Meta Data Analysis

Mapping non-coding RNAs (ncRNAs) in cancer research: Bibliometric trends, emerging themes, and implications for diagnostics and therapy

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Yasser Bustanji[1,2,3,*], Laila Al-Omari[4], Jalal Taneera[2,3], Shereen M. Aleidi[1,3,5], Ahmad Y. Abuhelwa[3,5], Zaid Nabulsi[2], Islam Hamad[6], Eman Y. Abu-Rish[1], Mohammad H. Semreen[3,5], Waseem El-Huneidi[2,3], Eman Abu-Gharbieh[1,2,3]

1. School of Pharmacy, The University of Jordan, Amman 11942, Jordan
2. College of Medicine, University of Sharjah, Sharjah 27272, United Arab Emirates
3. Research Institute of Medical and Health Sciences, University of Sharjah, Sharjah 27272, United Arab Emirates
4. Department of Medical laboratory sciences, Al- Ahliyya Amman University, Amman, Jordan
5. College of Pharmacy, University of Sharjah, Sharjah 27272, United Arab Emirates
6. Department of Pharmacy, Faculty of health sciences. American University of Madaba, Amman, Jordan

* ybustanji@sharjah.ac.ae

ABSTRACT

Non-coding RNAs (ncRNAs) have emerged as significant regulators in cancer biology, modulating gene expression via transcriptional, post-transcriptional, and epigenetic pathways. Their functions in apoptosis, autophagy, inflammation, and epithelial-mesenchymal transition (EMT) are essential to tumorigenesis, advancement, and metastasis. This study presents a bibliometric overview of global research trends, collaborative networks, and hotspots in cancer- related ncRNA research (2005– 2024). Bibliometric mapping was integrated with a targeted literature review, employing prevalent author- keywords as anchors to identify theme clusters. These clusters underscore research hotspots, while the integrated literature synthesis contextualizes the most actively studied biological themes, correlating publication patterns with established knowledge. The Scopus database was employed for data collecting, providing extensive coverage of peer-reviewed literature. Bibliometric tools, such as VOSviewer and Biblioshiny, were utilized to examine keyword co- occurrences, define conceptual clusters, and show international cooperation. China published the most ncRNA- related cancer papers and had highest total number of citations, whereas the United States ranked second in both publishing output and total citations but had a higher citation rate per article. Overall, these findings show the distribution of research production and citation patterns among leading contributing countries, with variances in average citation rates due in part to disparities in publishing volume. A focused literature review, directed by the analyses of the retrieved author keywords, revealed that the main research domains center on the regulatory roles of ncRNAs in apoptosis, autophagy, metastasis, inflammation, and clinical applications. Emerging themes, such as their involvement in angiogenesis and immune evasion, underscore the dynamic and evolving nature of this field.

INTRODUCTION

Non-coding RNAs (ncRNAs) have become essential regulators of gene expression and genomic integrity, transforming our comprehension of genomic functions. These RNA molecules, which do not encode proteins, constitute a considerable segment of the human genome and are categorized into many classes according to their size and function [1]. MicroRNAs (miRNAs) and long non-coding RNAs (lncRNAs) are among the most extensively studied classes of non-coding RNAs. miRNAs, approximately 20– 24 nucleotides in length, regulate gene expression post- transcriptionally by targeting messenger RNAs (mRNAs) for translational repression or destruction [2,3]. Dysregulated miRNAs, including oncogenic miR-21 and tumor- suppressive miR-34a, are involved in important cancer pathways such as PI3K/ AKT and TGF- β signaling [4,5]. Long non-coding RNAs (lncRNAs), characterized as transcripts exceeding 200 nucleotides, modulate gene expression via chromatin remodeling, transcriptional interference, and posttranscriptional processes [6]. For instance, HOTAIR facilitates metastasis by downregulating tumor suppressor genes [7], while MEG3 enhances p53 signaling and suppresses tumor development [8]. In addition to lncRNAs, other categories of non- coding RNAs, such as circular RNAs (circRNAs), PIWI-interacting RNAs (piRNAs), and small nucleolar RNAs (snoRNAs), further enhance the functional diversity of ncRNAs implicated in cancer biology [11].

CircRNAs, defined by their covalently closed configurations, function as miRNA sponges or engage with proteins to modulate signaling pathways, including Wnt/β-catenin, and have a role in drug resistance [6,7]. Other examples, such as circ- ITCH and ciRS-7, highlight their significance in oncogenesis. Simultaneously, piRNAs and snoRNAs preserve genomic stability and alter ribosomal RNA, respectively, highlighting their varied biological significance [8,9].

ncRNAs are essential to many cancer hallmarks, facilitating oncogenic transformation, metabolic reprogramming, immunological evasion, and resistance to therapy. miRNAs, such as the miR-17-92 cluster, facilitate MYC-driven proliferation [10], but lncRNAs like NEAT1 regulate the tumor microenvironment to inhibit immune responses [11]. Moreover, ncRNAs, including UCA1, promote chemotherapy resistance by activating pathways such as mTOR, hence complicating treatment strategies [12].

ncRNAs possess significant potential as biomarkers and therapeutic targets in clinical settings. Their stability in biological fluids and cancer- specific expression profiles render them appropriate for diagnostic and prognostic purposes. Circulating miR-21 and lncRNA PCA3 have been validated to diagnose lung and prostate malignancies early, respectively [13,14]. Moreover, ncRNA- based therapies, such as miRNA mimics, inhibitors, and antisense oligonucleotides aimed at lncRNAs like MALAT1, have demonstrated potential in both preclinical and clinical contexts [15]. Nonetheless, off-target effects and delivery constraints highlight the necessity for improved technologies, such as nanoparticles, to improve therapeutic efficacy [16].

Bibliometric studies have emerged as a crucial instrument in scientific research, offering quantitative assessments of published literature to recognize trends, patterns, and research influence within a certain topic [17-21]. Bibliometric analyses utilize statistical tools to assess the number, growth, and citation trends of academic works, thereby elucidating the intellectual framework of a discipline, showcasing prominent authors and organizations, and pinpointing nascent research domains [22,23].

As ncRNAs gain significance in cancer biology, it is essential to monitor the research efforts and identify therapeutically pertinent trajectories. The existing bibliometric studies regarding this topic have focused either on a single ncRNA subtype (e.g., lncRNAs or miRNAs) or on specific cancer types [24,25]. In contrast, the current study offers a broad and integrative overview that includes all ncRNA classes across diverse cancer types, enabling comparative insights not available in the existing literature. This manuscript includes bibliometric analysis combined with a focused literature review to investigate global research trends, collaborative networks, and thematic hotspots in cancer- related lncRNA research from 2005 to 2024. This study combines data mapping with biological interpretation to show how research trends connect with scientific discovery and to highlight lncRNAs as emerging biomarkers and therapeutic targets.

METHODS

Search Plan and Refining the Retrieved Documents

We searched the Scopus database on February 7, 2025, looking for worldwide research outputs from the past two decades with a focus on the roles non-coding RNA might play in cancer research. The search turned up using the following query: TITLE-ABS-KEY ("cancer" OR "tumor" OR "carcinoma" OR "neoplasm" OR "malignancy") AND TITLE ("non-coding RNA" OR "non coding RNA" OR "ncRNA") AND PUBYEAR > 2004 and PUBYEAR < 2025 AND (LIMIT-TO (SRCTYPE, "j")) AND (LIMIT- TO (PUBSTAGE, "final")) AND (LIMIT- TO (DOCTYPE, "ar")) AND (LIMIT- TO (LANGUAGE, "English")). We included only English-language peer-reviewed articles from 2005 to 2024. The search excluded press releases, reviews, letters, notes, editorials, conference papers, errata, and other non-primary research publications. The investigation also omitted book chapters and conference proceedings.

Data Export

The gathered documents were exported in CSV format to enable further analysis. The Scopus platform and Microsoft Office Excel 365 (Microsoft Corporation, Redmond, WA, USA) were employed to analyze bibliometric data, facilitating the retrieval of information related to various study domains and publishing journals. The dataset was manually screened to eliminate duplicates and correct inconsistencies in key fields, including country affiliation and publication year. Ambiguous or irrelevant records were excluded to maintain data accuracy [26].

Bibliometric Analyses and Visualization

In this study, we have utilized the most recent release of the Visualization of Similarities software (VOSviewer 1.6.20) [27,28] to analyze and visualize collaborations, keywords, and citations within the gathered papers. VOSviewer employed mapping techniques and cluster analysis to display the network of partnerships across countries, linkages between authors, and author keywords [22,28]. Furthermore, cluster density maps were created to illustrate the relationships among all keywords. The Biblioshiny application, a component of the Bibliometrix package, was employed for an in-depth study of author keywords [21,28,29]. This software facilitated identifying patterns and examining study focal points by assessing trends in author keywords. The assessments of the involved countries and keywords were thoroughly validated by manual review to ensure accuracy. Terms that were formerly categorized as separate words were combined utilizing a thesaurus file, thereby establishing a uniform nomenclature. These modifications were executed with both VOSviewer and Biblioshiny software tools [28].

RESULTS

Annual Production Analysis

A systematic search was conducted utilizing the designated search terms mentioned in the methodology to find papers referring to ncRNA and cancer research from 2005 to 2024. The search yielded 9,819 relevant articles. The bulk, including 5,395 documents or 55.0%, were published from 2018 to 2021. Figure 1 illustrates a graph depicting the yearly volume of research articles generated alongside their associated citation trends.

Evaluation of Contributing Journals

We successfully retrieved 9,819 articles from about 1,222 peer-reviewed journals listed in Scopus. Ninety-five journals were identified as having published twenty or more articles. Table 1 lists the ten most prolific journals. Among all, *Oncotarget* published the highest number of papers, totaling 334, which constitutes 3.4% of the overall count. All these ten journals in Scopus are classified within the Q1-Q2 journal categories.

Analysis of Articles

The set of retrieved articles has an *h*-index of 211 and have acquired a cumulative total of 368,049 citations. Each document has, on average, received 37.5 citations. Additionally, 1,979 documents have received 50 or more citations each. Table 2 displays the 10 most cited documents and their annual citation normalization.

Active Countries

The investigation of the search results indicated contributions from 81 countries within the Scopus database. Table 4 lists the ten countries with the highest publication output, whereas 31 countries have produced 20 or more publications. China produced the highest volume of ncRNA-related cancer papers (7,799 documents), receiving 262,957 citations (33.7 citations per document), whereas the United States placed second in publication production (946 documents) with a total of 77,191 citations (81.6 citations per document). The results highlight the distribution of research output and citation patterns among prominent contributing countries, with discrepancies in average citation rates partially attributable to differences in publication volume.

Bibliometric Mapping

International Collaboration

The VOSviewer software was utilized to examine publication and collaboration patterns among countries, providing insights via a network visualization map (Figure 2). This map depicts countries as spheres, with the size of each sphere according to the quantity of published papers (Figure 2A). Figure 2B illustrates that countries with larger spheres generally exhibit elevated citation counts for their publications. Of the 81 countries examined, 24 satisfied the criterion of publishing a minimum of 40 publications. The countries were categorized into three clusters, emphasizing each group's strong collaborations.

The first cluster includes 11 countries (red): Germany, the United Kingdom, the Netherlands, Australia, Brazil, Italy, Spain, France, Denmark, Sweden, and Switzerland. The second cluster (green) comprises Canada, Egypt, India, Iran, Japan, the Russian Federation, and Saudi Arabia. The third cluster (blue) comprises China, South Korea, Taiwan, the United States, and Hong Kong.

Authors from countries within the same cluster often work together, which could be due to common scientific interests. This visualization of international collaborations reveals patterns of publication trends and global cooperation. Interestingly, China and the United States had a robust collaboration partnership.

Analysis of Author Keywords and Hotspots Forecasting

A keyword association analysis was performed using VOSviewer and Biblioshiny as bibliometric tools to identify active research topics concerning the application of noncoding RNAs in cancer. This research concentrated on author keywords, utilizing a thesaurus file to standardize synonyms and establishing a minimum occurrence criterion of 100. Figure 3A displays the most frequent author keywords, each with a minimum frequency of 100 occurrences. Figure 3A depicts a network visualization map, with frequently recurring terms depicted as circular nodes. Spheres of identical color are linked, and their sizes correspond to the frequency of occurrence. The analysis categorized the author's keywords into four distinct clusters as described in Figure 3A. Cluster 1 (red) includes 13 terms: lncRNA, breast cancer, apoptosis, miRNA, lung cancer, cancer, prostate cancer, ovarian cancer, ceRNA, MALAT1, HOTAIR, autophagy, and inflammation. Cluster 2 (green) consists of terms such as proliferation, metastasis, colorectal cancer, invasion, epithelial-mesenchymal transition (EMT), glioma, and osteosarcoma. Cluster 3 (blue) comprises prognosis, gastric cancer, hepatocellular carcinoma, biomarker, diagnosis, and pancreatic cancer. Lastly, Cluster 4 (yellow) includes NSCLC, cervical cancer, bladder cancer, progression, and tumorigenesis. These clusters underscore the principal research domains and subjects related to ncRNA in cancer research, providing significant insights into the current trends throughout this field.

To further validate the conceptual structure, a conceptual map derived from Multiple Correspondence Analysis (MCA) was created utilizing Biblioshiny (Figure 3B). The MCA identified four thematic patterns that correspond closely with the VOSviewer groupings, notwithstanding variations in color schemes and visualization styles.

The central cluster (red) represents the core of ncRNA research, connecting major cancer types

(e.g., breast, lung, colorectal, hepatocellular, prostate, ovarian, cervical cancers, glioma, and osteosarcoma) with key ncRNA terms (miRNA, lncRNA, HOTAIR, MALAT1, TINCR) and regulatory mechanisms such as EMT. A second cluster (green) emphasizes clinical outcome–related themes, including biomarker, prognosis, and gastric cancer. A third cluster (blue) reflects mechanistic studies involving metastasis, invasion, proliferation, and apoptosis. The term diagnosis appears as an isolated theme, indicating a distinct and less integrated research focus.

The significant correlation between the VOSviewer and MCA findings validates the reliability of the observed thematic structures. The Biblioshiny MCA map functions as a complementary validation tool reinforcing the conceptual structure identified by the VOSviewer network analysis. However, subsequent assessments of research trends and hotspots were derived from the clustering results of VOSviewer.

Biblioshiny was employed to generate a thematic map for a more in- depth analysis of the retrieved keywords (Figure 3C). The thematic map offers an overview of the research landscape of ncRNAs in cancer. The map categorizes themes into four quadrants according to their centrality (relevance to the field) and density (degree of growth). The motor themes quadrant features prominent and impactful clusters, including "lncRNA," "prognosis," and particular malignancies such as "hepatocellular carcinoma," "gastric cancer," and "colorectal cancer." These subjects are fundamental and well- established, signifying their significance in ncRNA-related cancer research, especially with therapeutic consequences.

The status of motor themes like lncRNAs and prognosis indicates these areas advanced understanding and clinical relevance. Basic themes, such as cancer diagnosis and biomarkers, reveal foundational but underdeveloped aspects of the field, offering potential for further exploration. Emerging topics, including proliferation, metastasis, and apoptosis, suggest a transition towards integrating these processes into broader ncRNA research frameworks. Meanwhile, niche themes like miRNA biomarkers highlight their established significance within specific contexts but call for expanded translational applications.

In the basic theme quadrant, the cluster includes terms like "cancer," "diagnosis," and "bladder cancer" alongside "biomarker" and "miRNA." These themes are fundamental to the field but remain less developed in terms of research depth, highlighting their potential for further investigation. The “Emerging/ Declining” quadrant includes *proliferation*, *metastasis*, *apoptosis*, *invasion,* and *epithelial–mesenchymal transition (EMT),* which represent key biological processes in cancer. Their position in this quadrant reflects low centrality and density within the existing conceptual structure, suggesting that these themes are not well integrated into the central ncRNA research landscape. Lastly, the niche themes quadrant contains terms like "miRNA," "biomarker," and "diagnosis," suggesting that while these areas are well- developed within specific contexts, their broader relevance to the field is limited.

The research additionally examined the relationships among all significant keywords found in the titles and abstracts of academic journals. Figure 3D presents a cluster density map illustrating co- occurrence patterns among keywords extracted from titles and abstracts. A minimum threshold of 300 occurrences was applied for inclusion. Of the 39,015 terms identified, 227 met this criterion and were included in the visualization. In the density map, color intensity reflects the frequency of term occurrence, while areas with similar coloration indicate strongly connected and frequently co-occurring keywords.

Two complimentary methodologies were employed to support the assessment of author keywords. The initial method entailed creating a normalized overlay of keyword clusters according to the average year of publication with VOSviewer, as illustrated in Figure 4A. These graphic features color-coded clusters that denote author keywords, with yellow indicating the most recently published terms, providing an overview of the temporal evolution of keyword clusters.

The second method utilized Biblioshiny to visualize trending topics, illustrated in Figure 4B, which shows the chronological progression of significant phrases associated with ncRNA research in cancer research. The map highlights different author keywords according to their frequency of occurrence and period of projection. Significant keywords such as "autophagy," "inflammation," "hepatocellular carcinoma," "colorectal cancer," "breast cancer," and "lncRNA"

have demonstrated heightened study interest in recent years, as seen by their increased term frequencies in more recent periods. Keywords such as "proliferation" and "prognosis" exhibit enduring significance, underscoring their fundamental importance in cancer research related to ncRNAs.

Citations varied greatly by author keyword. The publication date was utilized to normalize citation numbers to account for publication age to provide a fair comparison across periods. The normalized author keyword citation network in Figure 4C considers publication age and considers publication age to standardize citation metrics. Each visualization cluster represents a word and is sized by its normalized citation count relative to its publication year. Keywords having different citation impacts are highlighted by a color gradient from dark blue to yellow. The author's keywords cRNA, autophagy, inflammation, and ovarian cancer exhibited the highest normalized citation counts, signifying their substantial influence and importance in the scientific literature. These data offer a thorough insight into the temporal trends, thematic focuses, and citation effects of author keywords in non-coding RNA cancer research. These contribute to the growing knowledge base and aid researchers in identifying key areas of interest and potential avenues for future research.

This study provides an integrated bibliometric and literature-based overview of ncRNA research in cancer from 2005 to 2024, mapping global trends, collaborations, and thematic hotspots. By combining systematic mapping with biological interpretation of high- frequency keyword clusters, we identified key research domains involving apoptosis, autophagy, inflammation, EMT, and metastasis, alongside emerging themes such as angiogenesis, immune evasion, and tumor microenvironment interactions. Unlike most prior studies that focus on a single ncRNA subtype or specific cancer, our analysis offers a broad comparative perspective encompassing all major ncRNA classes across diverse malignancies.

The findings show that while China leads in publication output, the United States contributes disproportionately to high- impact studies, reflecting the importance of international collaboration in shaping the field. ncRNAs—particularly lncRNAs and miRNAs—are increasingly recognized as critical regulators of cancer biology, with strong potential as diagnostic and prognostic biomarkers and as novel therapeutic targets. Future research should move beyond single- database dependence and incorporate clinical trials, translational, and patent data, thereby linking basic discovery to clinical application and strengthening the path toward ncRNA-based interventions in oncology.

Figures

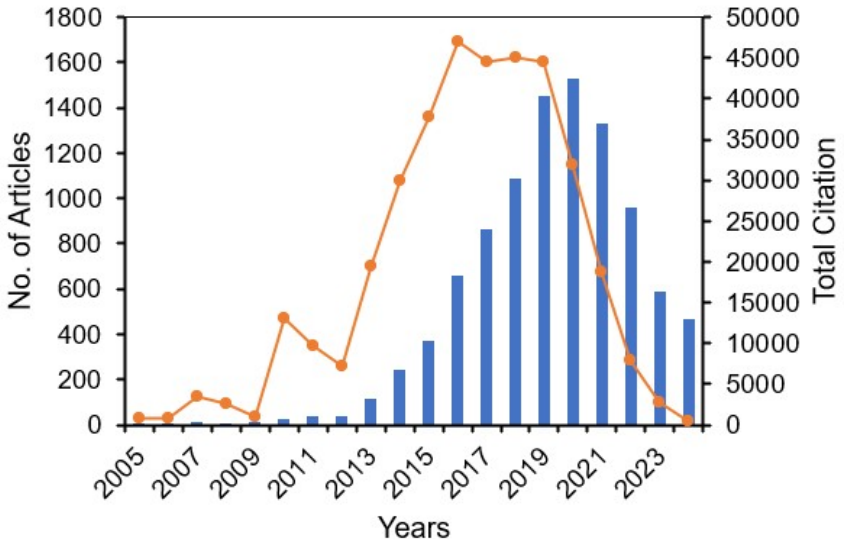


Figure 1: Annual scientific output and citation trend in non-coding RNA (ncRNA) cancer research. Bars represent the number of publications per year, while the line indicates the citation trend across the same period. The figure illustrates the growth of research activity in ncRNA-related cancer studies and the citation accumulation associated with earlier publications.

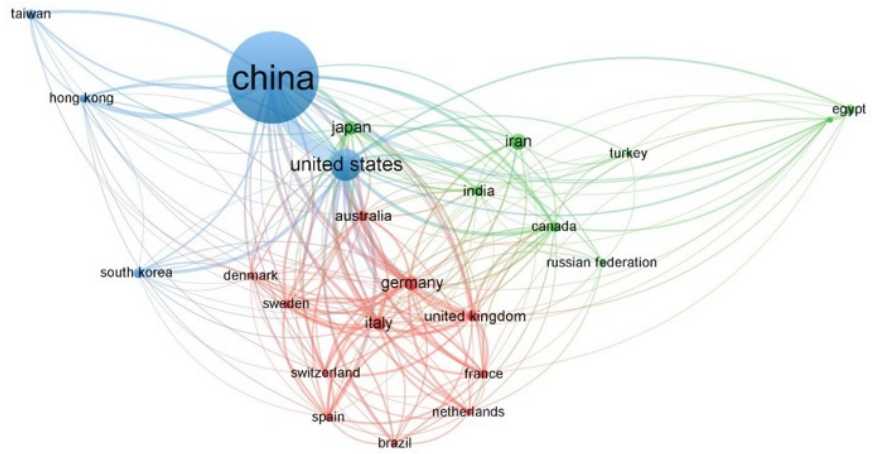


Figure 2A: International collaboration network in non-coding RNA (ncRNA) cancer research. Network visualization of country-level collaborations generated using VOSviewer. Each node represents a country, with node size proportional to research productivity or citation impact. Links between nodes indicate co-authorship collaborations, and colors represent clusters of closely collaborating countries. Panel (A) displays the network based on the number of published documents, while panel (B) illustrates the collaboration structure according to citation impact.

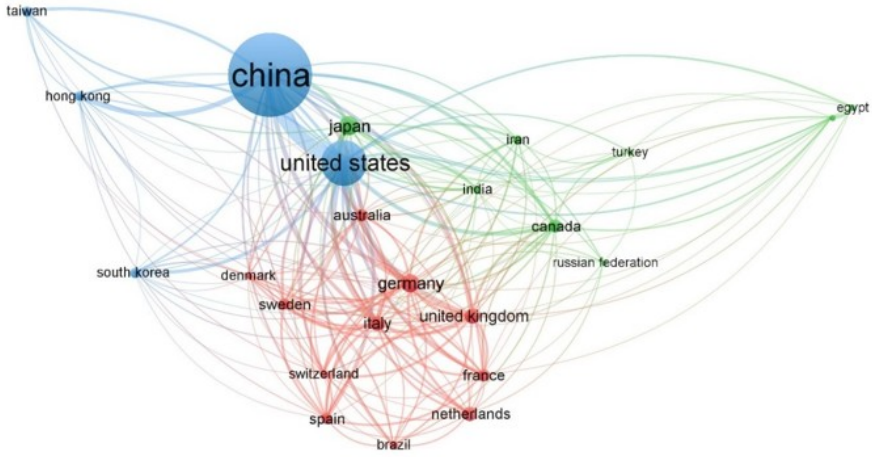


Figure 2B: International collaboration network in non-coding RNA (ncRNA) cancer research. Network visualization of country-level collaborations generated using VOSviewer. Each node represents a country, with node size proportional to research productivity or citation impact. Links between nodes indicate co-authorship collaborations, and colors represent clusters of closely collaborating countries. Panel (A) displays the network based on the number of published documents, while panel (B) illustrates the collaboration structure according to citation impact.

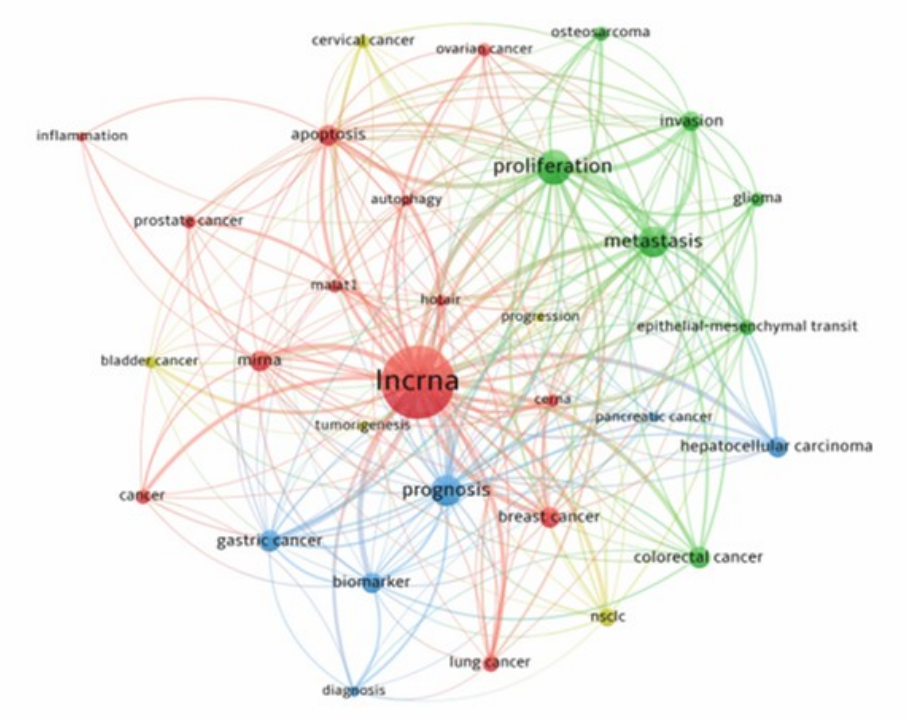


Figure 3A: Keyword co-occurrence and conceptual structure in non-coding RNA (ncRNA) cancer research. (A) Network visualization of the most frequently occurring author keywords generated using VOSviewer, including terms with at least 100 occurrences; node size represents keyword frequency and links indicate co-occurrence relationships. (B) Conceptual structure map generated by Multiple Correspondence Analysis (MCA) using Biblioshiny, illustrating thematic clustering of keywords based on conceptual similarity. (C) Thematic map derived from author keyword analysis in Biblioshiny, showing the distribution of research themes according to centrality and density. (D) Density visualization map of the most frequent terms extracted from titles and abstracts, including terms appearing at least 300 times, where color intensity reflects term frequency and areas of concentrated research activity.

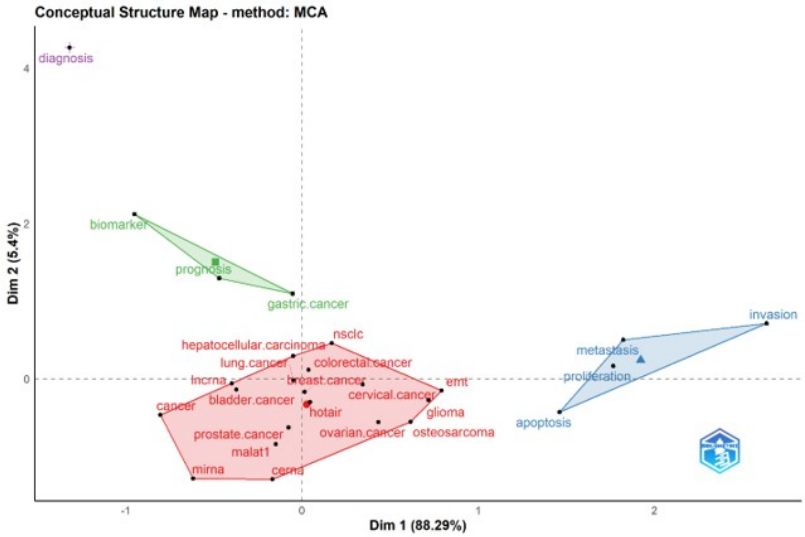
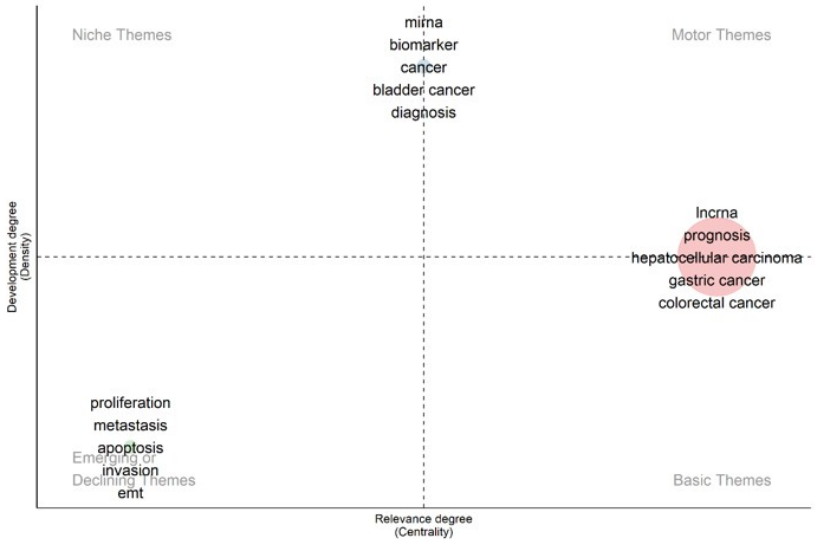


Figure 3B: Keyword co-occurrence and conceptual structure in non-coding RNA (ncRNA) cancer research. (A) Network visualization of the most frequently occurring author keywords generated using VOSviewer, including terms with at least 100 occurrences; node size represents keyword frequency and links indicate co-occurrence relationships. (B) Conceptual structure map generated by Multiple Correspondence Analysis (MCA) using Biblioshiny, illustrating thematic clustering of keywords based on conceptual similarity. (C) Thematic map derived from author keyword analysis in Biblioshiny, showing the distribution of research themes according to centrality and density. (D) Density visualization map of the most frequent terms extracted from titles and abstracts, including terms appearing at least 300 times, where color intensity reflects term frequency and areas of concentrated research activity.



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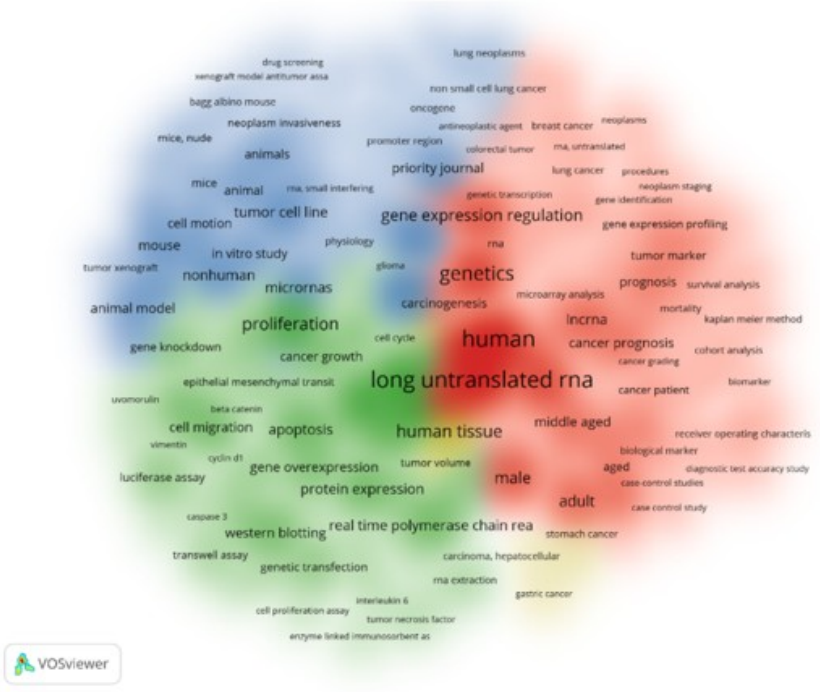

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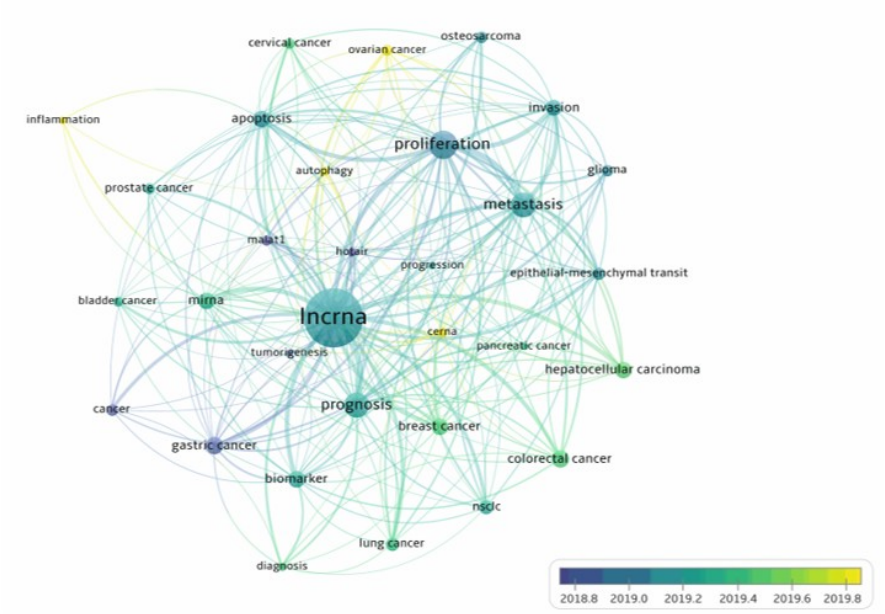
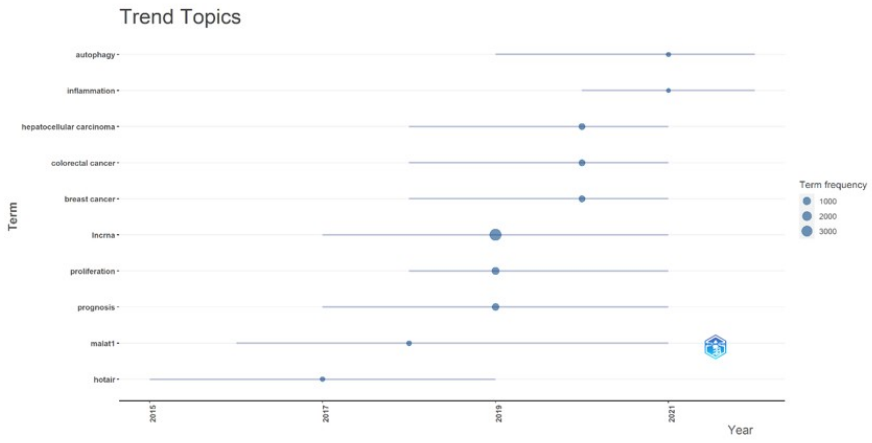


Figure 4A: Temporal trends and citation impact of key research topics in non-coding RNA (ncRNA) cancer studies. (A) Overlay visualization map of the most frequent author keywords generated using VOSviewer, where node size reflects keyword frequency and the color gradient represents the average publication year, highlighting the evolution of research topics over time. (B) Trend topics plot showing the temporal distribution and prominence of major author keywords across the study period, with bubble size indicating term frequency. (C) Overlay visualization map displaying the most frequent author keywords with a normalized citation overlay, where node size represents keyword frequency and the color gradient indicates relative citation impact across the literature.



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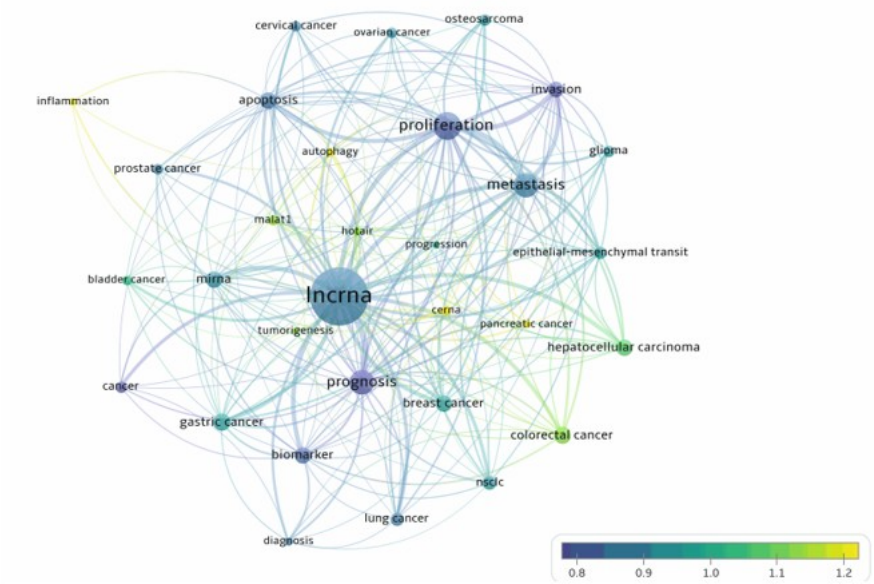

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Tables

Source	No of Publication	%	Total Citations	Scopus Percentile (Q)
Oncotarget	334	3.4	19285	73 (Q2)
European Review for Medical and Pharmacological Sciences	305	3.1	6540	64(Q2)
Oncology Letters	250	2.5	4743	65 (Q2)
OncoTargets and Therapy	203	2.1	5050	91 (Q1)
Scientific Reports	160	1.6	5414	92 (Q1)
Biomedicine and Pharmacotherapy	159	1.6	7601	91 (Q1)
Journal of Cellular Biochemistry	142	1.4	4914	86 (Q1)
Cell Death and Disease	140	1.4	8959	93 (Q1)
Biochemical and Biophysical Research Communications	137	1.4	6378	72 (Q2)
Aging	137	1.4	3058	78 (Q1)

Table 1: Most active journals publishing research on non-coding RNAs (ncRNAs) in cancer. The table lists the ten journals with the highest number of publications. For each journal, the number of publications, percentage contribution to the total output, total citations received, and Scopus percentile ranking (quartile classification) are presented, highlighting the leading publication venues and their citation impact within the field of ncRNA-related cancer research.

Paper	DOI	Total Citations (TC)	TC per Year	Normalized TC
Gupta RA, 2010, Nature [30]	10.1038/nature08975	4552	284.5	9.8
Iyer MK, 2015, Nat Genet [31]	10.1038/ng.3192	2209	200.8	21.7
Ørom UA, 2010, Cell [32]	10.1016/j.cell.2010.09.001	1530	95.6	3.3
Gutschner T, 2013, Cancer Res [33]	10.1158/0008-5472.CAN-12-2850	1394	107.2	8.3
Yuan J-H, 2014, Cancer Cell [34]	10.1016/j.ccr.2014.03.010	1377	114.8	11.2
Yap KL, 2010, Mol Cell [35]	10.1016/j.molcel.2010.03.021	1214	75.9	2.6
Faghihi MA, 2008, Nat Med [36]	10.1038/nm1784	1208	67.1	3.9
Kogo R, 2011, Cancer Res [37]	10.1158/0008-5472.CAN-11-1021	1204	80.3	4.9
Kino T, 2010, Sci Signal [38]	10.1126/scisignal.2000568	1093	68.3	2.4
Chu C, 2011, Mol Cell [38]	10.1016/j.molcel.2011.08.027	1029	68.6	4.17

Table 2: Top ten highly cited articles in non-coding RNA (ncRNA) cancer research. The table lists the ten most influential publications identified through Biblioshiny citation analysis. For each article, the authors, publication source, digital object identifier (DOI), total citation count (TC), average citations per year, and normalized citation score are provided.

Rank	Country	Number of Publications	Total Citations	% of Total documents	Citation /Document
1st	China	7799	262957	79.4	33.7
2nd	United States	946	77191	9.6	81.6
3rd	Iran	239	3273	2.4	13.7
4th	Germany	197	13707	2.0	69.6
5th	Japan	186	14063	1.9	75.6
6th	Italy	184	9457	1.9	51.4
7th	United Kingdom	127	8845	1.3	69.6
8th	India	102	2016	1.0	19.8
9th	Australia	97	6343	1.0	65.4
10th	South Korea	94	3886	1.0	41.3

Table 3: Most productive countries in non-coding RNA (ncRNA) cancer research. The table presents the ten leading countries contributing to the publication output in ncRNA-related cancer research. For each country, the number of publications, total citations, percentage contribution to the total documents, and average citations per document are reported.

DISCUSSION

ncRNAs are crucial in cancer biology, serving as significant regulators of gene expression at transcriptional, post- transcriptional, and epigenetic levels. Their dysregulation has been associated with the development, progression, and metastasis of various cancer types [39].

Bibliometric studies are essential for assessing research trends, recognizing significant publications, and revealing emerging scientific themes within a discipline [17]. This study examines two decades of progress in ncRNA research in cancer, offering a quantitative overview of global scientific output. We employed the Scopus database for data acquisition because of its broad coverage of peer-reviewed literature, strong citation-tracking features, and dependable indexing of high-impact journals [22]. The user-friendly interface, versatile analytical tools, and rich metadata of Scopus provide rapid data extraction, analysis, and visualization. Journals indexed in Scopus undergo rigorous peer- review processes and are categorized by subject matter, confirming their reputation and relevance [23].

The bibliometric analysis of research articles on ncRNA in cancer research from 2005 to 2024 indicates notable trends in scientific productivity and international contributions. The consistent yearly growth rate highlights the rising interest and progress in this domain, with most

publications (55.0%) occurring between 2018 and 2021. This increase underscores the swift advancement of ncRNA research in recent years, driven by progress in molecular biology, sequencing technology, and their ramifications for cancer diagnosis and treatment.

Publications in this field demonstrated both substantial productivity and notable impact. The Q1-Q2 ranking and comparable rankings of other leading journals signify the elevated scientific quality and impact of research in this domain. The elevated *h*-index of 211 and the notable average citation rate of 37.5 per document indicate considerable academic and clinical interest in the topic.

At the country level, China contributes a large volume of publications in ncRNA-related cancer research and accumulates a substantial number of total citations, while the United States shows a different citation distribution across a smaller body of publications. Variations in average citation rates may partly reflect differences in publication volume and research dissemination rather than research relevance alone.

Bibliometric mapping further highlights the importance of global cooperation, revealing three major clusters of collaborating countries and a particularly strong partnership between China and the United States. These patterns demonstrate that sustained international collaboration is essential for advancing ncRNA research in cancer and informing future research directions.

Author keywords analyses

The assessment of author keywords yields significant insights into the active research domains and emerging trends in investigating ncRNAs in cancer. The categorization of keywords into several groups underscores the varied focal points within this domain, encompassing individual ncRNAs, their functions in cancer biology, and clinical applications.

The thematic map (Figure 3C) provides a deeper perspective on the research landscape, dividing keywords into motor, basic, niche, and emerging/declining themes. The findings of the thematic map analysis indicate that lncRNAs have become a pivotal and progressive domain of research, especially in elucidating prognosis and their function in particular cancer types. This indicates that the field has attained considerable depth in this domain. Conversely, miRNAs are emphasized as fundamental yet require additional investigation to realize their potential in clinical applications.

The presence of *proliferation*, *metastasis*, *apoptosis*, *invasion*, and *EMT* in the "Emerging/Declining" quadrant of the theme map indicates low centrality and density, rather than a definitive temporal decline. In thematic mapping, this quadrant may signify topics that are still evolving and not yet conceptually established. Due to their essential roles in cancer biology, these processes are better understood as new mechanistic pathways that are being explored in ncRNA-related cancer research and are moving towards greater integration within the field's central themes.

This interpretation is additionally supported by the overlay visualization (Figure 4A), which illustrates that mechanistic processes such as proliferation, metastasis, apoptosis, and EMT are significantly associated with ncRNA-related terms and exhibit more recent average publication years, signifying heightened research focus and integration rather than thematic regression.

The existence of specialized topics such as miRNA biomarkers indicates the possibility of enhancing their influence via translational studies. This thematic map illustrates a dynamic and evolving research domain, featuring established fields like lncRNAs and prognosis and emerging prospects in mechanistic investigations and translational research. It underscores the significance of incorporating essential processes such as metastasis and apoptosis into broader ncRNA research frameworks to enhance their relevance. The map identifies patterns and gaps, offering significant insights to direct future research and enhance the clinical applications of ncRNAs in cancer.

Temporal analyses of keyword trends (Figure 4B) reveal a dynamic progression in ncRNA research. Studies focused on specific molecules of lncRNAs, including "MALAT1" and "HOTAIR," are significant in the earliest years of the timeline, underscoring their crucial significance in

catalyzing research on the participation of lncRNAs in cancer. Nonetheless, their frequencies diminish over time, indicating either a transition in emphasis towards other ncRNAs or the incorporation of these molecules into more extensive ncRNA research. The recent rise of complicated topics like "autophagy" and "inflammation" underscores a growing interest in comprehending how ncRNAs regulate these activities inside the tumor microenvironment.

The overlay visualization map of normalized citations (Figure 4C) offers further insights into the impact of different keywords. High-impact keywords like autophagy, inflammation, and ovarian cancer underscore research domains with substantial visibility and significance. These findings underscore the significance of these subjects in influencing the discipline and provide direction for future research efforts.

The analysis underscores the evolution of ncRNA research from fundamental discoveries to a more integrative and translational methodology. Future research should concentrate on underexamined domains, specifically the function of ncRNAs in essential processes such as autophagy and inflammation, while simultaneously progressing clinical applications, notably in biomarker creation and targeted therapeutics. By addressing these deficiencies and utilizing emerging themes, researchers might enhance the comprehension of ncRNAs in cancer and their prospective therapeutic implications.

Research trends and hotspots

VOSviewer and Biblioshiny were used to analyze co-occurring author keywords and identify research trends and hotspots within the collected literature. This analysis revealed four conceptual clusters comprising 32 primary keywords, which represent the major domains of interest and focal points of the retrieved studies (Figure 3 and Figure 4). To place these clusters into a meaningful biological framework, bibliometric mapping was complemented with a targeted literature review, using high-frequency keywords as anchors. This integrated approach underscores both established domains and emerging directions of lncRNAs in cancer research.

Cluster 1 keywords: LncRNAs in cancer: regulators of apoptosis, autophagy, and inflammation across diverse tumor types.

lncRNAs have emerged as crucial regulators in cancer biology, affecting essential processes such as apoptosis, autophagy, and inflammation in various cancer types, including breast, lung, prostate, and ovarian cancers [4,40,41]. These regulatory capabilities establish lncRNAs as crucial factors in tumor growth and prospective treatment targets. Apoptosis, or programmed cell death, is essential for preserving tissue homeostasis and removing damaged cells [42]. The dysregulation of apoptosis is a defining characteristic of cancer. LncRNAs are essential in regulating apoptotic pathways [43]. For instance, GAS5, a tumor suppressor lncRNA, suppresses cell proliferation and promotes apoptosis, with its downregulation found in breast and prostate malignancies [44].

Furthermore, autophagy, a cellular degradation mechanism vital for recycling damaged organelles and proteins, serves a dual function in cancer, either facilitating cell survival or inducing cell death. LncRNAs dramatically modulate autophagy in cancer cells. MALAT1 controls the progression of hepatocellular carcinoma (HCC) by affecting cell proliferation, autophagy, and apoptosis [45]. This lncRNA engages with miR-146a to modulate the PI3K/Akt/mTOR pathway, an essential signaling axis for cellular survival and autophagy [45]. These interactions highlight the function of lncRNAs in regulating autophagic mechanisms in cancer. Chronic inflammation, an acknowledged factor in cancer formation and progression, is another domain where lncRNAs significantly impact the tumor microenvironment. They govern the expression of pro-inflammatory cytokines, controlling inflammation linked with cancer [46]. The dual function as facilitators and suppressors of carcinogenesis indicates therapeutic potential in targeting lncRNA-mediated inflammatory pathways [47]. Moreover, lncRNAs demonstrate selectivity in their functions across various cancer types. In breast cancer, HOTAIR facilitates tumor development and metastasis by modifying chromatin states to activate oncogenic pathways [48]. Similarly, lncRNAs contribute to tumorigenesis in lung cancer by regulating processes such as proliferation and apoptosis [49]. LncRNAs are involved in regulating metastasis and chemoresistance in prostate and ovarian malignancies, highlighting their significance in cancer biology and treatment [50]. Competing endogenous RNA (ceRNA) networks introduce additional complexity to lncRNA functionality by serving as sponges for

microRNAs (miRNAs), thereby inhibiting the repression of target messenger RNAs (mRNAs) and forming regulatory networks that influence cancer progression [51,52].

Cluster 2 keywords: LncRNAs as drivers of cancer progression: insights into proliferation, metastasis, and EMT across diverse malignancies.

The role of lncRNAs in cancer research has become a vital focus, especially regarding their impact on tumor proliferation, metastasis, and EMT across numerous malignancies, such as colorectal cancer, glioma, and osteosarcoma [53].

The proliferation and invasion of cancer are essential traits of its progression, and lncRNAs have been demonstrated to influence these cellular processes significantly. ANRIL, lncRNA, enhances osteosarcoma cell proliferation, migration, and invasion, positioning it as a potential therapeutic target [54,55]. Likewise, lncRNA UCA1 promotes proliferation and diminishes apoptosis in osteosarcoma, facilitating tumor progression [56]. In colorectal cancer, lncRNA H19 facilitates EMT, a crucial process in cancer invasion and metastasis [57,58]. These findings highlight the significance of lncRNAs in governing mechanisms essential to cancer progression, underscoring their dual functions as indicators for illness and therapeutic targets. Metastasis, a defining characteristic of cancer, is regulated by lncRNAs, especially through their influence on EMT. The transition from an epithelial to a mesenchymal phenotype promotes cancer cells with migratory and invasive properties, which is crucial for metastasis. lncRNA NEAT1 facilitates EMT and metastasis in osteosarcoma by sequestering miR-483, thereby upregulating STAT3, a transcription factor essential for cellular motility [59]. These insights into lncRNA- mediated pathways underscore its therapeutic potential in restricting metastasis.

MALAT1, important lncRNA, is associated with unfavorable prognosis in glioma patients as it enhances cell proliferation and invasion [60]. The clinical value of lncRNAs is emphasized by their potential as diagnostic and prognostic biomarkers. The expression profiles of lncRNAs are associated with clinical outcomes in malignancies, including colorectal cancer and osteosarcoma [61]. The downregulation of lncRNA TUG1 suppresses proliferation and promotes apoptosis in osteosarcoma, indicating its potential as a therapeutic target [62]. Likewise, lncRNA SNHG1 facilitates carcinogenesis in osteosarcoma by modulation of miR-326, underscoring its significance in cancer advancement [63]. These findings connect genetic research with clinical application, providing a foundation for future therapeutic advancements.

Cluster 3 keywords: ncRNAs as biomarkers for prognosis, diagnosis, and therapeutic insights in gastrointestinal and hepatopancreatic cancers.

The expanding body of research on ncRNAs has confirmed their importance as biomarkers for prognosis, diagnosis, and treatment across multiple cancers, including gastric cancer, HCC, and pancreatic cancer [64,65]. These ncRNAs have been associated with essential processes like carcinogenesis, metastasis, and chemoresistance, offering the potential for their use in clinical cancer [31]. Among these cancers, gastric cancer illustrates the transformative capacity of lncRNAs in affecting disease development and patient outcomes. lncRNA LINC00941 has been recognized as a biomarker that enhances proliferation and metastasis in gastric cancer, associated with unfavorable clinical outcomes [66]. The lncRNA DANCR is similarly linked to increased tumorigenicity and functions as a prognostic marker [67]. The discovery of new lncRNAs like LINC02688, potentially facilitating early diagnosis, underscores the significance of lncRNA profiling in evaluating illness severity and customizing therapy approaches [65]. Furthermore, increased plasma concentrations of lncRNA HULC in HCC patients show its potential application as diagnostic and prognostic indicators [68]. Moreover, lncRNA- based signatures have been associated with prognosis and patient outcomes, providing a method to categorize patients according to recurrence risk and overall survival [69,70]. Incorporating lncRNA profiling into clinical practice may enhance diagnostic precision and guide personalized therapy approaches for patients.

Cluster 4 keywords: Role of ncRNAs in tumorigenesis and progression across NSCLC, cervical, and bladder cancers.

ncRNAs are pivotal in developing and progressing NSCLC, the most common form of lung cancer. Multiple studies have shown that lncRNAs and miRNAs are crucial regulators in the development and progression of NSCLC [71]. The lncRNA MALAT1 is often elevated in NSCLC,

correlating with increased tumor development, metastasis, and unfavorable prognosis [72]. Likewise, miR-21, a prominently examined oncogenic miRNA, is significantly upregulated in NSCLC, where it enhances proliferation, suppresses apoptosis, and promotes invasion via modulating PTEN and other tumor-suppressive targets [13]. These ncRNAs are essential for comprehending NSCLC biology and present exciting opportunities for targeted therapy and non-invasive diagnostic methods [73]. In cervical cancer, ncRNAs have become essential in modulating tumor advancement and treatment resistance. lncRNAs like HOTAIR facilitate cervical cancer progression by enhancing cell proliferation, invasion, and metastasis via interactions with chromatin remodeling complexes and downstream effectors, including Wnt/β-catenin signaling [74]. In contrast, tumor-suppressive miRNAs, such as miR-34a, are frequently downregulated, resulting in unregulated proliferation and diminished responsiveness to treatment [75]. Moreover, the interaction between ncRNAs and HPV oncoproteins (E6 and E7) undermines host cell regulatory networks, underscoring the critical function of ncRNAs in the etiology of cervical cancer [76]. Likewise, ncRNAs are essential to the progression of bladder cancer, functioning as oncogenes or tumor suppressors. The lncRNA UCA1 is significantly upregulated in bladder cancer and promotes carcinogenesis by augmenting proliferation, migration, and apoptosis resistance [77]. UCA1 functions as a ceRNA, binding and sequestering tumor-suppressive miRNAs such as miR-145, thereby relieving repression of oncogenic targets [78,79]. Conversely, miRNAs including miR-124 and miR-143, which are frequently downregulated in bladder cancer, exert tumor-suppressive effects by limiting cellular proliferation and invasion [77].

LIMITATION OF THE STUDY

One limitation of this study is its dependence on the Scopus database for bibliometric analysis, which, although extensive, omits relevant articles from other databases like Web of Science or Embase. This may lead to possible deficiencies in the dataset and the exclusion of important research contributions. Our search strategy restricted non-coding RNA terms to the title field to enhance specificity and reduce the inclusion of non-relevant articles. Although key ncRNA types (e.g., miRNA, lncRNA) frequently appear in author keywords and were therefore still captured, this approach may have excluded some relevant studies. Consequently, a limited number of relevant publications may not have been included in the dataset.

The analysis predominantly concentrates on published journal papers, excluding gray literature, conference proceedings, and preprints, which could offer significant insights into emerging patterns. A further restriction is a reliance on author keywords for presenting research trends, which may inadequately encompass the field's scope due to terminological discrepancies or the underrepresentation of specific subjects. Moreover, the study's emphasis on quantitative indicators, such as citation rates and *h*-index, may neglect qualitative dimensions, such as the societal or therapeutic implications of research.

CONFLICT OF INTEREST

The authors declare that they have no known financial or personal relationships with any individuals or organizations that could have influenced the work reported in this manuscript. There are no professional, financial, or personal interests of any kind related to any product, service, or company that could be perceived as affecting the content, analysis, or conclusions presented in this manuscript.

AUTHOR CONTRIBUTIONS

Conceptualization: YB., LAO.; methodology: YB., JT., AYA.; data collection and curation: ZN., IH., EYA.; formal analysis and bibliometric analysis: LAO., SMA.; visualization and software analysis: MHM., WEH., EAG; writing—original draft preparation: YB., LAO. writing—review and editing: all authors.; project administration: YB. All authors have read, revised, and approved the final version of the manuscript.

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Declaration of Generative AI and AI-Assisted Technologies

The authors used QuillBot and ChatGPT to improve language clarity and readability. All content

was subsequently reviewed and revised by the authors, who take full responsibility for the final version. No figures or images were generated or modified using AI tools.

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