Milk metabolites in relation with metabolomics: A perspective from scientometric analysis for trends and future

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Abstract. The composition and characteristics of milk change over the course of lactation. Metabolomics assesses milk quality, cow health, feeding systems, and potential adulteration. This review aimed to map the metabolic profile of fresh cow's milk. The data were collected from Scopus (2005-2025) using keywords: milk metabolomic, lactation stage, cow feed, location, cattle, bovine, cow's milk, and goat's milk. A total of 947 documents were obtained using R-Studio (Biblioshiny) and VOSviewer. Documents dominated by the articles (87.01%), followed by reviews (9.4%), book chapters, conference papers, and books. The highest number of publications (191) occurred in 2024. The top five Journals were Journal of Dairy Science, Animals, Food Chemistry, Food Research International, and Journal of Agricultural and Food Chemistry. The most productive countries were China, The USA, Italy, and Spain. Highly cited global and local documents were authored by Shabat et al. (2016) and Scano et al. (2014), respectively. Most of the analysis used NMR, GC-MS, and LC-MS. Milk metabolites are influenced by the cow's metabolism pathway in each lactation stage, feeds, and genetics. Choline, glycerophosphocoline, and glutamic acid were found as biomarkers for milk coagulation. Further research is needed to explore the milk nutrition, processing, quality, and safety of the milk products.

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1 Introduction

Milk characteristics and composition are important for dairy producers, as they directly impact processing and product quality. Breed, feed, climate, location, and handling practices influence milk composition [1]. The majority of people in the world consume milk that comes from cows [2]. Profiling of fresh cow milk metabolites are essential to optimize quality including nutrition and safety of milk products. The field of agriculture, food science, and dairy research have applied metabolomics as an accurate and frequently used analytical method. Metabolomics, the large-scale study of small molecules (metabolites), has gained prominence as a precise and comprehensive analytical tool in agricultural and food sciences. It enables the identification of biomarkers related to animal health, milk authenticity, and nutritional properties.

Previous studies have reported important factors and biomarker compounds related to animal health, production, authentication, and characterization of the functional properties of milk. Although numerous studies have examined milk metabolites, most are limited to specific geographic regions such as Europe, leaving gaps in global research coverage. The present study addresses this limitation through a bibliometric analysis of milk metabolomics research from 2005 to 2025. It aims to systematically identify key research trends, knowledge gaps, and future directions. The novelty of this work lies in its comprehensive mapping of the milk metabolomics landscape, highlighting the role of metabolomic tools in exploring milk heterogeneity and guiding future innovations in dairy science.

2 Experimental section

2.1 Methods

The data for this study were retrieved from the Scopus databases. The following search terms were used to identify articles relevant to milk metabolomics in the published literature: "milk metabolomic, lactation stage, cow feed, location, cattle, bovine, cow's milk, goat's milk". The steps to perform bibliometric study as shown in Figure 1. The dates of the publications ranged from 2005 to 2025. A total of 947 documents were collected.

The data were analyzed in R-tool (Biblioshiny from Bibliometric Library) was used to perform the systematic review analysis and visualize scientific literature trends [3]. The VOSViewer v. 1.6.6 software (Leiden University, Leiden, The Netherlands) was also employed to perform analysis and science mapping. The documents were analyzed about annual scientific production, top source documents, contributing countries, top ten authors, co-author's affiliations, distribution of documents type, top cited countries, research trends, the most relevant keywords, the most global cited documents and the most local cited documents for the documents which have been observed in this research.

3 Results and discussion

3.1 Main information

The time span for this research is from 2005 to 2025 (20 years), with the numbers of sources being 194. There are 947 documents in total including journal articles, books, book chapters, conference papers, erratums, and reviews, as can be seen in Figure 2.

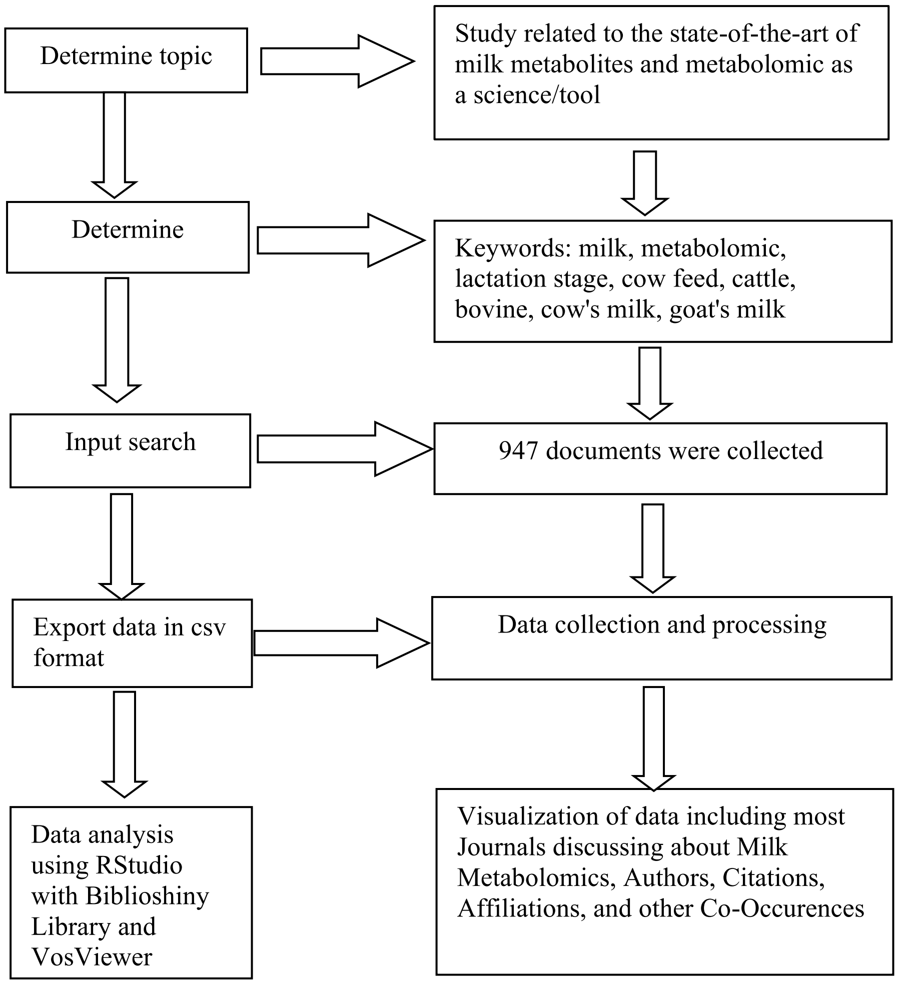

Fig. 1. Steps to perform bibliometric study in this research.

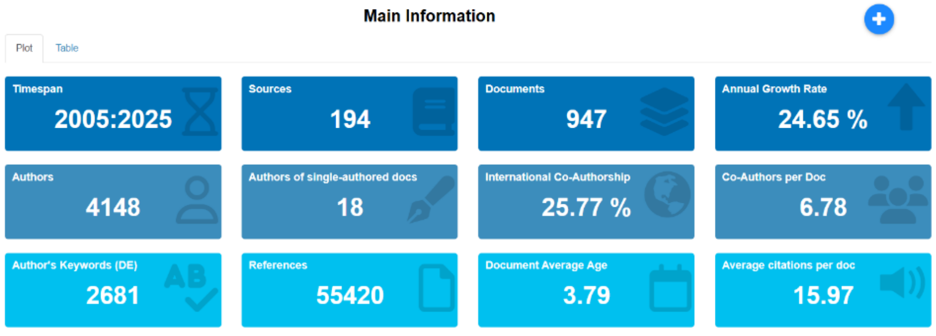

Fig. 2. Main information of time span, sources and numbers of documents on milk metabolomics in scopus.

3.2 Annual scientific production

Publications on the metabolomics of milk indicate a significant increase from 2005 to 2025, as described in Figure 3. The data search utilized keywords such as milk, metabolomics, lactation stage, cow feed, location, cattle, bovine, cow's milk, and goat's milk. Information collected over the last two decades reveals a notable upward trend, particularly starting from 2012. In this paper, it is reported that even though fatty liver is a temporary disease, it is a cause of other related metabolic disorders including ketosis, which is dangerous for cow health and milk production. Mechanisms in fatty liver occurring are not completely understood yet, thus the application of high-throughput 'omic' approaches such as metabolomic is essential in providing insight to improve mitigation strategies in reducing the fatality of fatty liver in dairy cows.

Between 2005 and 2009, there was no publication regarding milk and metabolomics. Subsequently, there was a gradual increase from 2011, with 2011 marks the initial stage of the development of science related to metabolomics in milk. The annual number of publications continued to rise, reaching 73 publications in 2020. In 2021, there were 111 publications, which dramatically rose in 2024 with 191 publications. This trend indicates a growing interest among researchers and academics in exploring metabolomics in milk and related scientific areas. The year 2024 witnessed the highest number of publications. It is anticipated that the number of publications will continue to rise by the end of 2025, reflecting a sustained interest in the field.

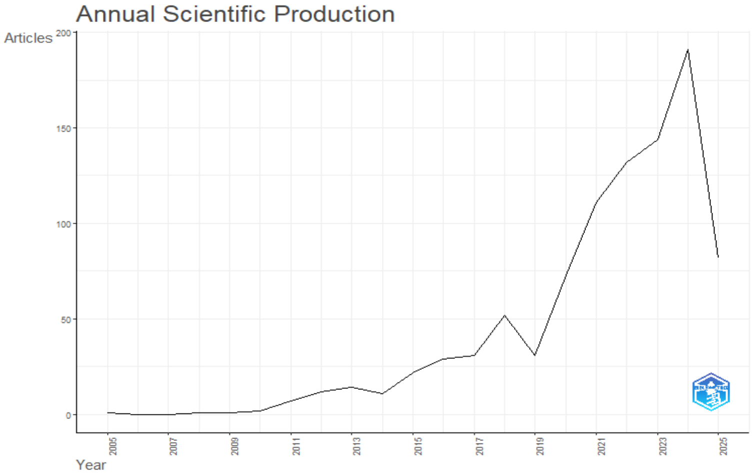

Fig. 3. Annual scientific production of publications on milk metabolomics.

The science of milk metabolomics is rapidly advancing due to the increasing need to comprehend the composition of metabolite compounds in milk and their implications for human health. Understanding metabolite compounds in milk confers the potential to significantly contribute to the development of healthier and more diverse dairy products. It also enhances our understanding of the impact of milk on human health, supporting advancements in the agricultural and livestock industries to improve the quality and safety of dairy products. Metabolomics analysis has proven instrumental in identifying bioactive metabolite compounds in various types of milk, including cow and goat milk, and human including breast milk and colostrum.

3.3 Top source documents

Search results on Scopus from 2005 to 2025 reveal that among the sources focusing on cow's milk metabolomics, ten stand out as the top source documents (Table 1). The Journal of Dairy Science leads with the highest number of publications, totaling 125 articles. The following are Animals (80 articles), Food Chemistry (61 articles), Food Research International (40 articles), Journal of Agricultural and Food Chemistry (40 articles), Nutrients (34 articles), Foods (33 articles), Food Bioscience (19 articles), Journal of Animal Science (18 articles), and LWT (17 articles). Starting from 2010, there were 125 articles on J. of Dairy Sciences with the highest number of citations (2802). Notably, these articles were published in the Journal of Dairy Science covering diverse topics, including inflammation and mastitis, the application of metabolomics and machine learning for lameness detection in dairy cattle, the examination of serum metabolome concerning buffalo ketosis incidence, and metabolomic analysis in plasma and sheep's milk.

Table 1. Top ten journals reporting research related to milk metabolites analysis.

Sources	Articles
Journal of dairy science	125
Animals	80
Food Chemistry	61
Food Research International	40
Journal of Agricultural and Food Chemistry	40
Nutrients	34
Foods	33
Food Bioscience	19
Journal of Animal Science	18
LWT – Food Science and Technology	17

3.4 Top ten authors and country production over time

Table 2 shows a list of top ten authors, with the number of publications ranging from 19 to 38 documents, who have made significant contributions to milk research with their own articles factionalized. Wang X and Wang Y are the most productive authors, with total citations of 161 and 190, respectively. The latest research related to the aroma compound of fermented cheese and the metabolic profile of raw milk, which is related to the health status of cows, while other scientists discussed the clinical condition of cow mastitis. Most of the corresponding authors come from China, the US, and Italy, with single-country publications or multi-country publications, as shown in the country production over time (Figure 4).

The field of metabolomics in China is rapidly advancing, evidenced by the growing number of authors engaging in research and contributing to scientific developments in milk metabolomics. According to a previous study, milk production in China has significantly increased from ten million metric tons in 2001 to nearly 39 million metric tons in 2009, attributed to the use of dairy animals with superior genetics, effective feeding practices, and efficient management [4]. This growth positions China as the third-largest milk producer globally, trailing behind the United States and India.

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Table 2. The top 10 authors on milk metabolomics.

Authors	Articles	Articles Fractionalized
Wang X	38	5.79
Wang Y	35	4.14
Wang J	32	4.19
Zhang Y	29	4.03
Zhang H	25	3.12
Li Y	24	2.92
Zhang J	24	3.42
Zhang X	22	2.74
Liu Y	20	2.93
Li X	19	2.10

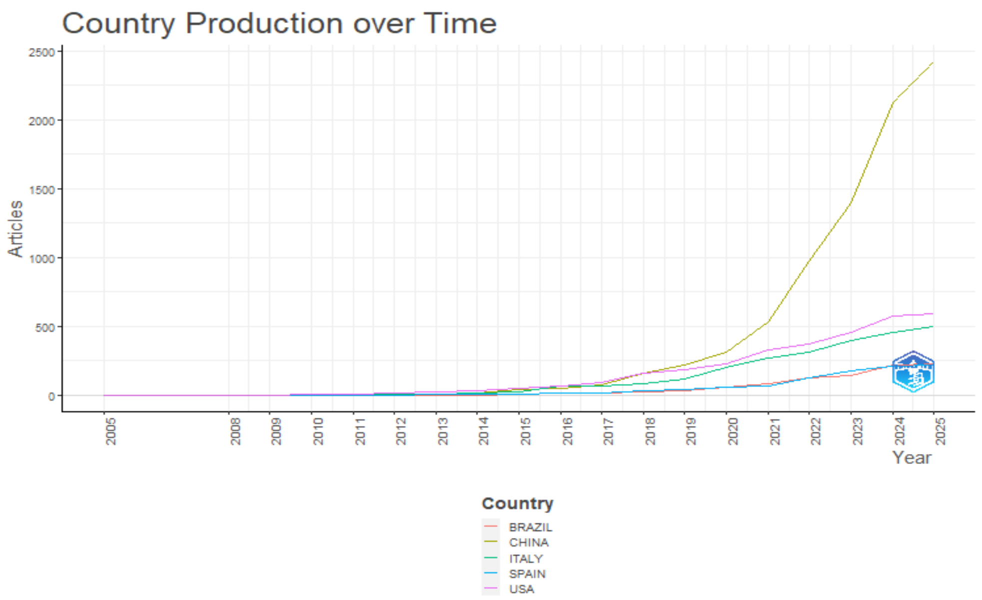

Fig. 4. Countries of the most corresponding authors on milk metabolomics.

3.5 Co-authors' affiliations

The documentation includes the university affiliation of all collaborating researchers, ensuring not only the recording of co-authors' affiliations but also providing visibility into researchers operating in different laboratories and in different countries (Figure 5). This certainly benefits each research affiliate by allowing them to record the scope of their research. The top ten affiliates based on publication distribution with The Inner Mongolian University (China) become the university that has the most publications discussing milk (138 articles), followed by the Northwest AANDF University (137 articles), China Agricultural University (104 articles), Institute of Animal Sciences (92 articles), Jiangnan University (85 articles), Universita Cattolica del Sacro Cuore (76 articles), University de Alberta (74 articles), Institutes of Animal Sciences (68 articles), University of Florida (61 articles), and Aarhus University (55 articles).

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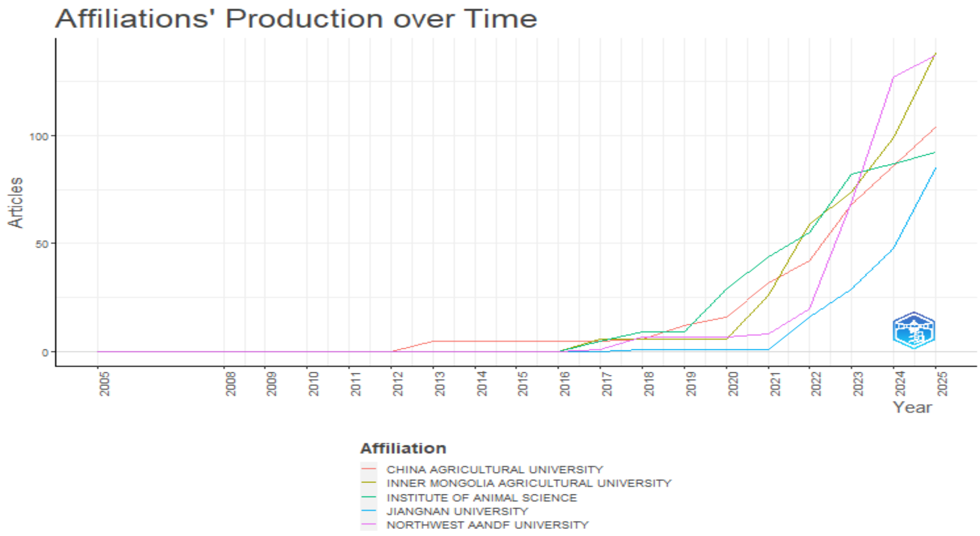


Fig. 5. Affiliations production over time on milk metabolomics.

3.6 Distribution of document types

Figure 6 shows the document search exploration on Scopus using keywords such as year, bibliography, and source resulted in 947 documents, there were 824 (87.17%) articles, 89 (9.40%) were in the form of reviews, 20 (2.11%) were book chapters, 7 (0.74%) were conference papers, 5 (0.53%) were books, and 2% of erratum. The largest proportion is 87.17% of document sources were from articles. The large number of research papers on milk metabolomics identifies the growing interest of researchers and academics in mapping developments in milk research.

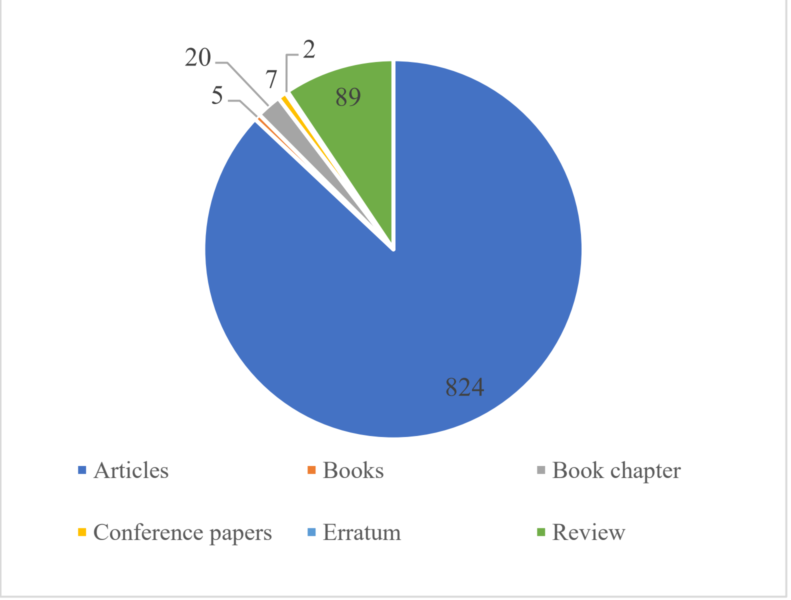


Fig. 6. Document types on milk metabolomics.

3.7 Top cited sources

Analysis of the R project found 116 sources that contributed to all documents. A total of ten documents had a high h-index (Table 3). The h-index data indicates that high quality publications are typically published in highly cited journals and are thus accessed by more readers. The most productive source of documents on milk metabolomics has an h-index range of 17 – 29. Journal of Dairy Science, Food Chemistry, Food Research International, Journal of Agricultural and Food Chemistry, and Nutrients rank the highest h-index. The Journal of Dairy Science has 2802 citations and an h-index of 29. It is followed by Food Chemistry (18), Food Research International (17), Journal of Agricultural and Food Chemistry (17), Nutrients (17), and Animals (15). Other Journals had h-index 9 and below.

Table 3. Information about the journal and their reputation.

Source	h_index	g_index	m_index	TC	NP	PY_start
Journal of dairy science	29	46	1.8125	2802	125	2010
Food chemistry	18	32	1.28571429	1108	61	2012
Food research international	17	30	1.30769231	938	40	2013
Journal of agricultural and food chemistry	17	33	1.0625	1106	40	2010
Nutrients	17	31	1.88888889	1002	34	2017
Animals	15	22	1.36363636	625	80	2015
Foods	9	14	1.5	236	33	2020
Journal of animal science	9	13	0.81818182	197	18	2015
Animal	8	15	0.57142857	248	16	2012
Food chemistry: x	8	10	2	111	12	2022

3.8 Research trends

Research trends and term frequency are shown in Figure 7. Based on Table 3, the majority of writers worldwide have written about metabolomics for highly esteemed journals, particularly the Journal of Dairy Science. The most popular keywords among writers are milk, metabolomics, animals, female, cattle, and male. Metabolite, non-human, controlled study, physiology, Nuclear Magnetic Resonance Spectroscopy, multivariate analysis, etc, are additional keywords. Most of the authors who were the five most influential authors in the metabolomics literature, selected these terms. The top five countries for research papers in the field of metabolomics are China, Brazil, Italy, Spain, and the US, where the five authors are based.

3.9 The most relevant words

In terms of the most relevant words, word analysis is carried out to obtain a basic structure for research development based on topic trends. From the search, a total of 3151 words were obtained (Figure 8). In the tree maps (Figure 9), the most left panel represents the most used words in the keywords. In this panel, female the first-top word (553 = 17.6%) being used by most of authors, followed by word ‘milk’ counting 345 (10.95%), and ‘metabolomics’ (407

= 12.92%) becoming the top three of the words among other search term identified in this research. All are other words counting for 6% and below.

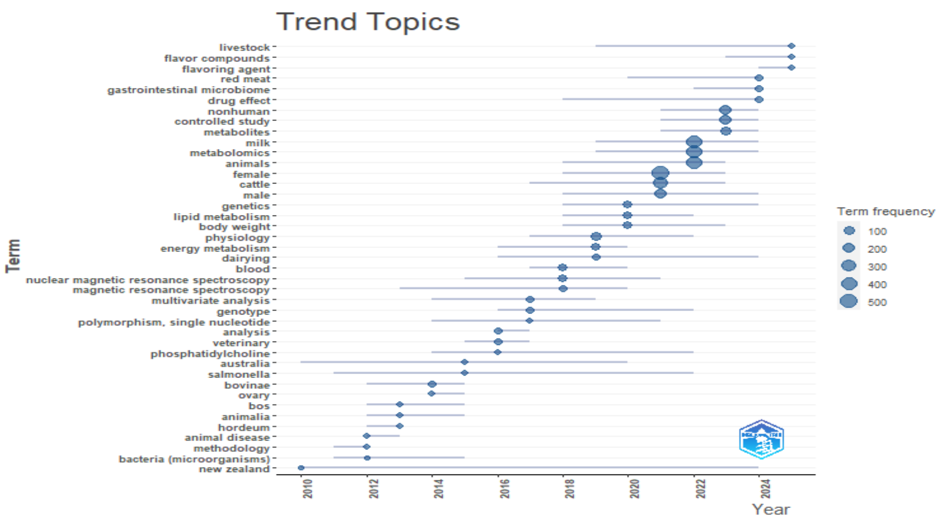
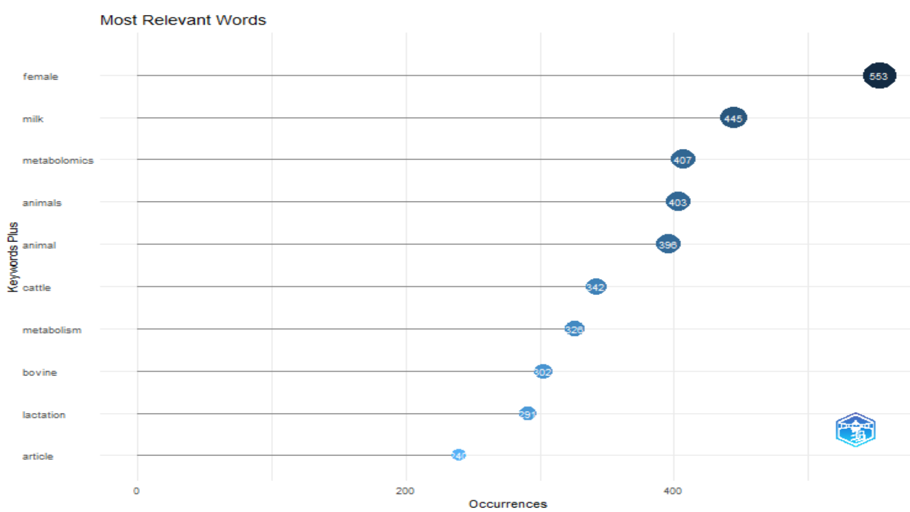


Fig. 7. Trend topics regarding milk metabolomics research from 2010 to 2024.



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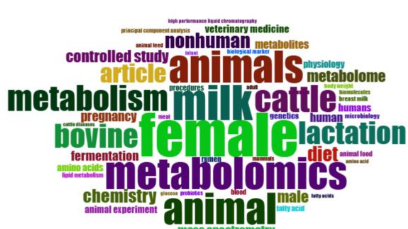

Fig. 8. Most relevant (and frequent) words (a) with wordcloud (b) from all documents observed.

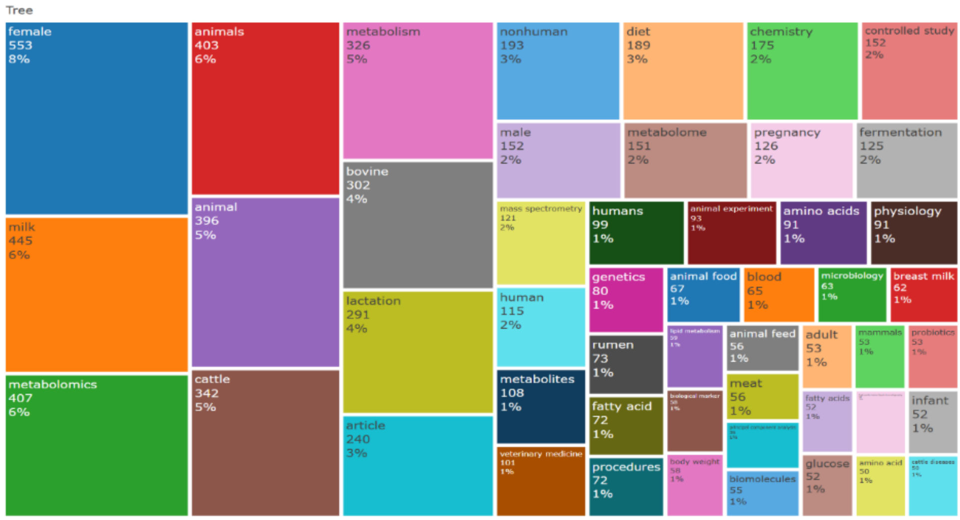

Fig. 9. Tree map showing the most frequent word used in all documents observed.

3.10. The most global cited documents and the most local cited documents

The most globally cited document was a paper written by Shabat et al. in 2016 [5] garnering the highest citation (562) for all of the papers discovered in this bibliometric research. He observed that components of the rumen microbiome are closely associated with cows' capacity to derive energy from their feed, referred to as feed efficiency. A diminished richness of microbiome gene content and taxa was closely associated with enhanced feed efficiency. The genes and species of the microbiome precisely predicted the feed efficiency phenotype of the animals. The targeted enrichment of microorganisms and metabolic pathways within each microbiome group enhanced energy and carbon allocation to the animal, concurrently reducing methane emissions into the atmosphere. This paper has driven developments in milk metabolomics followed by the second most global cited document written by Foroutan et al., [6] (180 citations) who reported the use of NMR-spectroscopy LC-MS and ICP-MS to get milk metabolites. Saleem et al. [7] followed by receiving 177 citations for his work on the metabolomic technique to elucidate the effects of grain diets on rumen health in dairy cows, indicating that various metabolomic platforms enable a more comprehensive understanding of metabolic causes and effects.

The most local cited documents talking about the specific topic that was discussed and researched. Scano et al. [8] acquired 40 local citations, examining a GC-MS based metabolomic methodology for defining goat's milk in comparison to cow's milk. Hailemariam et al. [9] ranks second with 29 local citations, identifying of predictive biomarkers of disease state in transition dairy cows, meanwhile Sundekilde et al. [10] ranks third, with 25 local citations, for demonstrating a strong association between milk metabolites and somatic cell counts in bovine milk through NMR metabolomics.

3.11. Metabolomics as tools for unravelling metabolite heterogeneity in milk and dairy products

Metabolomics, a relatively new analytical field, has revolutionized metabolite profiling and biomarker identification [11]. It allows targeted or untargeted analyses of metabolites in biofluids, providing insights into biological fingerprinting [12]. In dairy science, metabolites significantly impact milk production, quality, and composition, showing correlations with milk profiles in different breeds [8, 13]. Circadian rhythms, diet, and lactation stages influence milk metabolome, emphasizing its role in understanding milk's nutritional and functional properties. Chemicals found in milk include sugars (carbohydrates), lipids, proteins, minerals, vitamins, and other substances that are vital to the operation of most parts of the human body.

Dairy research has focused a lot of attention on the minerals, fatty acids, nucleotides, and bioactive peptides found in milk. Metabolites, which arise from different bodily metabolisms and are byproducts of cellular activity, are directly associated with phenotypes, indicating changes in biological status and functions. Numerous factors, including genetics, food, seasons, geographic origins, lactation stage, health state, processing, storage, contamination, and adulteration, can affect the amount and type of metabolites produced from milk. In addition to evaluating the quality of milk, milk metabolomics can be highly helpful in forecasting how the milk will react to various processing techniques. Dairy producers must always consider the technological characteristics of milk, especially in seasonal milking systems where changes in milk composition can affect the milk's functioning as cows pass through the early, mid, and late lactation stages. These characteristics will influence how milk behaves at various processing stages, which will ultimately affect the process' effectiveness and the calibre of the finished product. These characteristics might include, but are not restricted to, the milk's capacity to coagulate in acid and rennet, as well as its heat stability.

When referring to milk coagulation, Sundekilde et al. [14] examined the impact of cow milk metabolites on the technical qualities of milk in relation to milk coagulation. Two dairy herds were utilized. The results indicated that the different quantities of citrate, choline, carnitine, and lactose may be associated with the milk coagulation qualities. The scientists noted that there were differences in lactate, acetate, glutamate, creatinine, choline, carnitine, galactose 1-phosphate, and glycerolphosphocolines between non-coagulating and well-coagulating milks. These differences could serve as indicators of the quality of cheese milk. Similarly, Harzia et al. [15] discovered that there was a significant difference between non-coagulating and well-coagulating milks in terms of the levels of these mentioned metabolites, with the inclusion of glycerophosphocolines.

By analyzing the metabolome of milk, researchers can gain valuable insights into the biochemical variability of milk, monitor metabolite changes associated with milk production processes, and identify biomarkers for disease states in dairy cows [9]. These studies collectively highlight the significance of metabolomics in advancing our understanding of milk biology and its implications for nutrition, health, and dairy industry practices.

4 Conclusion

Over the past two decades, research in milk metabolomics has grown substantially, particularly after 2011, driven by advances in analytical technologies and the need to better understand milk's nutritional and functional components. Bibliometric analysis of 947 documents reveals that the field is dominated by contributions from China, the United States, and Italy, with a notable increase in publications in recent years. Metabolomics has proven to be a valuable tool for characterizing milk composition, identifying biomarkers for animal health and product quality, and ensuring food safety and authenticity. Despite the progress, this review acknowledges several limitations, such as the exclusive use of the Scopus database and reliance on specific keywords, which may have excluded relevant literature. Future research should address these gaps by incorporating additional data sources, expanding keyword strategies, and emphasizing underrepresented regions. Additionally, there is a need to integrate metabolomic findings into practical applications in dairy processing, product innovation, and sustainable livestock management.

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