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REVIEW

Global Trends in MPOX Research (2014–2025): A Bibliometric Analysis and Overview

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Abstract: The 2022 global monkeypox outbreak fuelled a surge in related research. In this study, a bibliometric analysis of 2,076 monkeypox-related articles indexed in the Web of Science Core Collection (from January 2014 to June 2025) was performed, and VOSviewer was used to visualize keyword co-occurrence networks and collaboration patterns among countries and institutions. Unlike existing studies, the latest data for 2024–2025 are incorporated; postoutbreak research trends, collaborative patterns, and PHEIC-driven resource aggregation effects are systematically incorporated; and gaps in dynamic and multifaceted analyses of the field are addressed. The results revealed a three-stage global research output: low accumulation (2014–2021), a sharp surge after 2022, and sustained high levels after a peak in 2023. The core research clusters focused on viral transmission dynamics and clinical interventions. Country contributions showed a pyramidal hierarchy, with the US leading, followed by China, India, and Saudi Arabia; government health agencies and academic institutions codominated collaborations. The findings confirm the role of the PHEIC in concentrating scientific resources, emphasizing the importance of strengthening international collaboration to address future epidemic challenges.

Keywords: MPOX, VOSviewer, co-occurrence networks, countries, institutions, outbreaks, bibliometric analysis, public health emergency

Introduction

Monkeypox (MPOX) infection, caused by the monkeypox virus (MPXV), is a zoonotic disease.[1] MPXV was first isolated in 1958 from crab-eating macaques in a research facility in Denmark.[2] The first human MPOX case was diagnosed in 1970 in a 9-month-old boy in the Democratic Republic of the Congo[3]—a country recognized as one of the core endemic regions for MPXV, alongside other Central and West African nations. Since 1970, human MPX cases have been formally documented in 11 countries in Africa, specifically Benin, Cameroon, the Central African Republic, Cote d' lvoire, the DRC, Gabon, Liberia, Nigeria, the Republic of the Congo, Sierra Leone and South Sudan.[4] Historically, the majority of reported human MPOX cases occurred in these African regions, with the first outbreak outside Africa emerging in the United States in 2003.[5] Following the reporting of the first MPOX case in the UK in May 2022, the MPOX outbreak evolved into a widespread global epidemic across multiple regions.[6] Owing to its rapid geographic expansion and increasing case numbers, the World Health Organization (WHO) declared MPOX a public health emergency of international concern (PHEIC) on 23 July 2022.[7] As of 31 July 2024, global surveillance systems have documented 102,997 human MPXV infections and 223 associated fatalities since the first human case was identified in 1970, reflecting the persistent public health burden posed by this pathogen over five decades of continuous circulation.[8] Notably, MPXV exhibits distinct genetic divergence, with two discrete clades responsible for driving outbreaks across Africa: the Central African (Congo Basin) clade and the West African clade. The Central African clade is associated with heightened virulence, featuring a reported case fatality rate (CFR) of 10%–11%, whereas the West African clade is less pathogenic, with a CFR ranging from 1% to 4%.[4] This clade-specific variation in pathogenicity has substantial implications for outbreak response and clinical management strategies. Although existing studies have advanced our

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understanding of the biological properties, epidemiological dynamics, and clinical care protocols of MPXV, few bibliometric investigations have focused specifically on MPOX. That said, bibliometric methodologies have been employed by researchers to analyse research progress in the field of analogous zoonotic viruses—most prominently COVID-19—wherein publication trends, interinstitutional collaboration networks, and emerging research hotspots have been explored.

MPXV is a member of the genus *Orthopoxvirus* within the family *Poxviridae*. The family *Poxviridae* comprises two subfamilies, the *Entomopoxvirinae* and the *Chordopoxvirina*e.[9] Within *Chordopoxvirinae*, viruses from four genera are known to cause human disease. Among these, the genera *Orthopoxvirus, Parapoxvirus*, and *Yatapoxviru*s have zoonotic potential.[10] The genus *Orthopoxvirus* notably includes four viruses that are pathogenic to humans, namely, MPXV, the variola virus (VARV, a causative agent of smallpox), the vaccinia virus (VACV, used historically in the smallpox vaccine), and the cowpox virus (CPXV). While generally rare, MPOX is a potentially severe disease.[11] MPXV infection shares similarities with smallpox infection in terms of clinical presentation (including the characteristic rash), lesion distribution, and disease progression.[12] These challenges are further exacerbated by restricted access to advanced diagnostic tools in endemic regions, nonspecific early manifestations—including fever and lymphadenopathy—that mimic other febrile conditions such as chickenpox and malaria, and inadequate laboratory capacity for confirmatory testing (notably polymerase chain reaction) in resource-limited settings.[4] Such constraints impede the timely identification of cases and compromise effective outbreak control. Disease severity is correlated with patient age and comorbidities, with reported case fatality rates reaching 11% and the highest risk observed in young children.[4,11] Currently, there is no specific vaccine approved solely for MPXV.[13,14] Consequently, patients infected with MPXV are treated with therapeutics originally developed for smallpox, although the efficacy of historically used smallpox vaccines against MPXV is limited.[15] The sustained global spread of monkeypox has led to substantial public health concerns and has spurred intensive research efforts worldwide, necessitating the synthesis of the burgeoning body of MPOX-related literature. Notably, bibliometric visualization tools—including VOSviewer—play a pivotal role in guiding future research directions: By converting fragmented literature data into intuitive networks, such as keyword co-occurrence maps or institutional collaboration diagrams, these tools empower researchers to rapidly identify research hotspots, uncover collaborative gaps, and prioritize understudied areas—thereby bridging the gap between raw literature data and evidence-based research planning. Integrating insights related to such tools into the framework of the current study serves to more closely align the research background with its methodology, providing a robust rationale for the adoption of visualization-driven bibliometric analysis.

This study conducted a comprehensive analysis of monkeypox-related research literature published between January 2014 and June 2025. To ensure clarity, the key objectives of the study are explicitly outlined as follows: 1) Analysing publication trends of MPOX-related literature over the study period, including annual publication volume and core source journals; 2) Exploring collaboration patterns among countries, institutions, and authors in the MPOX research field; and 3) Identifying keyword clusters to reveal research hotspots and evolutionary trends in MPOX studies.

By utilizing bibliometric visualization techniques, specifically focusing on keywords and source information, we constructed annual publication timelines and keyword, country, institutional, and author co-occurrence network maps. These visualizations provide an intuitive representation of the research dynamics and collaborative trends in monkeypox research over the past decade (from January 2014 to June 2025).

Materials and Methods

Data Source and Search Strategy

This bibliometric analysis utilized the Web of Science (WoS) Core Collection as the primary data source. Owing to its comprehensive interdisciplinary coverage, advanced citation analysis functionalities, and compatibility with bibliometric tools such as VOSviewer and R packages Bibliometrix/Biblioshiny, which enable robust network visualization and trend analysis, the WoS database was selected over alternative platforms, including Scopus and PubMed.

To identify relevant publications in the mpox (monkeypox) research field, a comprehensive search was performed using the following author keywords: “MPOX,” “MPXV,” “monkeypox,” or “monkeypox virus.” The search strategy

was applied to the WoS Core Collection database, with the time span set from January 2014 to June 2025 (H1). The retrieved records were exported in plain text format with full records and cited references for subsequent analysis.

Eligibility Criteria

Publications were selected on the basis of the following criteria: 1) Document type: Articles and Review Articles were included. Other document types, such as letters, editorial materials, early access, proceedings papers, and meeting abstracts, were excluded. 2) Language: Only English-language publications were included. 3) Time frame: The publication dates ranged from January 2014 to June 2025 (H1). 4) Thematic focus: The explicit thematic focus was mpox. The requisite thematic focus encompassed aspects such as clinical presentations, diagnostic methods, epidemiological features, viral evolution patterns, pathogenicity mechanisms, and prevention/control measures, including vaccine research. The explicit exclusions included all nonresearch outputs and retracted publications. The eligible records were exported in a plain text file with the full record content archived. The PRISMA flowchart outlining the identification, screening, eligibility, and inclusion process is presented in Figure 1.

Data Processing and Network Visualization for Literature Metrics

Data processing and analysis in this study were executed primarily through VOSviewer software by using the exported full-record literature data.[16] The annual publication volumes, spanning from January 2014 to June 2025 (H1), were first quantified and visualized via GraphPad Prism 9 software. Following data cleaning and optimization, default software parameters were implemented as follows: a frequency threshold of ≥5 occurrences was applied for high-frequency keywords, while a minimum output threshold of ≥5 publications was set for institutions and countries/regions. On the basis of the standardized dataset, four key networks were constructed and visualized: 1) a keyword co-occurrence network, 2) an international collaboration network, 3) an interinstitutional collaboration network, and 4) a researcher coauthorship network. These networks distinctly demonstrated the distribution patterns of prevalent terminology, current research hotspots, dominant trends in transnational collaboration, and institutional cooperation intensity patterns. Within the network diagrams, the node sizes are positively correlated with the occurrence frequency of represented elements across the literature corpus. Lines connecting nodes denote specific relationships between elements, with contextual interpretation determined by the network type. In keyword co-occurrence networks, lines indicate co-occurrence patterns within research contexts, whereas in national/institutional collaboration networks, lines explicitly represent the academic collaborative strength between entities.[17,18]

Results

Annual Trends Reveal Epidemic-Driven Research Patterns

A total of 2,076 publications meeting the screening criteria were included for subsequent analysis. The temporal distribution of the publications intuitively maps the trajectory of the evolution of the global epidemic, with research

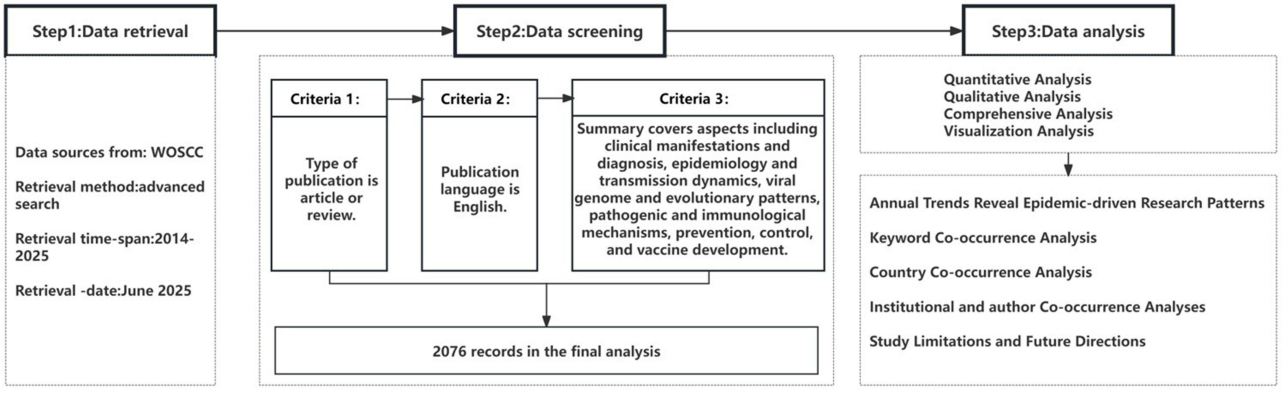

Figure 1 Flow chart of the inclusion and exclusion criteria.

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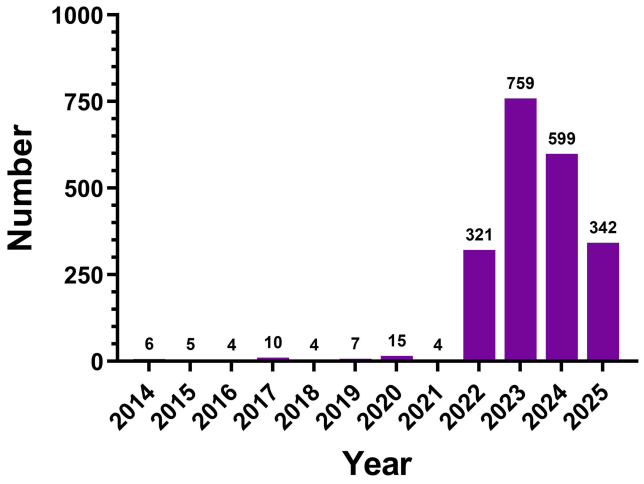

Figure 2 The numbers of published studies on MPOX from 2014 to 2025.

activity nearly stagnating between 2014 and 2021 (with only 55 publications recorded). In 2022, a sudden outbreak event triggered a surge in publications to 321, which exceeded the total of the previous eight years. The number of publications peaked at a historically high level of 759 in 2023 and slightly decreased to 599 in 2024. The first half of 2025 still had 342 papers published, which is significantly greater than the preoutbreak baseline (Figure 2). This three-phase "dormant–surged–plateaued" curve demonstrates the siphoning effect of public health emergencies on scientific research resources.

Practically, this insight informs policymakers and funding agencies on resource allocation: During postoutbreak "plateau" phases—such as 2024–2025—sustained investment in MPXV research is critical to prevent a regression to the pre-2022 "dormant" state, particularly for long-term research themes including viral evolution and zoonotic spillover monitoring. For global health authorities, the trend also underscores the necessity of establishing proactive rather than reactive research frameworks to prepare for potential MPXV resurgences.

Keyword Co-Occurrence Analysis

Keyword co-occurrence network analysis revealed that "monkeypox" (1,005 occurrences), "MPOX" (702 occurrences) and "monkeypox virus" (543 occurrences) dominated the network. Clustering revealed two primary research directions. The first direction focuses on viral transmission and pathogenesis, with high-frequency terms "virus" (235), "infection" (194), "outbreak" (170), and "transmission" (118) indicating studies in epidemiology (96) and evolutionary dynamics. The second direction emphasizes clinical treatment and vaccine development. The strong association of "HIV" (169) highlights the priority for protecting immunocompromised populations, whereas "smallpox" (143) and "vaccinia virus" (94) reflect investigations into MPOX pathogenesis and predictive models. Terms such as "vaccine" (82), "disease" (77), and "tecovirimat" (84) underscore the urgency of vaccine prevention and clinical interventions (Figure 3 and Table 1).

These findings have clear practical implications for multiple stakeholders: For clinicians and public health practitioners, the emphasis on "HIV" and "immunocompromised populations" reinforces the need for targeted screening and treatment protocols tailored to high-risk groups. For pharmaceutical authorities, the prominence of "vaccine" and "tecovirimat" signals sustained demand for advancing these interventions—particularly for viral variants that may diminish the efficacy of existing therapeutics. From a forwards-looking perspective, gaps in keyword frequency—such as limited terms related to paediatric cases or African regional transmission—highlight future research priorities: strengthening investigations into age-specific clinical outcomes and region-adapted prevention strategies to address underrepresented areas.

Country Co-Occurrence Analysis

The national research output has a three-tier pyramid structure. The United States is the main leader, with 522 publications (25.1% of the total). China (386 publications, 18.6%), India (214 publications), and Saudi Arabia (183

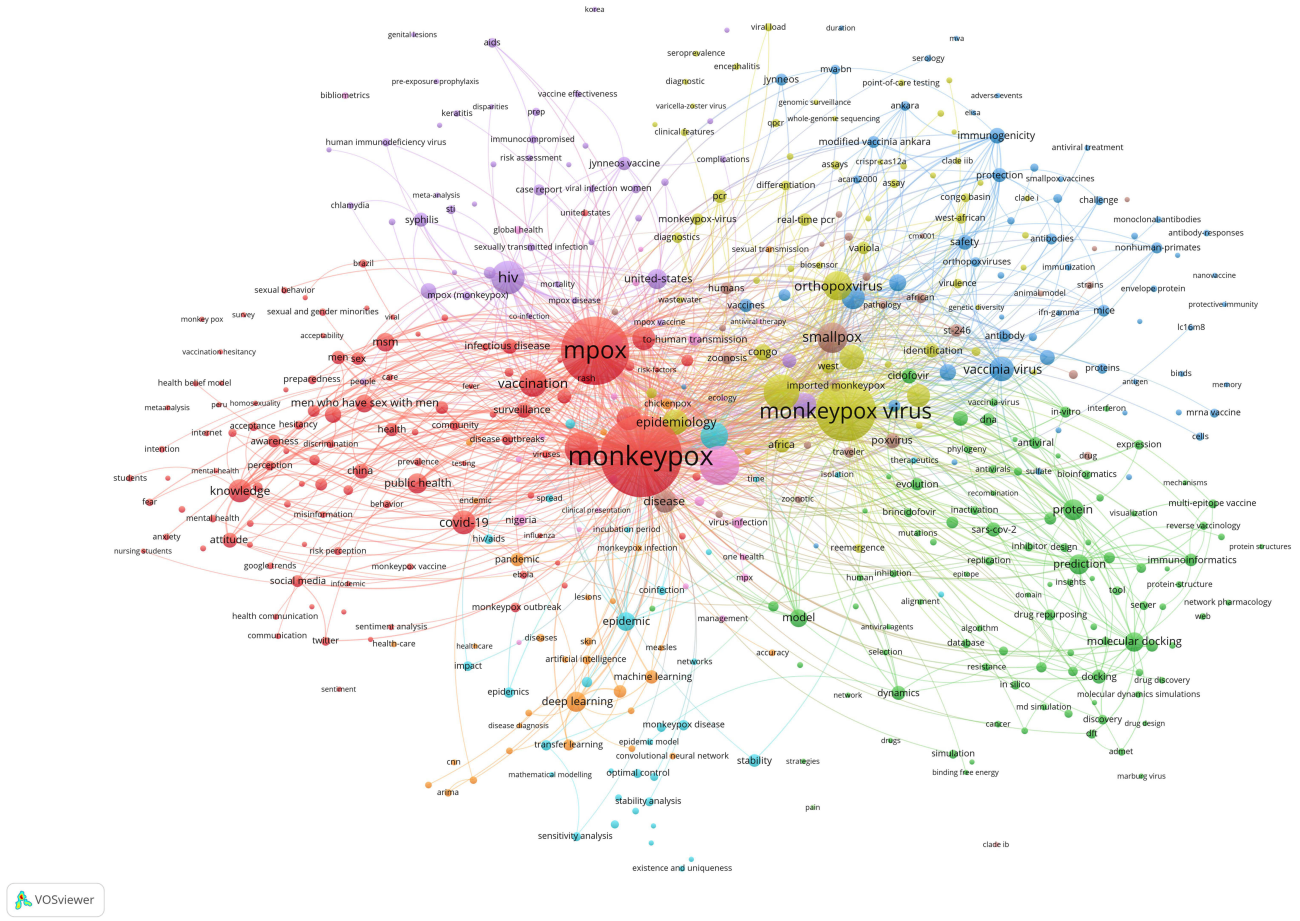

Figure 3 Visualization of the keyword co-occurrence network in monkeypox virus research, 2014–2025 (H1).

publications) form a second dominant tier (collectively 37.7%). Countries such as England (120), Italy (115), Spain (101), Pakistan (92), Germany (85), Nigeria (75), Canada (72), France (70), Egypt (68), Brazil (63), and Australia (60) constitute a broad participation tier (in aggregate 44.4%) (Figure 4 and Table 2).

This tiered structure provides actionable guidance for international collaboration: Global health authorities can leverage the leading research output of the US and China to coordinate multicentre initiatives—such as vaccine trials—while investing in capacity building for the "broad participation tier", particularly African nations, including Nigeria (a key MPXV-endemic region) and Egypt. Strengthening regional research in Africa not only addresses the imbalance in the

Table 1 Rank of the Keyword Co-Occurrence in Monkeypox Virus Research, 2014–2025 (H1)

Research Directions	Rank	Keywords	Counts
Viral transmission and pathogenesis	1	Virus	235
	2	Infection	194
	3	Outbreak	170
	4	Transmission	118
	5	Epidemiology	96

(*Continued*)

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Table 1 (Continued).

Research Directions	Rank	Keywords	Counts
Clinical treatment and vaccine development	1	HIV	169
	2	Smallpox	143
	3	Vaccinia virus	94
	4	Tecovirimat	84
	5	Vaccine	82
	6	Disease	77

current collaborative pyramid but also enhances on-the-ground surveillance for zoonotic spillover, a critical forwards-looking objective. For funding agencies, supporting cross-tier partnerships—for instance, pairing US institutions with Nigerian researchers—can expedite knowledge translation to endemic regions.

Institutional and Author Co-Occurrence Analyses

Research institutions comprise two dominant cohorts. Governmental health systems are dominated by the Centers for Disease Control and Prevention (CDC, US) (42 publications) and Japan's Ministry of Health, Labour and Welfare (41 publications). Academic institutions include King Saud University (49 publications), the Chinese Academy of Sciences (38 publications), Peking University (25 publications), the University of Chinese Academy of Sciences (24 publications), Sun Yat-sen University (24 publications), and Emory University (22 publications) (Figure 5 and Table 3).

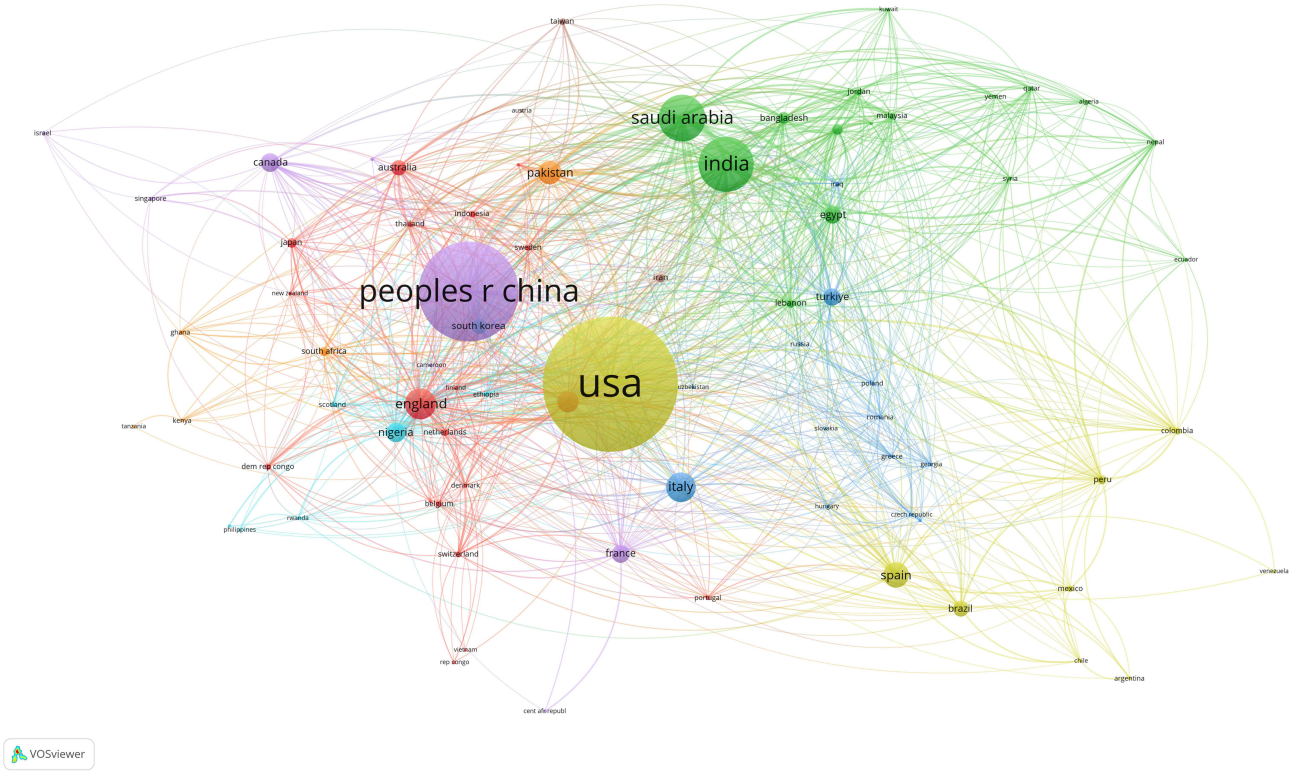

Figure 4 Visualization of the country co-occurrence network in monkeypox virus research, 2014–2025 (H1).

Table 2 Rank and Proportion of Country Co-Occurrences in Monkeypox Virus Research, 2014–2025 (H1)

Rank	Country	Counts	Proportion
1	The United States	522	25.10%
2	China	386	18.60%
3	India	214	37.70%
4	Saudi Arabia	183	
5	England	120	44.40%
6	Italy	115	
7	Spain	101	
8	Pakistan	92	
9	Germany	85	
10	Nigeria	75	
11	Canada	72	
12	France	70	
13	Egypt	68	
14	Brazil	63	
15	Australia	60	

Among the researcher clusters, the top three are Fabrizio Maggi (18 publications), Enrico Girardi (15 publications), and Valentina Mazzotta (15 publications). The next 10 scholars include Andrea Antinori, Kuldeep Dhama, Xiao Li, Min Liu, Ranjit Sah, Wenjie Tan, Chiranjib Chakraborty, Giulia Matusali, Emanuele Nicastri, and Silvia Nozza, who published 14, 13, 12, 12, 12, 12, 11, 11, 11 and 11 papers, respectively (Figure 6 and Table 4).

Practically, this analysis assists stakeholders in identifying key partners for collaborative initiatives: Policymakers aiming to develop evidence-based guidelines can engage leading institutions—such as the US CDC (for epidemiological data) or the Chinese Academy of Sciences (for vaccine research). For early-career researchers, collaborating with top scholars—including Fabrizio Maggi in clinical management or Kuldeep Dhama in viral pathogenesis—can accelerate advancements in understudied areas. Looking forward, fostering partnerships between governmental health systems (notably the US CDC) and academic institutions in low-resource regions can bridge the gap between research and on-the-ground implementation.

Discussion

This study employed tools such as VOSviewer to visualize bibliometric data from 2,076 publications. Through quantitative, qualitative, and integrative methodologies, the current status and trends in the field of monkeypox (MPOX) research were systematically evaluated.

Trends in the Field of Monkeypox Research

The transition of MPXV infection from a regional zoonosis to a global public health threat exemplifies the archetypal evolutionary trajectory of emerging infectious diseases in the era of globalization. The intercontinental spread of clade IIb in 2022, which was facilitated by transmission networks within communities of men who have sex with men (MSM),

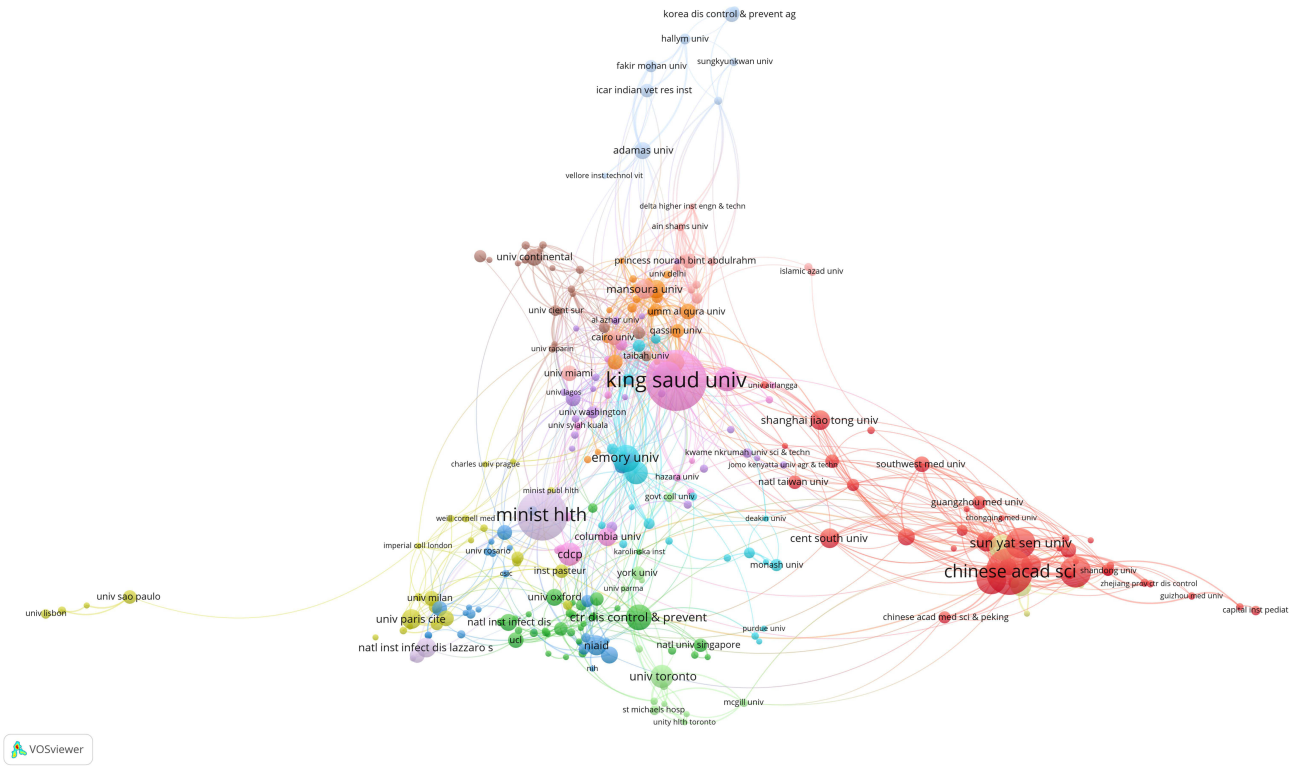

Figure 5 Visualization of the institutional co-occurrence network in monkeypox virus research, 2014–2025 (H1).

provided the first definitive evidence that MPXV could achieve sustained human-to-human transmission without the need for animal host intermediaries.[19] Concurrently, the 2023 outbreak of clade IIb in the Democratic Republic of the Congo (DRC) further revealed the evolutionary potential of the virus.[20] This outbreak resulted in a distinct shift in demographic distribution, with more than 50% of cases occurring in females—a notable contrast to the 2022 global epidemic, during which 98% of cases occurred in males.[21] MPXV transmission occurs through multiple pathways, including sexual contact (particularly among MSM), vertical mother-to-child transmission, and close household contact. Furthermore, its zoonotic nature enables spillover from natural reservoirs, such as rodents. Critically, viral genomic mutations (eg,

Table 3 Rank of the Institutional Co-Occurrence in Monkeypox Virus Research, 2014–2025 (H1)

Research Institutions	Rank	Institutional	Counts
Governmental health systems	1	Centers for Disease Control and Prevention	42
	2	Japan's Ministry of Health, Labour and Welfare	41
Academic institutions	1	King Saud University	49
	2	Chinese Academy of Sciences	38
	3	Peking University	25
	4	University of Chinese Academy of Sciences	24
	5	Sun Yat-sen University	24
	6	Emory University	22

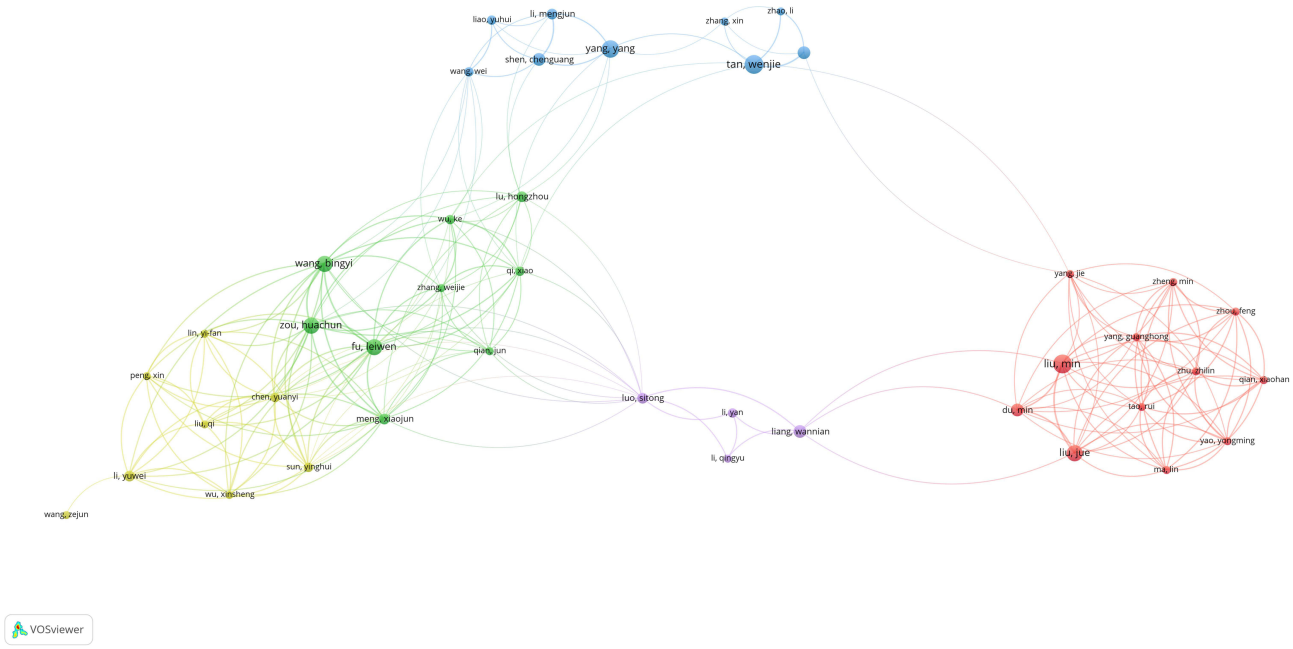

Figure 6 Visualization of the author co-occurrence network in monkeypox virus research, 2014–2025 (H1).

APOBEC3-driven mutations) coupled with diverse transmission routes collectively amplify the complexity of epidemic containment and control measures.[22]

Unlike most DNA viruses, MPXV uniquely completes its entire replication cycle independently within the cytoplasm, markedly reducing its reliance on host cell organelles.[23] Crucially, its genome exhibits functional compartmentalization,

Table 4 Rank of the Author Co-Occurrence in Monkeypox Virus Research, 2014–2025 (H1)

Rank	Author	Counts
1	Fabrizio Maggi	18
2	Enrico Girardi	15
3	Valentina Mazzotta	15
4	Andrea Antinori	14
5	Kuldeep Dhama	13
6	Xiao Li	12
7	Min Liu	12
8	Ranjit Sah	12
9	Wenjie Tan	12
10	Chiranjib Chakraborty	11
11	Giulia Matusali	11
12	Emanuele Nicastri	11
13	Silvia Nozza	11

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with conserved central genes maintaining core replication functions and terminal genes undergoing high-frequency mutations to adapt to host immune pressures.[24] Mutations mediated by APOBEC3 deaminase, identified in clade IIb, exemplify this adaptive strategy.[22] These mutations may not only increase human-to-human transmissibility but also generate variations, posing a risk of false-negative results with existing diagnostic assays.[25] This evolutionary strategy enables MPXV to overcome ecological niche constraints. Following its cross-species jump from African rodents to humans, the virus established transmission foci in nonendemic regions within only three years. This rate drastically exceeds the predicted evolutionary rate of orthopoxviruses, which is historically estimated at 6–12 accumulated SNPs per year.[26]

Significant disparities in susceptibility and clinical outcomes among different population groups necessitate precise stratification of prevention and control strategies. Immunocompromised individuals: HIV-coinfected individuals account for 40–90% of global cases.[27] They frequently present with large ulcerative necrotic lesions and multisystem complications (eg, rectal bleeding and encephalitis), increasing their potential as mobile sources of transmission. Children and older adults: During clade I outbreaks, paediatric case fatality rates reached 4.6%, primarily because of the absence of vaccine protection and secondary bacterial infections.[28] Older individuals, burdened by comorbidities, exhibit heightened susceptibility to severe complications, such as pneumonia and renal failure.[29] Sexually active populations: Within the MSM community, individuals reporting high sexual activity demonstrate a 120-fold higher transmission contribution than those with low activity. Female sex workers emerged as critical transmission hubs during the clade IIb outbreak, facilitating viral introduction from animal reservoirs into community households.[20]

Bibliometric evidence indicates that research output on MPXV expanded sharply following the 2022 global outbreak. Earlier studies (2014–2019) were dominated by epidemiological observations and animal reservoir investigations, whereas post-2020 research increasingly emphasized viral evolution, genomic diversity, and vaccine development. This temporal evolution of MPXV research reflects the broader pattern observed in outbreak-driven fields—where the transition from descriptive to molecular and translational studies parallels the global escalation of the disease.

Status and Quality of Authors, Journals and Research

As the world's second-largest contributor to global monkeypox research (18.6% of the total publications), China faces unique pressure from both local transmission and cross-border importation. Imported cases were identified in Chongqing, followed by local cases in Beijing. The spread of clade IIb to neighbouring countries, such as India and Thailand, is concerning and is compounded by the uncertain seroprotection levels conferred by historical smallpox vaccination among individuals born before 1982 in China.[30] Current smallpox vaccines (JYNNEOS and ACAM2000), which rely on cross-immunity, may exhibit waning efficacy against emerging variants.[31] The Rmix6 mRNA vaccine developed by Yan Jinghua et al demonstrated breakthrough potential. Animal studies revealed 100% survival and significantly elevated IFN-γ-secreting T-cell responses ($P<0.05$), confirming that multiantigen design can activate synergistic immunity.[32]

Notably, while leading contributors to global MPXV research—including Fabrizio Maggi and Kuldeep Dhama—have garnered widespread recognition for their seminal insights into viral evolution and clinical management strategies, the discourse on research contributions would be significantly enriched by greater balance, specifically through the acknowledgement of work originating from underrepresented regions. Foremost among these is Africa, the geographical epicentre of the MPXV. African research institutions and scholars have played an indispensable role in advancing MPXV knowledge: they have spearheaded efforts to document early outbreaks—such as conducting long-term epidemiological surveillance in the Democratic Republic of the Congo (DRC)[19]—and have deepened the understanding of region-specific transmission dynamics, including zoonotic spillover events involving local rodent populations. Integrating these regional contributions not only addresses critical gaps in the global research narrative but also highlights context-specific challenges—such as restricted access to advanced diagnostic tools in rural African settings—that are paramount to developing equitable, locally adaptable prevention and control strategies.

Research Hot Spots, Frontiers, and Future Trends

A concise comparison of MPXV research trends with those of other outbreak-driven fields, particularly Ebola and COVID-19, further contextualizes the scientific significance of MPXV studies and helps delineate unique research

priorities. In parallel with COVID-19 research, MPXV-related publications experienced a rapid surge in volume following the 2022 global epidemic, with a primary focus on unravelling transmission dynamics and accelerating vaccine development.[4] However, a key distinction emerges: unlike research on COVID-19—a respiratory virus characterized by high airborne transmissibility—MPXV research has centred heavily on sexual and zoonotic transmission pathways. This focus has, in turn, driven innovations in targeted interventions for high-risk groups, such as MSM communities. In contrast to Ebola, which is constrained by limited geographic spread but marked by high mortality rates, MPXV research confronts the unique challenge of balancing long-term zoonotic surveillance (to monitor spillover from animal reservoirs) with responsive measures for sustained human-to-human transmission. Such comparisons reveal that MPXV research occupies a critical middle ground, bridging gaps between "spillover-only" pathogens (such as Ebola) and "sustained pandemic" pathogens (such as COVID-19). As a result, it offers unparalleled insights into diseases that exhibit moderate transmission potential but have substantial global public health impacts.

Beyond vaccines, critical bottlenecks persist in the global response framework, including diagnostic technology limitations and inadequate interventions targeting high-risk groups.[33] Addressing these challenges requires—as a research priority—the development of broad-spectrum diagnostic assays and community integration by establishing integrated service models that combine sexual health clinics with monkeypox screening. The rapid spread of clade IIb within MSM networks exposed blind spots in traditional epidemiological surveillance.[27,33] Concurrently, the paediatric outbreak in the DRC underscores the urgent need for enhanced school health education and subsidized family screening programs.

The evolution of monkeypox fundamentally reflects a process of mutual adaptation between the virus and human society. Globalization accelerates pathogen dispersal, deforestation increases zoonotic spillover frequency, and shifting sexual behaviours alter transmission dynamics—these converging drivers create a "perfect storm" for emerging infectious diseases. Building a resilient next-generation pandemic defence system demands the deep integration of virology, social and behavioural science, and artificial intelligence-based prediction. This approach is not only essential for combating monkeypox but also constitutes vital preparation for future zoonotic pandemics.

This study's bibliometric analysis of MPXV research (2014–2025 H1) yields critical, unique insights to guide future research directions and policymaking. First, regarding research prioritization, the analysis identifies two core clusters—viral evolution, such as APOBEC3-driven mutations, and targeted interventions, including MSM-focused prevention—and highlights understudied areas, notably regional research in Africa and paediatric case management. This guidance empowers researchers and funding agencies to allocate resources to gaps that directly address real-world challenges, such as enhancing access to diagnostics in rural African settings and refining vaccine strategies for immunocompromised populations. Second, for policymaking, the analysis clarifies the need for stratified responses: identifying high-transmission groups—including high-activity MSM and female sex workers—and the geographic spread of clade IIb to China's neighbouring countries provides evidence for targeted public health measures, such as community-based screening at sexual health clinics and cross-border surveillance collaborations. Additionally, comparing MPXV research with that of Ebola and COVID-19 highlights that MPXV's "middle-ground" transmission characteristics demand policies balancing zoonotic spillover prevention—such as rodent population monitoring—and sustained human-to-human transmission control, including vaccine rollouts for high-risk groups. By synthesizing publication trends, collaborative networks, and research hotspots, this bibliometric analysis serves as a data-driven foundation to align future MPXV research with global health needs and ensure evidence-based, adaptable policies amid the virus's evolving threat.

Strengths and Limitations

This bibliometric and qualitative synthesis provides a comprehensive overview of MPXV research trends from 2014 to mid-2025, combining publication metrics with thematic and contextual analysis. However, several limitations warrant consideration. First, the analysis relied exclusively on the Web of Science Core Collection and English-language publications, potentially omitting relevant non-English or grey literature. Second, citation-based metrics may over-represent established authors and journals while undervaluing emerging contributions from developing regions. Third, bibliometric indicators alone cannot fully capture the translational value or societal impact of individual studies.

Despite these constraints, the integration of analytical tools such as VOSviewer and GraphPad enhances methodological robustness, enabling the identification of publication dynamics, research collaborations, and thematic frontiers. Collectively, these findings provide a data-driven foundation for evidence-based policymaking and targeted funding strategies in the evolving field of monkeypox research.

Conclusion

This study systematically applied bibliometric and visualization techniques to characterize global monkeypox (MPXV) research from 2014 to mid-2025, providing the first comprehensive mapping of publication dynamics, collaboration patterns, and thematic evolution. The results demonstrate a rapid transformation of the MPXV field, with a transition from a neglected zoonotic topic to a core focus of emerging infectious disease research following the 2022–2023 outbreaks.

These findings reveal that MPXV has evolved from a regionally confined zoonosis to a globally significant pathogen, following an archetypal trajectory of infectious disease emergence in the era of globalization. The 2022 spread of clade IIb across continents—driven primarily by transmission networks among men who have sex with men (MSM)—provided compelling evidence of sustained human-to-human transmission independent of animal reservoirs. The subsequent 2023 outbreak in the Democratic Republic of the Congo (DRC) highlighted the virus's ongoing adaptive evolution, marked by APOBEC3-driven mutations and demographic shifts in infection patterns. The analysis indicates that research activity mirrors these epidemiological transitions, shifting from descriptive surveillance to molecular, genomic, and immunological studies aimed at elucidating transmission dynamics, host interactions, and therapeutic development.

Keyword co-occurrence and clustering analyses identify two dominant research axes: viral evolution and targeted interventions. Studies increasingly emphasize APOBEC3-mediated mutagenesis, vaccine optimization, and protection of high-risk populations such as MSM and immunocompromised individuals. Comparative bibliometric patterns position MPXV research between Ebola and COVID-19—balancing zoonotic surveillance and sustained human-to-human transmission control. Future frontiers include the development of broad-spectrum diagnostic platforms, improved community screening systems integrated with sexual health services, and refined vaccine formulations that maintain efficacy against emerging viral variants.

This bibliometric and qualitative synthesis provides a robust, data-driven overview of MPXV research trends; however, certain limitations remain. The analysis relied solely on the Web of Science Core Collection and English-language records, potentially excluding relevant non-English or grey literature. Moreover, citation-based metrics may disproportionately favour established scholars and institutions. Despite these constraints, the integration of VOSviewer and GraphPad software ensures analytical precision and visual clarity, enabling the identification of major publication trends, collaboration patterns, and thematic frontiers. Collectively, these findings provide an evidence-based foundation to guide policymaking, funding allocation, and future global health preparedness strategies.

Data Sharing Statement

The original contributions presented in the study are included in this article.

Author Contributions

All the authors made significant contributions to the work reported, whether in the conception, study design, execution, acquisition of data, analysis and interpretation, or in all these areas; took part in drafting, revising or critically reviewing the article; gave final approval of the version to be published; agreed on the journal to which the article has been submitted; and agree to be accountable for all aspects of the work.

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Disclosure

The authors declare that they have no competing interests in this work.

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