



# Advances in Genetic Research in Systemic Lupus Erythematosus: Trend Analysis, Global Collaborations and Bibliometric Perspectives

Desti Rahmawati,<sup>1</sup> Isrovanigoro Isrovanigoro,<sup>1</sup> Alvin Kurniawan,<sup>1</sup> Danang Prasetyaning Amukti,<sup>1</sup> Nina Salamah,<sup>1</sup> Wirawan Adikusuma,<sup>2</sup> Rockie Chong,<sup>3</sup> Lalu Muhammad Irham<sup>4</sup>

## Abstract

Systemic lupus erythematosus (SLE) is a complex autoimmune disease affecting multiple organs and systems in the body. SLE manifestations result from lymphopenia, thrombotic thrombocytopenic purpura, thrombocytopenia, autoimmune haemolytic anaemia, myelofibrosis and leucopenia. SLE triggers the activation of both innate and adaptive immune responses. This process is initiated by T cells activating autoreactive B cells, leading to the accumulation of immune complexes in tissues. Consequently, an autoimmune cascade occurs, affecting either a single organ or causing widespread systemic complications. Bibliometric analysis used *Vosviewer* 1.6.16 and the *Biblioshiny R* tool to create and display bibliometric maps by obtaining relevant journals related to SLE through the *SciVerse Scopus* database from 1981 to 2025. The results obtained in the form of journal document types using English with keywords in the form of SLE which shows global trends. The United States is the country that produces the most research related to SLE genomics and the highest publication collaboration along with contributing citations at the global first level. *Lupus* was the journal source that discusses the most genomic studies in SLE disease and *Anhui Medical University* the affiliation with the highest number of documents (131). The increasing number of publications on genomics in SLE from 1981 to 2025 indicates a growing interest in researching and writing about this topic. This trend reflects the evolving understanding of SLE's genetic underpinnings and the potential for advancements in diagnosis, treatment and precision medicine.

**Key words:** Lupus erythematosus, systemic; Bibliometrics; Genomics.

1. Faculty of Pharmacy, Universitas Ahmad Dahlan, Yogyakarta, Special Region of Yogyakarta, Indonesia.
2. Research Centre for Computing, Research Organisation for Electronics and Informatics, National Research and Innovation Agency (BRIN), Cibinong Science Centre, Cibinong, Indonesia.
3. Department of Chemistry and Biochemistry, University of California, Los Angeles, Los Angeles, CA, USA.
4. Faculty of Pharmacy, Universitas Ahmad Dahlan, Yogyakarta, Special Region of Yogyakarta, Indonesia.

### Citation:

Rahmawati D, Isrovanigoro I, Kurniawan A, Amukti DP, Salamah N, Adikusuma W, et al. Advances in genetic research in systemic lupus erythematosus: trend analysis, global collaborations and bibliometric perspectives. *Scr Med*. 2025 Sep-Oct;56(5):1029-38.

### Corresponding author:

LALU MUHAMMAD IRHAM  
E: lalu.irham@pharm.uad.ac.id

Received: 27 January 2025  
Revision received: 22 February 2025  
Accepted: 22 February 2025

## Introduction

Systemic lupus erythematosus (SLE) is a multifaceted autoimmune disorder that has the potential to impact various body systems<sup>1</sup> and especially affecting young women.<sup>2</sup> The symptoms of SLE arise due to conditions such as thrombotic thrombocytopenic purpura (TTP), leucopenia, lymphopenia, thrombocytopenia, autoimmune

haemolytic anaemia (AIHA) and myelofibrosis.<sup>3</sup> SLE is a multifactorial condition influenced by genetic, epigenetic and environmental factors. It typically affects multiple organs, such as the skin, joints, kidneys, lungs, central nervous system and haematopoietic system and is often associated with numerous complications.<sup>4</sup>

Autoimmune disease of SLE leads to the activation of both innate and adaptive immune responses, driven by T cells stimulating autoreactive B cells<sup>5</sup> and lead to the accumulation of immune complexes in tissues, triggering an autoimmune response that can either affect a single organ or result in widespread systemic complications.<sup>6, 7</sup> Current treatment of SLE utilises agents with relatively non-selective immunosuppressive properties.<sup>8</sup> In the past few decades, SLE treatment has transitioned from relying on hydroxychloroquine, systemic glucocorticoids and traditional immunosuppressive drugs to the use of biologic therapies, with belimumab being the first and only biologic agent approved for SLE treatment so far.<sup>9</sup> However, hydroxychloroquine treatment is still the first-line treatment of choice and reduces disease activity, morbidity and mortality.<sup>10</sup>

Bibliometric analysis is increasingly recognised as a widely used method for assessing the credibility, quality and influence of scholarly publications.<sup>11</sup> Bibliometrics is an approach to analyse literature that evaluates the productivity and significance of publications in a specific research area using both quantitative and qualitative methods.<sup>12</sup> Bibliometrics uses citation ratios to evaluate research performance.<sup>13</sup> Mostly used to measure the influence or impact of a research article on future research.<sup>14</sup> Bibliometric analysis allows researchers to collect extensive data on various elements within a specific field of study, including authors, keywords, journals, countries, institutions and references. This method provides a comprehensive overview of the research landscape by examining these different components. Bibliometric studies can reveal patterns of collaboration, identify influential publications and detect emerging trends within a research area.<sup>15</sup> Bibliographic data contains information on genomic studies in SLE. Bibliometric analysis is conducted to determine whether SLE-related research is interesting to conduct.

Bibliometric mapping provides advantages for both the scientific community and the general public by transforming publication metadata into visual representations. These include visualising keywords to uncover research themes in specific fields, mapping author affiliations to determine the geographic scope of journals and charting institutional and international collaborations as a

means to identify emerging technologies that can be efficiently managed for deeper insights.

The purpose of writing the article was to provide an overview of research trends on SLE disease globally and contribute to writing articles related to SLE disease at the global level with a pharmacogenomic approach.

## Methods

### Database

In this study, *SciVerse Scopus* was used as the main database as it provides two search methods, namely basic search and advanced search, which enables comprehensive exploration with a high degree of validity. *Scopus* enables searches based on terms found in titles, title/abstracts, journal names, author names, affiliations or journal rankings.<sup>16, 17</sup>

### Indicators

The search indicators for bibliometric criteria in this study included: (1) Type of document and its language; (2) Development of SLE-related publications; (3) Most relevant source with SLE-related genetic research; (4) Most relevant affiliation with SLE-related genetic research; (5) Author's country related to SLE-related genetic research; (6) Country of production of scientific publications with SLE-related genetic research. Publication data including most active country, most relevant affiliation, author's country of origin, were retrieved and stored and then imported into *Biblioshiny* and *VOSviewer* 1.6.16 software for visualisation.<sup>18, 19</sup>

### Keywords

This study employed a systematic method to obtain relevant journals and publications. The keywords used in the bibliometric search used the phrases (title, abstract, keywords (SLE)) AND (title, abstract, keywords (Systemic AND Lupus AND Erythematosus) OR (title, abstract, keywords (Genomics))). Journal and publication searches obtained a total of 1115 documents. Only articles written in English (n = 1115) were included in further analysis.

# Results

A total of 816 articles were retrieved from the *Scopus* database between 1981 and 2025. Six thousand six hundred twenty authors were involved in making scientific articles. The analysis of the articles revealed that 816 were research articles and 235 were review articles. Additionally, the remaining documents consisted of 16 book chapters, 16 letters, 14 conference papers, 6 short surveys, 5 notes, 5 editorials and 2 erratum (Table 1).

**Table 1:** Key information on systemic lupus erythematosus (SLE) publication data related to genomics

Description	Results
<b>Key details regarding the data</b>	
Timespan	1981 - 2025
Sources (journals, books, etc)	465
Documents	1115
Average citations per document	46.14
Document average age (year)	12.20
Annual growth rate (%)	1.59
References	57722
<b>Document contents</b>	
Keywords plus (ID)	9422
Author's keywords (DE)	2293
<b>Authors</b>	
Authors (N)	6620
Authors of single-authored docs (N)	48
<b>Authors collaboration</b>	
Single-authored documents (N)	48
International co-authorships (%)	21.35
Authors per document (N - mean)	1.87
<b>Document type</b>	
Article	816
Review	235
Letter	16
Book chapter	16
Conference paper	14
Short survey	6
Note	5
Editorial	5
Erratum	2

## The keywords most often used by researchers

Analysis of the keywords used by the researchers revealed a total of 2297 keywords from all publications. After visual mapping with a minimum occurrence threshold of 5 times, 97 keywords were identified that met the criteria. The most frequently used keywords reflected the main fo-

cus of the research, including “systemic lupus erythematosus,” “lupus,” “autoimmunity” and “genetic,” reflecting the core of research related to genetics and immunological mechanisms in SLE (Figure 1). This visual mapping provides an in-depth insight into the trends in terminology used in research. These keywords not only indicate the dominant research topics, but also indicate the close relationship between the focus on genetics and the autoimmune aspects underlying SLE. This visualisation helps to identify areas of research that are of major concern to the scientific community, while also highlighting the potential for further development in this field (Figure 1).

## Growth of SLE-related genetic research publications

In the period 1981-2025, 816 documents focusing on genetic research related to SLE were collected. Publications first appeared in 1981 and showed a consistent increase over the following decade. This trend peaked in 2021, reflecting the growing attention to the role of genetics in understanding and treating SLE. Other years, such as 2021 and 2015, also show significant spikes in the number of publications, indicating active periods in research that may be driven by important discoveries or major research funding. The data displayed in Figure 2 provides a clear picture of this exponential growth, emphasising the importance of genetics as a foundation for understanding the molecular mechanisms underlying SLE and its potential in the development of more effective therapies. This surge in publications demonstrates not only the growing interest in SLE genetic research but also the expansion of global scientific collaboration. With the widespread use of genomics-based technologies, this trend is expected to continue to increase, paving the way for new innovations in the diagnosis, treatment and prevention of SLE.

## Sources that published the most genetic research related to SLE

There were 10 leading journals with the most relevant research related to genes associated with SLE. The first journal that provided publications related to genes associated with SLE was *Lupus* with 47 documents, followed by *Frontiers in Immunology* with 36 and the third was *Journal of Immunology* (n = 24) with studies related to genes associated with SLE (Figure 3).



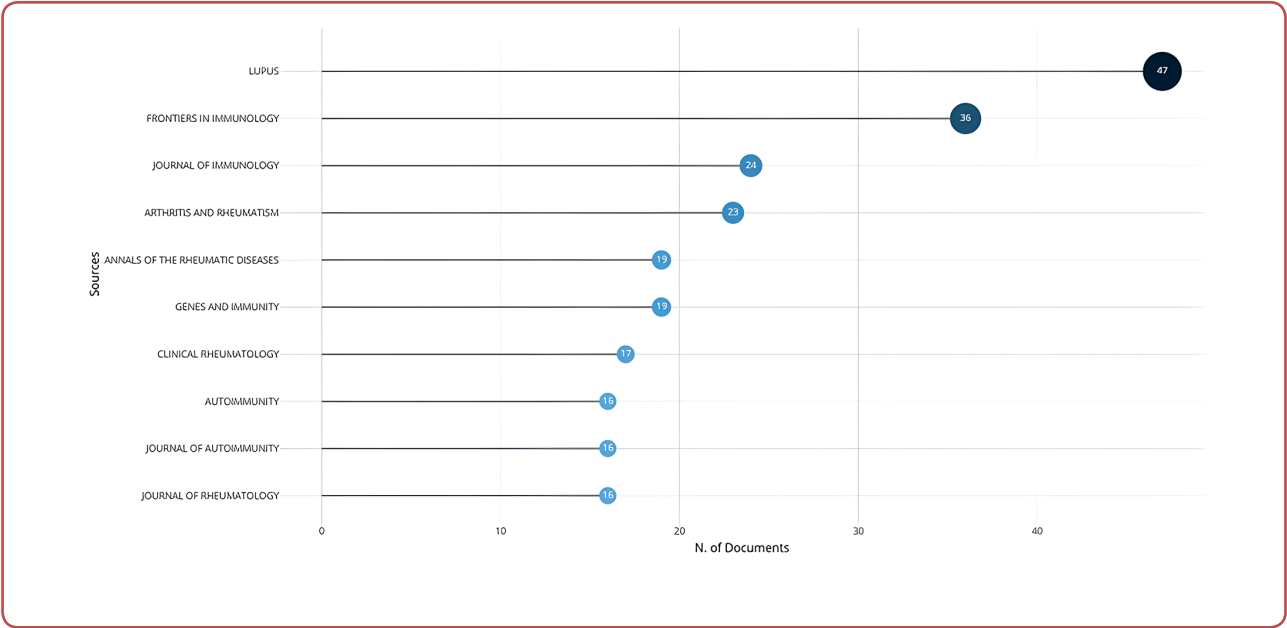


Figure 3: Most relevant sources of systemic lupus erythematosus (SLE) related studies

### Top 10 affiliates conducting SLE-related genetic research

In this study, there were 10 most affiliations that conducted research related to genes associated with SLE. *Anhui Medical University* became an af-

filiate with research related to genes associated with SLE with a total of 131 documents, followed by *Amgen the RA-MAP Consortium: Catherien Hilkens* with 107 documents and *University of California* with 85 documents (Figure 4).

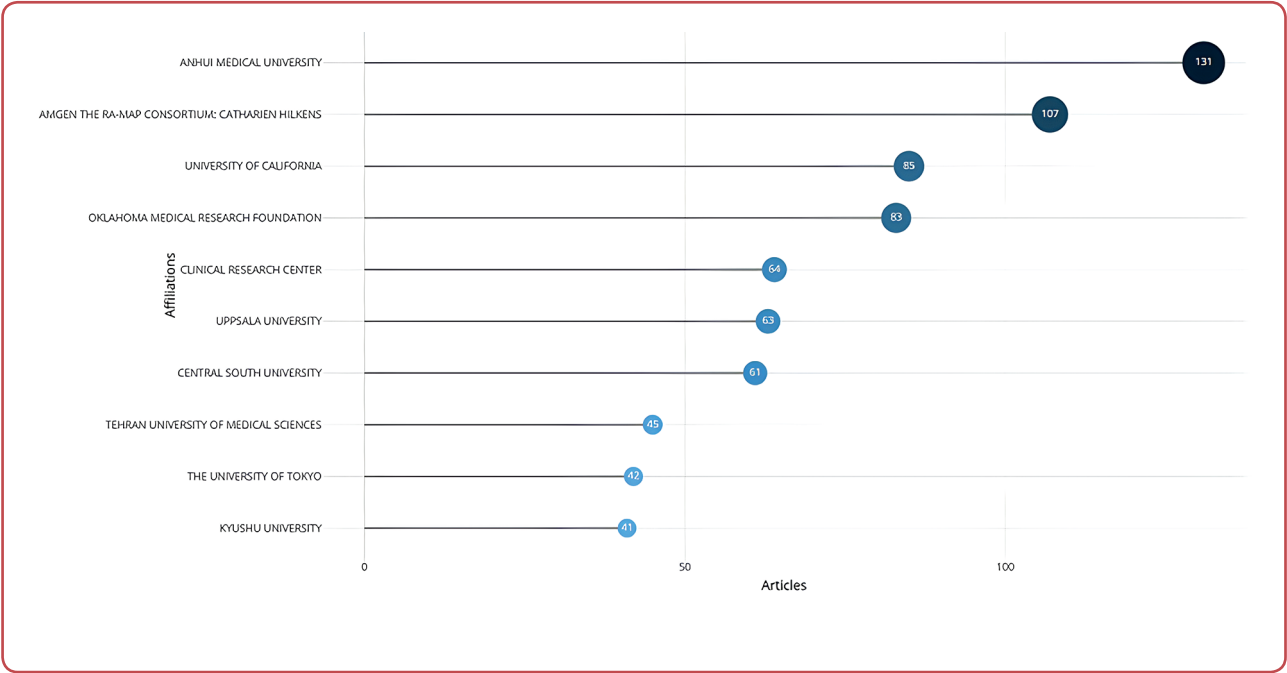


Figure 4: Top 10 affiliates conducting research on genes associated with systemic lupus erythematosus (SLE)



Top 10 countries contributing cited manuscripts

This study identified 10 countries with the highest citation counts for research on genes linked to SLE. The USA ranked first with 17915 citations, followed by Japan with 3078 citations and China

with 2778 citations. USA is the most cited country; authors from USA publish many articles in highly reputable journals (Figure 5).

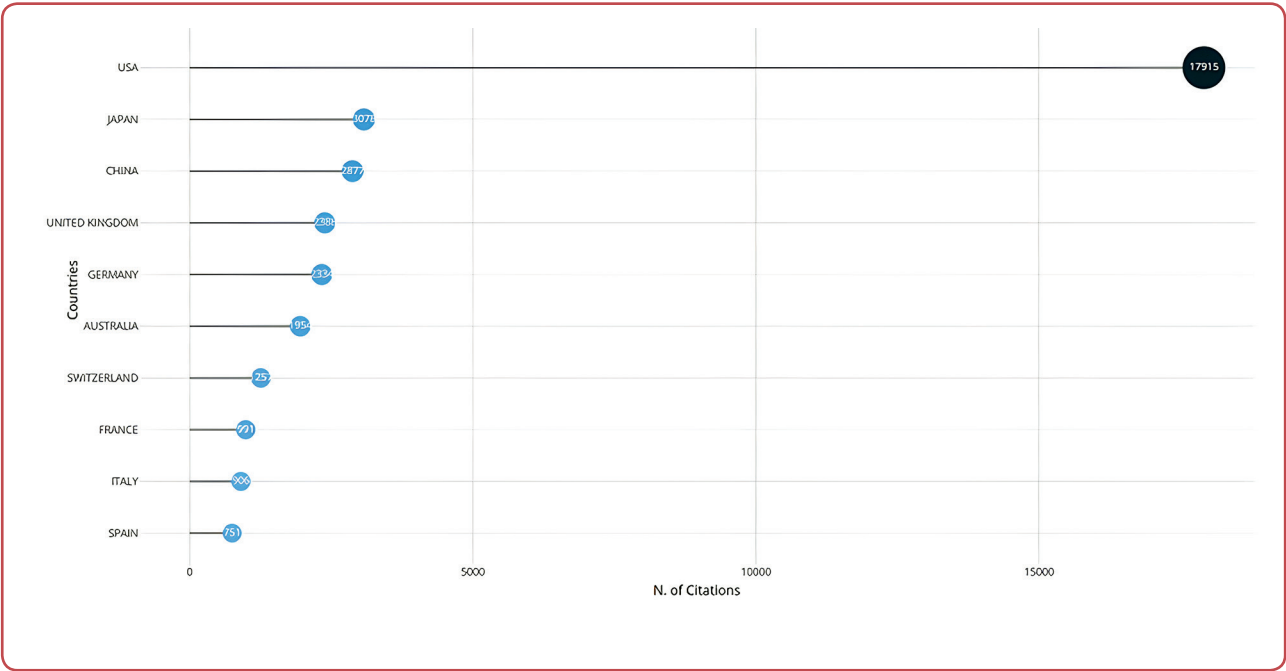


Figure 5: Top 10 countries with the most document citations

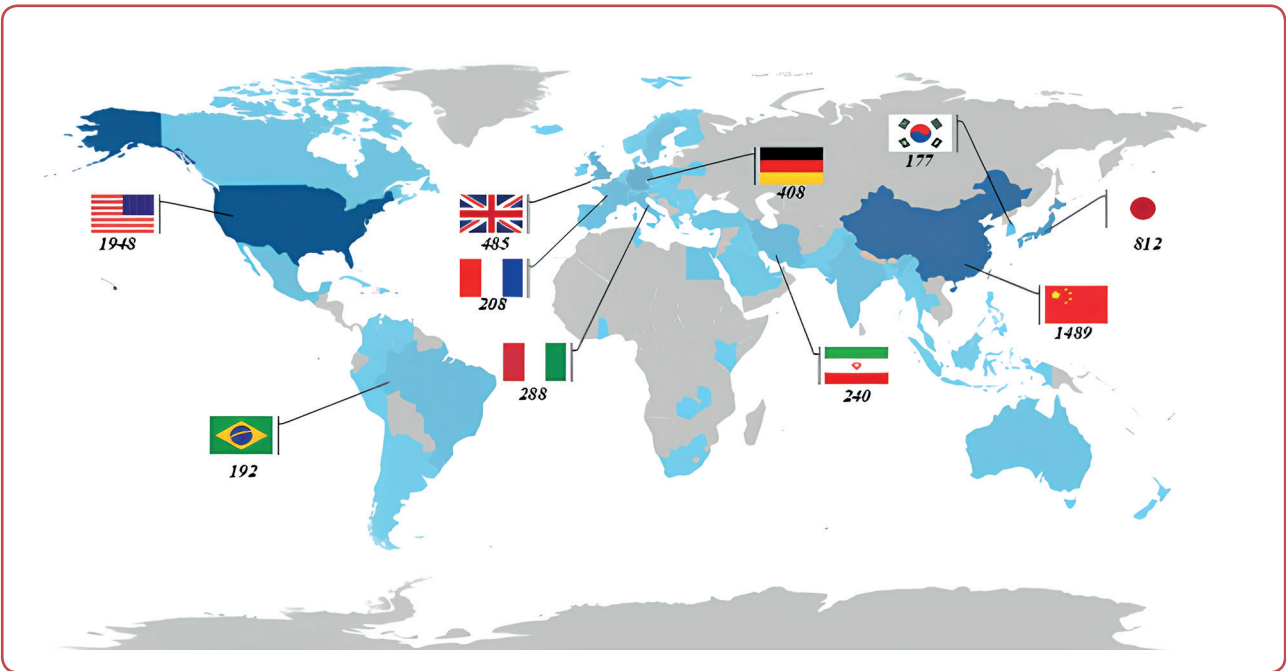


Figure 6: Top 10 countries with the most document authors

## Top 10 countries with the highest number of authors involved in genetic research related to SLE

This analysis reveals the 10 countries with the highest number of authors contributing to genetic research related to SLE. The United States led the way with the highest number of authors at 1948, confirming its dominant role in global SLE research. China came in second with 1489 authors, followed by Japan in third place with 812 authors. Other countries, such as the UK, Germany and Iran, were also noted to have made significant contributions despite the smaller number of authors compared to the top three countries. This data shows that SLE genetic research has a broad global scope, with substantial contributions from countries across continents. Figure 6 provides a clear visualisation of the distribution of the number of authors in each country, illustrating how major research centres in the world dominate scientific production in the field of SLE genetics. This high number of authors also reflects cross-institutional collaboration and commitment to scientific innovation, which plays a critical role in the development of therapies and a better understanding of SLE. The surge in participation from developing countries such as China also indicates a shift in the global research landscape, where more countries are taking an active role in clinically relevant genomics research. With this trend, it is expected that global author

contributions will continue to increase, accelerating new breakthroughs in the treatment of SLE.

## International collaboration related SLE study

This study highlights the importance of international collaboration in driving the progress of genetics research related to SLE. Publications can be categorised into two types: publications by one country alone, known as Single Country Publications (SCP) and publications resulting from collaboration between countries, or Multiple Country Publications (MCP). The data shows that the United States leads as the country with the largest contribution in publications, both in total number and international collaborations, confirming its position as the global centre of research in this field.

China and Japan came in second and third, with similarly significant contributions, reflecting their dedication to genome-based research. Countries such as the UK, Germany and Iran also show active participation, albeit with varying collaboration focus. This trend underscores that SLE genetics research depends not only on national initiatives, but also on global collaborations that enable the exchange of knowledge, technology and resources. Figure 7 provides a clear visualisation of the differences between SCPs and MCPs

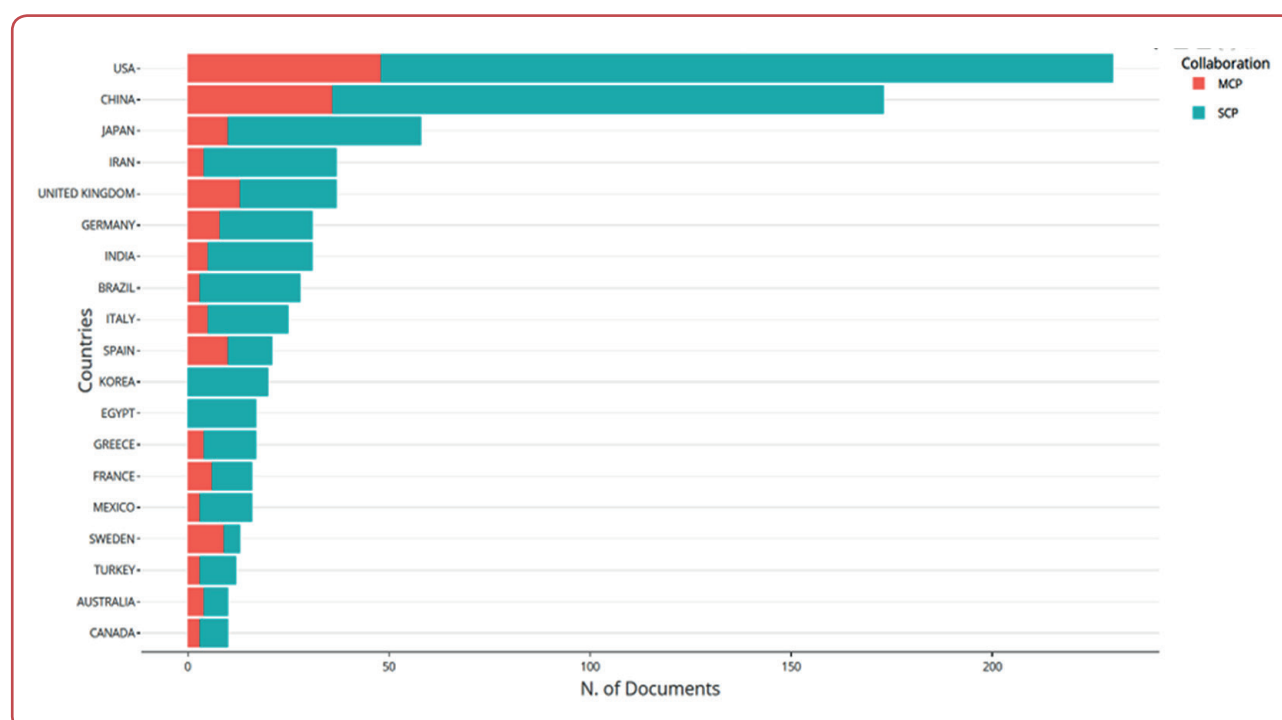


Figure 7: Visualisation of cross-country collaboration on publishing research on systemic lupus erythematosus (SLE)-related genes

in different countries. The United States not only excels in the number of SCP publications, but also shows strong MCP collaboration strengths with other countries. This signifies the importance of global research networks in accelerating innovative discoveries and advancing the understanding of SLE genetics. Such collaborations lay the foundation for better, globally relevant medical solutions.

Discussion

SLE is a disease with a strong and complex genetic component and clinical heterogeneity.<sup>20</sup> Bibliometric analysis in this study used literature from 1981 to 2025 data sources obtained as many as 465 and 1115 documents. The study was conducted in order to get an overview of research trends on SLE disease globally and how SLE disease is at the global level with a pharmacogenomic approach. Research on SLE disease has grown significantly in the last 10 years. This has an influence on the research trends carried out specifically on SLE disease.<sup>21</sup>

SLE is a multifaceted autoimmune disorder, with genetics being one of its contributing factors. Ge-

netic variations in *HLA-DR2* and *HLA-DR3* affect antigen presentation to T cells, which can trigger abnormal immune responses. The *HLA-DR3* gene is known to be a genetic marker associated with various autoimmune diseases, including SLE, while *HLA-DR2* is associated with diseases such as SLE, multiple sclerosis and rheumatoid arthritis.<sup>22, 23</sup> The irregular activation of T cells, which are crucial for regulating the immune system, leads to apoptosis dysregulation due to mutations in the *PTPN22* gene, heightening the risk of autoimmune conditions such as SLE.<sup>24, 25</sup> In SLE, the NF-κB pathway is also involved through the regulation of chronic inflammation. Mutations in the *TNFAIP3* gene, which encodes an inhibitory protein of the inflammasome pathway, lead to the activation of chronic inflammasome.<sup>26</sup> In addition, mutations in the IFN-γ pathway and genetic variations in *IRF5* increase disease risk by triggering uncontrolled inflammation.<sup>27</sup> These genetic elements contribute to systemic inflammation and tissue injury, potentially elevating the likelihood of developing SLE (Figure 8).

The increasing trend of research on SLE is evidenced by the growth of publications related to SLE genetics which reached the highest peak of publications in 2022 and the publication of the most articles published in *Lupus* with the most affiliations conducting research related to SLE

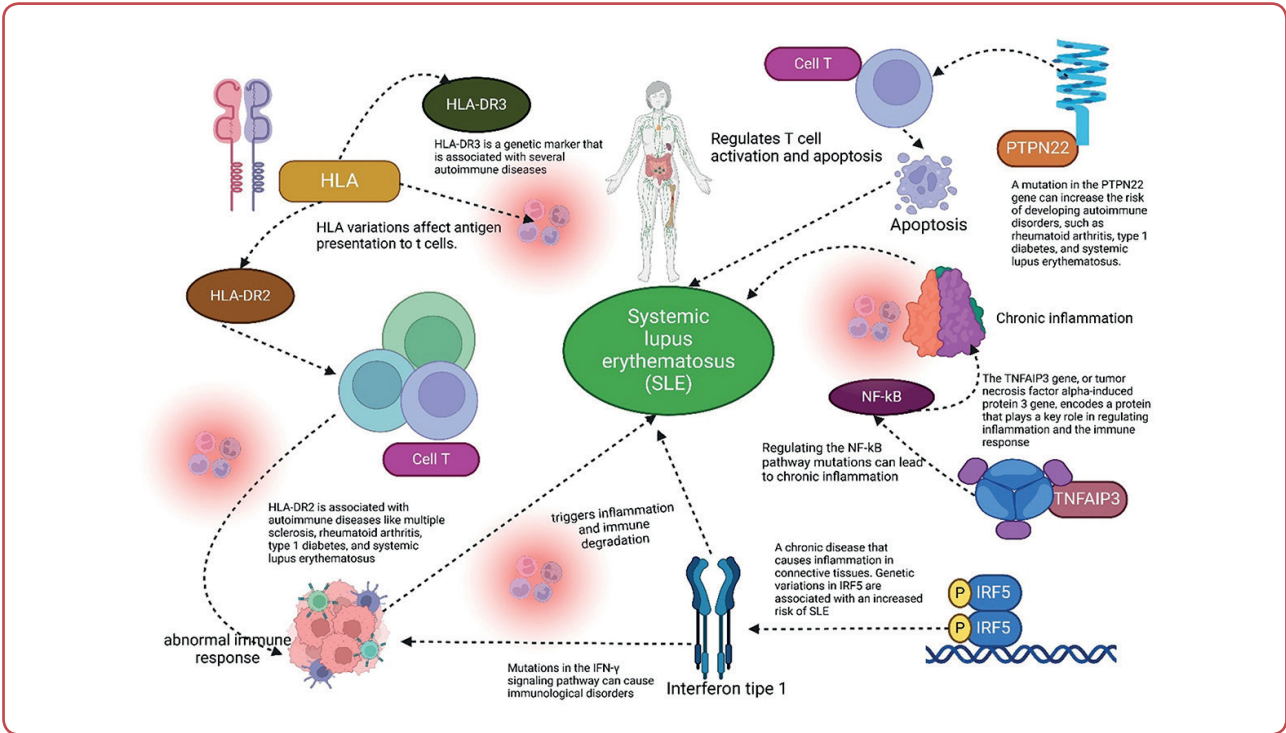


Figure 8: Mechanism of systemic lupus erythematosus (SLE)



written by *Anhui Medical University*. Some of the most frequently used keywords were systemic lupus erythematosus, lupus, single nucleotide polymorphism, genetic. Number of the keywords obtained with a minimum occurrence of 5 times was 2,297 and 97 keywords were obtained that met the threshold, then visualised with the *VOSviewer* application. This shows the extent of the use of keywords and the attachment between keywords. The more frequent the pairing between two words, the closer the relationship between the keywords.<sup>28</sup>

In (Figure 3) there were 10 journals that published the most genetic research related to SLE. *Lupus* is the first journal that provides the most publications about SLE disease, namely 47 articles. This number makes *Lupus* the most SLE genetic research journal publication that will be cited by other researchers.<sup>28</sup> Then, related to citations, there were also the top 10 countries that contribute to the manuscript. The USA became the country with the most citations, which amounted to 17915 and was followed by Japan by 3078, with a lot of citation manuscripts in the country making the country encouraged to publish related to genetics in SLE disease. The USA was also the country with the highest SLE genetic research authors, namely 1948 followed by China as much as 1489 and Japan, namely 812. The large number of publications and citations on SLE genetics from various countries, along with international collaborations, demonstrates growing research enthusiasm and trends.

## Conclusion

The increasing number of publications on genomics in SLE from 1981 to 2025 indicates a growing interest in researching and writing about this topic. This trend reflects the evolving understanding of SLE's genetic underpinnings and the potential for advancements in diagnosis, treatment and precision medicine. The USA was the country with the highest publication and citation of article manuscripts.

## Ethics

This study was a secondary analysis based on the currently existing data and did not directly involve with human participants or experimental animals. Therefore, the ethics approval was not required in this paper.

## Acknowledgement

None.

## Conflicts of interest

The authors declare that there is no conflict of interest.

## Funding

This review received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

## Data access

The data that support the findings of this study are available from the corresponding author upon reasonable individual request.

## Author ORCID numbers

Desti Rahmawati (DR):  
0009-0007-9637-7812  
Isrovanigoro Isrovanigoro (II):  
0009-0001-2876-3697  
Alvin Kurniawan (AK):  
0009-0008-4734-7948  
Danang Prasetyaning Amukti (DPA):  
0000-0002-4256-6534  
Nina Salamah (NS):  
0000-0001-5505-7336



Wirawan Adikusuma (WA):  
0000-0001-9165-690X  
Rockie Chong (RC):  
0000-0001-6736-9687  
Lalu Muhammad Irham (LMI):  
0000-0002-0091-4887

## Author contributions

Conceptualisation: II, DR, AK, DPA, LMI  
Methodology: LMI, DPA  
Formal analysis: DR, AK, II  
Data curation: DPA, LMI  
Writing-original draft: DR, II, AK  
Writing-review and editing: DPA, WA, RC, LMI

## References

1. Yao M, Zhang C, Gao C, Wang Q, Dai M, Yue R, et al. Exploration of the shared gene signatures and molecular mechanisms between systemic lupus erythematosus and pulmonary arterial hypertension: evidence from transcriptome data. *Front Immunol.* 2021;12(July):1–13. doi: 10.3389/fimmu.2021.658341.
2. Barber MRW, Drenkard C, Falasinnu T, Hoi A, Mak A, Kow NY, et al. Global epidemiology of systemic lupus erythematosus. *Nat Rev Rheumatol.* 2021;17(9):515–32. doi: 10.1038/s41584-021-00690-3.
3. Fayyaz A, Igoe A, Kurien BT, Danda D, James JA, Stafford HA, et al. Haematological manifestations of lupus. *Lupus Sci Med.* 2015;2(1). doi: 10.1136/lupus-2014-000078.
4. Islam MA, Khandker SS, Kotyla PJ, Hassan R. Immunomodulatory effects of diet and nutrients in systemic lupus erythematosus (SLE): a systematic review. *Front Immunol.* 2020;11(July):1–17. doi: 10.3389/fimmu.2020.01477.
5. Jenks SA, Cashman KS, Woodruff MC, Lee FEH, Sanz I. Extrafollicular responses in humans and SLE. *Immunol Rev.* 2019;288(1):136–48. doi: 10.1111/imr.12741.
6. Chalmers SA, Ramachandran RA, Garcia SJ, Der E, Herlitz L, Ampudia J, et al. The CD6/ALCAM pathway promotes lupus nephritis via T cell-mediated responses. *J Clin Invest.* 2022;132(1). doi: 10.1172/JCI147334.
7. Nakayamada S, Saito K, Nakano K, Tanaka Y. Activation signal transduction by  $\beta 1$  integrin in T cells from patients with systemic lupus erythematosus. *Arthritis Rheum.* 2007;56(5):1559–68. doi: 10.1002/art.22581.
8. Kirou KA, Dall'Era M, Aranow C, Anders HJ. Belimumab or anifrolumab for systemic lupus erythematosus? A risk-benefit assessment. *Front Immunol.* 2022;13(August):1–12. doi: 10.3389/fimmu.2022.980079.
9. Basta F, Fasola F, Triantafyllidis K, Schwarting A. Systemic Lupus Erythematosus (SLE) Therapy: The Old and the New. *Rheumatol Ther.* 2020;7(3):433–46. doi: 10.1007/s40744-020-00212-9. Epub 2020 Jun 2. PMID: 32488652; PMCID: PMC7410873.
10. Peng-Cheng L, Meng-Na L, Jian-Bin L, Shu-Jiao Y, Wu R. Advancements on the impact of hydroxychloroquine in systemic lupus erythematosus. *Heliyon.* 2024;10(9):e30393. doi: 10.1016/j.heliyon.2024.e30393.
11. Huang X, Jiang F, Ma Y, Zhu K, Wang Z, Hua Z, et al. A bibliometric analysis of endoplasmic reticulum stress and atherosclerosis. *Front Physiol.* 2024;15(June):1–20. doi: 10.3389/fphys.2024.1392454.
12. Wu F, Gao J, Kang J, Wang X, Niu Q, Liu J, et al. Knowledge mapping of exosomes in autoimmune diseases: a bibliometric analysis (2002–2021). *Front Immunol.* 2022;13(July):1–19. doi: 10.3389/fimmu.2022.939433.
13. Brandt JS, Hadaya O, Schuster M, Rosen T, Sauer MV, Ananth CV. A bibliometric analysis of top-cited journal articles in obstetrics and gynecology. *JAMA Netw Open.* 2019;2(12):E1918007. doi: 10.1001/jamanetworkopen.2019.18007.
14. Diane Cooper I. Bibliometrics basics. *J Med Libr Assoc.* 2015;103(4):217–8. doi: 10.3163/1536-5050.103.4.013.
15. Ke L, Lu C, Shen R, Lu T, Ma B, Hua Y. Knowledge mapping of drug-induced liver injury: a scientometric investigation (2010–2019). *Front Pharmacol.* 2020;11(June):1–14. doi: 10.3389/fphar.2020.00842.
16. Falagas ME, Pitsouni EI, Malietzis GA, Pappas G. Comparison of PubMed, Scopus, Web of Science, and Google Scholar: strengths and weaknesses. *FASEB J.* 2008;22(2):338–42. doi: 10.1096/fj.07-9492LSF.
17. Bakar A, Irham LM, Ningrum V. Publication trend on oral mucositis induced by chemotherapy 1978–2023: bibliometric analysis. *Scr Medica.* 2024;55(5):631–8. doi:10.5937/scriptamed55-51528.
18. van Eck NJ, Waltman L. Software survey: VOSviewer, a computer program for bibliometric mapping. *Scientometrics.* 2010;84(2):523–38. doi: 10.1007/s11192-009-0146-3.
19. Ai S, Li Y, Tao JY, Zheng H, Tian L, Wang Y, et al. Bibliometric visualization analysis of gut-kidney axis from 2003 to 2022. *Front Physiol.* 2023;14(June):1–21. doi: 10.3389/fphys.2023.1176894.
20. Bentham J, Morris DL, Cunningham Graham DS, Pinder CL, Tomblinson P, Behrens TW, et al. Genetic association analyses implicate aberrant regulation of innate and adaptive immunity genes in the pathogenesis of systemic lupus erythematosus. *Nat Genet.* 2015;47(12):1457–64. doi: 10.1038/ng.3434.
21. Quan L, Dai J, Luo Y, Wang L, Liu Y, Meng J, et al. The 100 top-cited studies in systemic lupus erythematosus: A bibliometric analysis. *Hum Vaccines Immunother.* 2024;20(1):1–16. doi: 10.1080/21645515.2024.2387461.
22. Graham RR, Ortmann W, Rodine P, Espe K, Langefeld C, Lange E, et al. Specific combinations of HLA-DR2 and DR3 class II haplotypes contribute graded risk for disease susceptibility and autoantibodies in human SLE. *Eur J Hum Genet.* 2007;15(8):823–30. doi: 10.1038/sj.ejhg.5201827.
23. Xue K, Niu WQ, Cui Y. Association of HLA-DR3 and HLA-DR15 Polymorphisms with risk of systemic lupus erythematosus. *Chin Med J (Engl).* 2018;131(23):2844–51. doi: 10.4103/0366-6999.246058.
24. Ostanek L, Ostanek-Pańska M, Bobrowska-Snarska D, Bińczak-Kuleta A, Fischer K, Kaczmarczyk M, et al. PTPN22 1858C>T gene polymorphism in patients with SLE: Association with serological and clinical results. *Mol Biol Rep.* 2014;41(9):6195–200. doi: 10.1007/s11033-014-3498-6.
25. Namjou B, Kim-Howard X, Sun C, Adler A, Chung SA, Kaufman KM, et al. PTPN22 Association in systemic lupus erythematosus (SLE) with respect to individual ancestry and clinical sub-phenotypes. *PLoS One.* 2013;8(8). doi: 10.1371/journal.pone.0069404.
26. Rosetti F, De La Cruz A, Crispín JC. Gene-function studies in systemic lupus erythematosus. *Curr Opin Rheumatol.* 2019;31(2):185–92. doi: 10.1097/BOR.0000000000000572.
27. Lazzari E, Jefferies CA. IRF5-mediated signaling and implications for SLE. *Clin Immunol.* 2014;153(2):343–52. doi: 10.1016/j.clim.2014.06.001.
28. Sianu R, Irham LM. [Study trends related to ulcerative colitis and genomics from 2000–2023.] *Lumbung Farm J Ilmu Kefarmasian.* 2024;5(1):76. doi: 10.31764/lf.v5i1.17728. Indonesian.