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Bibliometric analysis of studies on gene expression and RNA-seq in cattle species

Esma Gamze AKSEL[1,a*]***, Ahu CEPHE***[2,b]***, Funda İPEKTEN***[3,c]***, Gözde ERTÜRK ZARARSIZ***[4,d]***, Aytaç AKÇAY***[5,e]

[1] *Department of Genetic, Faculty of Veterinary Medicine, Erciyes University, 38280, Kayseri, Turkiye*
[2] *Institutional Data Management and Analytics Units, Erciyes University Rectorate, 38280, Kayseri, Turkiye*
[3] *Department of Biostatistics, Faculty of Medicine, Adıyaman University, 1302040, Adıyaman, Turkiye*
[4] *Department of Biostatistics, Faculty of Medicine, Erciyes University, 38280, Kayseri, Turkiye*
[5] *Department of Biostatistics, Faculty of Veterinary Medicine, Ankara University, 06070, Ankara, Turkiye*

0000-0002-0040-8933[a]*; 0000-0001-9374-4495* [b]*; 0000-0002-6916-9563*[c]*; 0000-0002-5495-7540*[d]*; 0000-0001-6263-5181*[e]

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ABSTRACT

The aim of this study is to examine the development of research articles on "gene expression and RNA-seq" in cattle species in the Web of Science (WOS) database between 2010 and 2023 using bibliometric mapping methods. Initially, 500 articles were screened using relevant keywords, and 353 articles suitable for analysis were analyzed using the Bibliometrix R package's shiny web application and some analyses were conducted using the VOSviewer application. The conducted analyses included subheadings such as main data information, annual scientific production, countries, and institution analysis, bibliographic coupling with sources, Bradford analysis, Lotka's law analyasis, highly cited articles, and most influential authors. According to the results obtained after the analysis, it was determined that the institution conducting the most studies in the relevant field is "Universidade De Sao Paulo", the country with the most publications is the USA, and the most published journal is "BMC Genomics". Keyword analysis revealed that the trending topics in recent years are mastitis, dairy cattle farming, and heat stress. The studies were categorized into different clusters related to the reproductive system, immune system and diseases, meat and dairy cattle production. It is recommended that researchers planning to work in this research area on cattle species should design their research, determine the journal to be published, or establish institutional connections by examining the reported study and planning accordingly.

Sığır türünde gen ifadesi ve RNA-dizileme alanında yapılan çalışmaların bibliyometrik analizi

ÖZET

Bu çalışmanın amacı; Web of Science (WOS) veri tabanında 2010-2023 yılları arasında sığır türünde "gen ifadesi ve RNA-dizileme" konusunun incelendiği araştırma makalelerinin bilimsel haritalama yöntemiyle gelişiminin incelenmesidir. Bu hususta ilgili anahtar kelimeler kullanılarak ilk taramada 500 adet makale incelenmiş ve analize uygun 353 makale Bibliometrix R paketinin Shiny web uygulaması ve bazı analizler VOSviewer uygulaması ile analiz edilmiştir. Yapılan analizler; ana veri bilgileri, yıllık bilimsel üretim, ülkeler ve kurum analizleri, kaynaklarla bibliyografik eşleştirme, Bradford analizi, Lotka kanunu analizi, en çok alıntı yapılan makaleler ve en etkili yazarlar gibi alt başlıkları içermektedir. Analiz sonrası elde edilen sonuçlara göre ilgili alanda en çok çalışma yapan ilişkili kurumun "Universidade De Sao Paulo" olduğu, en çok yayın yapan ülkenin ABD olduğu, en çok yayın yapılan derginin "BMC Genomics" olduğu belirlenmiştir. Anahtar kelime analizine göre son yıllarda öne çıkan konuların mastitis, süt sığırcılığı ve ısı stresi konuları olduğu belirlenmiştir. Çalışmaların reproduktif sistem, immun sistem ve hastalıklar, et ve süt sığır üretimi ile ilişkili olmak üzere farklı kümelere ayrıldığı belirlenmiştir. Sığır türünde bu araştırma alanında çalışma planlayacak araştırmacıların araştırmalarını tasarlama, yayınlanacağı dergiyi belirleme ya da kurumsal bağlantıların kurulmasında bildirilen çalışmayı inceleyerek planlama yapmaları önerilmektedir.

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* *Corresponding Author e-mail address:* gamzeilgar@erciyes.edu.tr

1. Introduction

Bibliometric research is a valuable method for quantitatively and qualitatively analysing publications covering a specific topic. This method was reported to help identify new and emerging research areas was widely used in the field of medical research (1). The implementation of the Human Genome Project in the early 2000s marked a turning point in molecular research, catalyzing exponential growth in studies focusing on DNA and RNA dynamics. Technological advancements have revolutionized data acquisition, rendering it not only more cost-effective but also enhancing data quality and accessibility. Identifying the studies conducted so far, particularly in the field of gene expression and RNA-seq in cattle species, and determining the most cited publications, sources, and authors will be crucial in guiding the planning of new research endeavors.

In the realm of gene expression and RNA sequencing in cattle species, numerous significant studies have emerged. Among these pioneering works, the study conducted by Cánovas et .al (2) stands out as it focused on SNP determination using the cattle milk transcriptome technique via RNA-seq. Following this seminal research, Huang et al. (3) delved into a transcriptomic analysis using RNA-seq in cattle embryos within the reproductive research area, while Mamo et al. (4) shed light on identified the reciprocal conversation between conceptus and endometrium during maternal recognition in cattle pregnancy through RNA-seq analysis. Additionally, McGettigan et al. (5) utilized RNA-seq to compare gene expression patterns in reproductive organs of female cattle. Bahrami et al. (6) reported the investigation of the miRNA-mRNA network during the folliculogenesis stage using a systems biology approach. Wang et al. (7) reported a study examining the effect of lipopolysaccharide stimulation on the miRNA and mRNA expression profile in cattle endometrial cells. Passaro et al. (8) reported another study investigating the transcriptomic response of embryos at the blastocyst stage in cattle embryos. Prakash et al. (9) reported a comparative transcriptomic analysis of spermatozoa from high and low-yielding hybrid bulls. Xu et al. (10) reported a study examining the relationship between metabolic and endocrine disorders with bovine ovarian follicular cysts. In addition to studies focusing on gene expression and reproductive mechanisms, research endeavors have also explored disease pathways and immune responses in cattle. Notably, Nalpas et al. (11) investigated the response of bovine macrophages to (*Mycobacterium bovis*), unveiling crucial insights through RNA-seq analysis; Liang et al. (12) conducted a transcriptomic analysis revealing regional and temporal differences in the development of the mucosal immune system in the small intestines of newborn calves; Pošćić et al. (13) reported a study examining breed and adaptive response at the transcriptome level in peripheral blood cells of cattle. Additionally, Barreto et al. (14) reported a comparative transcriptomic analysis of bovine papillomatosis; Scott et al. (15) reported a study on full-blood transcriptomic analysis in beef cattle, examining potential markers for resistance to respiratory diseases.

Some of the studies reported on the determination of developmental pathways of tissues such as muscle, fat, liver, related to animal feeding in cattle farming include: He et al. (16) reported a study examining transcriptional complexity in the *Longissimus Dorsi* muscle of cattle using the RNA-seq method; Sheng et al. (17) conducted a study analyzing intramuscular, subcutaneous, and perirenal fat tissue in cattle using the RNA-seq method; Liu et al. (18) investigated the transcriptome profile of muscle tissue in Angus and Luxi cattle; Tizioto et al. (19) reported a study associated with different residual feed intake supplements in liver tissue of Nelore cattle; Keogh et al. (20) conducted a study on limited and intermittent feeding in cattle using the RNA-seq method associated with insulin secretion and signaling pathways; Wærp et al. (21) reported an RNA-seq analysis of cattle fat tissue in heifers fed diets differing in energy and protein content. De Las Hera-Saldana et al. (22) reported a study on gene expression in the *Longissimus dorsi* and *semimembranosus* muscles of Hanwoo cattle using the RNA-seq method; Wu et al. (23) determined changes in gene expression associated with clinical ketosis in Holstein cows using RNA-seq analysis; Chen et al. (24) conducted a study on identifying biomarker genes for feed efficiency in beef cattle using machine learning methods applied to multi-tissue transcriptomic data; Li et al. (25) reported a study on transcriptional states and chromatin accessibility during proliferation and myogenic differentiation of bovine myoblasts. Studies conducted in dairy cattle farming include: Raven et al. (26) reported a study identifying 12 candidate genes associated with lactation volume, composition, and calving interval in dairy cattle, by assigning sequence variants and gene expression profiles in a targeted manner. Yang et al. (27) reported a study identifying differentially expressed genes in milk fat globules throughout lactation in dairy cattle. Ahmad et al. (28) reported a study demonstrating the genomic expression analysis of circular RNAs in dairy cattle mammary epithelial cells, highlighting differences in milk synthesis.

The reviewed literature mostly comprises studies conducted in the fields of reproductive biology, the immune system, dairy, and beef cattle farming. However, these studies represent only a subset of the researched field. Through bibliometric analyses, important trends, publications, institutions, journals, and authors can be identified within the examined research area, enabling the comprehensive evaluation of the development of this research area and facilitating the planning of future studies. Especially with the aid of integrated software tools with Scopus and Web of Science (WoS) databases, such analyses can be conducted. In the planned study, the aim is to identify gene expression and RNA-seq studies in cattle species within the Web of Science (WoS) database from 2010 to 2023 and to analyze these studies in terms of citation, country, author, institution, and keywords using bibliometric analyses.

2. Material and Methods

Determination of Data and bibliometric analysis

Ethics committee authorization is not required for this study. No funding was provided for the study. The database searches were carried out using the Web of Science (WoS) database on 20 January, 2024. The search query used to examine scientific publications is described as follows: (All Fields (AF)=("cattle" OR “cow” OR “bovine”) AND AF=(“gene expression”) AND AF=("RNA-seq”)). In particular, all searches are planned in all fields columns. It is planned in this way in order not to miss any article. The information about the selected literature was converted into a Plain Text File (.txt). During the conversion process to txt. format, the complete record of each entry, and its cited references were selected. This format was chosen because it includes full records and references to all features reported in the articles. Therefore, no other features were left out. Comprehensive analyses including content assessment, keyword examination, and research trends were performed using the bibliometrix package of R, version 4.1.4 (29), and VOSviewer software, version 1.6.20 (30). A total of 500 literature items on gene expression and RNA-seq studies in cattle from 2010 to 2023 through the WoS search query. In determining the keywords, especially the combination words that will cover the subject and that all articles can be identified should be determined correctly with AND, OR, NOT conjunctions. Otherwise, some articles belonging to the field to be analysed bibliometrically may be overlooked. In bibliometric analyses, at least the title and abstract parts of all articles should be examined manually after a general article search with keywords. In particular, it can be determined that some keywords are not directly related to the researched fields. This may change the results of the analysis. It is recommended that researchers pay attention to these issues. Among these, all literature items were examined in terms of title and abstract content, and items containing content related to "microbiological, RNA-seq, pig, human-derived, water buffalo, yak" were excluded. This filtering resulted in 356 articles and early-access article. The bibliometrix package, then filtered conference papers by year and language (English), resulting in a final set of 353 articles for analysis. The analyses performed included subheadings such as main data information, annual scientific production, country, and institution analysis, bibliographic coupling with sources, highly cited articles, most local cited references, and author production of overtime and keyword analysis.

3. Results

Quantitative analysis of publication

After applying year, language and document type filters in the Biblometrix programme, 353 articles and early-access articles from a total of 500 studies were included in the analysis (Table 1).

Table 1: Main data information

Table 1: *Temel veri bilgileri*

Main Information About Data	
Timespan	2010:2023
Sources (Journals, Books, etc)	122
Documents	353
Annual Growth Rate %	21,44
Document Average Age	5.18
Average citations per doc	18.73
References	17729
Document Contents	
Keywords Plus (ID)	1444
Author's Keywords (DE)	879
Authors	
Authors	2014
Authors of single-authored docs	2
Authors Collaboration	
Single-authored docs	2
Co-Authors per Doc	7.98
International co-authorships %	39.66
Document Types	
Article	312
Article; early access	41

The graph of the annual increase in studies from 2010 to 2023 is shown in Figure 1. Until 2014, the number of studies remained below 20, while in the following years an increase in these studies was observed. In particular number of studies reached a high level in 2022.

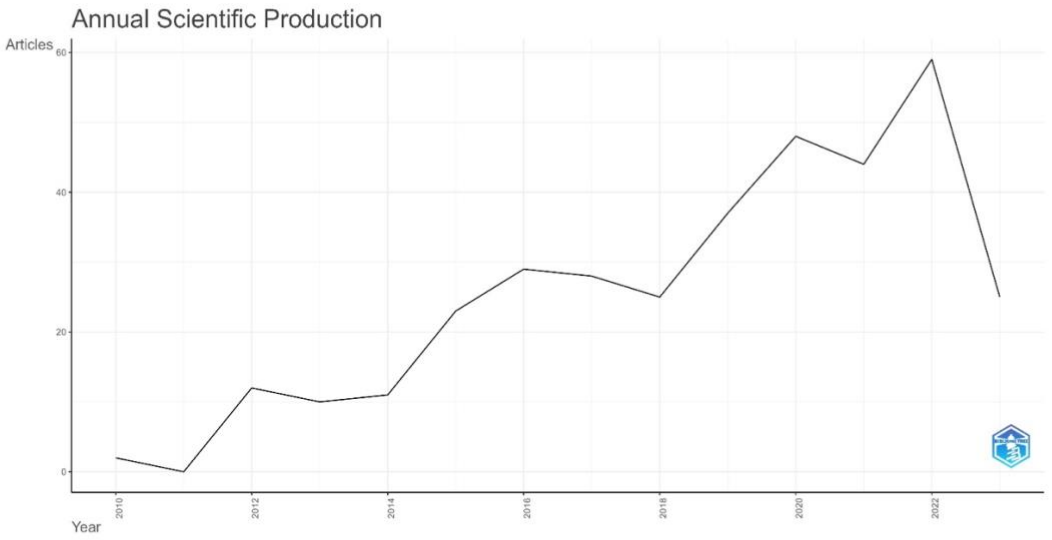

Figure 1: Annual number of publications in gene expression and RNA-seq studies in cattle

Şekil 1: *Sığırlarda gen ekspresyonu ve RNA-seq çalışmalarına ilişkin yıllık yayın sayısı*

Countries and institutions analysis

A total of 57 countries and 554 institutions were included in the research on RNA-seq and gene expression in cattle. The top 10 countries showed a global distribution including Asia, America, Europe, and Australia. The country with the highest number of publications was the USA (*n*=108), followed by China (*n*=104) and Brazil (*n*=39). A country analysis of collaborative authorship was performed to demonstrate international collaborations. For each country, the total strength and collaborative authorship connections with other countries were calculated. In the network visualisation, the font size represents the frequency of collaboration, and each circle represents the country of the author (Figure 2). The lines connecting the countries in the examined figure indicate the strength of the collaboration, while the nodes represent the number of collaborations from each country. Countries shown in the same colour represent a common area of research. The USA ranks first in the field of study with 108 publications and 88 total linkages.

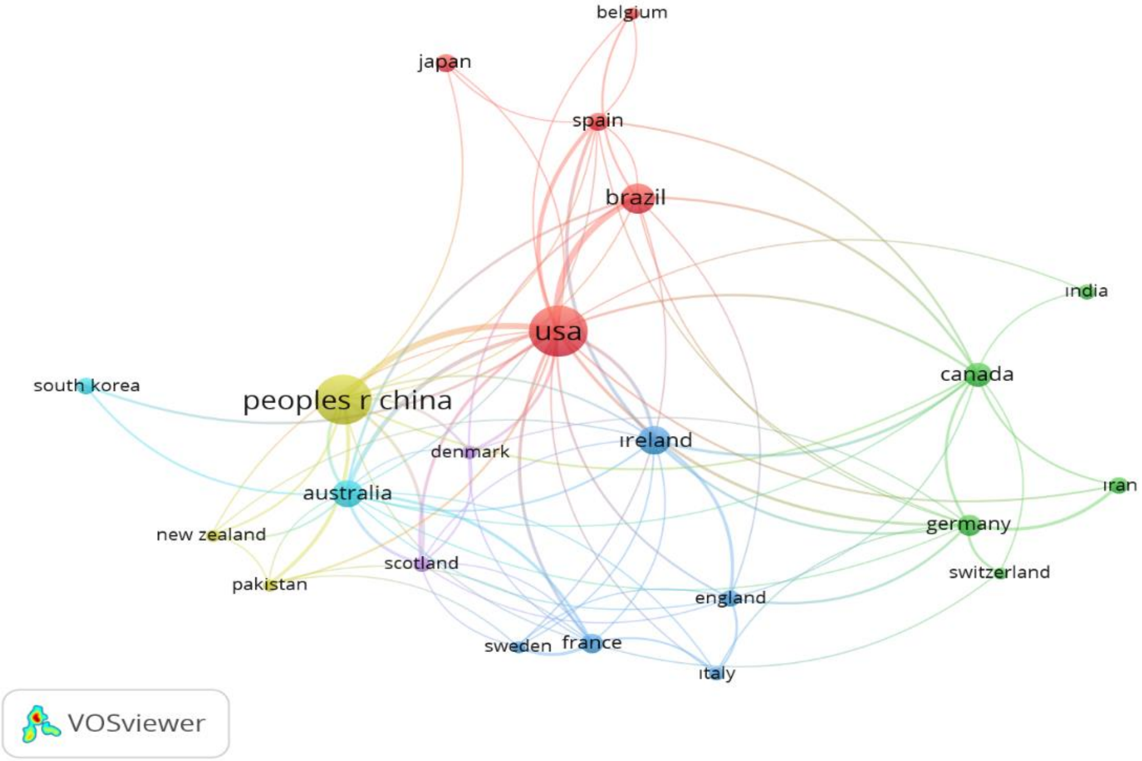

Figure 2: Map visualization of countries on research of gene expression and RNA-seq studies in cattle

Şekil 2: *Sığırlarda gen ekspresyonu ve RNA-seq çalışmaları araştırmalarına ilişkin ülkelerin harita görselleştirilmesi*

Taking into account the most relevant links identified by the authors of the respective articles, Universidade De Sao Paulo leads with the highest number of articles (n=39), as shown in Figure 3. It is closely followed by University College Dublin, with 38 articles, followed by INRAE with 26 articles. Figure 4 shows a three-domain graph using the Sankey plot that describes the interaction between institutions, countries and journals. The height of the nodes, shown as rectangles, corresponds to the frequency of a particular country, institution or journal within the collaborative network. Meanwhile, the width of the lines connecting the nodes is directly proportional to the number of links. The results show that America, Ireland, Brazil and China are the dominant countries.

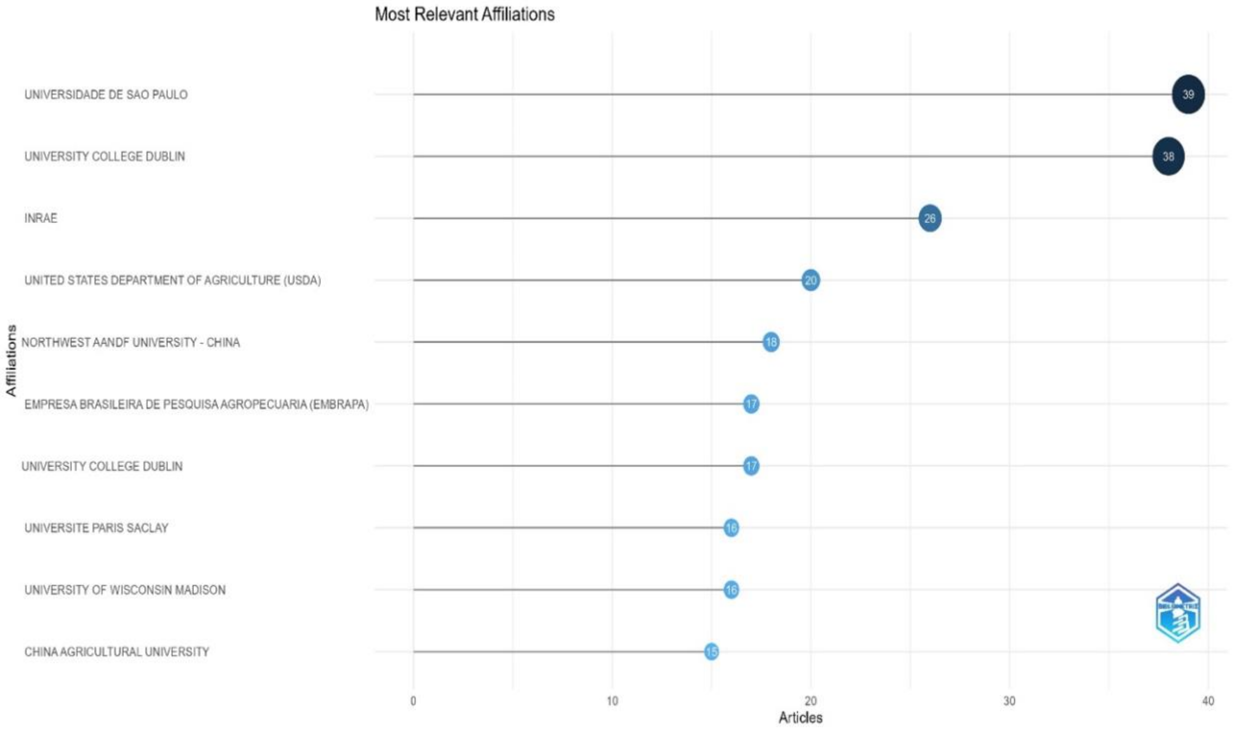

Figure 3: Most relevant institutions

***Şekil 3:** En ilgili kurumlar*

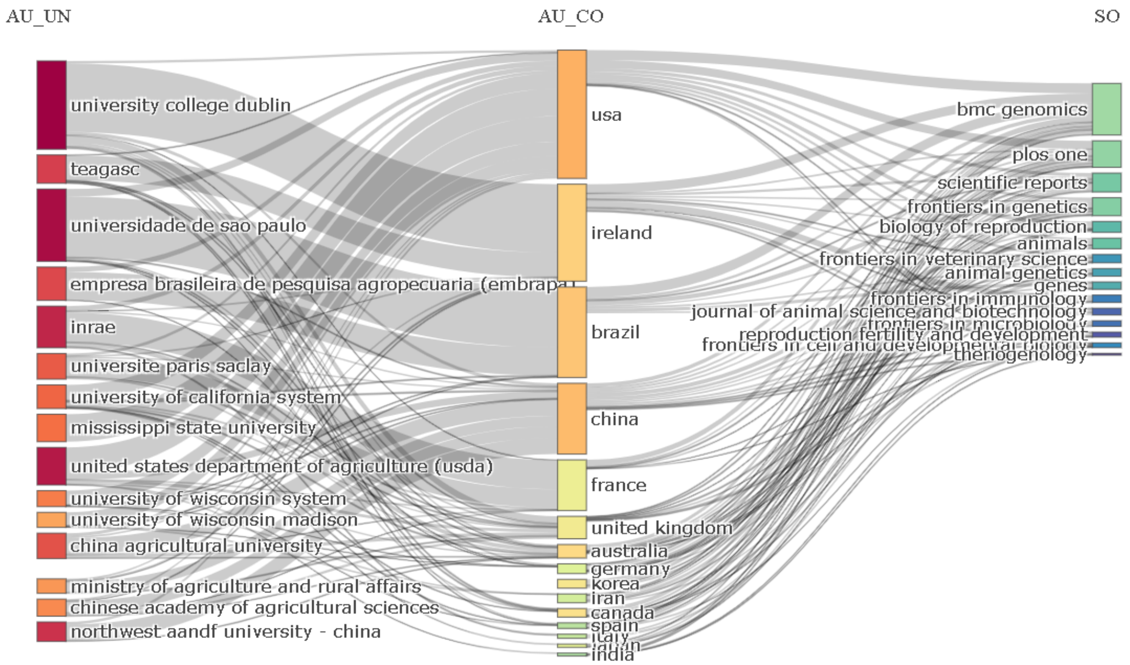

Figure 4: Three-field plot showing the network between institutions (left), countries (middle), and journals (right)

***Şekil 4:** Kurumlar (solda), ülkeler (ortada) ve dergiler (sağda) arasındaki ağı gösteren üç alanlı çizim*

Bibliographic Coupling with Sources

A total of 123 sources were generated from research articles using the full count method with a minimum threshold of 5. Only 15 sources met this criterion. For each of the 15 sources, the total strength of bibliographic coupling links with other sources was calculated (Table 3). The analysis revealed 105 links and a total link strength of 10988, forming 3 clusters of 15 items. The first cluster contained 7 elements, the second 5 items, and the third 3 items. The source with the highest total link strength is "BMC Genomics", followed by "PLoS One".

Table 3: The topmost 5 strong bibliographic coupling with sources

Tablo 3: *Kaynaklarla en güçlü 5 bibliyografik bağlantı*

Rank	Sources	Clusters	Links	Total link strength	Documents	Citations
1	BMC Genomics	1	14	5253	57	1998
2	PLoS One	2	14	2852	27	710
3	Frontiers in Genetics	1	14	2445	19	190
4	Scientific Reports	1	14	2351	17	279
5	Genes	1	14	1214	9	54

Among the top 10 journals, "BMC Genomics" stands out as the leading authoritative review journal in the field of gene expression and RNA-seq studies, with the highest Journal Impact Factor (JIF) as shown in Table 4. The latest recent impact factor for this journal: is 4.4, reflecting its importance at the academic forefront and providing insight into potential future development directions. Figure 6: shows the top 10 most locally cited journals. According to Table 4, it was determined that although the most articles were in BMC Genomics, PLoS One journal received also the most local citations (Figure 5).

Table 4: Top 10 journals with the most papers.

Tablo 4: *En çok makale içeren ilk 10 dergi*

Rank	Journals	Documents	JIF Percentile	JIF Quartile
1	BMC Genomics	57	78.1	Q1
2	PLoS One	27	65.1	Q2
3	Frontiers in Genetics	19	65.2	Q2
4	Scientific Reports	17	70.5	Q2
5	Animals	13	81.5	Q1
6	Biology of Reproduction	10	66.1	Q2
7	Genes	9	61.7	Q2
8	Animal Genetics	8	74.3	Q2
9	Frontiers in Veterinary Science	8	92.0	Q1
10	Frontiers in Cell and Developmental Biology	5	65.7	Q2

JIF: Journal Impact Factor

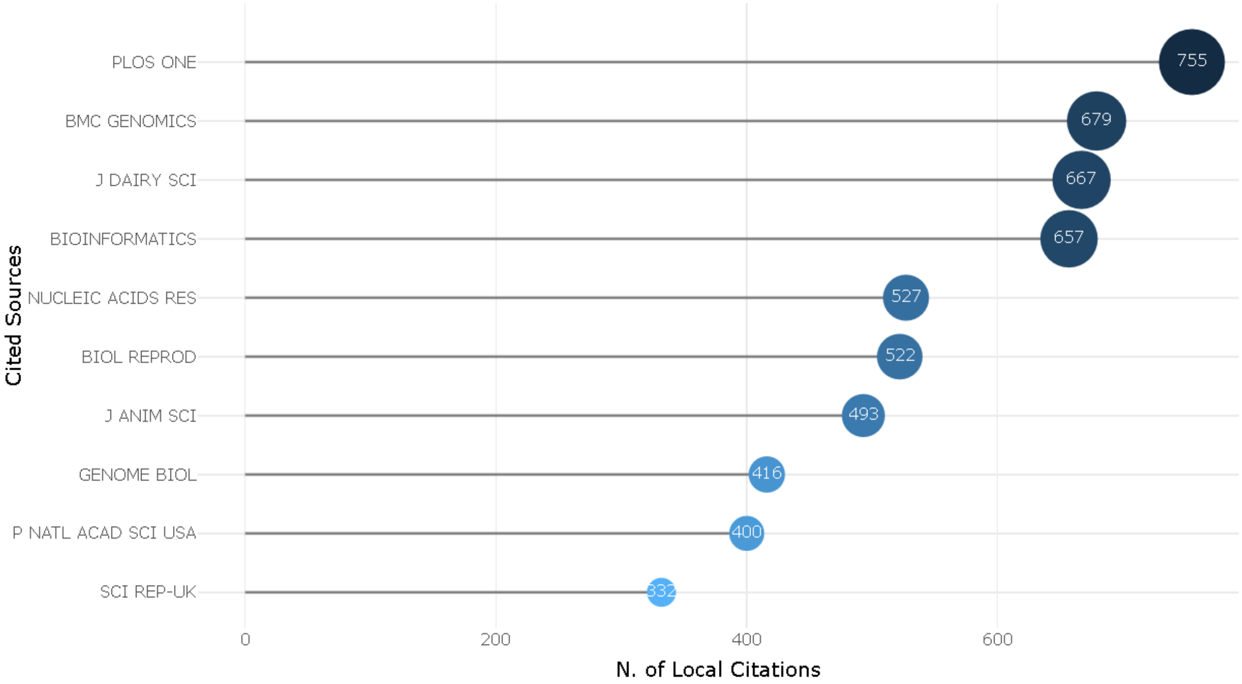

Figure 5: Most local cited sources

Şekil 5: *En çok yerel alıntı kaynağı*

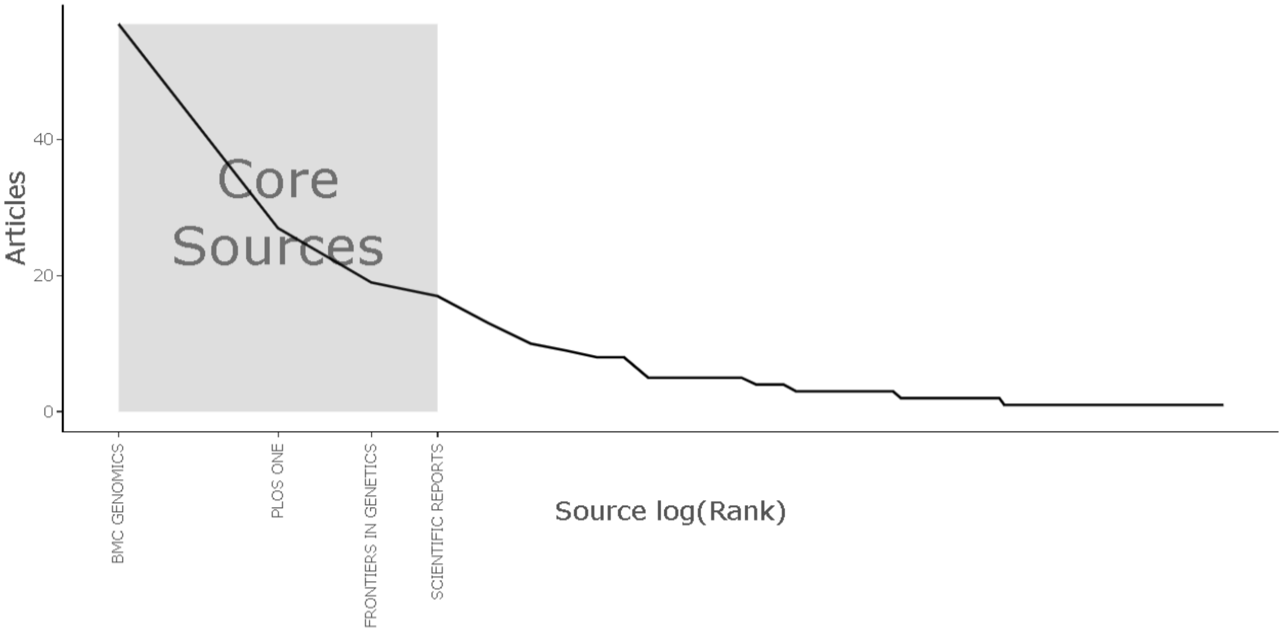

Figure 6: Determination of core journals with Bradford's law

Şekil 6: *Bradford's kanunu ile çekirdek dergilerin belirlenmesi*

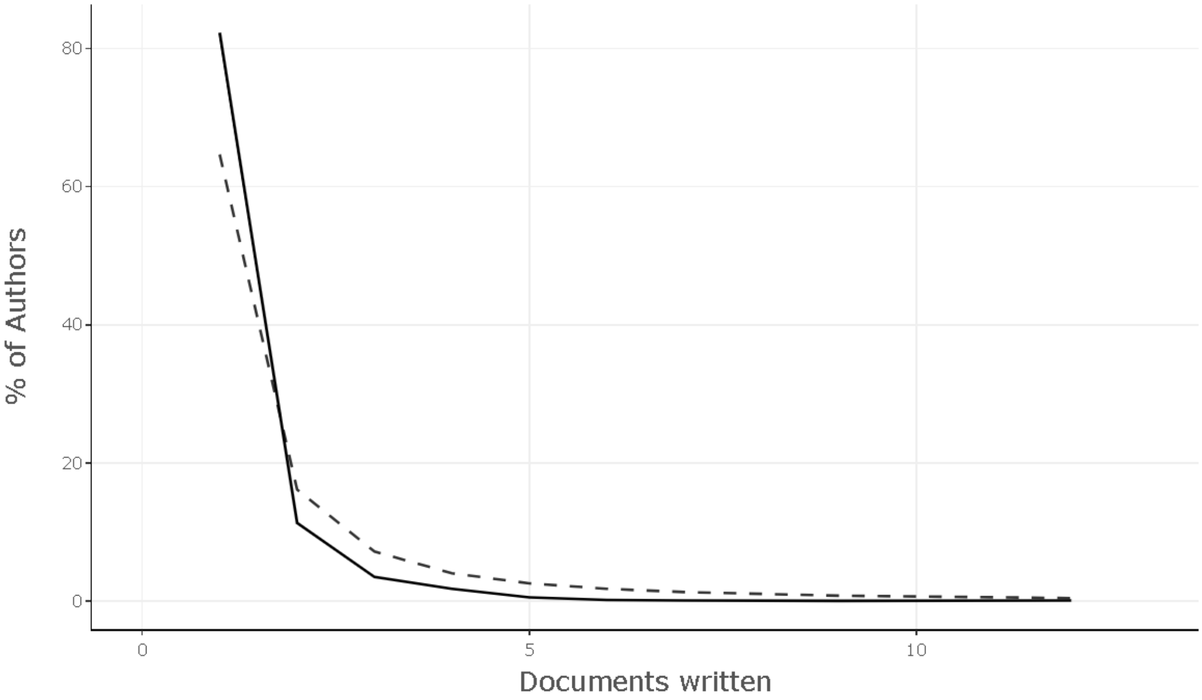

Figure 7: Lotka’s law analysis for author productivity
***Şekil** 7: Yazar üretkenliğinin Lotka kanununa göre analizi*

Figure 6 shows the first academic articles related to the study area in the Bradford region, where the distribution of articles across journals was examined. The journals in this central region are considered to the leading publications in the field of cattle gene expression and RNA-seq and serve as the primary outlet for the majority of articles related to this research. This graph is important for researchers trying to identify the most productive journals in the field of cattle gene expression and RNA-seq. Accordingly, core journals; BMC genomics, PLoS One, Frontiers in Genetics, Scientific Reports have been designated as journals. Figure 7 shows an analysis of the distribution of authors across articles according to Lotka's law. The distribution was found to follow this law.

Highly Cited Articles, References and Author Production of Over Time

Table 5 shows the top 5 most cited research articles. Bogliotti et al. (2018) "Efficient derivation of stable primed pluripotent embryonic stem cells from bovine blastocysts. " comes next. Published in 2018, this article has collected 153 citations in 5 years.

The reference articles with the most local citations are reported in Figure 8.

Table 5: The most global cited articles

Tablo 5: *En yüksek küresel atıf alan makaleler*

Rank	Title	Paper	Total Citations	TC per Year	Normalized TC
1	Efficient derivation of stable primed pluripotent embryonic stem cells from bovine blastocysts.	Bogliotti et al. (31)	153	21.86	6.59
2	Transcriptional profiles of bovine in vivo pre-implantation development.	Jiang et al. (32)	128	11.64	1.96
3	Long non-coding RNA ADNCR suppresses adipogenic differentiation by targeting miR-204.	Li et al. (33)	126	14.00	4.11
4	Transcriptome microRNA profiling of bovine mammary epithelial cells challenged with *Escherichia coli* or *Staphylococcus aureus* bacteria reveals pathogen directed microRNA expression profiles.	Jin et al. (34)	122	11.09	1.87
5	SNP discovery in the bovine milk transcriptome using RNA-Seq technology.	Cánovas et al. (2)	119	7.93	1.29

TC: Total citations

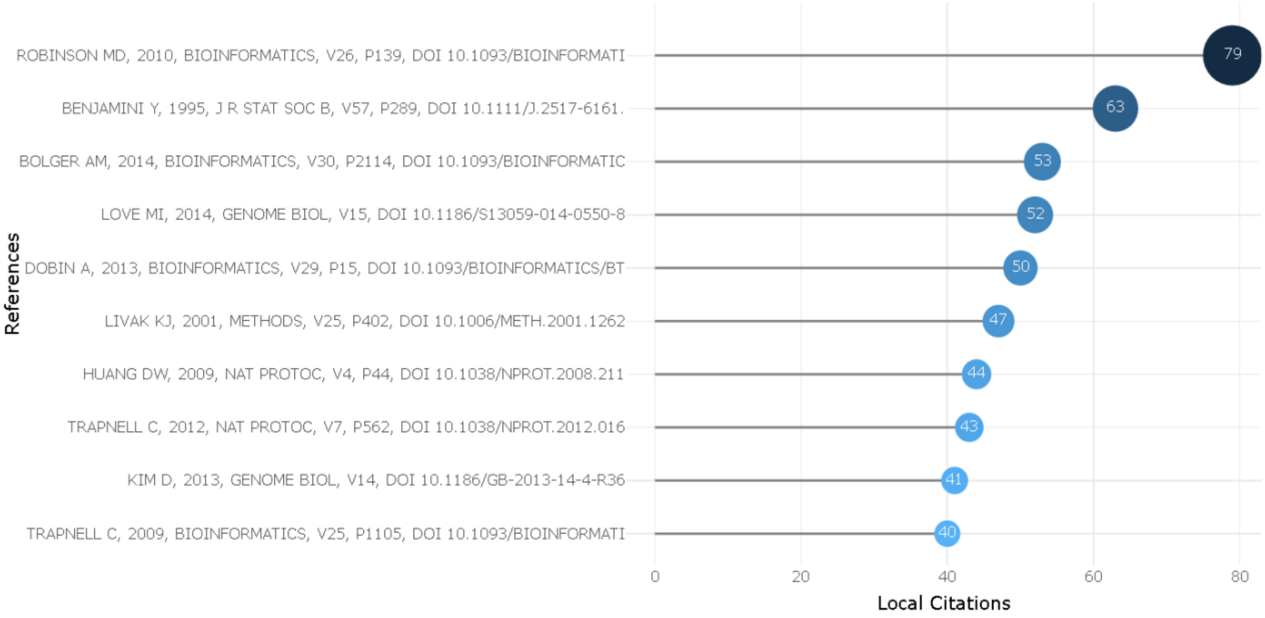

Figure 8: The most local cited references

Şekil 8: *En yüksek yerel atıf alan referanslar*

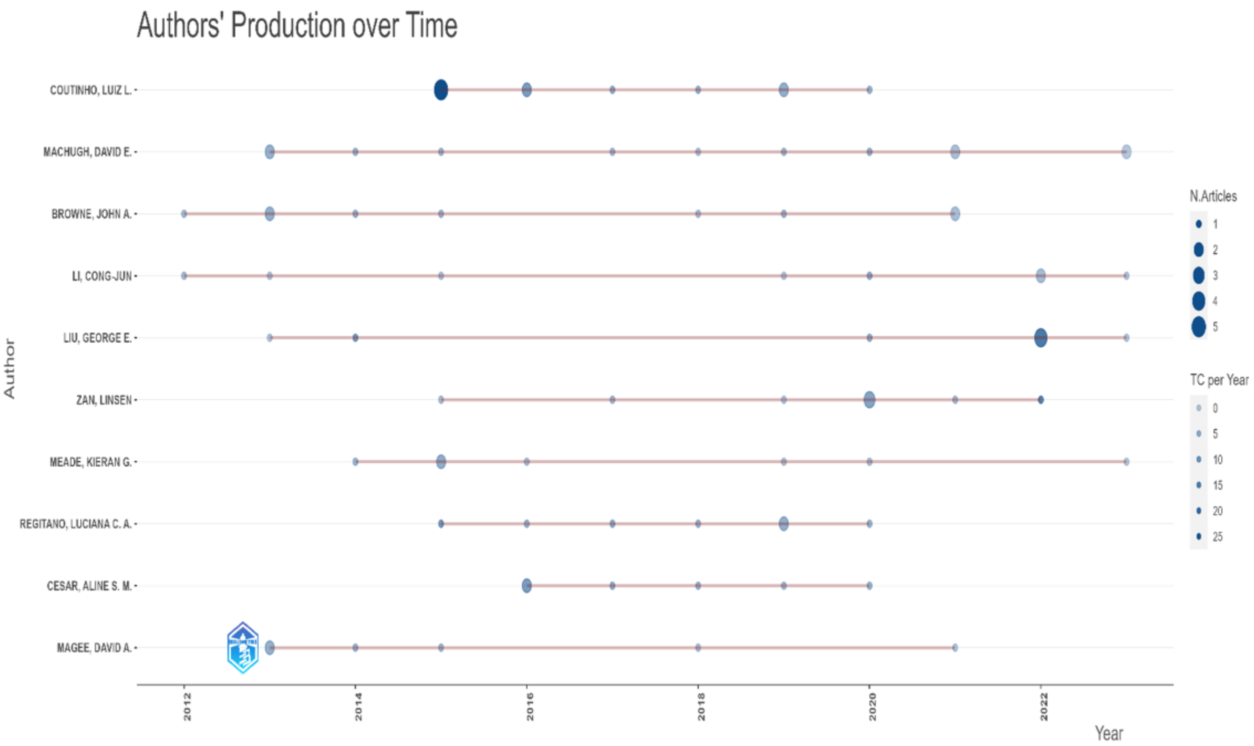

Figure 9: Production of the most productive authors over time

Şekil 9: *En üretken yazarların zaman içindeki üretimi*

Figure 9 shows, the most prolific authors in the field of gene expression and RNA-seq studies based on the number of publications attributed to each author. The size of the circles in the visualisation indicates the number of publications authored by an individual in a given year, while the density of the circles represents the number of citations received by the author the same year. As both the number of publications and the number of citations increase, the size and darkness of the circles increase proportionally. In particular, authors such as Li, CJ., Browne, JA. started their work on the topic in 2012, while other prolific authors concentrated their efforts in the following years. Coutinho LL continued their work until 2020 with a high number of articles in 2015 (Figure 9).

Keyword Analysis

Keyword analysis is essential for gaining insight into the key issues, focus areas and trends in a research area. Such analysis allows researchers to quickly identify the most discussed topics and key concepts. The word cloud highlights the most used keywords in the field, with terms such as "rna-seq", "transcriptome", "gene-expression", "bovine" and "cattle". This demonstrates the widespread use of rna-seq, and transcriptome data in the context of gene expression studies in cattle. The results of trending topics and co-occurance keyword analyses based on author keywords are reported in Figure 10 and Figure 11 respectively.

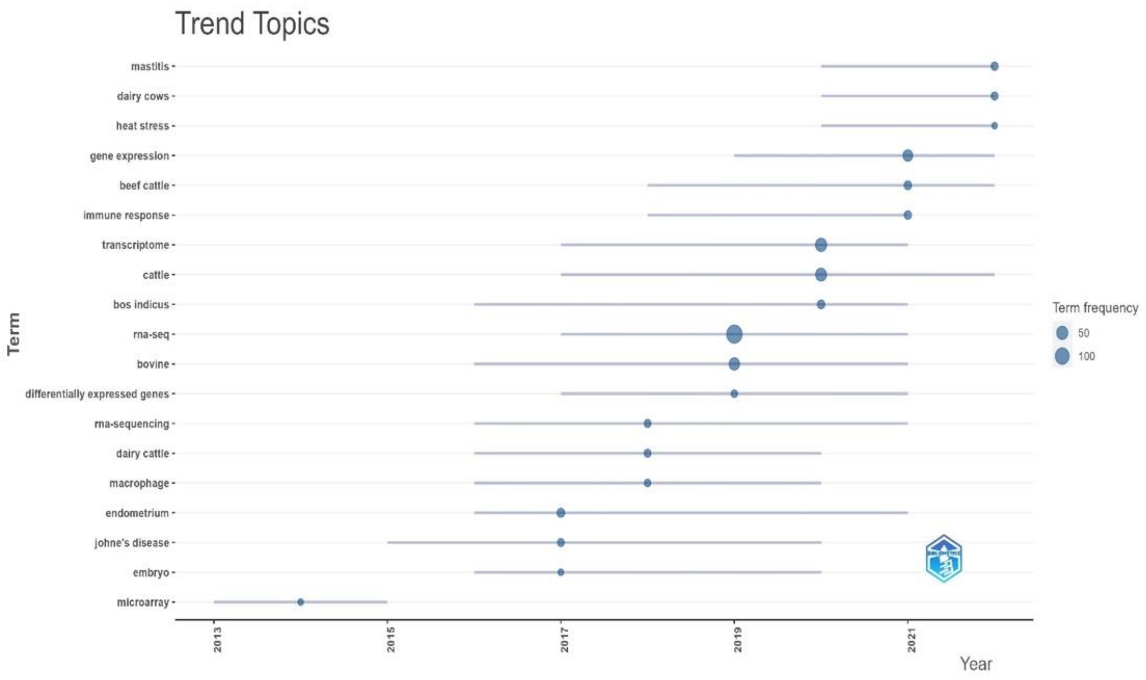

Figure 10: Trend topics across years for gene-expression and RNA-seq studies in cattle

Şekil 10: *Sığırlarda gen ifadesi ve RNA dizisi çalışmaları için yıllar içindeki trend konuları*

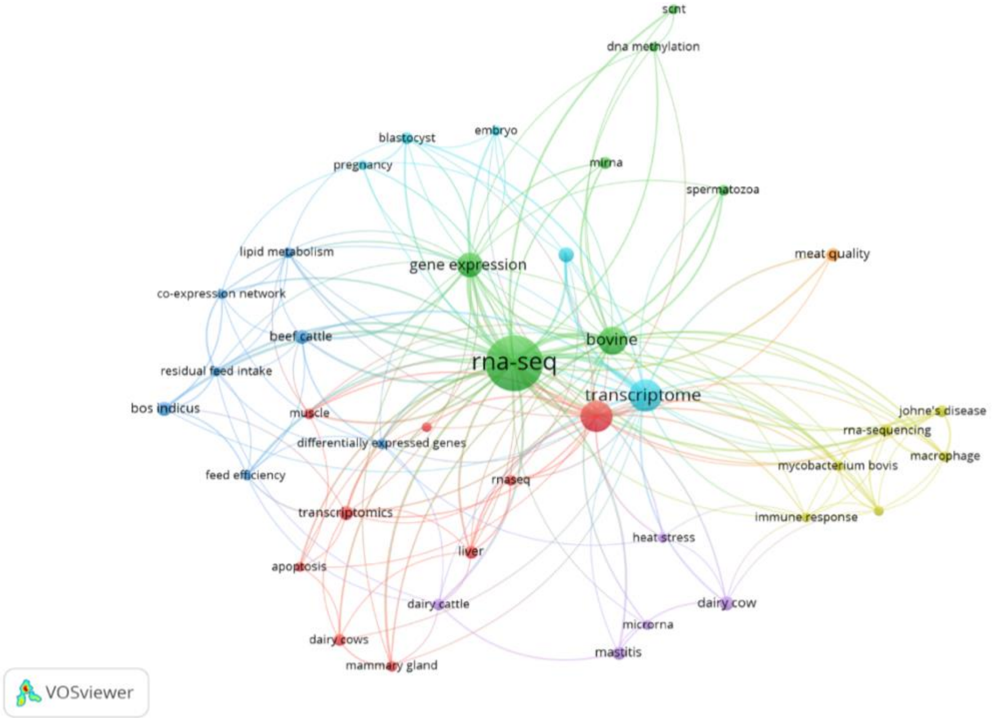

Figure 11: The result of a network of author keywords that co-occur in the field of gene expression and RNA-seq studies in cattle

Şekil 11: *Sığırlarda gen ifadesi ve RNA-seq çalışmaları alanında birlikte ortaya çıkan bir yazar anahtar kelimeler ağının sonucu*

4. Discussion and Conclusion

Bibliometric analyses allow for the statistical analysis and interpretation of articles accumulated over time and the summarisation of this information. While this analysis identifies potential research topics, trends and gaps in the research area, it can also show the impact of existing reported publications in the relevant subject area in the academic environment (35). In this study, research articles and early access articles published in the Web of Science journal search index between 2010 and 2023 on gene expression and RNA-seq studies in cattle species were collected and bibliometric analysis was performed. We used Bibliometrix and VOSviewer to understand the current literature in the research area and provide a globally accessible summary of studies conducted until 1 January, 2024. When the researches in the field of RNA-seq were examined in the Wos database, it was determined that there were a total of 58 publications between 2008-2010. However, it was determined that the first publications in RNA-seq and gene expression screening in cattle species started in 2010. While publications have increased since this year, it is observed that it has gained momentum since 2014. One of the main reasons for this is thought to be related to the references (bioinformatics studies) in Figure 8, where ‘the most cited local references’ are reported. In addition to technological developments in the field of RNA-seq, the development of bioinformatics algorithms in which differentiated gene expression analyses are performed has paved the way for researchers to obtain more unbiased publication results and indirectly suggests that publications may gain momentum.

In this study, 500 publications were identified from the WOS database between 2010 and 2023, and 353 articles were included in the analysis based on the content specified in the methods section. BMC Genomics, PLoS One, Frontiers in Genetics, Scientific Reports, Animals are reported as the top five journals with the most publications in this field. The fact that the determined journals are in Q1 and Q2 categories proves that the studies to be carried out in this field are high-level scientific studies. The top 10 journals with the highest number of publications in the field of gene expression and RNA-seq studies in cattle are as follows with WOS categories; Biotechnology & Applied Microbiology, Genetics & Heredity, Multidisciplinary Sciences, Reproductive Biology, Agriculture, Dairy & Natural Science, Veterinary Sciences, Agriculture, Dairy & Natural Science, Immunology. The reported research areas can be defined as cross-sectional areas of gene expression and RNA-seq studies in cattle species. According to Bradford's law, the top three journals with the most publications were "BMC Genomics", "PLoS One", and Frontiers in Genetics", while the three most cited journals were "PLoS One", "BMC Genomics" and "Journal of Dairy Science". Bogliotti et al., (30) were the most global cited authors in the related research field with 153 citations during the period analysed. In addition, it was concluded that the studies reported to have received high citations close to 2010 were pioneering due to the citations they received for the studies planned later.

The most productive authors over time were Coutinho LL, Li CJ, and Brown JA. It has been determined that the studies in which Countinho LL has been involved, especially in muscle development, polymorphism, gene expression (36), determination of variants on miRNA (37), transcriptional research on meat quality in different experimental designs (38- 42) as well as studies on reproductive organs in different experimental designs (43-46). Li CJ has been involved in studies in different perspectives ranging from transcriptomic profiling of organs in the digestive system such as rumen (47), duodenum (48) and butyrate-treated cells (49) in cattle, fat tissue development (50), epigenetic studies in which DNA methylation profiles (51) are monitored according to tissues and studies in which regulatory variants are examined in multiple tissue atlases (52). Brown JA, on the other hand, has been involved in reproductive studies and fertility genomics studies (53, 54) as well as some studies examining the responses in peripheral blood cells of cattle affected with *Mycobacterium avium* and *bovis* (11, 55-57). It was determined that the identified authors have been working and publishing in the relevant research field for many years. According to the author keyword analysis, "rna-seq", "transcriptome", "gene-expression", "bovine" and "cattle" best represent the studies. It is understood that the related words are in the front row because they are the basic words used by the authors to identify the subject at first glance. Although USA, China and Brazil were in the top three of the countries where the most articles were published, the most relevant affiliation institutes were Universidade De Sao Paulo from Brazil, University College Dublin from England, and INRAE from France. It is expected that these results are obtained in countries that are advanced in cattle breeding.

According to the trend topic analysis, while microarray studies were emphasised in the first years, topics such as Johne's disease, endometrium, macrophages, studies in 2015-2017, rna-seq, transcriptome studies in 2017-2018, immune response, and beef cattle between 2018-2020 were the trend topic. As of 2020, heat stress, dairy cattle, and mastitis are the trending topics. It is recommended that researchers design their research plans accordingly. It is predicted that studies on heat stress will increase, especially in terms of examining the effects of global climate changes on living things and taking the necessary measures. In addition, it is recommended that the studies to be planned especially on herd and beef cattle in the global food crises that may arise due to global climate change should be designed with this foresight in mind. In this regard, it may be recommended to perform transcriptomic analyses to determine the breeds resistant to temperature stress in which different tissues and organs are examined. It may be possible to determine up and down regulated gene expression, variants and molecular, biological and metabolic pathways associated with the mechanism under investigation. It may be suggested to design both descriptive and analytical comparisons of miRNA, lncRNA target mRNA interactions related to the mechanism to be investigated.

Seven different clusters were identified according to the results of keyword analysis in cattle species. These clusters were; spermatozoa, miRNA, DNA methylation - on epigenetic development genetics, mastitis - on dairy cattle, fat, muscle metabolism - on beef cattle, Johen's disease paratuberculosis - on immunity. In this regard, the article provides general guidance to researchers. For topic-specific studies, RNA-seq keywords and keywords observed as a result of cluster analysis can be used together to search the literature and determine the scope of the topics. The methods, bioinformatics algorithms and results can be evaluated from the articles obtained. For example, many researches can be designed at qualitative and quantitative levels of mRNA, miRNA, lncRNA with transcriptomic information to be obtained from different tissues in different cattle breeds, different developmental stages of the embryo, different disease patterns or different drug, feed, environment experimental designs.

This is the first planned bibliometric analysis in the field of gene expression and RNA-seq in bovine species. The results obtained in about 13 years of Web of Science accumulation show that studies in this field will increase every year. It may even be considered that the articles obtained are insufficient in terms of the scope of the subject of interest. In this direction, the results of keyword and trending topic analysis can be used in line with the above-mentioned recommendations in determining the field of study for new researchers, especially in the field of gene expression and RNA-seq in bovine species. The high quality of the journals in which the planned studies can be published can also provide motivation to the researchers. It can also make predictions about the quality of the studies that researchers will carry out in this field and with which institutions and organizations they can carry out their planned studies. Therefore, it is recommended that researchers plan their experimental designs in the field of gene expression and RNA-seq in bovine species after reviewing the reported analyses.

Conflict of Interest

The authors declared that there is no conflict of interest.

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Authors' Contributions

Motivation / Concept: Esma Gamze AKSEL, Aytaç AKÇAY
Design: Esma Gamze AKSEL, Ahu CEPHE, Aytaç AKÇAY
Control/Supervision: Gözde ERTÜRK ZARARSIZ
Data Collection and / or Processing: Esma Gamze AKSEL, Ahu CEPHE
Analysis and / or Interpretation: Esma Gamze AKSEL, Ahu CEPHE
Literature Review: Funda İPEKTEN, Gözde ERTÜRK ZARARSIZ
Writing the Article: Esma Gamze AKSEL, Funda İPEKTEN, Aytaç AKÇAY
Critical Review: Ahu CEPHE, Gözde ERTÜRK ZARARSIZ

Ethical Approval

Ethical statements have been obtained from the authors confirming that the data, information, and documents presented in this article have been obtained within the framework of academic and ethical rules and that all information, documents, evaluations, and results are presented by scientific ethics and moral rules.

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