 countries and documenting substantial resistance in common bacterial infections [6]. Together, these data show that the burden of AMR is linked to a consumption pattern that remains broad in geographic reach and significant in epidemiological terms [7,8].

Within agro-environmental systems, resistance emerges through interacting pressures rather than through a single source [9]. Antimicrobial use in livestock, manure handling, residue transport through water pathways, and chronic exposure of soil and aquatic microbiomes to low antimicrobial concentrations all contribute to selection and dissemination processes [10]. Global estimates for food-producing animals indicate an increase from 63,151 tonnes in 2010 to projected values above 100,000 tonnes by 2030, with additional growth expected in use intensity when standardised by animal biomass [11]. This trend places agricultural production at the centre of both resistance amplification and environmental spread.

Aquaculture adds another relevant pressure point within the broader agro-environmental continuum because antimicrobial inputs are directly connected with aquatic ecosystems [12,13]. Global consumption in this sector was estimated at 10,259 tonnes in 2017 and projected to rise to 13,600 tonnes by 2030, while the Asia-Pacific region accounted for the vast majority of total use and China alone represented more than half of global consumption [14]. These figures indicate that aquatic production systems are important not only for food supply, but also for the circulation of residues and resistance determinants in coastal and inland environments [15].

Environmental evidence quantifies the presence of pharmaceuticals in rivers at the global scale and supports the role of water as a pathway of exposure and a vector for dispersing selective pressure [16]. A 2022 global survey of 258 rivers across 104 countries detected 61 active pharmaceutical ingredients (APIs). It also reported that 25.7% of sites exceeded concentrations considered "safe" for the aquatic environment and identified a set of compounds with exceedances relevant for risk management [17]. In agro-environmental contexts, these findings matter because they integrate inputs from agricultural runoff, urban effluents, industrial discharges, and sanitation systems with insufficient treatment [18].

Urban sanitation and drainage systems, interacting with agricultural and peri-urban catchments, also reflect the population dimension of AMR and its connection with the environment [19,20]. A 2024 metagenomic analysis of untreated wastewater characterised the bacterial resistome across 79 sites in 60 countries and found systematic differences in the abundance and diversity of resistance genes between regions. This reinforces the need for comparable approaches across human health, animal health, and environmental management [21].

This landscape underpins the One Health approach as an operational framework to address health risks that emerge at the human-animal-plant-environment interface [22]. In 2015, WHO established a Global Action Plan on AMR with objectives focused on improving awareness, strengthening surveillance and research, reducing the incidence of infections, optimising antimicrobial use, and ensuring sustainable investment [23]. In 2022, the Quadripartite collaboration between FAO, UNEP, WHO and WOAH formalised the One Health Joint Plan of Action 2022 to 2026, which includes AMR as one of its workstreams and seeks to integrate capacities and systems across sectors [24]. In parallel, UNEP synthesised priority environmental actions across value chains in pharmaceutical manufacturing, agriculture, and health systems, with emphasis on effluents, waste, and the control of discharges that transport antimicrobials and resistance determinants [25].

Antimicrobial resistance within agro-environmental systems is also directly connected to the operational commitments of the 2030 Agenda. In particular, Sustainable Development Goal 3, Good Health and Well-being, through target 3.d, emphasises the need to reinforce capacities for early warning, risk prevention, and the management of health threats, including surveillance and response mechanisms relevant to antimicrobial resistance [26]. Likewise, Sustainable Development Goal 6, Clean Water and Sanitation, through target 6.3, promotes the improvement of water quality by reducing pollution, expanding wastewater treatment, and encouraging recycling and safe reuse, all of which are closely linked to the environmental circulation of antimicrobial residues and resistance determinants [27].

Given the multidimensional nature of this field, any effort to support integrated responses to antimicrobial resistance across the human, animal, and environmental interface in agro-environmental systems requires a broad, systematic, and reproducible understanding of its conceptual evolution and methodological consolidation over time. This need gives rise to the central research question guiding the study: what degree of scientific development has research on the One Health approach and antimicrobial resistance in agro-environmental systems reached, and how has this body of knowledge evolved over time?

From this central concern, twelve specific research questions were derived. First, how has scientific production on One Health and antimicrobial resistance in agro-environmental systems developed over time. Second, which document types dominate the field and what relative share each one represents within the study period. Third, which Scopus subject areas show the strongest association with this domain and how their distribution is configured. Fourth, which countries and institutions lead the scientific output and what relative contribution each one makes. Fifth, who the most influential authors are and how their publication trajectories and collaborative patterns can be described. Sixth, to what extent author productivity follows Lotka's Law and what this indicates about the concentration of scientific leadership. Seventh, which journals function as the main channels for the dissemination of research on One Health and antimicrobial resistance in agro-environmental systems. Eighth, how the journal nucleus is structured under Bradford's Law and how its zones of dispersion are distributed. Ninth, what level of international collaboration is observed among countries and institutions. Tenth, what Reference Publication Year Spectroscopy reveals about the historical roots of the field and the years of highest citation intensity. Eleventh, which seminal studies, methodological contributions, and policy frameworks in human, animal, and environmental health account for the citation peaks identified through RPYS. Twelfth, which emerging themes and future directions are indicated by keyword evolution and thematic mapping.

In response to this problem, the general objective of the study is to describe and quantitatively examine the development of research on the One Health approach and antimicrobial resistance in agro-environmental systems by identifying temporal, geographical, and thematic patterns, collaboration structures, and influential sources, with the aim of informing decision-making and supporting integrated strategies for health and environmental management.

Materials and methods

A bibliometric mapping design supported by statistical and mathematical procedures was employed to assess scientific production, citation performance, and collaboration structures related to the One Health approach and antimicrobial resistance in agro-environmental systems [28,29]. This analytical strategy made it possible to identify temporal trajectories, leading authors, institutions and countries, patterns of scientific cooperation, and emerging research fronts, while maintaining a clear focus on the interconnections among human health, animal health, plant health, and the environment across agroecosystems, livestock production, soils, water bodies, and aquaculture settings.

Following Luna-Morales et al. [30], the procedure was structured into four stages, as shown in Figure 1.

Figure 1. Bibliometric workflow followed in the study.

Source: Prepared by the author.

The study follows a quantitative, exploratory-descriptive, non-experimental, longitudinal, and retrospective design. Through this approach, the literature was traced from the earliest indexed records to the established search cut-off, thereby allowing the identification of shifts in publication dynamics, source concentration, collaboration intensity, and thematic restructuring, consistent with the analytical perspective proposed by García et al. [31].

The search was conducted in Scopus on 5 February 2026. This database was selected because of its broad multidisciplinary scope and the robustness of its metadata structure, particularly for authorship, institutional affiliation, country information, references, and keywords [32,33]. No restrictions were imposed on language or publication period so that retrieval of the domain could be as comprehensive as possible.

The canonical search string used was: TITLE-ABS-KEY ((“one health” OR “one-health” OR onehealth OR “una salud” OR “saúde única” OR ((human OR humans OR “human health”) W/3 (animal OR animals OR “animal health” OR livestock OR wildlife) W/5 (environment OR environmental OR ecosystem OR ecosystems OR plant OR plants))) AND (“antimicrobial resistance” OR “antimicrobial-resistant” OR amr OR “antibiotic resistance” OR “antibiotic-resistant” OR “antimicrobial drug resistance” OR “drug-resistant bacteria” OR “multidrug resistance” OR “multi-drug resistance” OR “antimicrobial resistance gene” OR “antimicrobial resistance genes” OR arg OR args OR “resistencia antimicrobiana” OR “resistência antimicrobiana”) AND (agroenvironmental OR “agro-environmental” OR “agri-environmental” OR agroecosystem OR agroecosystems OR “agro-ecosystem” OR “agro-ecosystems” OR “agricultural system” OR “agricultural systems” OR agriculture OR farming OR farm OR farms OR livestock OR “animal production” OR “plant production” OR “food production” OR crop OR crops OR soil OR soils OR manure OR slurry OR aquaculture OR “rural environment” OR agroambiental OR agroambientales OR “sistemas agroambientales”)).

The query retrieved 2,534 manuscripts, which were exported in CSV format for screening. Following retrieval, the record set was curated to ensure thematic relevance. At this stage, documents without an explicit link to the One Health approach or without a clear connection to antimicrobial resistance in agro-environmental contexts were excluded. Examples included resistance studies lacking a human-animal-environment interface component, or agricultural studies without a resistance dimension. Title, abstract, and keyword consistency was also checked to reduce semantic noise prior to mapping, yielding a final set of 2,515 records [34].

The metadata were subsequently standardised in Microsoft Excel in order to unify author names, institutional affiliations, and country designations, as well as to consolidate keywords through the integration of synonymous terms and the correction of spelling inconsistencies. This stage was essential for reducing distortions in productivity, citation, and collaboration metrics, while also strengthening the consistency and interpretive reliability of co-authorship, keyword co-occurrence, and bibliographic coupling networks [35].

The bibliometric analysis was conducted using bibliometrix version 5.4.0 in RStudio version 2026.05.0 and VOSviewer version 1.6.20. Bibliometrix was used to estimate productivity patterns across authors, countries, and institutions, calculate citation impact indicators and the h, g, and m indices, construct co-authorship networks, and assess the concentration of author productivity through Lotka’s Law. It also enabled the organisation of sources under Bradford’s Law and the application of Reference Publication Year Spectroscopy, with the aim of detecting historical roots and years marked by citation peaks [36]. VOSviewer, in turn, was used to generate maps of keyword co-occurrence, international collaboration, and bibliographic coupling, applying association strength normalisation to identify clusters and their thematic configuration around One Health, bacterial resistance, resistance genes, animal production, manure, soils, water, aquaculture, surveillance, biosecurity, and risk management within agri-food systems [37].

The integration of these procedures enabled the identification of the field’s intellectual structure, thematic evolution, cluster configuration, and collaboration patterns across authors, institutions, and countries. In parallel, a set of core operational indicators was established to enhance intersectoral comparability and to support a One Health interpretation of the evidence base. These indicators were consolidated in Table 1 through

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standardised expressions for antimicrobial use, the proportion of ESBL-producing isolates, and the relative abundance of resistance genes normalised against 16S rRNA.

Results and discussion

In Figure 2, the corpus comprises 2,515 documents from 1981 to 2026, distributed across 818 sources. It records an annual growth rate of 9.87%, 12,943 authors, and intensive co-authorship, at 6.7 authors per document, with 36.22% international collaboration. The dataset contains 4,720 keywords, 16,533 references, a mean document age of 4.15 years, and 27.78 citations per document.

These indicators describe a field with sustained expansion and recent output, where research is organised in large teams and transnational networks [38]. Dispersion across numerous sources suggests thematic and terminological fragmentation, which increases the value of comparable frameworks to map subdomains and reduce disciplinary silo bias [39]. The average citation level suggests a core set of guiding works that structure agendas in surveillance, environmental management, and animal production [40]. The observed collaboration supports integrated One Health approaches that translate evidence into intersectoral policy [41].

Figure 2. General bibliometric indicators of the corpus.

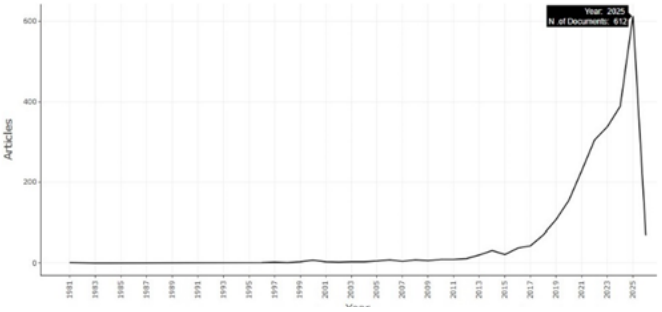
Timespan 1981:2026	Sources 818	Documents 2515	Annual Growth Rate 9.87 %
Authors 12943	Authors of single-authored docs 125	International Co-Authorship 36.22 %	Co-Authors per Doc 6.7
Author's Keywords (DE) 4720	References 16533	Document Average Age 4.15	Average citations per doc 27.78

Source: Summary of key information produced in Bibliometrix.

Figure 3 shows an almost flat series until 2015, followed by accelerated growth from 2018 onwards. The maximum occurs in 2025 with 612 documents. The 2026 value drops to 69, which is consistent with an incomplete year at the search cut-off.

The recent surge suggests the consolidation of an intersectoral agenda linked to the One Health approach, with integrated surveillance and regulatory pressure on antimicrobial use in agri-food chains [42]. This acceleration reflects expanding scientific and policy interest in antimicrobial resistance in agro-environmental systems, driven by the need to integrate human, animal, and environmental health within operational frameworks [43]. The increase also indicates diversification of approaches, with more studies on surveillance, risk assessment, and governance [21]. The field shifts from isolated contributions to an articulated agenda, where conceptual and methodological frameworks organise evidence and enable comparisons across sublines [44].

Figure 3. Annual scientific output.

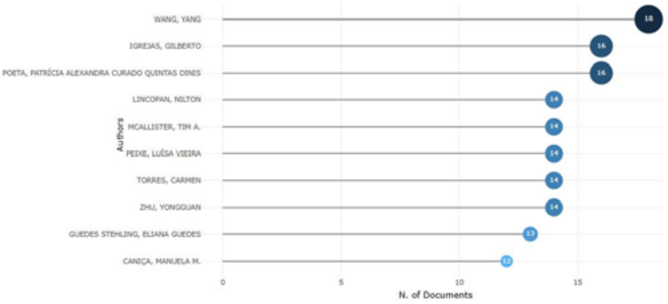


Source: Extracted from Bibliometrix.

In Figure 4, leading authorship shows moderate concentration. WANG, Yang ranks first with 18 documents. IGREJAS, Gilberto and POETA, Patrícia A. C. Q. Dinis each record 16. A second group stands at 14 documents. The top ten range spans 12 to 18.

This pattern suggests leadership by consolidated groups and sustained lines of work rather than isolated contributions. Concentration within a short set of authors often aligns with stable research agendas, international teams, and thematic continuity [45]. In a One Health field, such leadership tends to align shared vocabularies across animal production, the environment, and public health [21]. This alignment facilitates evidence accumulation and comparability across studies, as well as the standardisation of analytical frameworks [22]. It also shapes methodological diffusion and the prioritisation of problems within the agro-environmental domain [46].

Figure 4. Key authors.

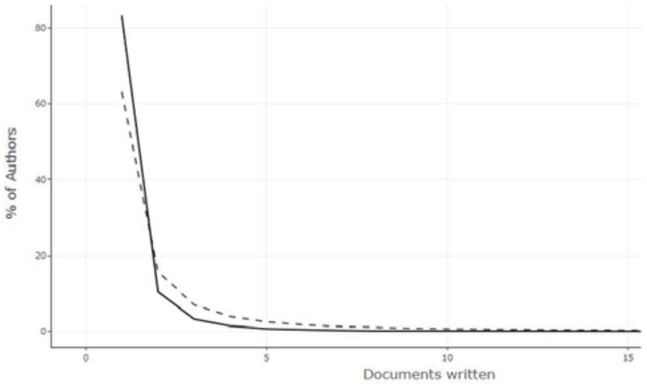


Source: Extracted from Bibliometrix.

In Figure 5, author productivity is asymmetric. 83.2% of authors publish a single document and 10.5% publish two. From three documents onwards, each category represents 3.2% or less, with residual presence up to 18 documents.

The fit to a power-law indicates that output is structured around a small core of researchers with continuity and a broad periphery entering the topic from health, veterinary science, ecology, and production systems [47]. The steeper slope relative to the theoretical model suggests episodic participation and author turnover, consistent with applied problems and short-cycle projects [48]. Within field dynamics, the core concentrates conceptual frameworks, surveillance protocols, and operational definitions of AMR in agroecosystems, which then diffuse into peripheral contributions [49].

Figure 5. Distribution of authors by productivity, Lotka's Law.

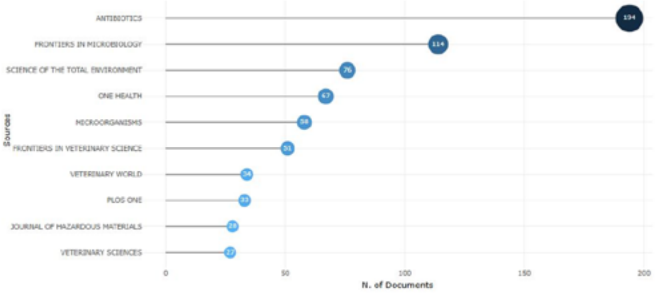


Source: Extracted from Bibliometrix.

In Figure 6, Antibiotics concentrates 194 documents, followed by Frontiers in Microbiology (114) and Science of the Total Environment (76). One Health contributes 67 and Microorganisms 58. The rest of the top ten ranges from 51 to 27 documents, with a veterinary and environmental emphasis.

Leadership by clinical, microbiological, veterinary, and environmental journals indicates a frontier field that links pathogen surveillance, antimicrobial use, and dissemination pathways across water, soil, and production systems [50]. The simultaneous presence of One Health-focused titles and high-impact environmental outlets indicates progressive integration of compartments and methods, from molecular microbiology to risk assessment [51]. This pattern also reinforces that the agenda disseminates through established channels where terminology, surveillance designs, and comparable metrics become standard for health and agro-environmental decision-making [52].

Figure 6. Leading journals.

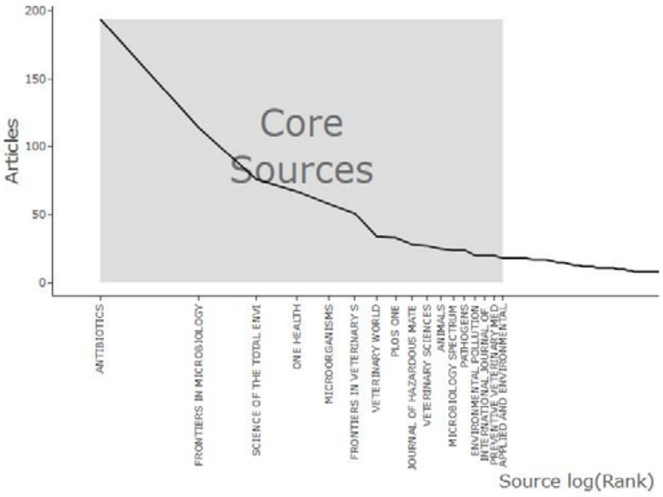


Source: Extracted from Bibliometrix.

In Figure 7, Bradford's Law identifies 17 core journals that collectively contain 833 articles. Output then redistributes into two peripheral zones with comparable article volumes, accompanied by a strong expansion in the number of sources, from an intermediate ring to a long tail.

This core–periphery structure indicates that knowledge dissemination is organised around a stable set of journals that validate approaches, terminology, and metrics [53]. The long tail reflects the entry of additional disciplines and audiences, where AMR is analysed through microbiology, veterinary science, environmental research, and agri-food management [54]. This arrangement concentrates cross-cutting debates in the core and distributes specialised studies across the periphery, sustaining One Health integration between surveillance, environmental dissemination routes, and production practices in agri-food chains [55].

Figure 7. Article dispersion, Bradford's Law.

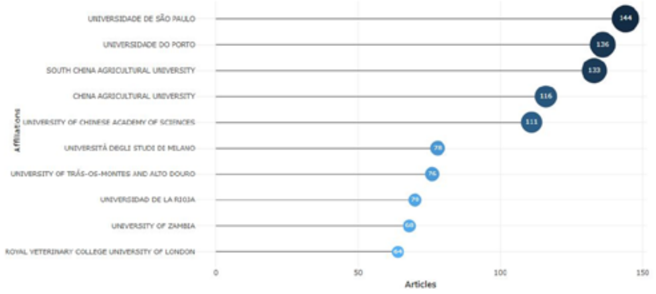


Source: Extracted from Bibliometrix.

In Figure 8, Universidade de São Paulo (144) and Universidade do Porto (136) lead, followed by South China Agricultural University (133) and China Agricultural University (116). The University of Chinese Academy of Sciences records 111. The top ten includes Università degli Studi di Milano, the University of Trás-os-Montes and Alto Douro, Universidad de La Rioja, the University of Zambia, and the Royal Veterinary College, University of London.

Institutional leadership reflects sustained capacity to integrate microbiology, veterinary science, and environmental sciences within a single analytical framework [56]. The joint presence of Chinese agricultural universities and Ibero-American centres suggests that AMR in production systems and its environmental footprint is addressed as both a public health problem and an agri-food governance issue [14]. These institutions articulate surveillance networks, exposure studies in water and soils, and risk assessment across value chains, linking experimental evidence to health and environmental management [40].

Figure 8. Leading institutions.

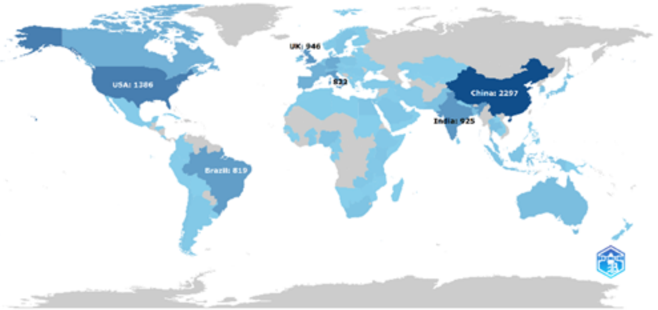


Source: Extracted from Bibliometrix.

In Figure 9, China leads with 2,297 articles, followed by the United States with 1,386, the UK with 946, and India with 925. Italy (822) and Brazil (819) form the next group. Germany, Spain, Portugal, Canada, and France complete the top ten. The map covers 117 countries.

Concentration in China, the United States, the UK, and India suggests that the agenda rests on intensive production systems, laboratory capacity, and established surveillance programmes [21]. The presence of Europe and Brazil in the upper tier reflects active dialogue across public health, veterinary science, and the environment, where resistance is examined alongside dissemination routes through water, soils, and food chains [41]. This scientific geography reinforces the cross-border nature of the One Health approach and explains why integrated frameworks gain centrality to connect microbiological evidence with health and agro-environmental decisions [43].

Figure 9. Output by country.

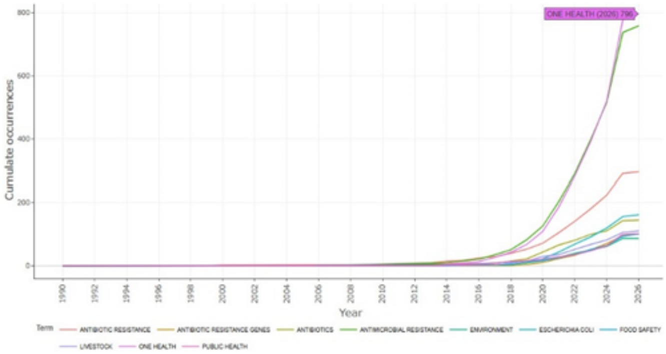


Source: Extracted from Bibliometrix.

In Figure 10, cumulative term dynamics accelerate from 2018; One Health and antimicrobial resistance dominate and reach 796 and 758 occurrences in 2026. Antibiotic resistance reaches 296.

The simultaneous rise of terms related to One Health, antimicrobial resistance, livestock, food safety, and environmental matrices indicates that the literature is integrating production practices, exposure routes, and downstream impacts within a shared analytical space [20]. The continued visibility of resistance genes also points to a transition towards genomic and resistome-based surveillance, instead of relying exclusively on descriptive reports of resistant isolates [6]. This pattern supports a research agenda oriented towards comparability across compartments and towards interventions that connect animal management, environmental monitoring, and public health response [52].

Figure 10. Term frequency over time.

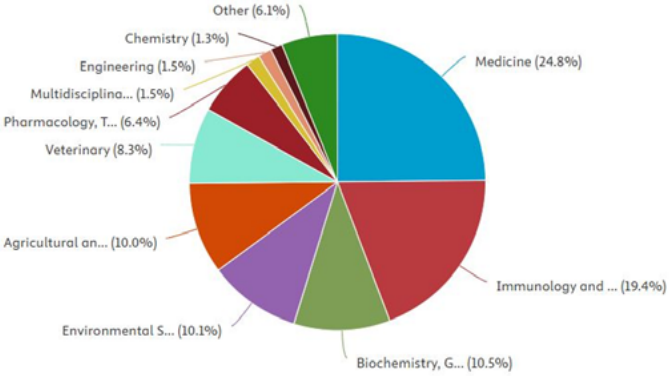


Source: Extracted from Bibliometrix.

In Figure 11, Scopus classifies output into areas dominated by Medicine (24.8%) and Immunology and Microbiology (19.4%). Biochemistry, Genetics and Molecular Biology follows (10.5%), then Environmental Science (10.1%), Agricultural and Biological Sciences (10.0%), Veterinary (8.3%), and Pharmacology, Toxicology and Pharmaceutics (6.4%). Other accounts for 6.1%.

This distribution shows a strong biomedical base centred on pathogens, immune response, and therapeutics [22]. The weight of environmental and agro-biological sciences indicates integration of contamination pathways, manure management, soils, and water alongside animal production and food safety [39]. Veterinary science acts as a bridge between clinical research and production systems, consistent with One Health [8]. Disciplinary convergence reinforces shared frameworks for surveillance, risk assessment, and intervention design across the agri-food chain [49].

Figure 11. Publications by subject area.

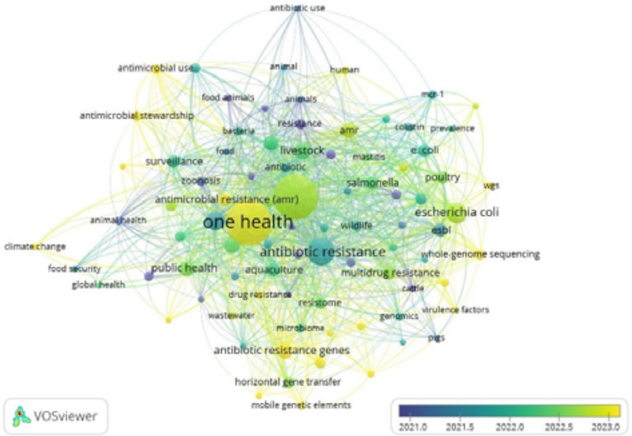


Source: Extracted from Scopus.

In Figure 12, the co-occurrence map positions One Health and antibiotic resistance as central nodes connected with AMR, livestock, poultry, surveillance, and public health. The network integrates pathways such as wastewater and molecular modules such as the resistome, resistance genes, horizontal transfer, whole-genome sequencing, and mcr-1, organised around *Escherichia coli*.

The linking pattern shows that the agenda does not treat resistance as an isolated clinical phenomenon. It connects animal production, food safety, and public health with environmental reservoirs and genomic tools [15]. The proximity between surveillance, stewardship, and sequencing reflects emphasis on early detection and the traceability of lineages and genes [48]. The prominence of *Escherichia coli*, colistin, and mcr-1 points to sentinel markers for monitoring selective pressure in agri-food chains [57]. This structure strengthens a shared language across sectors and supports coordinated decisions in biosecurity, effluent management, and prudent antimicrobial use [50].

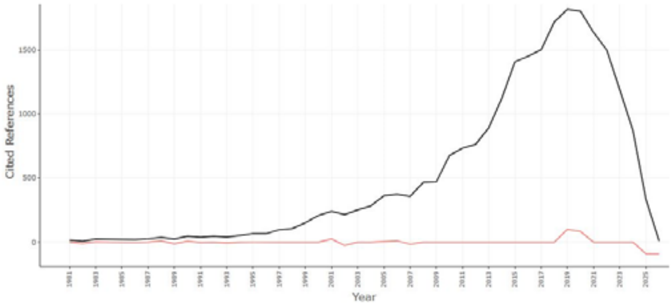
Figure 12. Keyword co-occurrence.



Source: Extracted from VOSviewer.

In Figure 13, RPYS shows a marked intensification in cited references from 2010 onwards, with a maximum in 2019 (1,818) and high values in 2020 (1,802) and 2018 (1,718). Deviation from the five-year moving median increases between 2014 and 2019 and becomes negative after 2021.

Figure 13. Annual distribution of cited references.

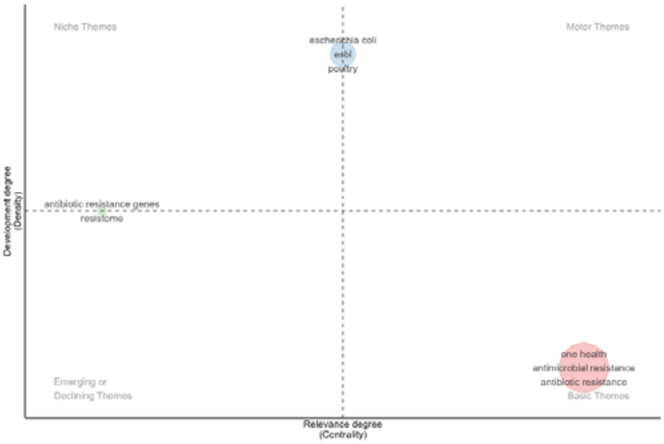


Source: Extracted from Bibliometrix.

In Figure 14, the thematic map places One Health, antimicrobial resistance, and antibiotic resistance as basic themes, with high centrality and low density. A second axis groups *Escherichia coli*, ESBL, and poultry as a motor theme, with high density and connectivity. In the low-centrality quadrant, antibiotic resistance genes and the resistome appear as more specialised themes with weaker integration into the broader field.

Figures 13 and 14 depict a field organised around a broad conceptual base and a smaller set of specialised molecular lines. The concentration of cited references after 2010 indicates that recent reviews, surveillance frameworks, and intersectoral action plans have structured the domain. At the same time, the thematic map places *Escherichia coli*, ESBL, and poultry in a dense and connected cluster, suggesting that applied evidence tends to accumulate around sentinel organisms and production contexts where selection pressure becomes measurable through operational indicators [12, 40, 13]. By contrast, the resistome and resistance-gene cluster reflects a more specialised analytical layer that is advancing rapidly, although with weaker integration into the wider policy and management debate [48, 18, 16].

Figure 14. Thematic map.



Source: Extracted from Bibliometrix.

Table 1 summarises three indicators that are comparable across the human, animal, and environmental compartments. It standardises data extraction and facilitates cross-study comparisons.

These three indicators reinforce a One Health reading because they link processes that occur in different compartments yet form a single epidemiological continuum [47]. Use intensity in animal production is associated with the emergence and amplification of resistance in commensal and pathogenic bacteria circulating along the food chain [17]. The presence of ESBL phenotypes in *Enterobacterales* is interpreted as a signal of sustained selective pressure and horizontal gene transfer, with direct implications for therapeutic efficacy [38]. The relative abundance of resistance genes in agro-environmental matrices evidences persistence and recirculation of the resistome, supporting the concept of active environmental reservoirs rather than passive recipients [2].

Table 1. Priority operational indicators to assess antimicrobial resistance under a One Health approach in agro-environmental systems.

Indicator	Measure	Formula	Variables and units	Source
Intensity of antimicrobial use in animal production (AMU)	Selective pressure driven by antimicrobial consumption in livestock production.	$AMU = \frac{\sum_i m_i}{PCU}$ $PCU = \sum_k (N_k \cdot W_k)$	AMU [$\mathrm{mg \cdot PCU^{-1}}$] ratio between mass used and biomass exposed m_i [mg] mass of active ingredient i used in the period $\sum_i m_i$ [mg] sum of masses of all active ingredients i PCU [kg] corrected animal biomass (Population Correction Unit) N_k: number of animals in category k W_k: [$\mathrm{kg \cdot animal^{-1}}$] standard weight or slaughter weight for category k	[57]
Proportion of ESBL producers in *Enterobacterales* (ESBL%)	Frequency of ESBL in agri-food chains and environmental discharges.	$\%ESBL = \left(\frac{n_{\mathrm{ESBL}}}{n_{\mathrm{Ent}}}\right) \cdot 100$	ESBL% [%] proportion nEnt: total number of isolates confirmed as Enterobacterales evaluated nESBL: isolates with phenotypic confirmation of ESBL according to reference protocol (synergy with inhibitor or other validated method) 100: conversion factor to percentage	[5]
Relative abundance of resistance genes normalised to 16S (RAARG)	Resistome intensity adjusted for bacterial biomass. Useful for water, soil, manure, and effluents.	$RA_{\mathrm{ARG}} = \frac{C_{\mathrm{ARG}}}{C_{16S}}$	RAARG [1] normalised ratio CARG [$\mathrm{copies \cdot L^{-1}}$ in liquids, $\mathrm{copies \cdot g^{-1}}$ in solids] absolute abundance of the target resistance gene (qPCR or quantitative metagenomics) C16S [$\mathrm{copies \cdot L^{-1}}$ in liquids, $\mathrm{copies \cdot g^{-1}}$ in solids] absolute abundance of the 16S rRNA gene as a proxy for bacterial biomass	[22]

Source: Prepared by the author.

Conclusions

The study confirms sustained scientific development on One Health and antimicrobial resistance in agro-environmental systems, with a shift towards surveillance and risk management at the human, animal, plant, and environmental interface. This evolution answers the central research question by evidencing an increasingly integrated agenda.

The field's structure combines a moderate concentration of leadership and a core set of journals that establishes standards, alongside an interdisciplinary periphery that broadens applications. Lotka's and Bradford's laws clarify the distribution of productivity and sources, enabling the identification of priority actors and publication channels for disseminating findings and strengthening inter-institutional collaboration.

Influential references, identified through RPYS, position guidelines, policy frameworks, and multicentre studies as anchors of the domain. Keyword dynamics and the thematic map delineate applied fronts in production matrices and sentinel organisms such as *Escherichia coli*, as well as frontier lines linked to resistomes and genomic surveillance.

The agenda requires compartment-compatible metrics and coordinated actions on prudent use, biosecurity, and the control of manures, effluents, and hydrological and edaphic pathways. This mapping provides a reproducible basis for prioritising research and supporting intersectoral decision-making.

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