Black Sea Journal of Agriculture
doi: 10.47115/bsagriculture.1296263

Open Access Journal
e-ISSN: 2618 – 6578

Research Article
Volume 6 - Issue 5: 485-491 / September 2023

BIBLIOMETRIC ANALYSIS OF NEXT-GENERATION SEQUENCE APPLICATIONS IN LIVESTOCK

Selçuk KAPLAN[1], Yasin ALTAY[2]*

[1]*Tekirdag Namık Kemal University, Faculty of Agriculture, Department of Agricultural Biotechnology, 59030, Tekirdağ, Türkiye*
[2]*Eskisehir Osmangazi University, Faculty of Agriculture, Department of Animal Science, 26160, Eskisehir, Türkiye*

Abstract: Bibliometric analyzes are widely used in many fields. However, there are still insufficient bibliometric studies evaluating animal science studies from different perspectives. Therefore, we performed the comprehensive bibliometric analysis of 335 documents scanned in the Web of Science (WoS) database in next-generation sequence applications in livestock between 2009 and 2023. According to the analysis results, this field has been increasing interest recently. The fact that the studies (45.07% of total) were carried out by international large research groups with the participation of many researchers shows that the collaborative working culture in this field is developed. BMC Genomics, Animals and Frontiers in Genetics are among the most preferred journals in studies in this field, and 14, 10 and 10 articles have been published, respectively, to date. The number of citations per article indicates the high impact of the articles published in this field. It has been determined that the three most frequently used keywords in next-generation sequence studies in the field of livestock are "identification", "diversity" and "expression". Overall, studies about next-generation sequence applications in livestock seem to be very popular among the scientific community in recent years.

Keywords: Bibliometrics, Next-generation sequence, Genome, SNP, Livestock

***Corresponding author:** Eskisehir Osmangazi University, Faculty of Agriculture, Department of Animal Science, 26160, Eskisehir, Türkiye
E mail: yaltay@ogu.edu.tr (Y. ALTAY)
Selçuk KAPLAN https://orcid.org/0000-0003-1101-2296
Yasin ALTAY https://orcid.org/0000-0003-4049-8301

Received: May 12, 2023
Accepted: July 23, 2023
Published: September 01, 2023
Cite as: Kaplan S, Altay Y. 2023. Bibliometric analysis of next-generation sequence applications in livestock. BSJ Agri, 6(5): 485-491.

1. Introduction

DNA is the fundamental source of life and has the heredity information of all known organisms, from prokaryotes to eukaryotes (Dahm and Banerjee, 2019). James Watson and Francis Crick discovered the double helix structure of DNA in 1953 (Watson and Crick, 1953). The discovery of DNA structure has led to significant changes in biology and genetics (Hood and Galas, 2003; Waters, 2008). In the late 1970s, Frederick Sanger and colleagues developed a new DNA sequencing method called The Sanger Dideoxynucleotide Sequencing Method (Sanger et al., 1977). Frederik Sanger was awarded the second Nobel Prize in Chemistry in 1980 with this method. This method has become a standard method in clinical genetics (Totomoch-Serra et al., 2017). Moreover, the Sanger method has been widely used in forensic and medical sciences (Alex et al., 2020). However, a critical limitation of the Sanger method is high cost, low analytical sensitivity, sequencing fidelity and limited read length (Schuster, 2008; Altimari et al., 2013).

The human genome project was completed in 2003 with a budget of approximately $3 billion over 15 years using the Sanger Sequencing method (Olson, 2002; Lallar and Phadke, 2016). However, the Human Genome Project has led to a search for new technologies due to its high cost and long duration (Van Dijk et al., 2014). Therefore, The National Human Genome Research Institute (NHGRI) has launched a funding program to reduce the cost of human genome sequencing to $1,000 over ten years (Chan, 2005; Schloss, 2008). Thus, high-throughput sequencing technologies have been developed following technological developments in the last two decades (Kim et al., 2014).

The first Next Generation Sequencing (NGS) technology was developed and introduced in 2005 (Margulies et al., 2005). To date, commercial companies such as Illumina and Roche have introduced many different Next Generation Sequencing (NGS) technologies to remove the limitations of Sanger sequencing (Morozova and Marra, 2008; Tipu and Shabbir, 2015). Despite the widespread use of the Sanger Method in DNA sequencing for the last 30 years, the NGS technology developed in 2005 started a new era in DNA sequencing (Voelkerding et al., 2009). While the human genome can be sequenced in one day with NGS technologies, it took about ten years to draft it using the Sanger Sequence method (Behjati and Tarpey, 2013). Today, with the widespread use of NGS technologies, there has been a significant decrease in DNA sequencing costs (Goodwin et al., 2016; Park and Kim, 2016). Thus, NGS technologies can be used in many fields, such as personalized medicine, cancer genomics, forensics and clinical microbiology (Rasheed, 2020).

The discovery of NGS allowed rapid and high throughput whole genome sequencing of individuals (Pareek et al., 2011; Schneeberger and Weigel, 2011). Therefore, NGS technology has significantly influenced genomics approaches that address the entire genome or defined regions (Koboldt et al., 2013). In this regard, genome-wide association studies (GWASs) that have been ongoing since 2007 play a significant role in determining the individual-specific differences of single nucleotide polymorphisms (SNPs) (Pouladi et al., 2016; Young, 2019). In recent years, it has been seen that GWAS studies with NGS have increased to elucidate the genomic architecture associated with important yield traits in livestock (Bordbar et al., 2020; Jiang et al., 2014). Moreover, these high-throughput technologies and approaches can effectively predict animal phenotype and breeding values for genomic selection (Goddard and Hayes, 2009; Toghiani et al., 2017).

The term "bibliometrics" was described by Pritchard in 1969 (Pritchard, 1969). Bibliometrics is a qualitative and quantitative analysis of scientific literature (Osareh, 1996). Today, the bibliometric study is one of the valuable tools used to understand the growth and trends of the scientific literature (Akhavan et al., 2016; Zahra et al., 2021). The bibliometric analysis uses various metrics such as publications, citations and journals to evaluate a particular field of study (Mishra et al., 2018; Thanuskodi, 2010).

In this study, we aimed to identify current trends and approaches to the Next-Generation Sequence applications in livestock with bibliometric analysis.

2. Materials and Methods

2.1. Materials

The material of this study consists of 335 documents scanned in the Web of Science (WoS) database in animal husbandry between 2009 and 2023 (Table 1). In obtaining the data from the Web of Science (WoS) database, appropriate keywords and journals related to the subject of animal husbandry were identified, in addition to the "next-generation sequence" and "livestock" keywords. The data were downloaded in plain text format (Full Record and Cited References) from the Web of Science (WoS) database and re-checked for suitable subjects.

Table 1. Document structure of primary data

Document Types	Number
Article	278
Article; Book Chapter	2
Article; Data Paper	1
Article; Early Access	1
Article; Proceedings Paper	4
Meeting Abstract	1
Proceedings Paper	1
Review	44
Review; Book Chapter	3

2.2. Bibliometric Analysis

Bibliometric analysis is a sociometric and network analysis method that reveals the social network of scientific studies in a particular field (Önder and Tirink, 2022). This method helps to determine the effectiveness of qualitative and quantitative research methods. As a result, it can influence the trends, policies, collaboration areas, and funding support for future research on the relevant topic. Therefore, the bibliometric analyses performed in this study have reached significant insights for future studies in this field.

2.3. Data Analysis

The data was formatted using R software's "convert2pdf" package (R Core Team, 2016). For statistical analysis related to the topics covered, both the "bibliometrics" package in R software and the "bibloshiny" application were utilized (Aria and Cuccurullo, 2017). The document structure of primary data is given in Table 1.

3. Results and Discussion

The primary data shows articles are the most common document type among 335 documents. Articles constitute 83% of all documents. It is seen that the second most common document type after articles are reviews, which constitute 13% of all documents. Moreover, the remaining document types such as book chapter and proceedings paper make up a small percentage of the total documents. According to the comprehensive bibliometric data analysis of the whole data, the data shows an overall upward trend in articles published each year. Between 2009 and 2011, the production of articles was relatively low, and it is seen that the total number of articles was 11. However, there has been a rapid increase in article production, with 23 articles published in 2012. It is seen that the number of articles published per year peaked at 44 articles in 2021. In 2023, it is seen that there are only 6 articles as of April, but data for the whole year is not available yet. The number of articles published between 2009 and 2023 is given in Figure 1.

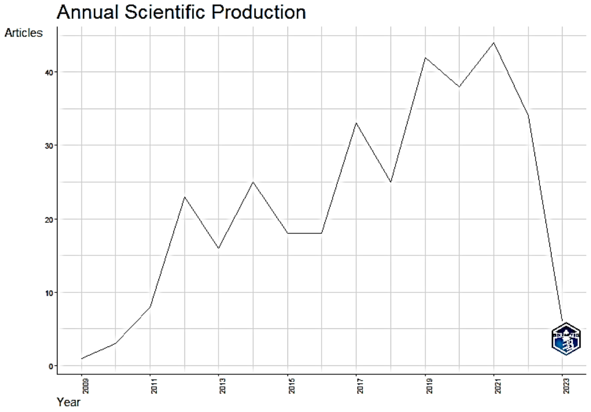

Figure 1. Number of articles published between 2009 and 2023 of next-generation sequence applications in livestock.

The collaborative studies about next-generation sequence applications in livestock are given in Figure 2. The analysis revealed that 2323 authors have contributed to this field. Among them, it is seen that only 9 authors published a single-authored paper. Thus, it demonstrates that collaborative research is widespread in this field. The 8.3 authors per article indicate that large research groups generally conducted the study. Moreover, the international co-authorship constitutes 45.07% of the articles produced, which shows intense participation in the research from different countries.

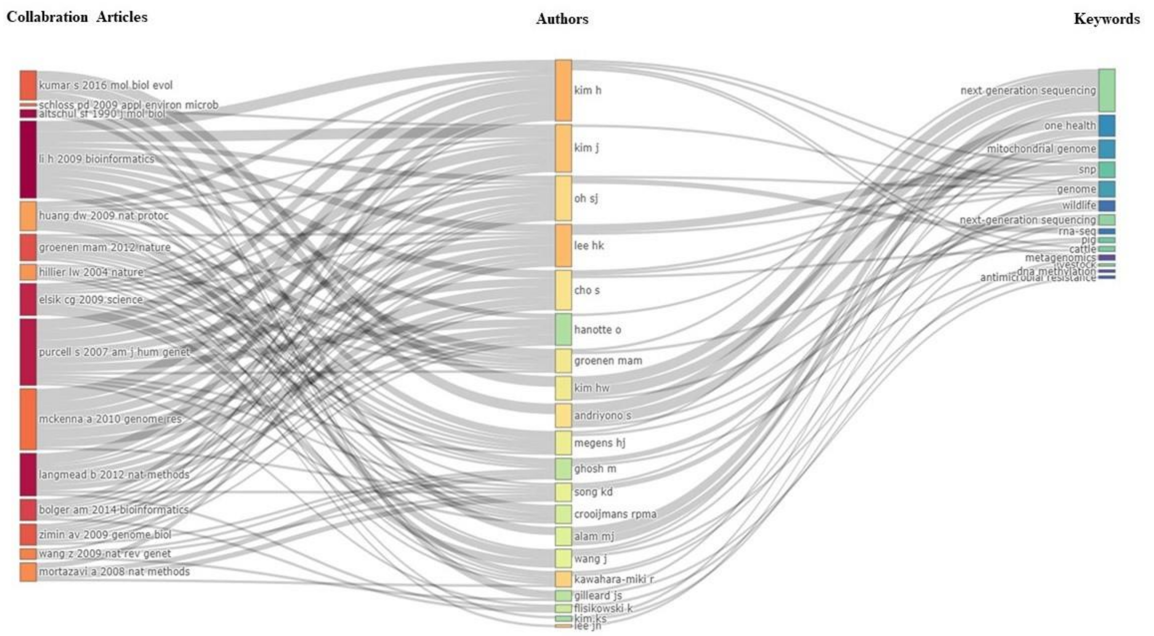

Figure 2. Collaborative studies about next-generation sequence applications in livestock.

Figure 3 provides information about the most published journals. Among the published articles, BMC Genomics ranks first with 14 articles. Frontiers in Genetics, Animals, PLOS ONE and Livestock Science follow BMC Genomics with 10 articles each. The most cited local sources are given in Figure 4. Analysis revealed that among the cited articles, PLOS ONE ranks first with 757 articles. Afterwards, BMC Genomics and Nature 423,371 received the most citations, respectively. According to the analysis results, PLOS ONE and BMC Genomics are among the most preferred journals in next-generation sequence applications in livestock.

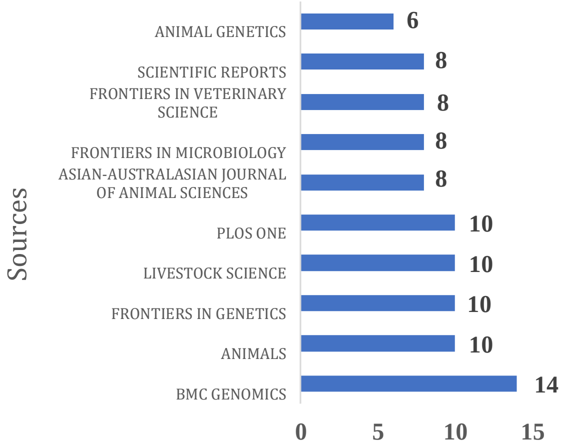

Figure 3. The most published articles in journals about next-generation sequence in livestock.

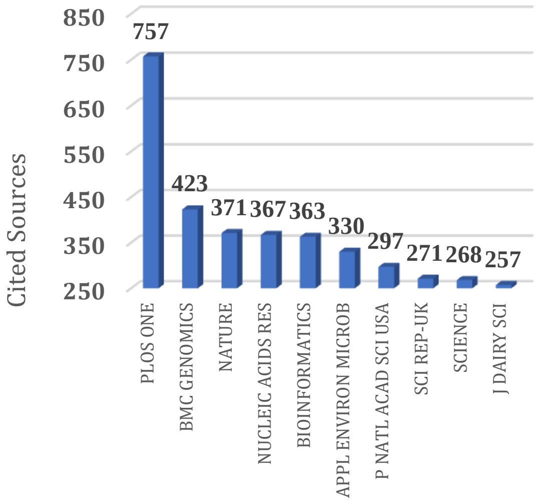

Figure 4. The most cited journals about next-generation sequence in livestock.

Figure 5 provides information about the number of articles published by various authors. According to data, Kim H and Kim HW have the highest number of articles among the most relevant authors in this field. Kim Y is the author with the 3rd most publications in this field.

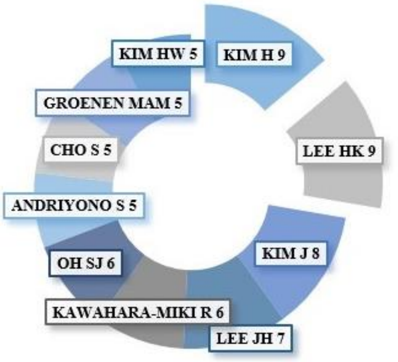

Figure 5. The most productive authors about next-generation sequence in livestock.

The articles published in different institutes from 2009 to 2023 are given in Figure 6. In this context, The National Institute of Animal Science had no articles between 2009 and 2011. However, an increasing graph is observed in the number of articles until 2019 in other years. 17 articles were published in The National Institute of Animal Science in 2023. Seoul National University has the highest number of articles in total. 38 articles were published in this university in 2023. There are no publications in Tokyo Agricultural University between 2009 and 2012. The publications that started in 2013 reached 14 articles in 2017. In 2023, the number of articles was determined as 14. There were no publications in the University of Bern between 2009 and 2016. However, the number of articles increased continuously in the following years, reaching 14 publications in 2021. The number of articles published remained stable in 2022 and 2023, with 14 publications. Although Edinburgh University appeared to have the least number of articles in the first years, the number of articles published has increased continuously from 2012 to 2023, reaching 18. There was no article published in the University of Illinois until 2012. However, there was an increase in the number of publications in the following years, and 16 articles were published every year from 2019 to 2023.

Figure 7 provides information about the trending topic keywords that appeared in scientific studies during each year between 2012 and 2022. According to the analysis results, “identification” was used 41 times in scientific studies conducted between 2014 and 2019 and became the most used keyword. In the studies conducted between 2016 and 2021, the keyword “diversity” was used 34 times and became the 2nd most used. The “expression” keyword was used 23 times in studies between 2014 and 2020 and became the 3rd most used keyword. Considering the keywords used, it is seen that they are generally related to gene research in this field.

The country-based collaborative studies are given in Figure 8. The analyses reveal that the most collaborative scientific studies in the world are done in the United States of America (USA), China and Germany. However, it was determined that the least collaborative work was done in Japan. When the collaborative work of countries with each other is evaluated, it is seen that the USA carries out collaborative work with all countries. It is also seen that Germany, France and China are working together. So, there is strong scientific cooperation between these countries. Much collaborative work is also between England and USA based on their scientific cooperation.

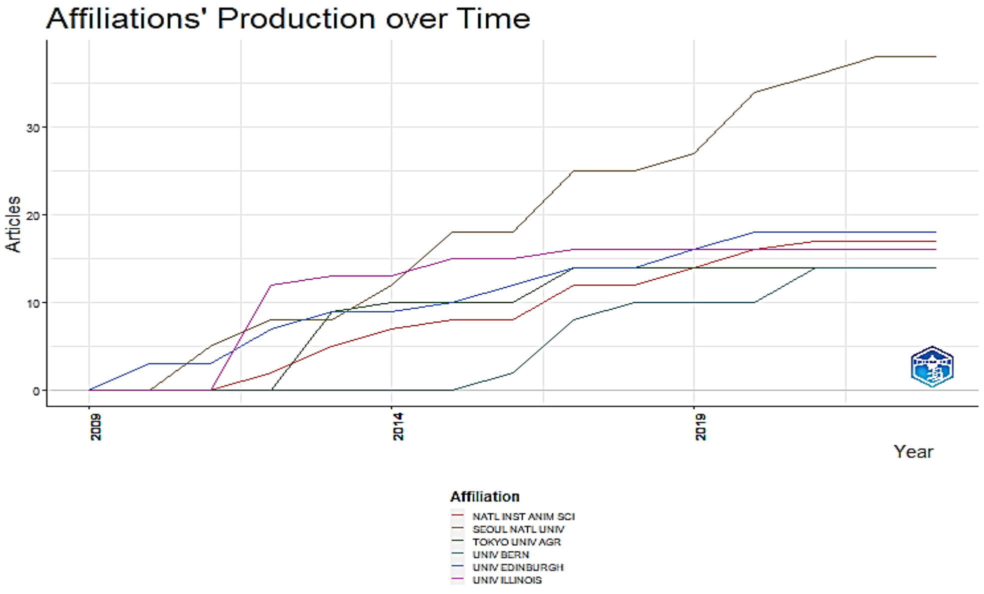

Figure 6. Scientific research institutions that publish the most articles about next-generation sequence in livestock.

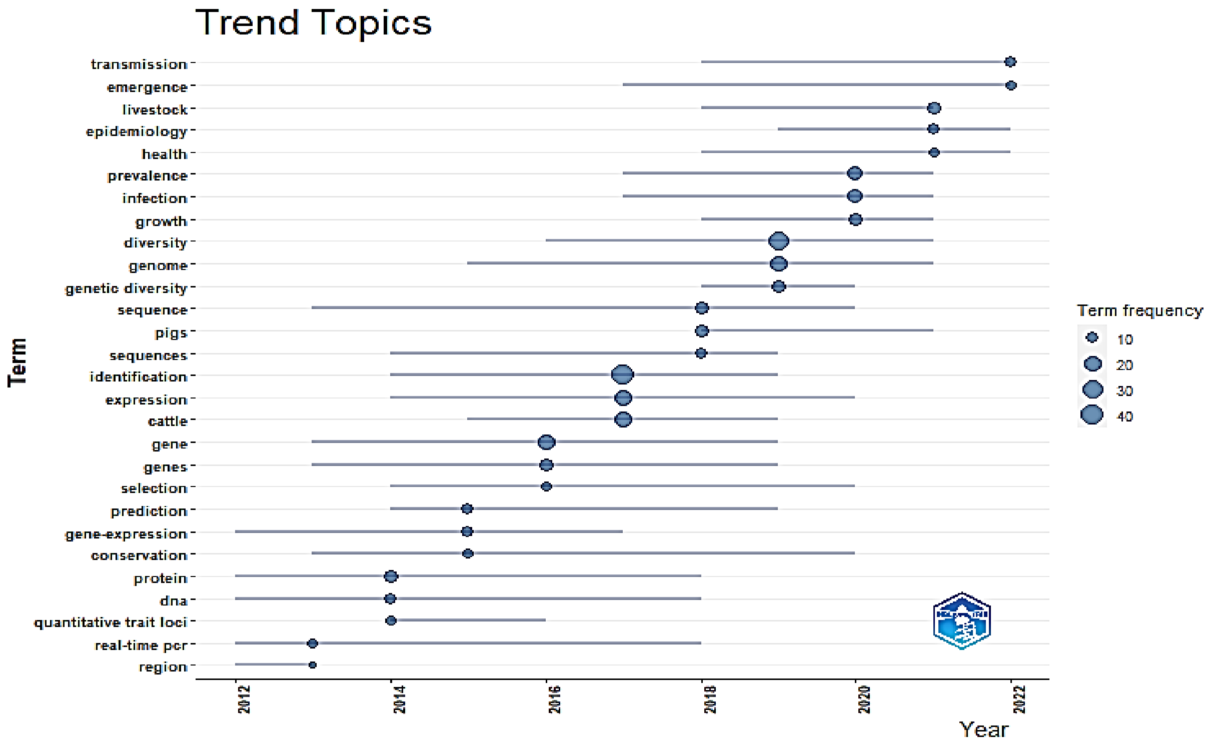

Figure 7. Trend topics keywords in scientific studies about next-generation sequence in livestock.

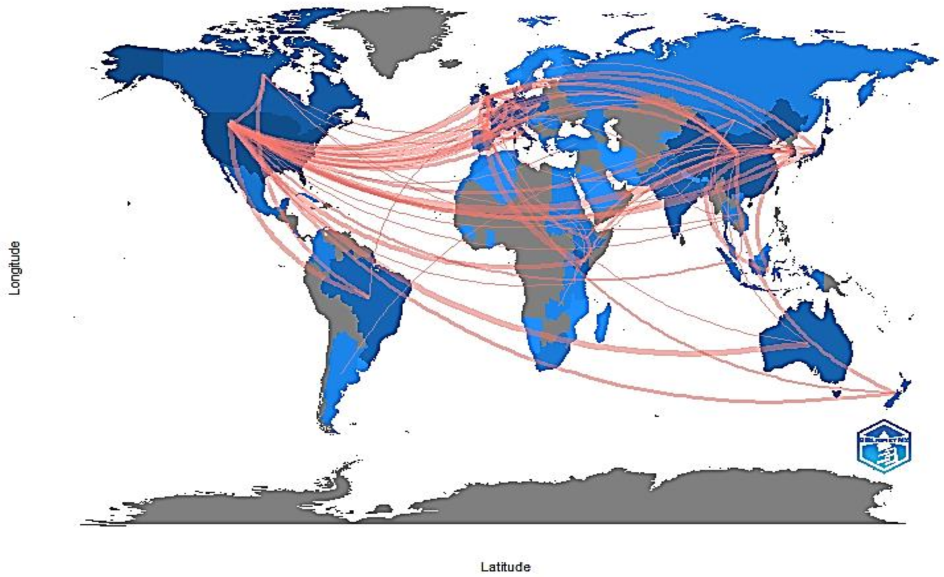

Figure 8. Country-based collaborative studies.

4. Conclusion

The mean age of the document in this study is 5.34 years, indicating that there have been recent new studies and trends in this field. The annual increase in documents is 13.65%, which shows that there has been an increasing demand for studies over the years. 23.03 citations to each document show the scientific impact of these studies. The fact that only 9 of the documents produced by 2323 authors are published documents shows that collaborative studies based on scientific cooperation are common in this field. Moreover, the number of authors per document produced, an average of 8.3, indicates that large research groups generally carry out the studies. Overall, this study presents an in-depth overview of the latest studies on next-generation sequence applications in Livestock. Thus, this perspective is expected to guide future studies in this field.

Author Contributions

The percentage of the author(s) contributions is presented below. All authors reviewed and approved the final version of the manuscript.

	S.K.	Y.A.
C	50	50
D	50	50
S		100
DCP	20	80
DAI	20	80
L	50	50
W	50	50
CR	50	50
SR	50	50
PM	50	50
FA	50	50

C=Concept, D= design, S= supervision, DCP= data collection and/or processing, DAI= data analysis and/or interpretation, L= literature search, W= writing, CR= critical review, SR= submission and revision, PM= project management, FA= funding acquisition.

Conflict of Interest

The authors declared that there is no conflict of interest.

Ethical Consideration

Ethics committee approval was not required for this study because of there was no study on animals or humans.

References

Akhavan P, Ebrahim NA, Fetrati MA, Pezeshkan A. 2016. Major trends in knowledge management research: a bibliometric study. Scientometrics, 107: 1249-1264.

Alex A, Brundha M, Prathap L. 2020. Sanger sequencing and its recent advances-a review. PalArch's J Archaeol Egypt/Egyptol, 17(7): 698-705.

Altimari A, de Biase D, de Maglio G, Gruppioni E, Capizzi E, Degiovanni A, D'Errico A, Pession A, Pizzolitto S, Fiorentino M. 2013. 454 next generation-sequencing outperforms allele-specific PCR, Sanger sequencing, and pyrosequencing for routine KRAS mutation analysis of formalin-fixed, paraffin-embedded samples. Onco Targets Therap, 2013: 1057-1064.

Aria M, Cuccurullo C. 2017. Bibliometrix: An R-tool for comprehensive science mapping analysis. J Informet, 11(4): 959-975.

Behjati S, Tarpey PS. 2013. What is next generation sequencing? Arch Diseas Childhood Educ Pract, 98(6): 236-238.

Bordbar F, Jensen J, Du M, Abied A, Guo W, Xu L, Gao H, Zhang L, Li J. 2020. Identification and validation of a novel candidate gene regulating net meat weight in Simmental beef cattle based on imputed next-generation sequencing. Cell Proliferation, 53(9): e12870.

Chan EY. 2005. Advances in sequencing technology. Mutat Res/Fundam Molec Mechan Mutagenesis, 573(1-2): 13-40.

Dahm R, Banerjee M. 2019. How we forgot who discovered DNA: why it matters how you communicate your results. BioEssays, 41(4): 1900029.

Goddard ME, Hayes BJ. 2009. Mapping genes for complex traits in domestic animals and their use in breeding programmes. Nature Rev Genetics, 10(6): 381-391.

Goodwin S, McPherson JD, McCombie WR. 2016. Coming of age: ten years of next-generation sequencing technologies. Nature Rev Genetics, 17(6): 333-351.

Hood L, Galas D. 2003. The digital code of DNA. Nature, 421(6921): 444-448.

Jiang L, Liu X, Yang J, Wang H, Jiang J, Liu L, He S, Ding X, Liu J, Zhang Q. 2014. Targeted resequencing of GWAS loci reveals novel genetic variants for milk production traits. BMC Genomics, 15(1): 1-9.

Kim KM, Park JH, Bhattacharya D, Yoon HS. 2014. Applications of next-generation sequencing to unravelling the evolutionary history of algae. Int J Systematic Evolut Microbiol, 64(Pt_2): 333-345.

Koboldt DC, Steinberg KM, Larson DE, Wilson RK, Mardis ER. 2013. The next-generation sequencing revolution and its impact on genomics. Cell, 155(1): 27-38.

Lallar M, Phadke SR. 2016. Human genome project and after. Genetic Clin, 9(1): 9-15.

Margulies M, Egholm M, Altman WE, Attiya S, Bader JS, Bemben LA, Berka J, Braverman MS, Chen YJ, Chen Z. 2005. Genome sequencing in microfabricated high-density picolitre reactors. Nature, 437(7057): 376-380.

Mishra D, Gunasekaran A, Papadopoulos T, Dubey R. 2018. Supply chain performance measures and metrics: a bibliometric study. Benchmarking Int J, 25(3): 932-967.

Morozova O, Marra MA. 2008. Applications of next-generation sequencing technologies in functional genomics. Genomics, 92(5): 255-264.

Olson MV. 2002. The human genome project: A player's perspective. J Molec Biol, 319(4): 931-942.

Önder H, Tirink C. 2022. Bibliometric analysis for genomic selection studies in animal science. J Inst Sci Tech, 12(3): 1849-1856.

Osareh F. 1996. Bibliometrics, citation analysis and co-citation analysis: A review of literature I. Libri, 46: 149-158.

Pareek CS, Smoczynski R, Tretyn A. 2011. Sequencing technologies and genome sequencing. J Appl Genet, 52: 413-435.

Park ST, Kim J. 2016. Trends in next-generation sequencing and a new era for whole genome sequencing. Int Neurourol J, 20(Suppl 2): S76.

Pouladi N, Bime C, Garcia JG, Lussier YA. 2016. Complex genetics of pulmonary diseases: lessons from genome-wide association studies and next-generation sequencing. Translat Res, 168: 22-39.

Pritchard A. 1969. Statistical bibliography; an interim bibliography. Eric, London, UK, pp: 69.

Rasheed M. 2020. Next generation sequencing as an emerging technology in rare disease genetics. J Islamabad Medic Dental College, 9(1): 1-3.

Sanger F, Nicklen S, Coulson AR. 1977. DNA sequencing with chain-terminating inhibitors. Proc National Acad Sci, 74(12): 5463-5467.

Schloss JA. 2008. How to get genomes at one ten-thousandth the cost. Nature Biotechnol, 26(10): 1113-1115.

Schneeberger K, Weigel D. 2011. Fast-forward genetics enabled by new sequencing technologies. Trends Plant Sci, 16(5): 282-288.

Schuster SC. 2008. Next-generation sequencing transforms today's biology. Nature Methods, 5(1): 16-18.

Team RC. 2016. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. http://www. R-project. org/.

Thanuskodi S. 2010. Journal of Social Sciences: A bibliometric study. J Soc Sci, 24(2): 77-80.

Tipu HN, Shabbir A. 2015. Evolution of DNA sequencing. J Coll Physicians Surg Pak, 25(3): 210-215.

Toghiani S, Chang LY, Ling A, Aggrey SE, Rekaya R. 2017. Genomic differentiation as a tool for single nucleotide polymorphism prioritization for Genome wide association and phenotype prediction in livestock. Livestock Sci, 205: 24-30.

Totomoch-Serra A, Marquez MF, Cervantes-Barragán DE. 2017. Sanger sequencing as a first-line approach for molecular diagnosis of Andersen-Tawil syndrome. F1000 Res, 6(1016): 1016.

Van Dijk EL, Auger H, Jaszczyszyn Y, Thermes C. 2014. Ten years of next-generation sequencing technology. Trends Genet, 30(9): 418-426.

Voelkerding KV, Dames SA, Durtschi JD. 2009. Next-generation sequencing: from basic research to diagnostics. Clin Chem, 55(4): 641-658.

Waters CK. 2008. Beyond theoretical reduction and layer-cake antireduction: How DNA retooled genetics and transformed biological practice. Oxford Press, Oxford, UK, pp: 262.

Watson JD, Crick FH. 1953. The structure of DNA. Cold Spring Harbor symposia on quantitative biology, New York, US.

Young AI. 2019. Solving the missing heritability problem. PLoS Genet, 15(6): e1008222.

Zahra AA, Nurmandi A, Tenario CB, Rahayu R, Benectitos SH, Mina FLP, Haictin KM. 2021. Bibliometric analysis of trends in theory-related policy publications. Emerging Sci J, 5(1): 96-110.