Journal of Infection and Public Health 18 (2025) 102631

Contents lists available at ScienceDirect

Journal of Infection and Public Health

journal homepage: www.elsevier.com/locate/jiph

Review

Understanding and addressing the global impact: A systematic review and cross-sectional bibliometric analysis of Langya henipavirus and pre-existing severe henipaviruses

Jian-Di Li [a,1], Yu-Qing Liu [a,1], Rong-Quan He [b], Zhi-Guang Huang [a], Wan-Ying Huang [a], Hong Huang [c], Zhi-Hong Liu [d,2,*], Gang Chen [a,2,*]

[a] *Department of Pathology, The First Affiliated Hospital of Guangxi Medical University, Nanning, Guangxi Zhuang Autonomous Region 530021, China*
[b] *Department of Medical Oncology, The First Affiliated Hospital of Guangxi Medical University, Nanning, Guangxi Zhuang Autonomous Region 530021, China*
[c] *Department of Respiratory and Critical Care Medicine, The First Affiliated Hospital of Guangxi Medical University, Nanning, Guangxi Zhuang Autonomous Region 530021, China*
[d] *Department of Infectious Diseases, The First Affiliated Hospital of Guangxi Medical University, Nanning, Guangxi Zhuang Autonomous Region 530021, China*

ARTICLE INFO

Article history:
Received 25 August 2024
Received in revised form 15 December 2024
Accepted 22 December 2024

Keywords:
Langya henipavirus
Hendra virus
Nipah virus
Bibliometric analysis
Vaccine

ABSTRACT

In 2022, Langya henipavirus was identified in patients with fever in eastern China. This study provides an overview of the scientific landscape, highlights research focus areas, and outlines potential future investigations. The relevant scientific literature was systematically searched and reviewed via advanced bibliometric techniques. Over the past two decades, henipavirus research has increased at an annual rate of 8.82 %. The United States leads in research output, with the Australian Animal Health Laboratory as the top institution. Most articles are published in the *Journal of Virology*, identified as the most influential journal along with researcher Wang LF. Current research focuses on “zoonosis,” “vaccine,” and “pathogenesis,” whereas future areas may include “molecular docking,” “immunoinformatics,” “climate change,” “antibodies,” “vaccines,” “glycoprotein,” and “ephrin-b2.” This study details henipavirus research, highlighting key players, trends, and future directions. These insights will guide future efforts to address the risks posed by novel Henipaviruses, such as Langya.

Contents

---

[*] Corresponding authors.
E-mail addresses: Liuzh308@163.com (Z.-H. Liu), chengang@gxmu.edu.cn (G. Chen).
[1] Contributed equally as the first author
[2] Contributed equally as the corresponding author.

https://doi.org/10.1016/j.jiph.2024.102631

Introduction

Langya henipavirus (also known as Langya virus or LayV), a novel member of the *Henipavirus* genus within the family *Paramyxoviridae* and the order *Mononegavirales*, has quickly become a focal point in the field of viral research [1,2]. Langya henipavirus exhibits a distinct profile, particularly in terms of host specificity and receptor binding characteristics [3,4], that differentiates it from other established henipaviruses like Hendra and Nipah. These latter viruses have been the cause of catastrophic outbreaks with significant fatality rates in Australia, Southeast Asia, and South Asia since the late 20th century [5–7]. The zoonotic potential of these viruses has been a significant concern, prompting a global vigilance for their emergence and spread [8]. Langya henipavirus's emergence is not just another addition to the *Henipavirus* family; it signifies a new dimension in the threat landscape of zoonotic diseases, demanding a reevaluation of our understanding and preparedness [9]. Langya henipavirus shares genetic similarities with other henipaviruses but presents distinct features that warrant further investigation [10]. Its discovery underscores the importance of surveillance efforts in identifying novel viral threats and highlights the need for proactive measures to mitigate potential spillover events [11]. As a single-stranded RNA virus, Langya henipavirus may exhibit a mutation rate comparable to that in severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) [12], which has profound implications for its potential to evolve and adapt in the human population. Therefore, further research is imperative to comprehensively understand the characteristics and risks associated with Langya henipavirus, paving the way for effective prevention and control strategies.

Bibliometric analysis serves as a valuable tool in assessing the scientific landscape surrounding emerging infectious diseases such as Langya henipavirus [13–15]. By analyzing publications related to Langya henipavirus, researchers can gain insights into the extent of research activity, key contributors, geographic distribution, and thematic trends [16]. This information not only aids in understanding the current state of knowledge but also guides future research directions and resource allocation to address gaps in understanding and preparedness.

In this study, we present a comprehensive bibliometric analysis of Langya henipavirus research, encompassing publications from various scientific disciplines and geographic regions. Through a systematic literature review and analysis, we aim to provide a comprehensive overview of the scientific landscape surrounding Langya henipavirus, identify areas of research focus, and delineate potential avenues for future investigations. Our findings contribute to the collective knowledge base on Langya henipavirus and inform strategies for enhanced surveillance, prevention, and control of emerging henipaviruses.

Materials and methods

Literature search

Historical documents of global significance were meticulously retrieved from the esteemed Web of Science Core Collection (WOSCC), employing a refined search strategy incorporating keywords such as "henipavirus," "Hendra virus," "Nipah virus," "Langya henipavirus," and "LayV." Our inclusion criteria were stringent, requiring that documents be indexed in WOSCC and demonstrate relevance to Langya henipavirus, Hendra virus, or Nipah virus in their titles or abstracts. To maintain the integrity of the review process, retracted and duplicated studies were systematically excluded by manual methods. Initial screening utilized sophisticated character-matching algorithms implemented in R software (version 4.2.1), followed by meticulous manual examination by two independent scientists employing a double-blind methodology. This meticulous approach ensured the comprehensive evaluation of each document, enhancing the reliability and credibility of our review findings. Additionally, the PubMed database was incorporated to mitigate potential biases.

Bibliometric analysis

Using the "bibliometrix" R package (version 4.1.3), we meticulously extracted metadata from a comprehensive selection of 1546 documents spanning the years 1998–2024. Most of the content (83.96 %) consists of scholarly articles and reviews, reflecting the field's academic depth. We obtained a total of 2096 keywords, 5157 authors, 32256 references, and contributions from 412 distinct journals. Subsequently, employing advanced mathematical and statistical methodologies within the "bibliometrix" R package, we conducted a quantitative exploration of the research landscape surrounding Langya henipavirus and pre-existing severe henipaviruses. Leveraging the power of science mapping techniques, we delved into key dimensions, including scientific output, literature citation patterns, international collaboration dynamics, thematic evolution trajectories, and emergent frontier topics, to elucidate the evolving contours of scholarly discourse within the academic community.

To assess the productivity and impact of journals and authors, we employed robust metrics such as the H-index and G-index. The H-index, denoting the number H such that an author has H papers each cited at least H times, and the G-index, representing the highest number of top G publications with at least G^2 citations, provide nuanced insights into the scholarly influence wielded by key stakeholders in the field. To further enrich our analysis, we constructed a dynamic cooccurrence map of keywords across temporal dimensions via the VOSviewer software (version 1.6.18), facilitating a granular exploration of thematic trends and shifts over time [17,18]. Moreover, leveraging the capabilities of CiteSpace (version 6.3. R1), we conducted rigorous keyword clustering and citation burst detection analyses, leveraging thresholds such as a Q-score > 0.3 and an S-score > 0.7 to ensure the structural integrity and credibility of our findings [19–21].

Results

Scientific output and research performance

With stringent inclusion and exclusion criteria, the current study undertook a cross-sectional exploration within the research domain of Langya henipavirus and pre-existing severe henipaviruses via WOSCC and PubMed (Fig. 1 and Supplemental Figure 1). Over the past two decades, scientific output within the field of henipaviruses has exhibited a consistent upward trajectory, with an annual growth rate of 8.82 % (Fig. 2**A**). The cumulative publication count was accurately modeled via the following formula:

$$y = 6.26 \times 10^6 - 6.29 \times 10^3 x + 1.58x^2 \ (R^2 = 0.999)$$

The United States emerged as the foremost contributor to henipavirus research, followed by Australia and India (Fig. 2**B**). Notably, the Australian Animal Health Laboratory, the University of Texas

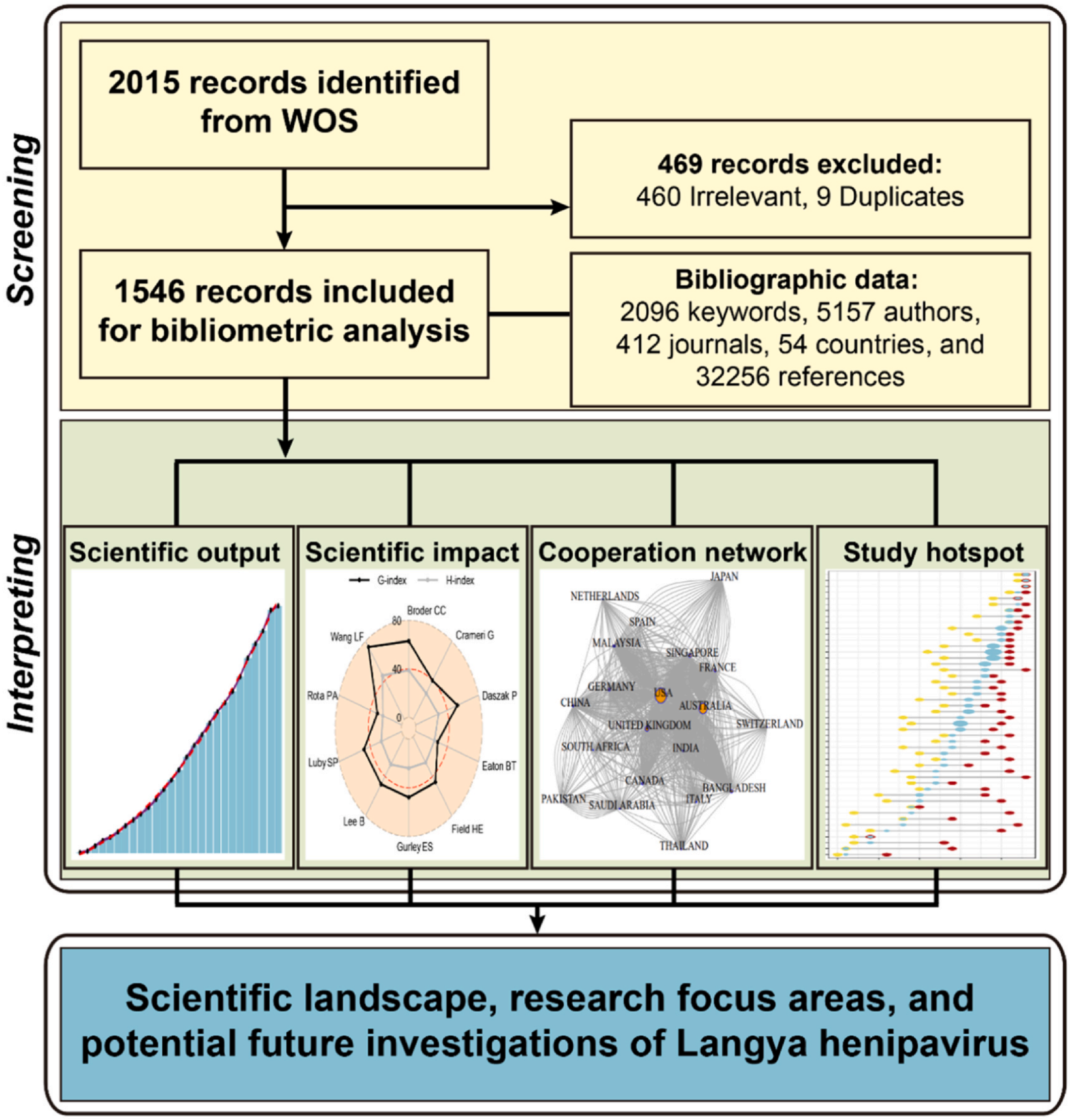

Fig. 1. Flow diagram for the comprehensive bibliometric analysis of Langya henipavirus and pre-existing severe henipaviruses.

Medical Branch, and the Centers for Disease Control and Prevention (CDC) emerged as the three most prolific scientific institutions (Fig. 2**C**). The Australian Animal Health Laboratory exhibited a particularly noteworthy annual article output, whereas the CDC displayed promising growth trends, poised to potentially surpass the former shortly (Fig. 2**D**). The leading publishing outlets in this domain included the *Journal of Virology*, *PLoS One*, and *Emerging Infectious Diseases* (Fig. 2**E**). Among these, the *Journal of Virology* stood out for its notably higher annual publication count, a trend anticipated to persist for the foreseeable future (Fig. 2**F**). The noteworthy authors within the field included Wang LF, Broder CC, and Daszak P, who emerged as the top three most prolific contributors (Fig. 2**G**).

Scientific impact of journals and authors

Applying Bradford's Law, we delineated the core publishing zones within the research domain of Langya henipavirus and pre-existing severe henipaviruses (Fig. 3**A**, Table 1). Notably, the *Journal of Virology* had the highest total number of citations among these core zones (Fig. 3**B**). Wang LF emerged as the most locally cited scientist within this field (Fig. 3**C**). In terms of individual publications, the average number of citations per document was 36.86 %, with Chua KB's study in *Science* being the most locally cited reference (Fig. 3**D**) [22]. Evaluating the H-index and G-index metrics, both the *Journal of Virology* and Wang LF were identified as the most

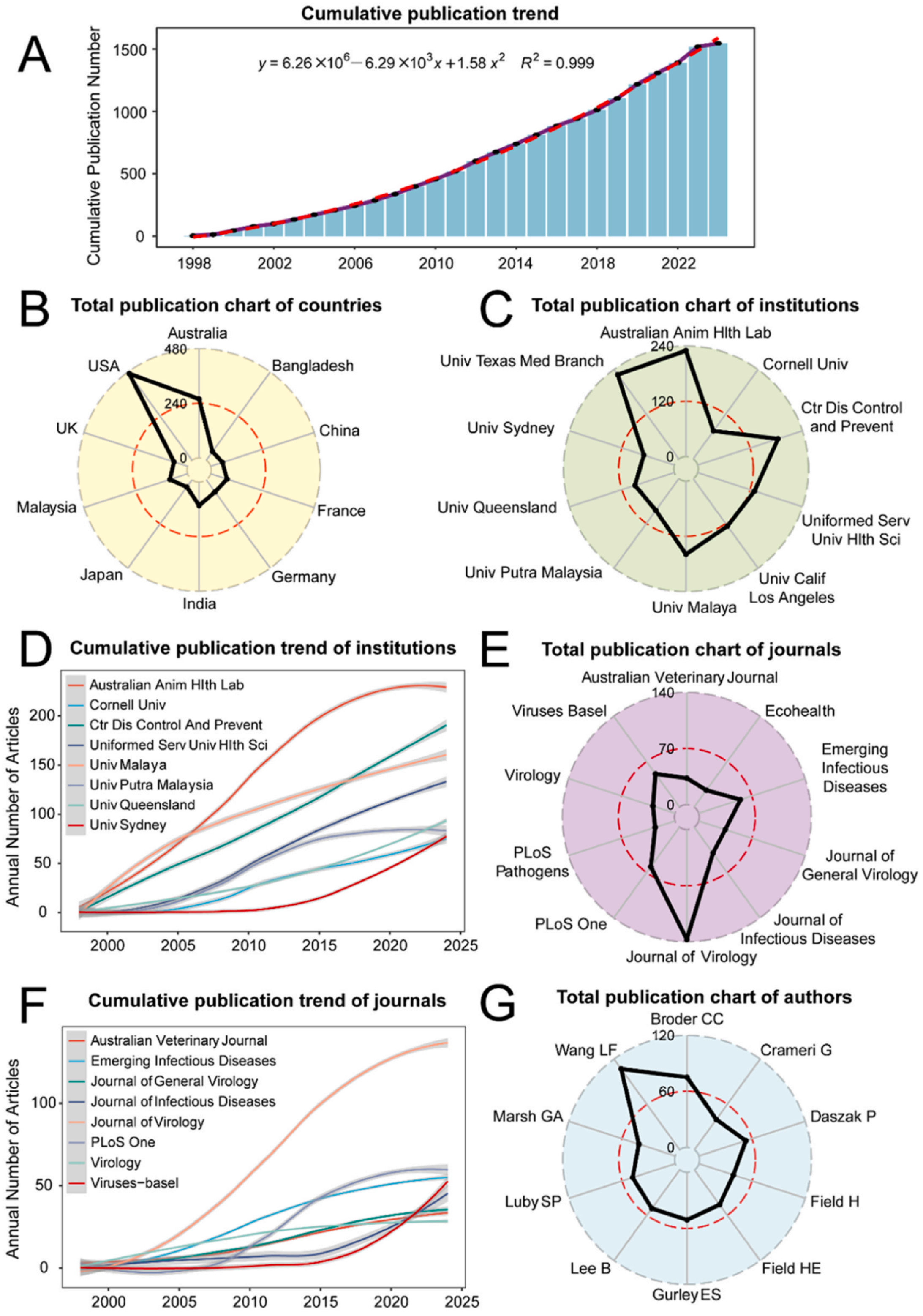

Fig. 2. Overview of research output in the field of Langya henipavirus and pre-existing severe henipaviruses (A) Cumulative publication trends of Langya henipavirus and pre-existing severe henipaviruses, including Nipah virus and Hendra virus (B) Scientific output by country (C, D) Institutional contributions to scientific output (E, F) Scientific output across journals (G) Contribution of individual authors to scientific literature.

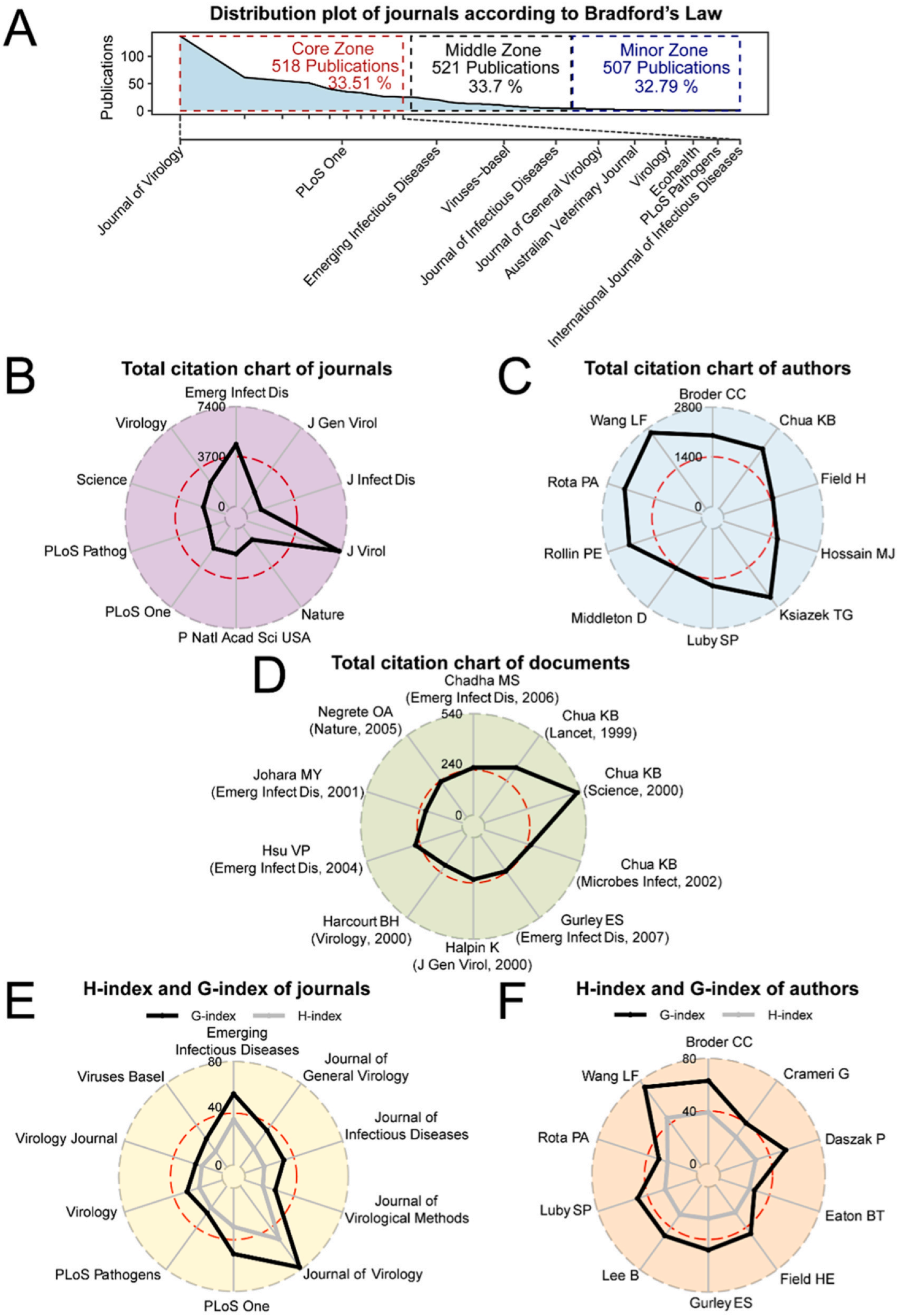

Fig. 3. Analysis of citations in the field of Langya henipavirus and pre-existing severe henipaviruses (A) Applying Bradford's Law, the core publishing zones were identified within the research domain of Langya henipavirus and pre-existing severe henipaviruses. (B) Total citations received by journals. (C) Total citations received by authors. (D) Total citations received by documents. (E, F) H-index and G-index were utilized to evaluate the productivity and impact of journals and authors. An author has an H-index if H of their papers has at least H citations each. The G-index is the highest number of top G publications that together have at least G^2 citations.

Table 1

Core publishing sources in the research field of Langya henipavirus and pre-existing severe henipaviruses.

Journal	Category	JCR IF (2022)	JCR quartile	ISSN	EISSN	Region
Journal of Virology	Virology	5.4	Q2	0022–538X	1098–5514	USA
PLoS One	Multidisciplinary sciences	3.7	Q2	1932–6203	1932–6203	USA
Emerging Infectious Diseases	Infectious diseases; immunology	11.8	Q1	1080–6040	1080–6059	USA
Viruses-Basel	Virology	4.7	Q2	/	1999–4915	Switzerland
Journal of Infectious Diseases	Microbiology; infectious diseases; immunology	6.4	Q2	0022–1899	1537–6613	USA
Journal of General Virology	Virology; biotechnology and applied microbiology	3.8	Q2	0022–1317	1465–2099	England
Australian Veterinary Journal	Veterinary sciences	1.1	Q3	0005–0423	1751–0813	Australia
Virology	Virology	3.7	Q3	0042–6822	1089–862X	USA
Ecohealth	Environmental Sciences	2.5	Q3	1612–9202	1612–9210	USA
PLoS Pathogens	Microbiology; virology; parasitology	6.7	Q1	1553–7366	1553–7374	USA
International Journal of Infectious Diseases	Infectious diseases	8.4	Q1	1201–9712	1878–3511	England

JCR., Journal Citation Reports; IF., Impact Factor; ISSN., International Standard Serial Number; EISSN., Electronic International Standard Serial Number

influential journal and researchers, respectively, within the research community (Fig. 3**E** and Fig. 3**F**).

Cooperation networks of institutions and scientists

The intricate tapestry of global scientific collaboration has fostered a paradigm shift in research dynamics, exemplified by the burgeoning rate of international coauthorships, which has soared to a remarkable 40.43 %. This study delved into the forefront of collaborative endeavors, spotlighting key players such as the United States, and spearheading pioneering research on Langya henipavirus and its relationship with pre-existing severe henipaviruses (Fig. 4**A**). Notably, the Australian Animal Health Laboratory emerged as a nexus of collaborative synergy, intricately interwoven with diverse scientific institutions (Fig. 4**B**). Furthermore, a compelling narrative unfolds through the intimate collaborative ties between Wang LF and their esteemed counterparts (Fig. 4**C**).

Research hotspots and frontier directions in the field of henipaviruses

In the historical documents of Langya henipavirus and pre-existing severe henipaviruses retrieved from WOSCC, the most frequently occurring keywords were identified as “zoonosis,” “bat,” “vaccine,” “encephalitis,” and “pathogenesis” (Fig. 5**A**). These terms demonstrated a significant degree of overlap with those identified in PubMed (Supplemental Figure 2**A**), highlighting a high level of similarity between the two databases. Notably, thematic clustering analysis revealed that “zoonosis,” “one health,” “epidemiology,” “flying fox,” and “horse” formed a cohesive motor theme, representing well-developed and highly relevant topics within the field (Fig. 5**B**). Conversely, keywords such as “encephalitis,” “innate immunity,” “pathology,” “molecular docking,” and “virology” were categorized into a niche theme, highlighting more isolated research areas. Noteworthy emerging themes included “bat virus,” “COVID-19,” “diagnosis,” and “Ebola virus,” whereas fundamental concepts such as “Nipah virus,” “Hendra virus,” “henipavirus,” “paramyxovirus,” and “vaccine” were grouped in the basic theme, indicative of future developmental trajectories.

A time-sliced cooccurrence map of keywords was subsequently constructed (Fig. 6). This map revealed that “Langya henipavirus” was associated with keywords such as “vaccine,” “immunoinformatics,” and “molecular docking.” The log-likelihood ratio clustering analysis yielded 12 distinct clusters, included topics such as “fusion protein,” “emerging infectious disease,” “West Nile virus,” “molecular docking,” “monoclonal antibody,” and “Langya henipavirus” (Fig. 7**A**). The Q-score of 0.5608, which exceeds the threshold of 0.3, and the S-score of 0.9193, surpassing 0.7, indicate that the clustering structure is both significant and reliable. Within the “Langya henipavirus” cluster, specific keywords such as “vaccine construction,” “immunoinformatics,” “China,” and “protein-protein docking” were prominently featured. Additionally, a timeline of keyword bursts spanning 1998–2024 revealed significant research hotspots, including “molecular docking,” “Ebola virus,” “molecular dynamics,” “public health,” and “reverse genetics,” with “molecular docking” exhibiting the highest citation burst strength (citation burst strength = 4.2677) (Fig. 7**B**). This timeline map also visually depicts the temporal evolution of keywords across various clusters (Fig. 7**C**). On the basis of quantile years of publication in WOSCC, trend topics predicted for the henipavirus research field included “molecular docking,” “molecular,” “dynamics,” “immunoinformatics,” “climate change,” “antibodies,” “SARS-CoV-2,” “Ebola virus,” “vaccine,” “glycoprotein,” and “ephrin-b2” (Fig. 7**D**). This aligned with the trends identified in PubMed, where “neutralizing antibodies,” “molecular docking,” and “glycoprotein” were also highlighted as emerging topics. Additionally, PubMed shed light on new topics such as “Ghana virus,” “public health,” “antiviral,” and “biosecurity” (Supplemental Figure 2B).

Discussion

To the best of our knowledge, we performed the first comprehensive systematic review and bibliometric analysis of Langya henipavirus and its pre-existing counterparts, Hendra and Nipah viruses. We present a nuanced and multifaceted portrait of the scholarly landscape surrounding Langya henipavirus and pre-existing severe henipaviruses, shedding light on key patterns, trends, and emerging frontiers that shape the trajectory of scientific inquiry in this critical domain.

We note an annual growth rate of 8.82 % in scholarly output related to henipavirus research over the past two decades, highlighting sustained interest in this field. This trend likely stems from significant public health concerns, as evidenced by the prominence of terms such as “zoonosis,” “bat,” and “vaccine” within the literature. A positive correlation between time and research output is suggested by our modeling, which may be a reflection of heightened global awareness of henipaviruses and their potential impact on human health. Notably, *Henipavirus* is one of the most perilous zoonotic virus groups in the Asia-Pacific region since the dawn of the 21st century [23]. Hendra virus and Nipah virus, among the identified species, are particularly virulent pathogens responsible for human outbreaks associated with high fatality rates [4,24,25]. Hendra virus was first recognized amidst an outbreak of respiratory and neurological ailments affecting horses and humans in Hendra, a suburb situated near Brisbane, Australia [26]. Nipah virus was first identified in Malaysia and Singapore, subsequently leading to encephalitis outbreaks among pig farmers, with recurring occurrences

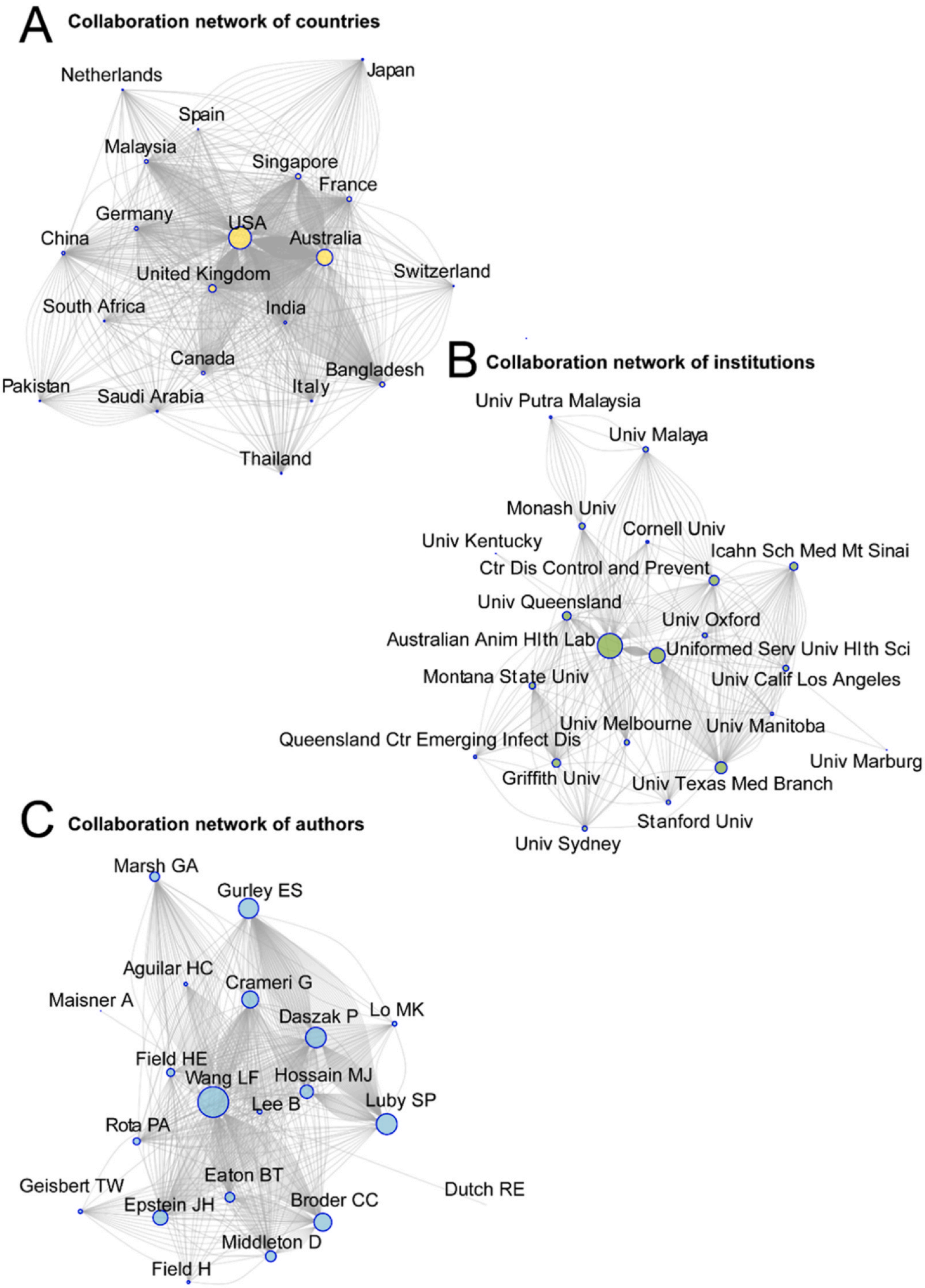

Fig. 4. Examination of international collaboration dynamics in the field of Langya henipavirus and pre-existing severe henipaviruses (A) Network analysis illustrating international collaborations between countries. (B) Network analysis highlighting collaborative relationships between institutions. (C) Network analysis depicting collaborative ties between authors.

reported nearly every year in Bangladesh and India [27,28]. These viruses have been classified as biosafety level 4 (BSL-4) pathogens, denoting the highest level of laboratory safety isolation and often representing the most dangerous and refractory viruses [29]. In 2022, a previously unknown zoonotic henipavirus, designated Langya henipavirus, was first identified in patients exhibiting fever in eastern China [1,30]. Although no severe symptoms or documented cases of human-to-human transmission have been reported thus far [30], recognizing the possibility of future mutations that could lead to changes in its epidemiological characteristics is crucial.

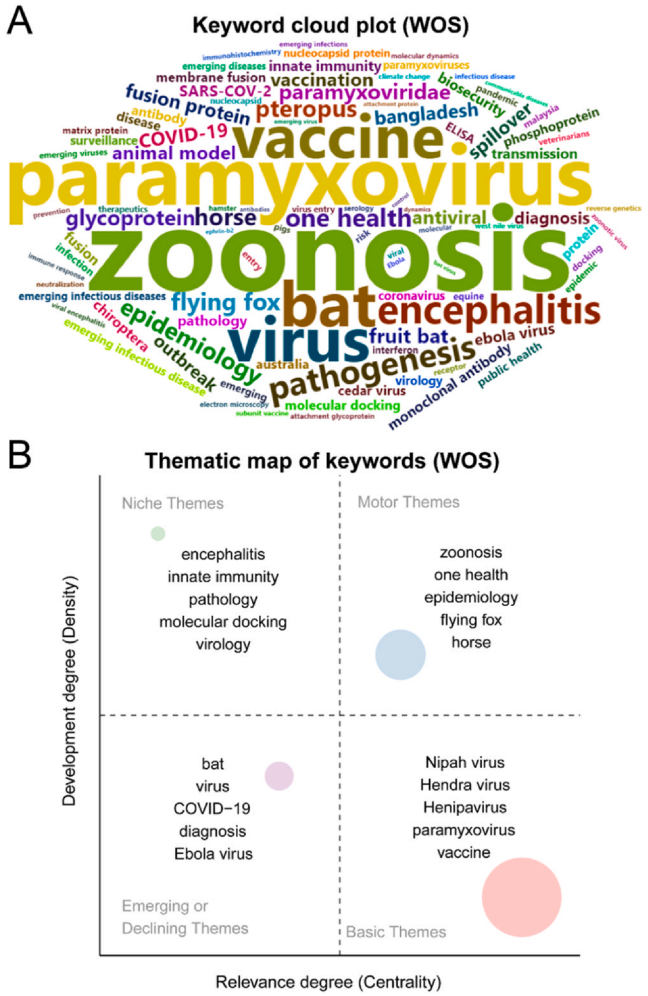

Fig. 5. Keyword analysis in the research field of Langya henipavirus and pre-existing severe henipaviruses (A) Top keywords in henipavirus research from Web of Science (B) Thematic map: organizing keywords into four quadrants based on development potential and relevance. Motor themes denote well-developed and highly relevant topics within the field, such as “zoonosis”; whereas niche themes encompass isolated research areas, namely “encephalitis”. Basic themes, such as “vaccine”, represent highly relevant topics with relatively low maturity, indicating potential avenues for future research exploration. The circle size reflects the number of keywords within each cluster.

Consequently, research focused on emerging henipaviruses, including Langya henipavirus, is progressively intensifying to monitor potential risks.

Geographically, the United States has emerged as the leading contributor to henipavirus research, followed by Australia and India. This triumvirate of countries is mirrored in the most prolific institutions, where the Australian Animal Health Laboratory leads, followed by the University of Texas Medical Branch and the CDC. These institutions have played crucial roles in identifying, monitoring, and managing henipavirus outbreaks, particularly those caused by the Hendra and Nipah viruses [31–34]. In 2020, researchers at the Australian Animal Health Laboratory conducted a pioneering first-in-human randomized controlled trial, focusing on the use of monoclonal antibodies to target glycoproteins in henipaviruses [35]. This innovative study laid the groundwork for the prevention of henipavirus infections. Efforts by the CDC team include risk assessment, pathogen detection, prognostic follow-up, immune response evaluation, and vaccine development for henipaviruses [36–41]. Notably, the CDC’s growing trend suggests that it may soon surpass Australian institutions in annual article output.

The *Journal of Virology* stands out for its a higher annual publication count, positioning it as a central hub for disseminating research on henipaviruses. The high total citation count and H-index further corroborate its influence within the research community. Wang LF’s status as the most locally cited scientist suggests that their work has had a significant impact on guiding subsequent research endeavors [25,42–44]. Chua KB’s study in *Science* represents a foundational work in the field, garnering the highest number of local citations and shaping the understanding of Nipah virus characteristics and implications [22].

Keyword analyses reveal research hotspots and emerging themes, with terms such as “molecular docking,” “molecular,” “immunoinformatics,” “vaccine,” “glycoprotein,” and “ephrin-b2” featuring prominently. These findings suggest that molecular studies, particularly those focusing on viral dynamics and vaccine development, are at the forefront of current research efforts. A recombinant vesicular stomatitis virus-vectored vaccine has been designed to induce long-lasting immunity against Nipah virus [45]. More importantly, the first-in-human trial targeting the G glycoprotein in Hendra and Nipah viruses with monoclonal antibodies has commenced [35]. Researchers have successfully developed the first postexposure passive antibody therapy for Nipah virus [46]. A recent study revealed that the attachment glycoprotein G of Langya henipavirus is antigenically distinct from that of Hendra and Nipah viruses [10]. Given the potential pandemic threat of Langya henipavirus, immunoinformatics has been employed to design novel multiepitope-based vaccines [47]. Moreover, molecular docking may aid in the discovery of novel antiviral drugs [48–50], particularly in the design of multiepitope vaccines for Langya henipavirus [51]. Recently, mRNA-based vaccines have demonstrated significant advantages in the rapid development of vaccines against emerging pathogens [52]. Furthermore, nanovaccines stand out because of their capacity to increase immunogenicity and stability, offer broad protection against a variety of viral strains, and minimize adverse effects [53]. As artificial intelligence advances, large language models have the potential to expedite identification, design, and educational outreach for vaccines targeting emerging infectious diseases [54–56]. However, no approved vaccines or specific antiviral medications are currently available for Langya henipavirus. To advance vaccine research for emerging infectious diseases like Langya henipavirus, a multi-faceted approach is essential. For instance, immunoinformatics can be utilized to predict epitopes, which are crucial for immune recognition. Additionally, reverse vaccinology can guide the design of vaccines from surface proteins, enhancing our understanding of the virus’s structure and function [57]. Immune simulation predicts immune responses [47], while ensuring equitable global vaccine access is vital for global health security [58]. Regulatory innovation and platform vaccine approval can expedite the process, making emergency vaccine development and authorization more efficient in the face of new threats.

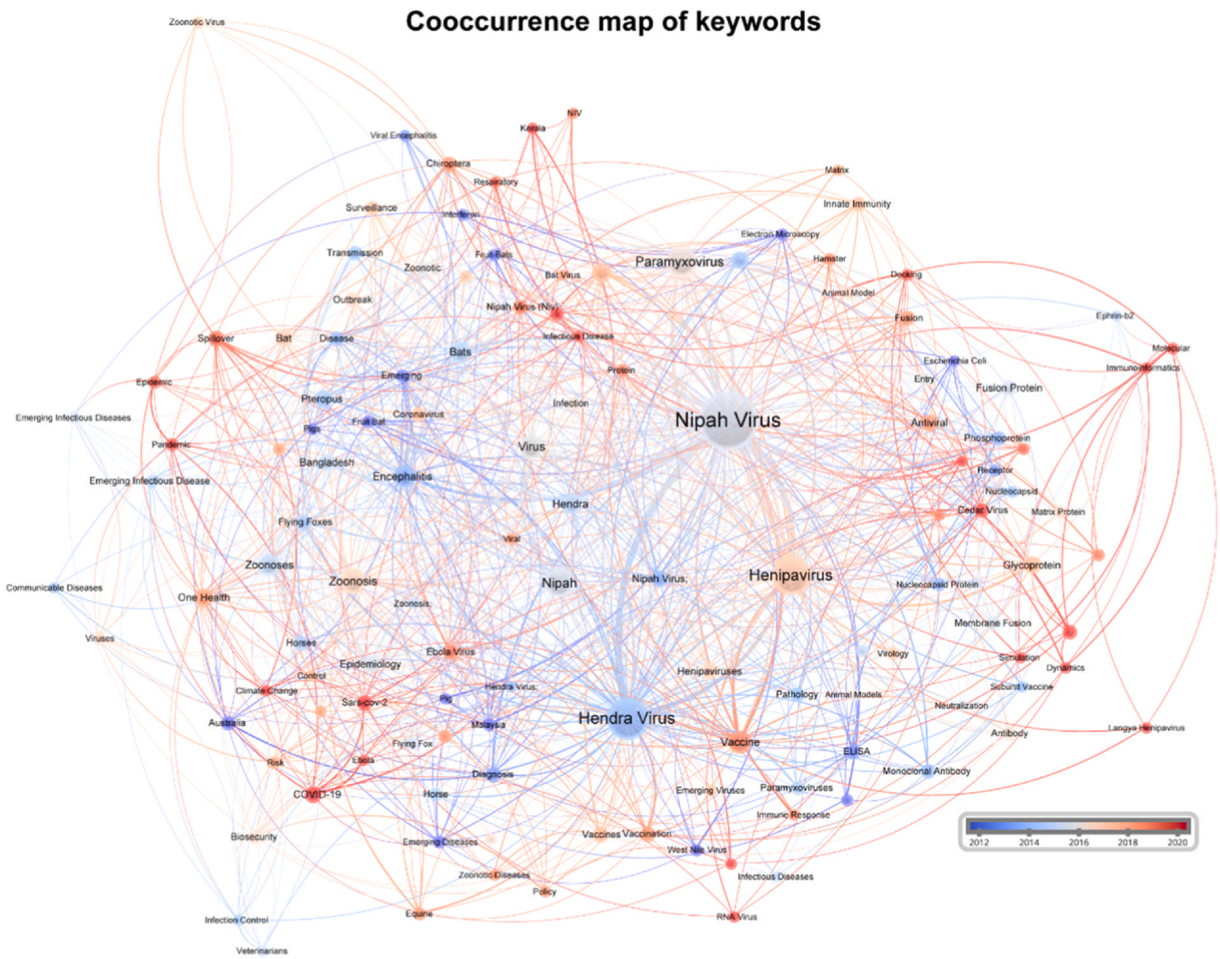

Fig. 6. Cooccurrence mapping of keywords in the research field of Langya henipavirus and pre-existing severe henipaviruses. This map revealed that "Langya henipavirus" was associated with keywords such as "vaccine," "immunoinformatics," and "molecular docking.".

Our study also highlights the need for pathological research to better understand the biology of emerging henipaviruses, improve diagnostic capabilities, and develop effective interventions to prevent and control infections. Keywords such as "encephalitis," "pathology," and "virology" were clustered in the niche theme, reflecting a relatively isolated research area. Pathology detection is key to characterizing emerging infectious disease pathogens [22,59,60]. In 2002, on the basis of a series of 32 fatal human cases of infection, the pathology and pathogenesis of Nipah virus were comprehensively described [61]. According to their findings, endothelial cell and neuron infection, vasculitis, and thrombosis are critical to the lethal nature of Nipah virus. In 2009, scientists from the Australian Animal Health Laboratory replicated the pathological morphology of Nipah virus infection via a ferret model, characterized by multisystemic vasculitis [46]. Systemic infection and acute encephalitis have been identified as major pathogeneses of Hendra virus [62], which shares similarities with Nipah virus. The pathological characteristics and pathogenesis of Langya henipavirus remain unclear.

Although this study provides an extensive overview of the scientific discourse on Langya henipavirus, we are aware of the constraints inherent in our bibliometric analysis, especially our initial reliance on databases like Web of Science, which could potentially exclude regional literature. To mitigate this, we have broadened our scope to incorporate PubMed, thereby enriching the comprehensiveness of our research. We understand that each database possesses distinct advantages and limitations. Nevertheless, through rigorous search methodologies and stringent selection criteria, we are confident in presenting a reliable portrayal of the research domain.

In conclusion, this study provides a detailed picture of henipavirus research, identifying key players, trends, and future directions. The findings underscore the importance of continued research, international collaboration, and a focus on molecular studies and public health strategies to combat henipaviruses effectively. In the ongoing struggle against emerging infectious diseases in the context of a shifting global landscape [63], the findings of this study are poised to significantly inform and direct subsequent research

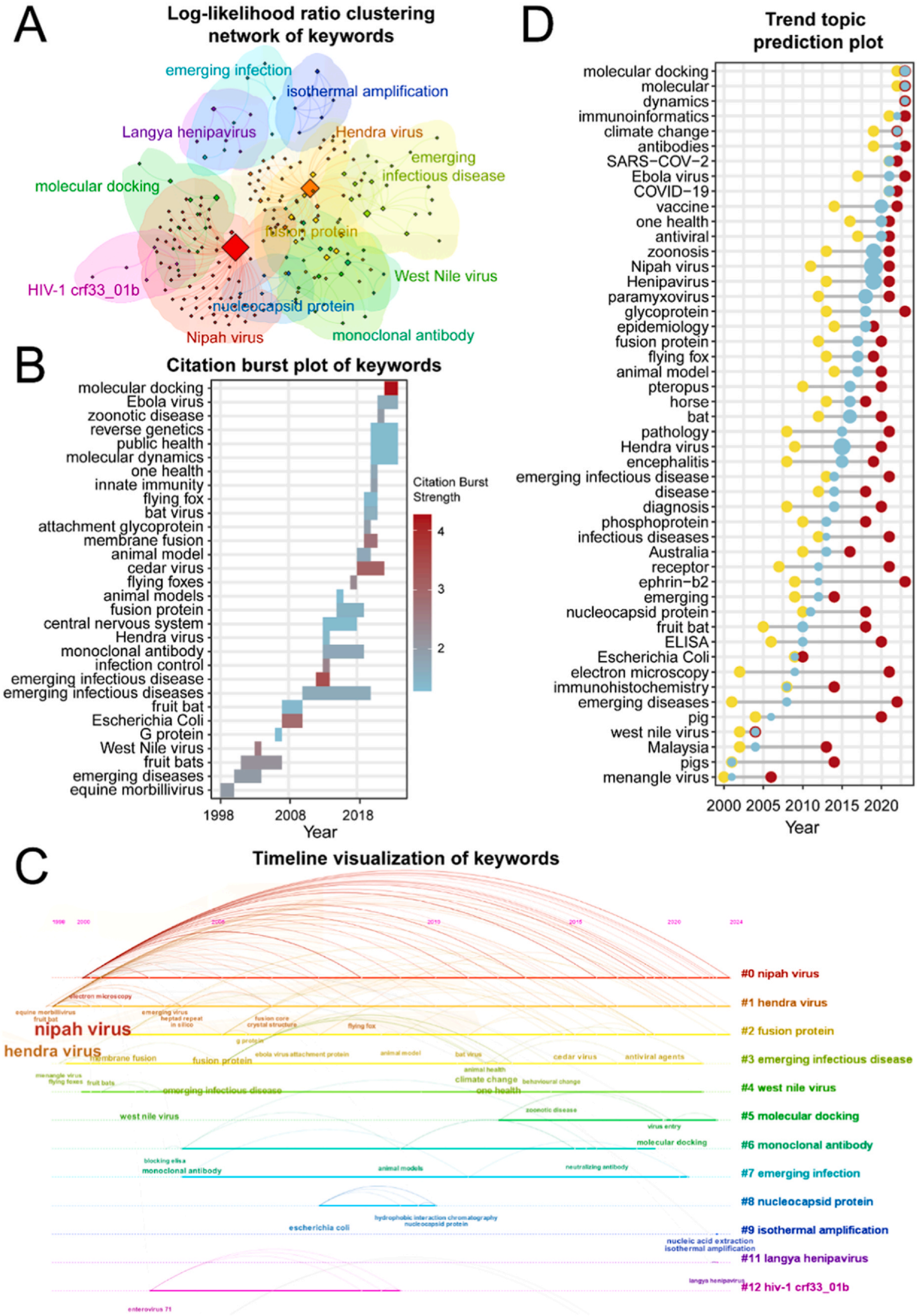

Fig. 7. Keyword clustering and frontier hotspot detection in the research field of Langya henipavirus and pre-existing severe henipaviruses (A) Log-likelihood ratio clustering analysis reveals 12 credible and well-structured clusters from henipavirus-related keywords. (B) Citation burst analysis reveals significant research hotspots. (C) Timeline map depicts the temporal evolution of keywords across various clusters. (D) Trend topics was predicted for the henipavirus research field based on the quantile years of publication. Yellow, blue, and red circles represent the first, second, and third quantile years of papers published, respectively. The size of the blue circle reflects occurrence frequency of keywords.

initiatives, bolstering our collective defense against the threats posed by novel henipaviruses, such as Langya henipavirus.

Authors' contributions

Li JD was responsible for data collection, data analysis, and visualization. Li JD and Liu YQ were responsible for reviewing the literature and writing the first draft. He RQ and Huang ZG were responsible for the design of the project. Huang WY, Huang H, and Liu ZH polished the article. Chen G was responsible for supervision and project management. All authors contributed to the final version of the manuscript and approved it for publication.

Funding

The present study was supported by the Innovation Project of Guangxi Graduate Education (JGY2023068), Guangxi Higher Education Undergraduate Teaching Reform Project (2022JGA146), Guangxi Medical University Undergraduate Education and Teaching Reform Project (2023Z10), Guangxi Medical High-level Key Talents Training "139" Program (2020), and Guangxi Graduate Education Innovation Program project (Project No. YCSW2023220).

Declaration of Competing Interest

The authors declare that they have no conflicts of interest.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.jiph.2024.102631.

References

[1] Zhang XA, Li H, Jiang FC, Zhu F, Zhang YF, Chen JJ, et al. A Zoonotic Henipavirus in Febrile Patients in China. N Engl J Med 2022;387:470–2. https://doi.org/10.1056/NEJMc2202705

[2] Wang Z, McCallum M, Yan L, Gibson CA, Sharkey W, Park YJ, et al. Structure and design of Langya virus glycoprotein antigens. Proc Natl Acad Sci USA 2024;121:e2314990121. https://doi.org/10.1073/pnas.2314990121

[3] Zhang JT, Hu ZY, Tang F, Liu YT, Tan WL, Ma XF, et al. Decoding the RNA viromes in shrew lungs along the eastern coast of China. NPJ Biofilms Micro 2024;10:68. https://doi.org/10.1038/s41522-024-00543-3

[4] Quarleri J, Galvan V, Delpino MV. Henipaviruses: an expanding global public health concern? Geroscience 2022;44:2447–59. https://doi.org/10.1007/s11357-022-00670-9

[5] Wang Z, Amaya M, Addetia A, Dang HV, Reggiano G, Yan L, et al. Architecture and antigenicity of the Nipah virus attachment glycoprotein. Science 2022;375:1373–8. https://doi.org/10.1126/science.abm5561

[6] Ang LT, Nguyen AT, Liu KJ, Chen A, Xiong X, Curtis M, et al. Generating human artery and vein cells from pluripotent stem cells highlights the arterial tropism of Nipah and Hendra viruses. e2530 Cell 2022;185:2523–41. https://doi.org/10.1016/j.cell.2022.05.024

[7] Chadha MS, Comer JA, Lowe L, Rota PA, Rollin PE, Bellini WJ, et al. Nipah virus-associated encephalitis outbreak, Siliguri, India. Emerg Infect Dis 2006;12:235–40. https://doi.org/10.3201/eid1202.051247

[8] Gómez Román R, Tornieporth N, Cherian NG, Shurtleff AC, L'Azou Jackson M, Yeskey D, et al. Medical countermeasures against henipaviruses: a review and public health perspective. Lancet Infect Dis 2022;22:e13–27. https://doi.org/10.1016/s1473-3099(21)00400-x

[9] Isaacs A, Low YS, Macauslane KL, Seitanidou J, Pegg CL, Cheung STM, et al. Structure and antigenicity of divergent Henipavirus fusion glycoproteins. Nat Commun 2023;14:3577. https://doi.org/10.1038/s41467-023-39278-8

[10] Guo Y, Wu S, Li W, Yang H, Shi T, Ju B, et al. The cryo-EM structure of homotetrameric attachment glycoprotein from langya henipavirus. Nat Commun 2024;15:812. https://doi.org/10.1038/s41467-024-45202-5

[11] Thien DH, Tran HB, Uyen NNP, Thao HLP, Tam HTM, Quan NK, et al. A comprehensive review of Langya virus and framework for future zoonotic disease control. Rev Med Virol 2024;34:e2520. https://doi.org/10.1002/rmv.2520

[12] Kockler ZW, Gordenin DA. From RNA World to SARS-CoV-2: The Edited Story of RNA Viral Evolution. Cells 2021;10. https://doi.org/10.3390/cells10061557

[13] Sofyantoro F, Frediansyah A, Priyono DS, Putri WA, Septriani NI, Wijayanti N, et al. Growth in chikungunya virus-related research in ASEAN and South Asian countries from 1967 to 2022 following disease emergence: a bibliometric and graphical analysis. Glob Health 2023;19:9. https://doi.org/10.1186/s12992-023-00906-z

[14] Xavier-Santos D, Padilha M, Fabiano GA, Vinderola G, Gomes Cruz A, Sivieri K, et al. Evidences and perspectives of the use of probiotics, prebiotics, synbiotics, and postbiotics as adjuvants for prevention and treatment of COVID-19: A bibliometric analysis and systematic review. Trends Food Sci Technol 2022;120:174–92. https://doi.org/10.1016/j.tifs.2021.12.033

[15] Sweileh WM. Global research activity on mathematical modeling of transmission and control of 23 selected infectious disease outbreak. Glob Health 2022;18:4. https://doi.org/10.1186/s12992-022-00803-x

[16] Zhang MD, Huang WY, Luo JY, He RQ, Huang ZG, Li JD, et al. The 'whole landscape' of research on systemic sclerosis over the past 73 years. Autoimmun Rev 2024;23:103538. https://doi.org/10.1016/j.autrev.2024.103538

[17] Nath RD, Chowdhury MAF. Shadow banking: a bibliometric and content analysis. Financ Innov 2021;7:68. https://doi.org/10.1186/s40854-021-00286-6

[18] van Eck NJ, Waltman L. Software survey: VOSviewer, a computer program for bibliometric mapping. Scientometrics 2010;84:523–38. https://doi.org/10.1007/s11192-009-0146-3

[19] Sabe M, Pillinger T, Kaiser S, Chen C, Taipale H, Tanskanen A, et al. Half a century of research on antipsychotics and schizophrenia: A scientometric study of hotspots, nodes, bursts, and trends. Neurosci Biobehav Rev 2022;136:104608. https://doi.org/10.1016/j.neubiorev.2022.104608

[20] Cortese S, Sabé M, Chen C, Perroud N, Solmi M. Half a century of research on Attention-Deficit/Hyperactivity Disorder: A scientometric study. Neurosci Biobehav Rev 2022;140:104769. https://doi.org/10.1016/j.neubiorev.2022.104769

[21] Sabé M, Sulstarova A, Chen C, Hyde J, Poulet E, Aleman A, et al. A century of research on neuromodulation interventions: A scientometric analysis of trends and knowledge maps. Neurosci Biobehav Rev 2023;152:105300. https://doi.org/10.1016/j.neubiorev.2023.105300

[22] Chua KB, Bellini WJ, Rota PA, Harcourt BH, Tamin A, Lam SK, et al. Nipah virus: a recently emergent deadly paramyxovirus. Science 2000;288:1432–5. https://doi.org/10.1126/science.288.5470.1432

[23] Singh RK, Dhama K, Chakraborty S, Tiwari R, Natesan S, Khandia R, et al. Nipah virus: epidemiology, pathology, immunobiology and advances in diagnosis, vaccine designing and control strategies - a comprehensive review. Vet Q 2019;39:26–55. https://doi.org/10.1080/01652176.2019.1580827

[24] Devnath P, Wajed S, Chandra Das R, Kar S, Islam I, Masud H. The pathogenesis of Nipah virus: A review. Micro Pathog 2022;170:105693. https://doi.org/10.1016/j.micpath.2022.105693

[25] Eaton BT, Broder CC, Middleton D, Wang LF. Hendra and Nipah viruses: different and dangerous. Nat Rev Microbiol 2006;4:23–35. https://doi.org/10.1038/nrmicro1323

[26] Mahalingam S, Herrero LJ, Playford EG, Spann K, Herring B, Rolph MS, et al. Hendra virus: an emerging paramyxovirus in Australia. Lancet Infect Dis 2012;12:799–807. https://doi.org/10.1016/s1473-3099(12)70158-5

[27] Gazal S, Sharma N, Gazal S, Tikoo M, Shikha D, Badroo GA, et al. Nipah and Hendra Viruses: Deadly Zoonotic Paramyxoviruses with the Potential to Cause the Next Pandemic. Pathogens 2022;11. https://doi.org/10.3390/pathogens11121419

[28] Alam AM. Nipah virus, an emerging zoonotic disease causing fatal encephalitis. Clin Med (Lond) 2022;22:348–52. https://doi.org/10.7861/clinmed.2022-0166

[29] Li H, Kim JV, Pickering BS. Henipavirus zoonosis: outbreaks, animal hosts and potential new emergence. Front Microbiol 2023;14:1167085. https://doi.org/10.3389/fmicb.2023.1167085

[30] Choudhary OP, Priyanka, Fahrni ML, Metwally AA, Saied AA. Spillover zoonotic 'Langya virus': is it a matter of concern? Vet Q 2022;42:172–4. https://doi.org/10.1080/01652176.2022.2117874

[31] Update: outbreak of Nipah virus–Malaysia and Singapore, 1999. MMWR Morb Mortal Wkly Rep 1999;48:335–7.

[32] Outbreak of Hendra-like virus–Malaysia and Singapore, 1998-1999. MMWR Morb Mortal Wkly Rep 1999;48:265–9.

[33] Hsu VP, Hossain MJ, Parashar UD, Ali MM, Ksiazek TG, Kuzmin I, et al. Nipah virus encephalitis reemergence, Bangladesh. Emerg Infect Dis 2004;10:2082–7. https://doi.org/10.3201/eid1012.040701

[34] Nikolay B, Salje H, Hossain MJ, Khan A, Sazzad HMS, Rahman M, et al. Transmission of Nipah Virus - 14 Years of Investigations in Bangladesh. N Engl J Med 2019;380:1804–14. https://doi.org/10.1056/NEJMoa1805376

[35] Playford EG, Munro T, Mahler SM, Elliott S, Gerometta M, Hoger KL, et al. Safety, tolerability, pharmacokinetics, and immunogenicity of a human monoclonal antibody targeting the G glycoprotein of henipaviruses in healthy adults: a first-in-human, randomised, controlled, phase 1 study. Lancet Infect Dis 2020;20:445–54. https://doi.org/10.1016/s1473-3099(19)30634-6

[36] Montgomery JM, Hossain MJ, Gurley E, Carroll GD, Croisier A, Bertherat E, et al. Risk factors for Nipah virus encephalitis in Bangladesh. Emerg Infect Dis 2008;14:1526–32. https://doi.org/10.3201/eid1410.060507

[37] Goldsmith CS, Ksiazek TG, Rollin PE, Comer JA, Nicholson WL, Peret TC, et al. Cell culture and electron microscopy for identifying viruses in diseases of unknown cause. Emerg Infect Dis 2013;19:886–91. https://doi.org/10.3201/eid1906.130173

[38] Sejvar JJ, Hossain J, Saha SK, Gurley ES, Banu S, Hamadani JD, et al. Long-term neurological and functional outcome in Nipah virus infection. Ann Neurol 2007;62:235–42. https://doi.org/10.1002/ana.21178

[39] Arunkumar G, Devadiga S, McElroy AK, Prabhu S, Sheik S, Abdulmajeed J, et al. Adaptive Immune Responses in Humans During Nipah Virus Acute and Convalescent Phases of Infection. Clin Infect Dis 2019;69:1752–6. https://doi.org/10.1093/cid/ciz010

[40] Welch SR, Spengler JR, Genzer SC, Coleman-McCray JD, Harmon JR, Sorvillo TE, et al. Single-dose mucosal replicon-particle vaccine protects against lethal Nipah virus infection up to 3 days after vaccination. Sci Adv 2023;9:eadh4057. https://doi.org/10.1126/sciadv.adh4057

[41] Lo MK, Feldmann F, Gary JM, Jordan R, Bannister R, Cronin J, et al. Remdesivir (GS-5734) protects African green monkeys from Nipah virus challenge. Sci Transl Med 2019;11. https://doi.org/10.1126/scitranslmed.aau9242

[42] Marsh GA, Wang LF. Hendra and Nipah viruses: why are they so deadly? Curr Opin Virol 2012;2:242–7. https://doi.org/10.1016/j.coviro.2012.03.006

[43] Broder CC, Xu K, Nikolov DB, Zhu Z, Dimitrov DS, Middleton D, et al. A treatment for and vaccine against the deadly Hendra and Nipah viruses. Antivir Res 2013;100:8–13. https://doi.org/10.1016/j.antiviral.2013.06.012

[44] Irving AT, Ahn M, Goh G, Anderson DE, Wang LF. Lessons from the host defences of bats, a unique viral reservoir. Nature 2021;589:363–70. https://doi.org/10.1038/s41586-020-03128-0

[45] Woolsey C, Borisevich V, Fears AC, Agans KN, Deer DJ, Prasad AN, et al. Recombinant vesicular stomatitis virus-vectored vaccine induces long-lasting immunity against Nipah virus disease. J Clin Invest 2023;133. https://doi.org/10.1172/jci164946

[46] Bossart KN, Zhu Z, Middleton D, Klippel J, Crameri G, Bingham J, et al. A neutralizing human monoclonal antibody protects against lethal disease in a new ferret model of acute nipah virus infection. PLoS Pathog 2009;5:e1000642. https://doi.org/10.1371/journal.ppat.1000642

[47] Fahira A, Amin RS, Arshad U, Khan MI, Shah Syed AA, Alshammari A, et al. Chimeric vaccine design against the epidemic Langya Henipavirus using immunoinformatics and validation via immune simulation approaches. Heliyon 2023;9:e17376. https://doi.org/10.1016/j.heliyon.2023.e17376

[48] Wu C, Liu Y, Yang Y, Zhang P, Zhong W, Wang Y, et al. Analysis of therapeutic targets for SARS-CoV-2 and discovery of potential drugs by computational methods. Acta Pharm Sin B 2020;10:766–88. https://doi.org/10.1016/j.apsb.2020.02.008

[49] Zaib S, Akram F, Waris W, Liaqat ST, Zaib Z, Khan I, et al. Computational approaches for innovative anti-viral drug discovery using Orthosiphon aristatus blume miq against dengue virus. J Biomol Struct Dyn 2023;41:8738–50. https://doi.org/10.1080/07391102.2022.2137238

[50] Dinesh TV, Malgija B, Ponraj MR, Muralakar P, Thathapudi JJ, Kandasamy R, et al. Design of novel pyrimidine based remdesivir analogues with dual target specificity for SARS CoV-2: A computational approach. Int J Biol Macromol 2023;242:124443. https://doi.org/10.1016/j.ijbiomac.2023.124443

[51] Ahmad S, Nazarian S, Alizadeh A, Pashapour Hajialilou M, Tahmasebian S, Alharbi M, et al. Computational design of a multi-epitope vaccine candidate against Langya henipavirus using surface proteins. *J Biomol Struct Dyn*: 1-18 2023. https://doi.org/10.1080/07391102.2023.2258403

[52] Priyanka, Chopra H, Choudhary OP. mRNA vaccines as an armor to combat the infectious diseases. Travel Med Infect Dis 2023;52:102550. https://doi.org/10.1016/j.tmaid.2023.102550

[53] Priyanka, Abusalah MAH, Chopra H, Sharma A, Mustafa SA, Choudhary OP, et al. Nanovaccines: A game changing approach in the fight against infectious diseases. Biomed Pharm 2023;167:115597. https://doi.org/10.1016/j.biopha.2023.115597

[54] Choudhary OP, Priyanka. ChatGPT in travel medicine: A friend or foe? Travel Med Infect Dis 2023;54:102615. https://doi.org/10.1016/j.tmaid.2023.102615

[55] Moayedpour S, Broadbent J, Riahi S, Bailey M, H VT, Dobchev D, et al. Representations of lipid nanoparticles using large language models for transfection efficiency prediction. Bioinformatics 2024;40. https://doi.org/10.1093/bioinformatics/btae342

[56] Wang Q, Feng Y, Wang Y, Li B, Wen J, Zhou X, et al. AntiFormer: graph enhanced large language model for binding affinity prediction. Brief Bioinform 2024;25. https://doi.org/10.1093/bib/bbae403

[57] da Silva MK, Campos DMO, Akash S, Akter S, Yee LC, Fulco UL, et al. Advances of Reverse Vaccinology for mRNA Vaccine Design against SARS-CoV-2: A Review of Methods and Tools. Viruses 2023;15. https://doi.org/10.3390/v15102130

[58] Md Khairi LNH, Fahrni ML, Lazzarino AI. The Race for Global Equitable Access to COVID-19 Vaccines. Vaccin (Basel) 2022;10. https://doi.org/10.3390/vaccines10081306

[59] de Wit E, Prescott J, Falzarano D, Bushmaker T, Scott D, Feldmann H, et al. Foodborne transmission of nipah virus in Syrian hamsters. PLoS Pathog 2014;10:e1004001. https://doi.org/10.1371/journal.ppat.1004001

[60] Chua KB, Goh KJ, Wong KT, Kamarulzaman A, Tan PS, Ksiazek TG, et al. Fatal encephalitis due to Nipah virus among pig-farmers in Malaysia. Lancet 1999;354:1257–9. https://doi.org/10.1016/s0140-6736(99)04299-3

[61] Wong KT, Shieh WJ, Kumar S, Norain K, Abdullah W, Guarner J, et al. Nipah virus infection: pathology and pathogenesis of an emerging paramyxoviral zoonosis. Am J Pathol 2002;161:2153–67. https://doi.org/10.1016/s0002-9440(10)64493-8

[62] Wong KT, Robertson T, Ong BB, Chong JW, Yaiw KC, Wang LF, et al. Human Hendra virus infection causes acute and relapsing encephalitis. Neuropathol Appl Neurobiol 2009;35:296–305. https://doi.org/10.1111/j.1365-2990.2008.00991.x

[63] Choudhary P, Shafaati M, Abu Salah MAH, Chopra H, Choudhary OP, Silva-Cajaleon K, et al. Zoonotic diseases in a changing climate scenario: Revisiting the interplay between environmental variables and infectious disease dynamics. Travel Med Infect Dis 2024;58:102694. https://doi.org/10.1016/j.tmaid.2024.102694