More mpox data are needed to better respond to the Public Health Emergency of International Concern

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On Aug 14, 2024, WHO re-declared mpox (formerly known as monkeypox) as a Public Health Emergency of International Concern (PHEIC) making it the second infectious disease that has caused two independent PHEICs in the 21st century, the first being Ebola. Monkeypox virus could be traditionally divided into three major clades based on their genetic diversity, namely clades I, IIa, and IIb.[1] A newly emerged clade of monkeypox virus, clade Ib, was considered to initiate this PHEIC[2] (not clade IIb, the causative agent responsible for the last PHEIC between 2022 and 2023).[3] Although most confirmed and suspected cases to date have been in Africa, especially in the Democratic Republic of the Congo, imported cases have been detected in Sweden and Thailand;[4] hence, mpox might re-spread globally. Since monkeypox virus clade I is typically associated with more severe clinical symptoms and a higher case fatality rate (10·6%) than clade II,[5] it also poses a higher risk to public health than the clade IIb virus. In response to the current PHEIC, rapid viral genomic sequencing in conjunction with the timely sharing of data—including but not limited to viral genome sequences and corresponding epidemiological and clinical data—are vital for assessing the epidemic trends in real time and will undoubtedly benefit the development of vaccines and the formulation of effective prevention and control policies.[6] Hence, understanding how well mpox-related data are currently shared from Africa is vitally important, and can be simply assessed by the availability and timeliness of publicly available monkeypox virus genome data from the region. By comparison with the last mpox PHEIC, we aimed to determine areas of genomic surveillance and data sharing where improvement is needed, to facilitate timely policy optimisation in the future to better respond to the current, and any future, PHEICs.

As of Aug 14, 2024, 62 complete monkeypox virus genomes

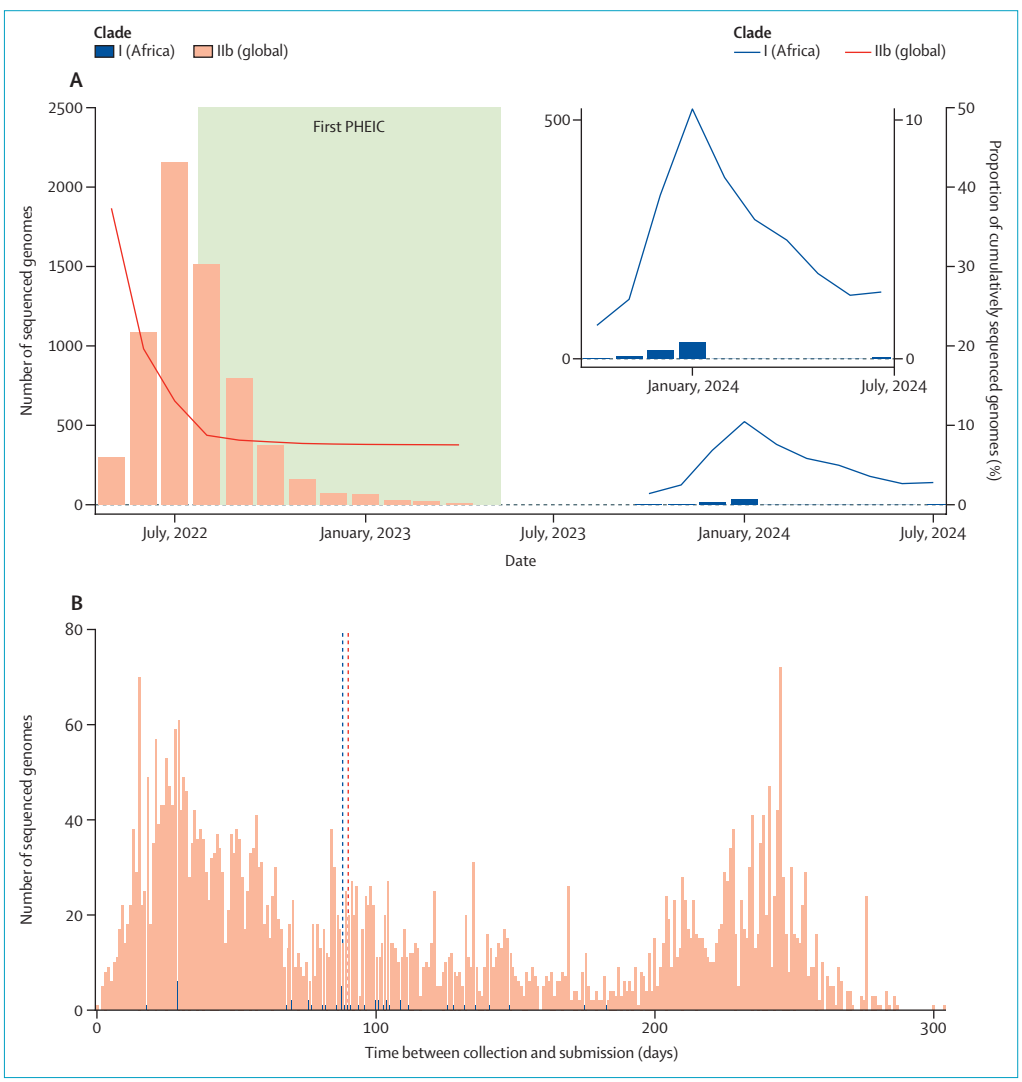

Figure: **Genomic data submitted to GISAID between two PHEICs caused by monkeypox virus**
(A) Bar plot indicates the number of publicly available monkeypox virus genomes collected in each month. Lines indicate the proportion of cumulatively sequenced monkeypox virus genomes over time, which is determined by dividing the cumulative number of publicly available monkeypox virus genome sequences up to each month by the cumulative number of confirmed cases during the same period. The box indicates the PHEIC during 2022–23. (B) Distribution of time intervals between sample collection date and submission date of genomic sequence for different monkeypox virus complete genome datasets. Dashed vertical lines indicate the median time interval for each dataset. For the clade IIb dataset, only complete genomes with submission date between the first identification of mpox in the UK (May, 2022) and the end of the first mpox PHEIC (May 11, 2023) were included (n=4753). For the clade I dataset, only complete genomes from Africa that had a collection date after October, 2023, were included (n=62). Monkeypox virus genomic sequences and associated metadata (such as collection and submission dates) to generate this figure were downloaded from GISAID on Aug 17, 2024. We used Nextclade (version 3.8.2)[7] for clade assignment. Only monkeypox virus genomes with length ≥170 kb were considered as complete genomes and were used for following statistics. For part A, to ensure we did not miss any clade I monkeypox virus genome sequences shared from Africa since October, 2023, we also checked the NCBI database using the same criteria (collection date since October, 2023) and using Nextclade for clade assignment. We then compared names of virus isolates from clade I between datasets from NCBI and GISAID to ensure that no monkeypox virus genomes belonging to clade I reported from Africa since October, 2023, were missing. All monkeypox virus complete genomes reported from Africa since October, 2023, were assigned to clade I. The number of confirmed cases per month per region was downloaded from WHO.[8] GISAID=Global Initiative on Sharing All Influenza Data. NCBI=National Center for Biotechnology Information. PHEIC=public health emergency of international concern.

For **WHO's announcement on Aug 14, 2024** see https://www.who.int/news/item/14-08-2024-who-director-general-declares-mpox-outbreak-a-public-health-emergency-of-international-concern

For the **GISAID website** see https://gisaid.org/

collected from Africa since October, 2023 (the date of the initial outbreak in the Democratic Republic of the Congo) have been made publicly available. They all belong to clade I and account for 2·8% of 2219 confirmed cases in Africa during this period. This proportion is much lower than that during the last PHEIC of clade IIb monkeypox virus (6581 genome sequences [7·5%] from 87 329 confirmed cases; figure A). Furthermore, all complete genomes for the ongoing PHEIC are from three countries, with 59 from the Democratic Republic of the Congo (with 5160 confirmed cases), and two from Uganda (with ten confirmed cases) and one from Kenya (with five confirmed cases), despite 15 African countries having reported confirmed or suspected cases of mpox since 2024.[8] Additionally, we identified a clear gap in data from Africa between February and June, 2024 (figure A), despite onward transmission of mpox during that time. The lack of adequate reporting of data during this period could be due to several reasons, for instance, insufficient awareness regarding the importance of timely data sharing, even if genomic surveillance has been conducted and relevant data have been generated. Another reason might be limited funding and related resources (eg, infrastructures and technical personnel) required for sequencing and data sharing. Yet, the few sequenced monkeypox virus genomes from Africa makes the determination of whether novel variants have emerged among these countries impossible. Despite these challenges, efforts made by clinicians, researchers, and health-care professionals in Africa on rapid sequencing and prompt data sharing merit great recognition. The median interval between sample collection and genome submission for monkeypox virus samples collected after October, 2023 in Africa is 88 days, which is even faster than the median 90-day interval observed for clade IIb monkeypox virus samples up to the end of the last PHEIC (figure B); indicative of the rapid response to the epidemic in Africa.

Given the pivotal role of the first 100 days in establishing scalable mechanisms for disease management and containment,[4] more publicly available data about epidemics could enable the scientific community to evaluate the epidemic situation in real time and thereby adjust prevention and control policies accordingly to control the epidemic and end this PHEIC as soon as possible. Failure to fill these gaps might exacerbate the risk of undetected or hidden viral transmission and the emergence of novel variants, thereby complicating efforts to mitigate the spread of mpox. Considering the numerous challenges faced by Africa (eg, large-scale infections and limited funding and infrastructure for genomic surveillance), multifaceted international support, such as funding and technical infrastructure and platforms for sequencing and data sharing, as well as professional training, are necessary. Moreover, streamlining policy barriers on timely data sharing should be prioritised where feasible.

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GFG and LW designed and coordinated the study. LW collected data, performed analysis, designed the figure, and wrote the first draft of the manuscript. GFG and LW reviewed and revised the manuscript. GFG and LW accessed and verified the underlying study data and had final responsibility for the decision to submit for publication. We declare no competing interests. All data used in this study are publicly available from the Global Initiative on Sharing All Influenza Data (GISAID) database. We thank researchers from the originating laboratories and the submitting laboratories where genetic sequence data were generated and shared via the Global Initiative on Sharing All Influenza Data and National Center for Biotechnology Information, enabling this research. This work was supported by the National Key R&D Program of China (2022YFF1203203), and the Strategic Priority Research Program of the Chinese Academy of Sciences (XDB29010202).

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1 Happi C, Adetifa I, Mbala P, et al. Urgent need for a non-discriminatory and non-stigmatizing nomenclature for monkeypox virus. *PLoS Biol* 2022; **20:** e3001769.
2 Vakaniaki EH, Kacita C, Kinganda-Lusamaki E, et al. Sustained human outbreak of a new MPXV clade I lineage in eastern Democratic Republic of the Congo. *Nat Med* 2024; published online June 13. https://doi.org/10.1038/s41591-024-03130-3.
3 Tan W, Gao GF. Neglected zoonotic monkeypox in Africa but now back in the spotlight worldwide. *China CDC Wkly* 2022; **4:** 847–48.
4 The Lancet. Mpox: the need for a coordinated international response. *Lancet* 2024; **404:** 725.
5 Bunge EM, Hoet B, Chen L, et al. The changing epidemiology of human monkeypox—a potential threat? A systematic review. *Plos Neglect Trop D* 2022; **16:** e0010141.
6 The Lancet. Genomic sequencing in pandemics. *Lancet* 2021; **397:** 445.
7 Aksamentov I, Roemer C, Hodcroft EB, Neher RA. Nextclade: clade assignment, mutation calling and quality control for viral genomes. *J Open Source Softw* 2021; **6:** 3773.
8 WHO. 2022–24 Mpox (Monkeypox) outbreak: global trends. World Health Organization, 2024. https://worldhealthorg.shinyapps.io/mpx_global/ (accessed Sept 15, 2024).

Antimicrobial resistance: now is the time to revisit global commitments

Antimicrobial resistance (AMR) and the inability to treat infections affects everyone, especially individuals in low-income and middle-income countries (LMICs) and the most vulnerable groups, such as very young children, older adults, and refugees. Effective antimicrobials are key for human and animal health and should be viewed as common global goods.

The 2024 high-level meeting on AMR in the UN General Assembly is a timely opportunity to revisit global commitments to curb the increasing resistance. We must do our best to ensure that world leaders maintain political attention on this issue and increase their efforts to counteract AMR, in response to the UN General Assembly political declaration.

For more on the **2024 high-level meeting on AMR** see https://www.who.int/news-room/events/detail/2024/09/26/default-calendar/un-general-assembly-high-level-meeting-on-antimicrobial-resistance-2024