

## Three Decades of Bibliometric Analysis of the Rising Tide of Cefquinome as a Fourth-Generation Cephalosporin Exclusively for Veterinary use

Manar Alhawil<sup>1</sup>, Mohamed S. Ahmed <sup>2</sup>, Sherief M. Abdel-Raheem <sup>3</sup>, Mustafa Shukry <sup>1</sup>, Sameer Alhojaily <sup>1</sup> and Mahmoud Kandeel <sup>1\*</sup>

<sup>1</sup>Department of Biomedical Sciences, College of Veterinary Medicine, King Faisal University, 31982 Al-Ahsa, Saudi Arabia

<sup>2</sup>Department of Clinical Sciences, College of Veterinary Medicine, King Faisal University, 31982 Al-Ahsa, Saudi Arabia

<sup>3</sup>Department of Public Health, College of Veterinary Medicine, King Faisal University, 31982 Al-Ahsa, Saudi Arabia

\*Corresponding author: [mkandeel@kfu.edu.sa](mailto:mkandeel@kfu.edu.sa)

Article History: 25-337

Received: 21-Dec-25

Revised: 19-Feb-26

Accepted: 22-Feb-26

Online First: 07-Mar-26

### ABSTRACT

Cefquinome, a fourth-generation cephalosporin for veterinary use, is vital for treating bacterial infections in food-producing animals. This study provided a bibliometric analysis of global cefquinome research to identify key contributors, publication trends, collaborations, and emerging themes. We conducted a comprehensive bibliometric analysis using the Scopus database, extracting 171 documents published between 1991 and July 2025. Analysis included publication trends, citation metrics, author and institutional contributions, country collaboration networks, and thematic evolution using VOSviewer and Biblioshiny visualization tools. The dataset revealed a 4.85% annual growth rate, with publications surging after 2011. China accounted for 40.4% of corresponding authorships. Cefquinome research clustered around four main thematic areas: (1) pharmacokinetics and PK/PD optimization, (2) antibiotic resistance and microbiological studies, highlighting *Staphylococcus aureus* and *Escherichia coli*; (3) clinical and veterinary applications, especially mastitis and respiratory diseases; and (4) analytical and formulation innovations, including HPLC detection, sustained release, and liposome systems. Thematic evolution showed a shift from clinical trials toward mechanistic and modeling studies in resistance and bioavailability. Cefquinome research has matured from basic characterization toward sophisticated resistance-focused investigations, driven primarily by Asian institutions responding to livestock production demands. Future research should strengthen international collaboration, explore environmental impacts, and investigate antimicrobial alternatives to preserve cefquinome's clinical effectiveness while addressing global antimicrobial resistance challenges.

**Keywords:** Cephalosporins, Bibliometric analysis, Veterinary medicine, Scopus, VOSviewer, Antimicrobial resistance.

### INTRODUCTION

Cefquinome is a fourth-generation cephalosporin antibiotic developed exclusively for veterinary use (Thomas et al. 2006). It exhibits a broad spectrum of antimicrobial activity against both Gram-positive and Gram-negative bacteria, including those producing  $\beta$ -lactamases (Papich 2016). It is widely used in the treatment of respiratory infections (Qu et al. 2019; Somogyi et al. 2023), mastitis (Omar et al. 2025), endometritis (Li et al. 2025), septicemia (Ahmad et al. 2015), and other bacterial diseases and applications in cattle, pigs, horses and other animals (Cheng et al. 2020; Elbadawy et al. 2021). In addition, it is used in treating infections in wild birds (Zhao et al. 2017) and fish (Shan

et al. 2018). It also attracted the focus of combination with other substances for improved efficacy (Zhang et al. 2025).

In veterinary medicine, cefquinome is used in handling several microorganisms, including *Staphylococcus aureus* (Li et al. 2019; Gao et al. 2021; Jiang et al. 2022), *Escherichia coli* (Yu et al. 2017; Zhang et al. 2021; Gao et al. 2025), *Streptococcus agalactiae* (Yang et al. 2023), *Staphylococcus xylosus* (Zhou et al. 2018), *Streptococcus equi* (Lee et al. 2020), *Streptococcus uberis* (Li et al. 2025), *Actinobacillus pleuropneumoniae* (Zhang et al. 2020), *Klebsiella pneumoniae* (Qu et al. 2019), *Pasteurella multocida* (Somogyi et al. 2023), *Mannheimia haemolytica* (Alvarez et al. 2023) and *Streptococcus suis* (Somogyi et al. 2023).

**Cite This Article as:** Alhawil M, Ahmed MS, Abdel-Raheem SM, Shukry M, Alhojaily S and Kandeel M, 2026. Three decades of bibliometric analysis of the rising tide of cefquinome as a fourth-generation cephalosporin exclusively for veterinary use. International Journal of Veterinary Science 15(3): 868-878. <https://doi.org/10.47278/journal.ijvs/2026.033>

Over the past three decades, research on cefquinome has expanded significantly, encompassing pharmacodynamics (Lee et al. 2020), pharmacokinetics (Lee et al. 2020), microbial susceptibility testing (Zonca et al. 2011), clinical outcomes (Swinkels et al. 2013), drug residues (Liu et al. 2023) and environmental impacts (Qiu et al. 2022). However, the body of literature is dispersed across multiple journals, institutions, and countries, with diverse thematic focuses evolving over time. This complexity calls for a systematic approach to synthesize existing knowledge and identify knowledge gaps, leading to informed decision-making in both clinical practice and further research.

Bibliometric analysis is a quantitative approach used to evaluate scientific publications, map research trends, and identify key contributors and collaborations (Kumar 2025). Despite increasing research on cefquinome, no comprehensive bibliometric review has been conducted. In this context, we provided up-to-date bibliometric information on important antibiotics and antiviral agents in the veterinary field (Alsuhaibani et al. 2025; Naji et al. 2025a; Naji et al. 2025b).

This study addresses that gap by analyzing cefquinome research. The objective of this study was to conduct thorough analysis of the global publication and citation trends of cefquinome and to rank prominent authors, institutions, countries and journals in the cefquinome literature, to investigate international and institutional collaborations in cefquinome research, to conduct thematic mapping of the predominant research areas along with their development over the study timeframe, and to identify emerging and declining research domains that could be promoted further based on the prospective veterinary antimicrobial research. The findings provide an overview of cefquinome research, highlight influential contributors, and reveal emerging areas that may guide future studies in veterinary medicine and antimicrobial pharmacology.

## MATERIALS AND METHODS

### Study design

This analysis used bibliometric methods to systematically explore worldwide patterns in cefquinome research from 1991 to July 27, 2025.

### Data sources and search strategy

A comprehensive bibliometric approach was used to map global research on cefquinome. Data were extracted from peer-reviewed literature indexed in Scopus database covering the period 1991– July 27, 2025. The search query included “(TITLE(cefquinome) AND (LIMIT-TO (DOCTYPE,"ar"))) AND (LIMIT-TO (LANGUAGE,"English"))”. To maintain analytical consistency, only original research articles were included; conference proceedings, editorials, notes, and book chapters or other publications were excluded.

### Data extraction and preprocessing

Bibliographic metadata was downloaded and standardized for consistency. Keywords Plus, author keywords (DE), cited references and authorship data were extracted for each publication. Data were cleaned and harmonized before quantitative and network analysis. Data

was exported from Scopus and filtered through the Scopus query by removing the unidentified authors and institutes. The exported file was checked for inconsistencies. No duplicate records were found in the exported data. Fractional authorship and international co-authorship rates were calculated to assess collaboration patterns.

### Bibliometric analysis

Annual publication trends were quantified, including calculation of growth rates, document age, and average citation impact. Journal sources, authors and affiliations were ranked based on volume and fractionalized counts. Country-level scientific production and collaboration networks were mapped using co-authorship analysis, centrality scores and frequency tables. Corresponding author countries, research output, and cross-country co-authorships were analyzed.

### Thematic mapping and clustering

Research topic evolution was described using trend analysis of keywords and frequency metrics. Data visualization tools—including VOSviewer and thematic mapping—were employed to perform topic clustering, centrality/density capture, and motor, core, niche, and emerging theme identification.

### Citation analysis

Global citation data were retrieved for all included papers. Most globally cited papers were identified and summary metrics—total citation count, average citations per year, normalization for publication date—were calculated. DOI-based tracking ensured access to full bibliographic records.

### Visualization and reporting

All Figs and network visualizations were created using Biblioshiny and VOSviewer (van Eck and Waltman 2010; Darvish 2020).

## RESULTS

### Data description

The dataset includes 171 documents from 93 unique sources published between 1991 and 2025, showing a consistent annual growth rate of 4.85%. These works featured an average age of 9.46 years and gained an average of 14.09 citations per document, reflecting enduring relevance in the field. The references cited totaled 4749. Keywords Plus numbered 1427 with 353 distinctive author keywords. Collaborative patterns reveal an average of 5.9 co-authors per document and 17.54% international co-authorship (Table 1).

### Annual scientific production

Annual scientific production in cefquinome research showed a gradual increase over more than three decades. Throughout the 1990s, output was very modest, rarely exceeding one article per year and with some years such as 1993, 1996, 1999, and 2000 registering no publications at all. After 2000, output began to rise, with a clear surge in productivity starting in 2011, when publications first reached double digits. The most active years were 2014 to 2018, with consistent peaks of 13 to 15 articles annually,

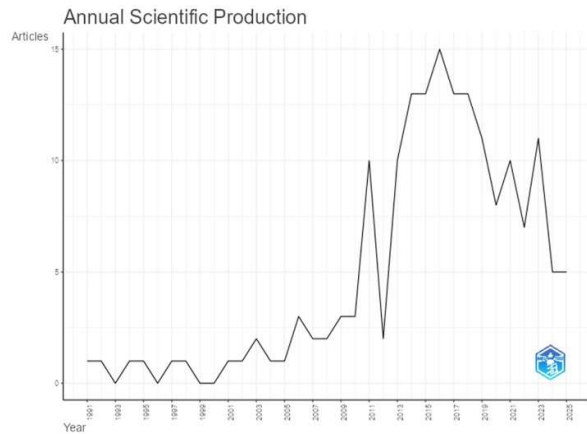
marking a period of rapid expansion and heightened research interest. Activity remained high into the early 2020s, averaging between 7 and 11 articles per year, and even in 2024 and 2025, the field sustained output with 5 articles each year (Fig. 1).

**Table 1:** Summary of data on cefquinome research

Description	Results
<b>Main Information About Data</b>	
Timespan	1991:2025
Sources	93
Documents	171
Annual Growth Rate %	4.85
Document Average Age	9.46
Average citations per doc	14.09
References	4749
<b>DOCUMENT CONTENTS</b>	
Keywords Plus (ID)	1427
Author's Keywords (DE)	353
<b>AUTHORS</b>	
Authors	684
Authors of single-authored docs	4
<b>AUTHORS COLLABORATION</b>	
Single-authored docs	5
Co-Authors per Doc	5.9
International co-authorships %	17.54
<b>DOCUMENT TYPES</b>	
article	171

**Most relevant resources**

Research on cefquinome is concentrated in a few key journals. The Journal of Veterinary Pharmacology and Therapeutics leads with 27 articles, making it the primary publication venue. Antimicrobial Agents and Chemotherapy and Frontiers in Microbiology both published 7 articles, reflecting the interest in microbial and pharmacological aspects. BMC Veterinary Research and Frontiers in Veterinary Science each contributed 5 articles. Other details are shown in Fig. 2.



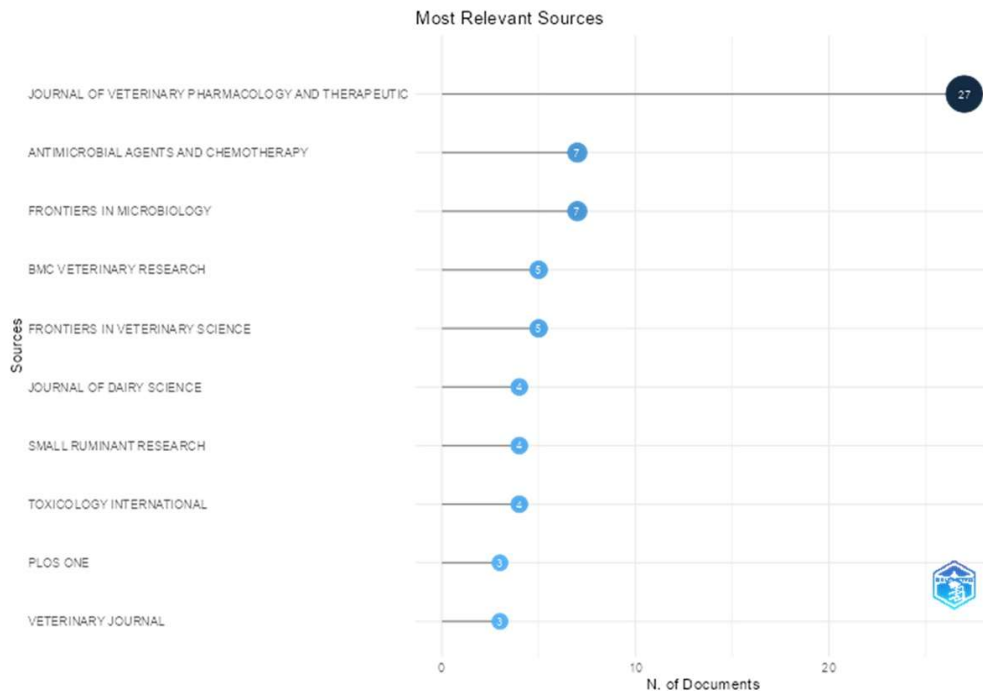
**Fig. 1:** Annual Scientific Production.

**Most relevant authors**

The research landscape is driven by prolific authors such as Ding H, who contributed 15 articles, followed by Zhang L (10), and Sun J (9), showing leadership in advancing cefquinome knowledge. Several others—including Uney K, Hao Z, and Shan Q—produced between 6 and 8 articles each, maintaining strong fractional scores, which indicates frequent lead or corresponding authorship roles (Fig. 3).

**Most relevant affiliations**

South China Agricultural University leads institutional contributions with an impressive 164 publications, highlighting it as a major research hub for cefquinome studies. Qingdao Agricultural University (41) and Huazhong Agricultural University (24) follow as significant centers. Other universities such as University of Selcuk and China Agricultural University underscore diverse geographic involvement (Fig. 4).



**Fig. 2:** Most Relevant Sources.

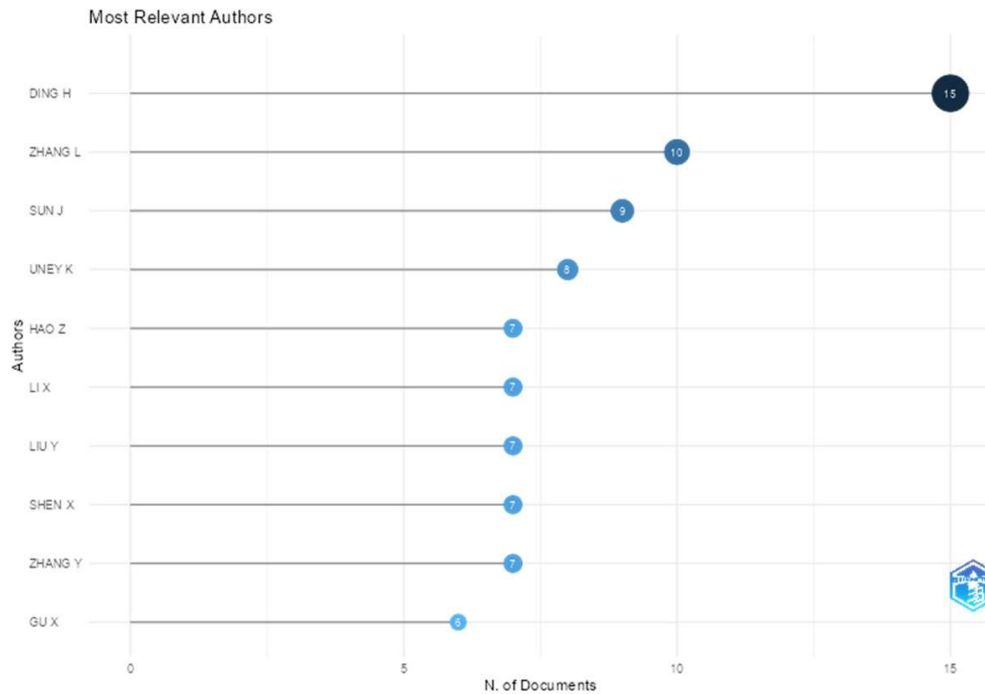


Fig. 3: Most Relevant Authors.

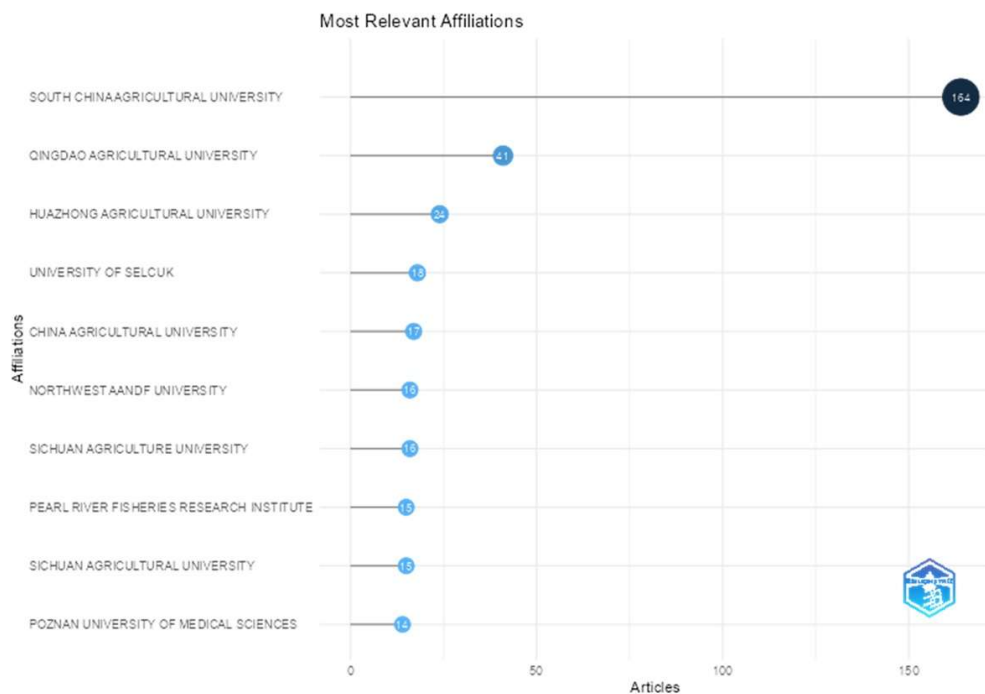


Fig. 4: Most Relevant Affiliations.

**Corresponding author countries**

China was the dominant country for corresponding authors with 69 articles, making up 40.4% of the total, and 63 were single-country publications. Egypt contributed 10 articles (5.8%), with 4 of these being multi-country collaborations. Germany, India, and Turkey each produced 8 articles (4.7%), but Turkey had one multi-country paper (12.5% MCP), while Germany and India had none. Belgium published 5 studies, with 1 involving international collaboration (20% MCP rate). Notably, countries such as the Netherlands, France, Italy, New Zealand, Pakistan and the USA were involved only in multi-country collaborations, with a 100% MCP rate for their single

articles (Fig. 5).

**Country scientific production and collaboration world map**

China dominated cefquinome scientific production. Germany was second, followed by Egypt, Turkey, and India. Other active countries included the USA, Belgium, and the UK. Other details are displayed in Fig. 6.

Collaboration analysis reveals bilateral partnerships, particularly between China and the USA (6 joint works), Egypt and Saudi Arabia (3), and several European country pairings such as Belgium-Italy and Germany-Netherlands (Fig. 6).

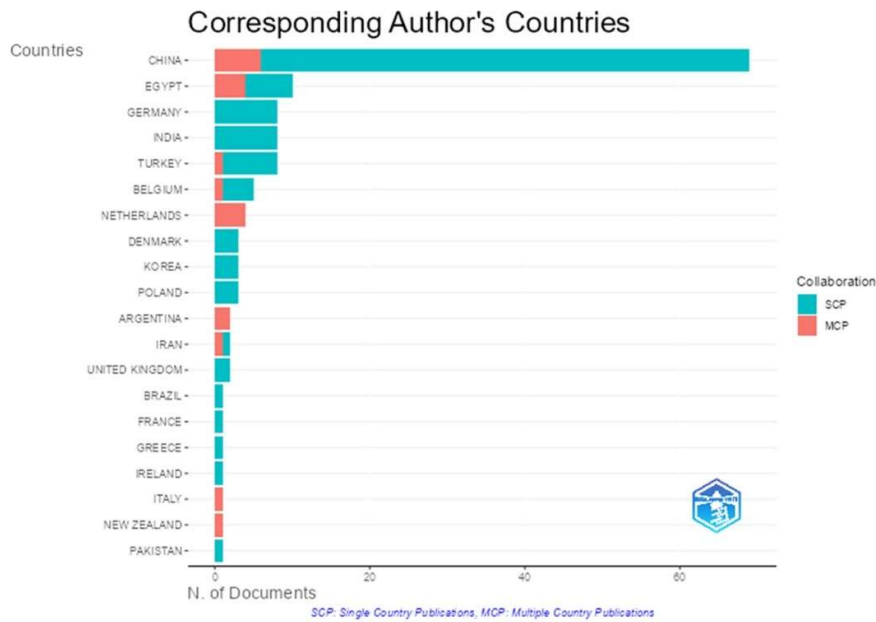


Fig. 5: Corresponding Author Countries.

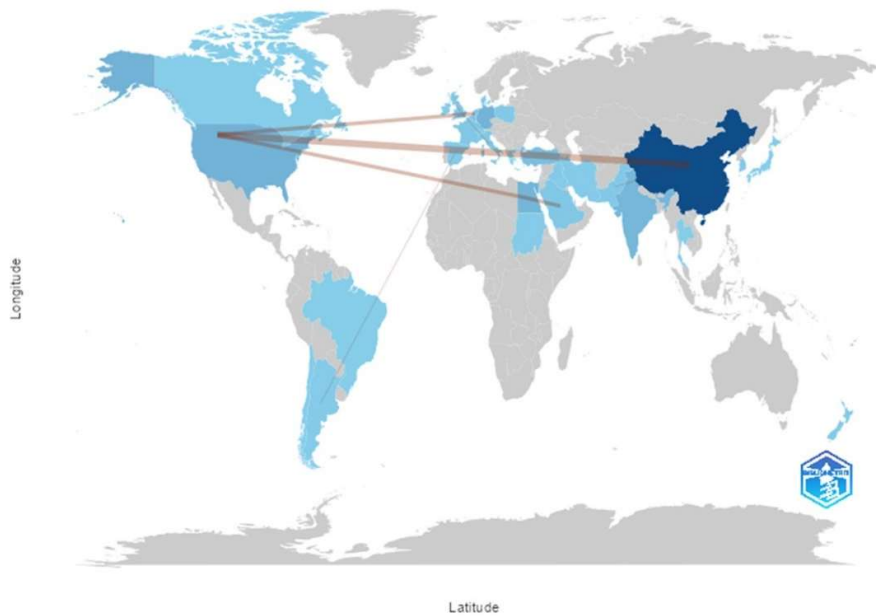


Fig. 6: Country Scientific Production and Collaboration World Map.

**Trend topics**

Trend topics in cefquinome research have shifted and grown over time, with certain subjects gaining distinct prominence. "Cefquinome" was the most frequent keyword, found in 89 articles and peaking in importance from 2015 to 2021. Other notable themes included "pharmacokinetics" (30 times), rising sharply from 2015 onward, and "cephalosporins," which appeared consistently between 2015 and 2019. Research around "mastitis," "antibiotic," "Escherichia coli," and "buffalo calves" showed steady interest. Technical topics like "PK/PD," "HPLC," and "bioavailability" emerged strongly in the late 2010s, marking methodological advances. "*Staphylococcus aureus*" appeared more in recent years (2016–2021), drawing attention to resistance and infections (Fig. 7).

**Most global cited papers**

The most cited papers in cefquinome research cover a

range of foundational and innovative topics. Cavaco et al. (2008, 127 citations) is highly influential for work on resistance gene (Cavaco et al. 2008). Limbert et al. (1991, 105 citations) established key pharmacokinetics insights (Limbert et al. 1991), while Shpigel et al. (1997, 82 citations) advanced treatment protocols for mastitis in cows (Shpigel et al. 1997). Thomas et al. (2006, 60 citations) presented data on microbial susceptibility patterns (Thomas et al. 2006). Uney et al. (2011, 55 citations) contributed a validation method by HPLC (Uney et al. 2011). Moro et al. (2019, 54 citations) brought attention to sensor technology for drug monitoring (Moro et al. 2019) (Table 2).

**Relationships among countries, institutions, sources, and research topics**

The relationships among countries, institutions, journals, and research topics in cefquinome studies form a

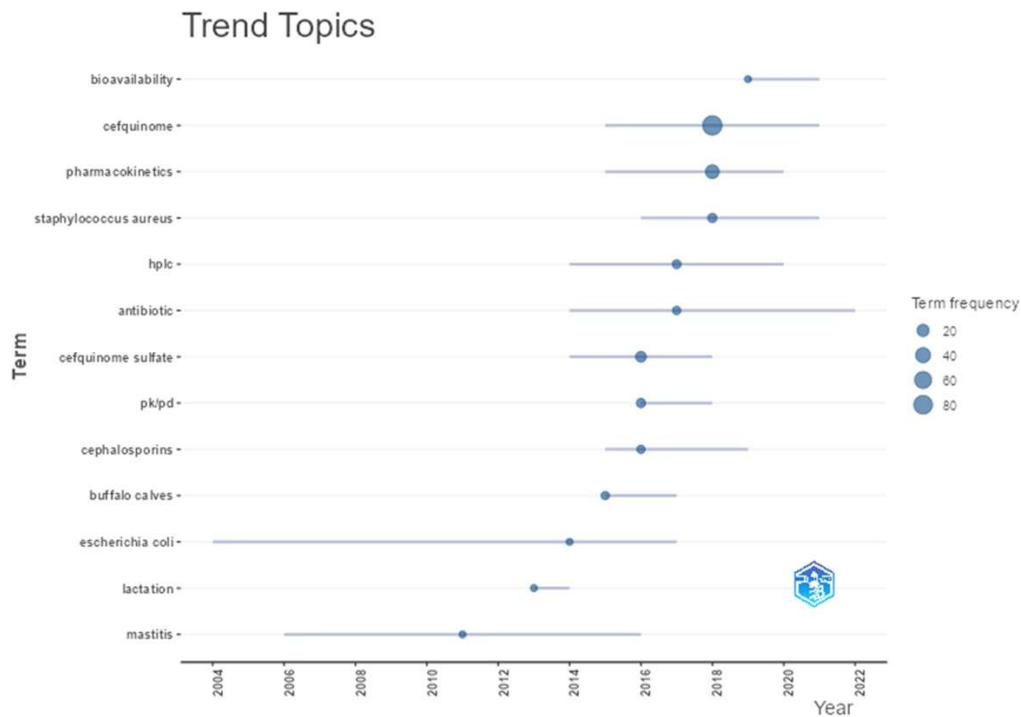


Fig. 7: Trend Topics.

Table 2: Most global cited papers, TC: total citations

Paper	DOI	Total Citations	TC per Year	Normalized TC
CAVACO LM, 2008, ANTIMICROB AGENTS CHEMOTHER	10.1128/AAC.00354-08	127	7.05555556	1.45142857
LIMBERT M, 1991, ANTIMICROB AGENTS CHEMOTHER	10.1128/AAC.35.1.14	105	3	1
SHPIGEL NY, 1997, J DAIRY SCI	10.3168/jds.S0022-0302(97)75941-1	82	2.82758621	1
THOMAS E, 2006, VET MICROBIOL	10.1016/j.vetmic.2005.12.019	60	3	1.47540984
UNEY K, 2011, ANTIMICROB AGENTS CHEMOTHER	10.1128/AAC.01126-10	55	3.66666667	2.15686275
MORO G, 2019, SENS ACTUATORS, B CHEM	10.1016/j.snb.2019.126786	54	7.71428571	4.56923077

complex and interconnected web. Leading universities—such as South China Agricultural University, Southwest University, and Qingdao Agricultural University—have strong ties to core journals like the Journal of Veterinary Pharmacology and Therapeutics and Frontiers in Microbiology, driving a high volume of research output. These institutions frequently collaborate with other domestic and international universities, notably those in Europe, Asia and North America. Topics such as cefquinome, pharmacokinetics, PK/PD, and antibiotic resistance act as central thematic bridges, frequently appearing together and linking diverse research clusters. The visualizations show how institutions channel their scientific output into specific journals, which then help disseminate studies that focus on recurring keywords and clinical problems, such as mastitis and *Escherichia coli* (Fig. 8).

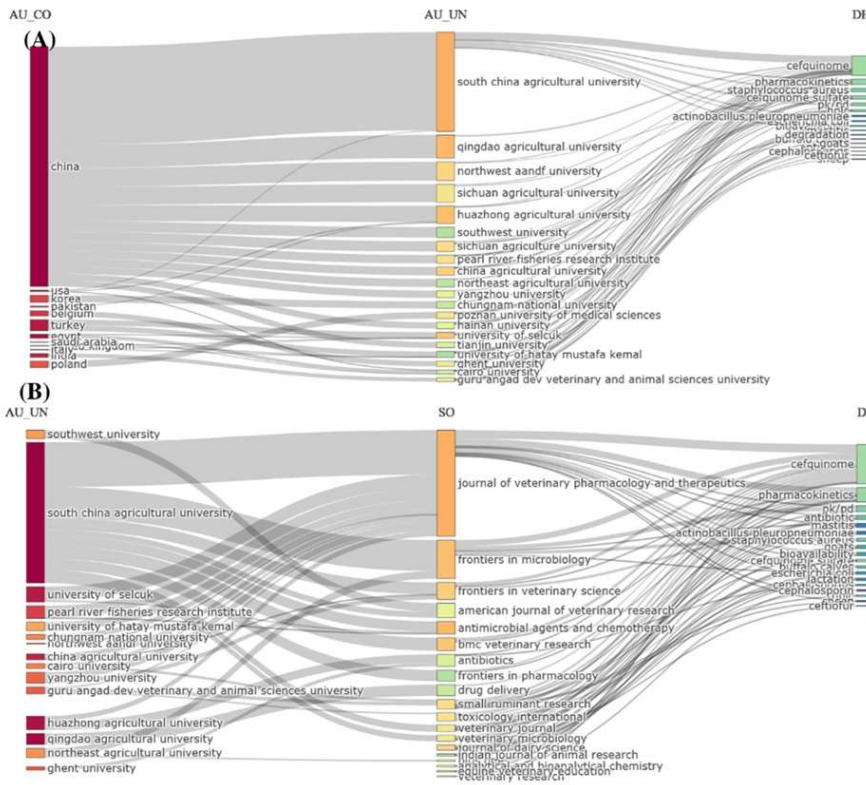
#### Core, niche, and emerging themes in cefquinome research

The motor themes (e.g., antibiotic, cephalosporin, PK/PD, *Staphylococcus aureus*, *Escherichia coli*, sustained release, and intramuscular administration) represent the most influential areas, focusing on pharmacokinetic–pharmacodynamic optimization, dosing strategies and therapeutic applications in livestock. Basic

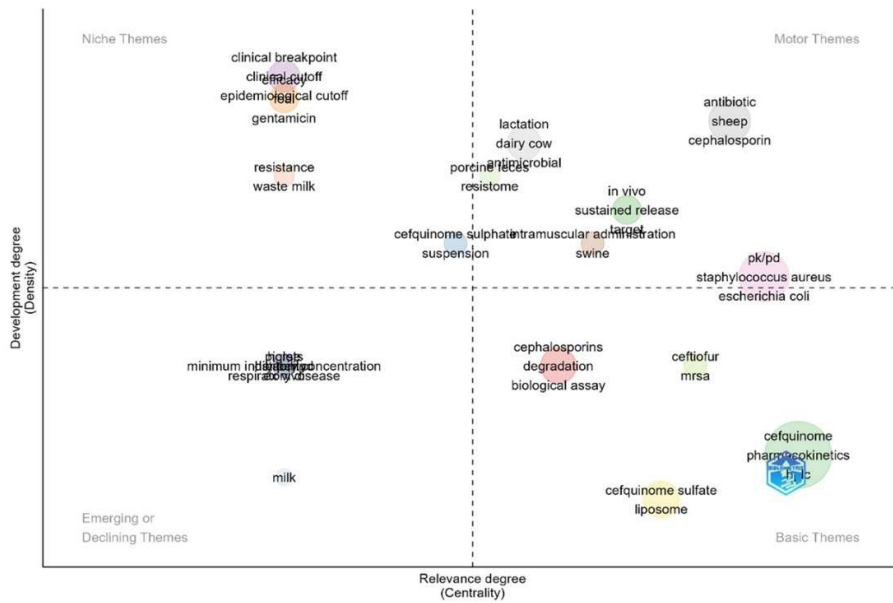
themes such as cefquinome, pharmacokinetics, liposome, ceftiofur, and MRSA indicate the foundation of ongoing studies centered on drug delivery systems and comparative  $\beta$ -lactam antibiotic analysis. Niche themes like clinical breakpoint, epidemiological cutoff, and resistance highlight specialized investigations in antimicrobial resistance and regulatory standards, while emerging or declining themes including milk and respiratory disease suggest earlier research directions that are now being replaced by more advanced mechanistic and modeling approaches (Fig. 9).

#### Thematic clustering and evolution

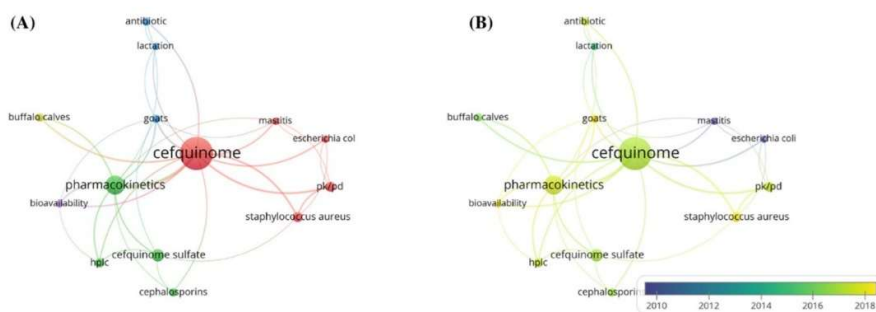
Clustering of topics in cefquinome research reveals two main hubs: “cefquinome” and “pharmacokinetics,” which link to several related keywords such as antibiotics, PK/PD, HPLC, and clinical conditions like mastitis, *Escherichia coli*, and *Staphylococcus aureus*. These clusters show a tight overlap between drug-focused and clinical research interests, with connections extending to bioavailability, lactation, and cephalosporin classes. Evolution is tracked using color-coded timeline (Fig. 10B): earlier topics like mastitis and *Escherichia coli* appear in darker shades, while recent themes such as bioavailability, PK/PD, and cefquinome sulfate move toward lighter yellows and greens (Fig. 10).



**Fig. 8:** Relationship among Countries, Institutions, Sources, and Research Topics.



**Fig. 9:** Core, Niche, and Emerging Themes.



**Fig. 10:** Thematic Clustering and Evolution.

## DISCUSSION

This bibliometric analysis of 171 cefquinome publications from 1991 to 2025 reveals a field that gained momentum after 2011, coinciding with global concerns about antimicrobial resistance. The dramatic shift in publication volume—from sporadic single articles in the 1990s to consistent double-digit output after 2011—reflects both growing livestock production pressures and heightened scientific scrutiny of veterinary antibiotics (Enshaie et al. 2025).

Chinese institutions dominate the research landscape. This concentration makes practical sense: China's massive livestock industry, serving nearly one-fifth of humanity's protein needs (Shi et al. 2023), requires comprehensive veterinary pharmaceutical research. The 40.4% of publications with Chinese corresponding authors directly correlate with the country's investment in animal health research. This highlights the importance of China in research related to drugs used in food animals, which was evident with streptomycin (Naji et al. 2026) and florfenicol (Naji et al. 2025b). Other bibliometric analysis that focuses on gut health and antimicrobial uses in veterinary medicine similarly ranks China as the leading country (Colombino et al. 2021). This strongly correlates with the ranking of countries associated with cefquinome research. Another review, which addressed the issue of antimicrobial resistance in food animals, named China – along with India – as the world's hottest hotspots of resistance development and transmission (Van Boeckel et al. 2019). The leading role of these two countries in the emergence of resistance lies in their scale of farming operations, and excessive exposure of animals to antimicrobials through their use as growth promoters. In terms of veterinary antibiotic use, China's share in 2017 was the largest at around 45% (Tiseo et al. 2020). Projections show that China will continue to maintain its ranking in the next decade, thus confirming its leading role in veterinary antimicrobial consumption. However, starting from 2020, China prohibited the use of antibiotics growth promoters (Wen et al. 2022).

The research evolved predictably from foundational pharmacokinetics toward PK/PD integration and resistance monitoring. Early studies addressed basic questions—drug distribution, safe dosing, tissue clearance times. As these fundamentals became established, researchers shifted toward optimizing treatment protocols and tracking resistance emergence. The focus on mastitis and *Escherichia coli* (Cavaco et al. 2008; Zhao et al. 2017) reflects ongoing clinical challenges in dairy production, where treatment failures drive repeated research cycles.

Journal distribution reveals the field's dual identity: clinical need meets pharmacological rigor. The *Journal of Veterinary Pharmacology and Therapeutics* leads with 27 articles, while *Antimicrobial Agents and Chemotherapy* and *Frontiers in Microbiology* contribute significantly, showing that pharmacology and antimicrobial characteristics of cefquinome are the most predominant research.

While no previous bibliometric analysis examined cefquinome specifically, our findings align with broader veterinary antimicrobial literature patterns. Studies analyzing antibiotic research in livestock consistently show Asian dominance, particularly from China and India (Tiseo

et al. 2020; Mulchandani et al. 2023).

Our finding that pharmacokinetics and PK/PD integration dominate thematically echoes patterns in bibliometric analyses of other veterinary antimicrobials like fluoroquinolones and macrolides. However, cefquinome research shows less emphasis on environmental fate compared to antibiotics approved for both human and veterinary use, possibly because its veterinary-only status reduces certain regulatory pressures.

The prominence of mastitis as a recurring theme underscores practical pressures driving research. As one of dairy production's costliest diseases, mastitis forces continuous re-evaluation of treatment strategies (Stanek et al. 2024). The cyclic research attention every few years likely reflects outbreak patterns or shifts in pathogen susceptibility (Bruno et al. 2025).

An environmental study showed that cefquinome has significant environmental impact due to its high mobility and persistence after substantial veterinary use in food animals (Qiu et al. 2022). It can be highly dispersed in the ecosystem, especially in crops requiring high amounts of irrigation. Temperature, light and pH have been shown to strongly affect degradation kinetics, with higher temperatures accelerating degradation and more acidic environments showing more stability, reflecting the environmental impact on cefquinome half-life (Qiu et al. 2022). This is in agreement with the current global efforts in combating the environmental impact of antibiotics e.g. penicillin (Goodarzi et al. 2024), aminoglycosides (Coates et al. 2022), tetracyclines (Amangelsin et al. 2023) and quinolones (Yang and Wu 2023).

This study provides the first comprehensive bibliometric overview of cefquinome research, employing rigorous methods including publication trends, citation analysis, keyword evolution and network visualization. Using Scopus ensured broad coverage across veterinary medicine, pharmacology and microbiology.

However, limitations exist. Restricting searches to Scopus excluded studies in other databases, potentially underrepresenting regional research. Language bias affects findings, as non-English publications remain underrepresented. Excluding conference proceedings and grey literature may have omitted emerging findings. Citation counts reflect timing and networks as much as scientific merit, and recent publications lack time to accumulate citations. Bibliometric analysis describes past research rather than identifying crucial knowledge gaps.

## Conclusion

The present bibliometric analysis regarding cefquinome investigations, covering thirty-three years is the first and showcases a well-established and developing research field. Thematic shifts comprised of landmark issues as pharmacokinetics, clinical studies, followed by efforts to PK/PD optimization, resistance and advanced analytical methods research. While this analysis characterizes a significant step in the effort for providing evidence-based information for understanding research trends, the most productive authors or institutions and the collaboration network, also identifies under-researched areas as the environmental effects of cefquinome residues. These findings are significant as highlighting cefquinome application is substantially important due to the rising

development of antimicrobial-resistant bacteria populations becoming a severe threat globally. Thereby, the provided study supports future guiding suggestions for researchers for evidence-based policies, and sustainable approaches to protecting cefquinome effectivity in animals.

### DECLARATIONS

**Funding:** This work was supported by the Deanship of Scientific Research, Vice Presidency for Graduate Studies and Scientific Research, King Faisal University, Saudi Arabia (Grant No. KFU254018).

**Acknowledgement:** We appreciate the financial support from the Deanship of Scientific Research, Vice Presidency for Graduate Studies and Scientific Research, King Faisal University, Saudi Arabia (Grant No. KFU254018).

**Conflict of Interest:** The authors declare no conflict of interest.

**Data Availability:** Data can be requested from the corresponding author upon reasonable request.

**Ethics Statement:** Not applicable.

**Author's Contribution:** Conceptualization (MA, MSA, SMA, MS, SA, MK); Data curation (MA, MSA, SMA); Formal analysis (MS, SA); Funding acquisition (MSA); Investigation (MSA); Methodology (MA, MSA, SMA, MS, SA, MK); Project administration (SA); Resources (MK); Software (MK); Writing - original draft (MK); Writing - review and editing. (MA, MSA, SMA, MS, SA).

**Generative AI Statement:** The authors declare that no Gen AI/DeepSeek was used in the writing/creation of this manuscript.

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