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Recurrent Mpox: divergent virulent clades and the urgent need for strategic measures including novel vaccine development to sustain global health security

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Abstract

In August 2024, the Africa CDC and WHO declared Mpox a Public Health Emergency of Continental Security and a Public Health Emergency of International Concern, respectively, following a devastating global outbreak driven by newly emerged virulent clades I (Ia, IIb) and II (IIa, IIb) of the Mpox virus. These new clades are genetically and phylogenetically distinct from previously known strains, with the re-emerging variants originating from the Democratic Republic of the Congo (DRC) and rapidly spreading to neighbouring regions and across the globe. The ongoing epidemic is characterized by alarming morbidity and mortality, and the newly identified clades are linked to significant changes in the epidemiology of the disease, resulting in worse clinical outcomes. Sexual transmission has emerged as a key factor in sustaining the spread of the virus, particularly among sexually active young adults, facilitating the virus's spread beyond Africa. To combat the growing threat, there is an urgent need for the development of a polyvalent vaccine that incorporates the diverse circulating clades as part of other mitigation measures.. Widespread vaccination with such a vaccine could help achieve herd immunity and complement other infection prevention and control strategies to effectively mitigate the impact of this global health crisis.

Keywords Mpox, Recurrent, New, Virulent, Clades I and II, Threat, Global, Health, Security, Counter measures

Introduction

Mpox, formerly known as monkeypox is an infectious viral disease caused by monkeypox virus (MPXV). Its re-emergence poses a threat to global health [1]. It was declared a public health emergency of continental security (PHECS) and public health emergency of international concern (PHEIC) by both the Africa Centers for Disease Control and Prevention (Africa CDC) [2] and the World Health Organization (WHO) under the international health regulation (IHR) 2005 [3–5] on the 13th and 14th of August 2024. These declarations were prompted by the swift and extensive spread of highly virulent strains that emerged from previously circulating clades and showed notable human-to-human transmissibility

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[6–9]. Mpox has been classified as PHEIC by the WHO for the second time since the 2022 declaration, suggesting that the threat to global public health security has not yet been eliminated [3]. Mpox was first found in the DRC, but since then, it has spread to nearby non-endemic African nations and farther around the world [2, 3]. Concerns about the racial and stigmatizing language connected with the name Monkeypox, led the WHO to change the name to "Mpox" in 2022 [1]. Since January 2022, cases have been reported in over 120 countries, and as of August 2024, there were over 100,000 confirmed cases and 200 deaths worldwide [10]. The continued spread and significant global impact of Mpox underscore the pressing need for ongoing prevention efforts and international collaboration to stop its spread [11].

This review aims to provide in-depth knowledge by consolidating recent research findings on Mpox transmission dynamics, biosafety and biosecurity measures, and disease outcomes. It seeks to narrow existing knowledge gaps, shed light on the evolving epidemiology of the disease, and explore vaccine options. Furthermore, it advocates for the reinvigoration and effective implementation of infection prevention and control (IPC) measures to mitigate the ongoing public health threat.

Mpox has likely existed in Sub-Saharan Africa for thousands of years, originating from zoonotic transmission of the MPXV from infected animals to humans [12]. Seasonal outbreaks of Mpox have been documented in Africa for over 50 years, yet responses by governments of endemic countries and global health partners have remained inadequate, despite repeated warnings from African researchers [13–15]. The Africa CDC has highlighted a worsening situation, reporting significantly higher figures than those stated by the WHO. As of 2024, an estimated 15,000 new Mpox cases and 461 deaths have been recorded across the continent—a staggering 160% increase compared to 2023, with mortality rates surging to 19% [16]. Mpox represents an alarming resurgence and a re-emerging public health challenge that threatens both continental and global health security [2–4, 13–15]. The virus was first identified in Copenhagen, Denmark, in 1958 among monkeys imported from Singapore for research purposes. These monkeys developed a smallpox-like illness, characterized by cutaneous pustular eruptions, leading to the name "monkeypox" [17, 18].

Epidemiological trends and geographic expansion of Mpox outbreaks

Mpox ground zero

The first documented human case occurred on September 1, 1970, in a 9-month-old boy from Basankusu, DRC. He was the only member of his family unvaccinated against smallpox [4, 19, 20]. Within a year, six additional cases were reported in Liberia, Sierra Leone, and Nigeria [21]. Between 1970 and 1979, 47 human cases were identified, 38 of which were in Zaire (now DRC). The number of Mpox cases rose to 338 between 1981 and 1986 in the DRC and exceeded 400 cases between February 1996 and October 1997 [22, 23]. The eradication of smallpox in the region, with the last case reported in 1970, coincided with decreased herd immunity following the discontinuation of smallpox vaccination which conferred cross immunity to the MPXV. This appears to have increased human susceptibility to severe Mpox disease [24].

West and central DRC mpox outbreak (Clade Ia)

Historically, recurrent Mpox outbreaks were predominantly confined to endemic regions, primarily in the West and Central DRC, which served as the epicenter [13, 14, 24–26]. However, the 2024 outbreak in the DRC marked a significant change in transmission dynamics, with approximately 12,569 suspected Mpox cases and 581 fatalities, resulting in a case fatality rate (CFR) of 4.6% [27]. Notably, the outbreak extended into previously unaffected regions, with cases reported across 156 health sectors in 22 out of 26 provinces—the highest case count recorded to date. A considerable proportion of cases were attributed to sexual transmission, indicating a shift in transmission dynamics and variability in clinical presentations. Against the backdrop of ongoing conflict in the DRC, Mpox has evolved into a substantial public health emergency [27].

Eastern DRC mpox outbreak (Clade Ib) and spread to the neighboring countries and other regions of the world

Clade Ib is endemic in the South Kivu province in the Eastern Democratic Republic of the Congo. The outbreak began in 2023 and by 2024 has spread to neighboring countries, including Rwanda, Burundi, Tanzania, Kenya, and other global regions [28]. At the same time, during the summer of 2024, Clade Ia outbreaks occurred in neighboring countries including the Republic of the Congo (ROC) and the Central African Republic (CAR), where Clade I Mpox had historically been endemic. Some of these outbreaks were epidemiologically related to transmission from the DRC [28]. By mid-2024, sustained local transmission led to further geographic expansion into non-endemic regions, spreading rapidly among adults through close physical contact, including sexual contact within networks of sex workers and their clients [29]. Other means of transmission include household exposure, and nosocomial spread, exacerbated by inadequate access to personal protective equipment (PPE) in healthcare settings. As of late 2024, more than 50,000 suspected Mpox cases and approximately 1,000 deaths

had been reported, with 13,000 laboratory-confirmed cases and 40 associated fatalities [29].

Global Mpox outbreaks (Clade IIa)

Clade IIa is endemic in and mainly circulating in Guinea, Liberia and Côte d'Ivoire but later has spread among neighbouring African countries. The first recorded outbreak beyond these regions occurred in 2003 in the United States, affecting Illinois, Indiana, Kansas, Missouri, Ohio, and Wisconsin. This outbreak, the first in the Western Hemisphere, was linked to the importation of MPXV-infected rodents from Ghana [30].

Global outbreak Clade IIb lineage A

Clade IIb caused the 2017–2019 outbreak in Nigeria and the 2022–2023 devastating global human mpox outbreaks that occurred in about 116 countries with 92,000 confirmed cases and171 deaths [31]. This outbreak continued to 2024 and to this day. Since the 2022 multi-country outbreaks caused by Clade IIb, have been reported in previously non – endemic African countries and beyond. Outbreaks have involved Central African nations such as the Central African Republic, Cameroon, and Gabon. East African nations like Kenya, Uganda, Rwanda, and Burundi; and West African nations, including Nigeria, Sierra Leone, Senegal, Côte d'Ivoire, Liberia, and Benin Republic [30]. These global outbreaks were due to the divergent Clad IIb from previously circulating clade in the West African countries and rapidly spreading across sub- Saharan African countries and beyond to involve Europe, the Americas and then all the six WHO regions (just short from being declared a pandemic). The 2022 global outbreak was declared PHEIC by the WHO. Following the 2024 global outbreak with continental and global health threat, a second declaration was made by the Africa CDC and the WHO describing it as PHECS [2] and PHEIC [3–5] respectively. The mode of transmission the MPXV for these global outbreaks is predominantly through sexual contact and networks primarily but not limited to men who have sex with men (MSM) driving person to person transmission especially in adults [32]. Other risk factors include male sex especially those between 20–41 years of age, having multiple sex partners, bisexual, female sex workers, person living with advanced HIV disease and having anogenital lesions. In addition, nonsexual contact with infected persons and animals play a role in transmission in adults. In children, the driver of transmission include close contact with infected patients, animal exposure and Varicella Zoster Virus (VZV) infection [32]. Nigerian travellers introduced the disease into Israel, Singapore and the United Kingdom between 2018- 2019 [33, 34]. The rapid spread of Mpox outside of Africa to all the six WHO regions is becoming increasingly concerning. It is associated with milder illness and lower mortality compared to Clade I [32].

The emergence of new clades and sub-lineages, changes in the age groups that are affected, and evolving modes of transmission are some of the epidemiological changes that mark these outbreaks. There has been a notable shift in both major clades from zoonotic to human-to-human transmission, especially through sexual interaction, resulting in a variety of disease outcomes [28, 30, 35, 36].

Virology and genetic divergence

Previously considered a strictly zoonotic viral infection, Mpox is caused by the *Monkeypox virus* (MPXV), an enveloped double-stranded DNA virus of the *Poxviridae* family, subfamily *Chordopoxvirinae*, and the *Orthopoxvirus* genus. This genus also includes *Variola minor* and *Variola major* (smallpox viruses), as well as *Vaccinia*, *Cowpox*, *Camelpox*, *Goatpox*, and *Deerpox* viruses [37, 38]. MPXV exists as two genetically distinct clades: Clade I (formerly Congo Basin or Central African clade) and Clade II (West African clade) [39]. The evolved MPXV strains, divergent from the previously circulating Clades I and II, exhibit significant differences in epidemiological and clinical characteristics. The case fatality rate for Clade I can reach up to 10%, but Clade II has a case fatality rate of less than 1% [21, 32, 40]. Clade II is further subdivided into Clade IIa and Clade IIb. Clade I, predominantly observed in Central African countries such as the DRC, historically affected children and adolescents and is associated with more severe disease outcomes compared to Clade II. Cameroon remains the only country known to harbour both Clade I and Clade II [25].

Clinical manifestations and transmission dynamics

While Mpox can remain asymptomatic, symptomatic cases present with flu-like symptoms, high fever, and vesiculopapular rashes that are centrifugally distributed, including on the palms and soles. Other symptoms include headache, myalgia, sore throat, systemic blisters, and lymphadenopathy, especially in the inguinal region. Notably, Mpox differs from smallpox in that it is characterized by lymphadenopathy at the onset of fever [23, 25]. Mpox is transmitted through the *Monkeypox virus* (MPXV) via animal-to-human or human-to-human transfer. Natural reservoirs of the virus include non-human primates such as chimpanzees, sooty mangabeys, and cynomolgus monkeys, as well as small mammals like squirrels, mice, rabbits, hamsters, and porcupines [1, 3, 10, 41]. The most common cause of human infections is zoonotic spillover [7–10, 13, 14]. Humans can contract the disease from animals by eating contaminated meat, coming into close contact with the body fluids or flesh of sick animals, or exposure to contaminated objects and

surfaces. The most common way that human-to-human transmission occurs is through close physical contact with infected individuals or their bodily fluids [25, 32, 33].

According to recent researches, sexual transmission is rapidly becoming the major driver in the global spread of Mpox [7, 31, 32, 42–48]. This trend draws attention to the new biological characteristics and changing epidemiological patterns of the re-emerging mutant clades. Additionally, the virus that causes Mpox can spread from mother to fetus during pregnancy. This can lead to unfavorable obstetric outcomes, such as miscarriage, especially when viral loads are high. Therefore, it is crucial to reduce the risk of MPXV infection during pregnancy [32, 42].

The WHO has identified outbreaks in a number several countries that were brought on by different clades of the MPXV, each with unique routes of transmission and varying levels of risk. MPXV continues to circulate in endemic areas, causing periodic waves of epidemics and an increasing spread beyond the DRC to previously unaffected African countries and regions across the globe. The increase in foreign travel, urbanization, commercialization, and sexual transmission has all contributed to this development [7–9, 32]. These findings highlight the role of sexual transmission in the global spread of MPXV. The currently occurring 2022–2024 epidemic is especially concerning because of its rapid spread and transmission. Genetically modified clades Ia, Ib, and IIb are the cause of these outbreaks, which have been described as the most virulent to date. These clades exhibit new biological characteristics with improved epidemiological patterns, and heightened pathogenicity. These factors have fuelled a series of devastating outbreaks in Africa and beyond since July 2024, posing a significant threat to global health security [7–9, 34, 43].

The present Mpox outbreaks have introduced a new epidemiological trend that is different from what is previously known. Sexual contact is the predominant route of transmission, especially among adults who engage in risky sexual behaviors including inconsistent use of condoms, having multiple sexual partners, or men having sex with men (MSM) [15, 32, 43, 44, 48, 49]. Physical contact with infected individuals also remains a significant risk factor. The outbreaks caused by clade Ib in the DRC have primarily affected young adults aged 20–45 years and are spreading rapidly [7, 37]. Furthermore, at least 20 non-endemic African nations as well as other regions of the world have reported an alarming rise in suspected or confirmed cases. Since many of these individuals have no history of travel to endemic regions, community transmission within human populations is likely to be ongoing [46].

Strategies for epidemic control and mitigation

To curb the spread of the epidemic, strengthening infection prevention (IPC) programmes, improved health care access, improved surveillance, early detection in human and treatment in human and livestock as part of mitigation measures as well as mass vaccination programme to achieve herd immunity. Improving healthcare access and implementing mass vaccination efforts are also critical components of mitigation measures aimed at achieving herd immunity. The African continent requires over 10 million vaccine doses; however, only about 200,000 doses are currently available due to numerous challenges [2]. These challenges include unpredictable financial resources, limited global availability and production of Mpox vaccines, logistical delays in fulfilling orders, and legal agreements surrounding vaccine donations versus direct procurement. Additionally, the availability of the antiviral agent tecovirimat and other effective antiviral drugs remains limited and costly, further complicating containment efforts [2].

The rising global attention toward Mpox stems from the increasing daily cases in endemic regions and widespread epidemics across non-endemic areas, creating a demand for comprehensive and updated information.

Discussion

The emergence and re-emergence of highly dangerous new clades of the MPXV circulating in endemic regions such as the DRC, other parts of Africa, and globally, highlight the urgent need for prophylactic vaccination strategies. These should prioritize individuals at high risk and entire populations in endemic regions to achieve herd immunity against the various known circulating clades.

Continuous mutations of previously circulating clades in these endemic areas have resulted in the emergence of virulent, divergent sub-lineages with distinct genomes and new epidemiological characteristics globally. Genomic studies [8, 9, 50] have identified unique mutational profiles, clades with sub-lineages, altered phylogenies, and expanded transmission patterns. These include sustained human-to-human transmission, extended age susceptibility, and previously unobserved trends.

The genetic diversity of these mutant clades has been attributed to factors such as recombination, mutations, gene loss, gene gain, and other genomic modifications [7–9, 47]. Furthermore, the emergence of more virulent MPXV clades may be linked to bio-modifications during the virus's adaptation from zoonotic to human hosts. This transition underscores a lethal virus-host interaction, driving the current epidemiological shifts and amplifying the global public health threat [49].

The MPXV undergo slow but steady microevolution, driven by amino acid point mutations, to adapt to human

hosts. This process contributes to their divergence into sub—lineages with distinct geographic and demographic profiles [51, 52].

Ecosystem modifications and viral adaptability, particularly during the spread outside their zoonotic hosts, appear to favour recombinant mutations in MPXV clade I [9]. Notably, studies by Masirika et al. on the Kamituga subgroup of the clade I revealed highly mutative proteins with patterns of consensus in-frame deletions, frame shift variants, synonymous variants, and amino acid substitutions [9].

The newly emergent virulent MPXV clade Ib displays epidemiological variability and adverse clinical outcomes, likely due to a higher incidence of recombinant single nucleotide polymorphism (SNP) pairs—approximately 5.1-fold higher than those observed in MPXV IIb. This suggests a higher super infection rate, which sustains ongoing genetic recombination in MPXV Ib infected populations. Furthermore, the MPXV Ib strain has generated more recombinant variants and subgroups than the MPXV IIb strain [6].

Some researchers attributed the changing epidemiology and disease outcomes to Apolipoprotein B mRNA editing enzyme catalytic polypeptide 3 (APOBEC3)-type mutations in the clade IIb. These mutations may accelerate viral evolution, enabling the divergent strains to sustain efficient human-to-human transmission, as observed in the current outbreaks [7, 8].

The Clade I *Kamituga* MPXV cluster genome, for instance, possesses a unique C9L gene that encodes a Kelch-like protein. This protein acts as a critical antagonist to the host's innate immune response, impairing its effectiveness. Additionally, the genome contains an RNA G-quadruplex (RG4), which induces unstable structural changes in the Clade I MPXV genome during evolution [15]. These characteristics, along with other factors, position the emergent sub lineages of Clade I MPXV as having a unique pathogen-favouring mutational profile.

Conversely, research on the mutant divergent Clade IIb highlights the accumulation of APOBEC3-type mutations. These mutations represent a host defence mechanism, targeting the viral genome during replication when single strands are exposed. This process leads to nucleotide changes, such as cytosine-to-thymine or guanine-to-adenine substitutions in favour of human-to-human transmission [8, 9].

These genetic developments significantly contribute to the changing epidemiological and clinical characteristics of MPXV infections. Furthermore, the overwhelming role of the sexual route—particularly involving men who have sex with men (MSM) and heterosexual intercourse as the primary driver of transmission for the new sub lineages has been extensively documented [6–8, 15, 32, 36, 53].

Epidemiological risk factors for MPXV include male gender, age (predominantly 20–42 years), multiple sexual partners, being gay or bisexual, engaging in MSM activities, and living with HIV [9, 48]. Co-existing infections, such as hepatitis B and C, especially among people who inject drugs illegally, have also been identified as contributing factors to disease spread and outcomes [54, 55].

The DRC, along with neighbouring East and West African countries, continues to serve as a reservoir for clusters of self-sustaining, emerging, and re-emerging MPXV sub-lineages exhibiting mutational antigenic variability. Vaccination remains part of the cornerstones for curbing these recurrent waves of dangerous epidemics, which pose significant challenges to both continental and global health security [2, 3].

Vaccines have demonstrated enormous protective effects on human and animal health [13, 56]. However, Africa faces significant challenges in achieving adequate equitable vaccine coverage for the at-risk populations. These include limited financial resources, logistical and supply chain constraints, global vaccine shortages, regulatory and vaccine licensure issues, and insufficient budgetary allocations to healthcare by some African leaders [2].

To ensure effective protection, complete vaccination at the recommended dose and interval must be prioritized. The current protocol involves administering two doses, spaced four weeks apart, to confer cross immunity against MPXV [13].

The Centers for Disease Control and Prevention (CDC) presently recommends Mpox vaccination for populations at increased risk, including, bisexual men and gay men, MSM with multiple recent sexual partners, MSM living with HIV, individuals with known or suspected exposure to Mpox disease patient, women with male sexual partners at risk, and healthcare workers handling orthopoxviruses [57].

Researchers have documented that the smallpox vaccines currently in use for mpox provide approximately 80–85% cross-protection [58, 59]. However, these vaccines must be re-engineered to a polyvalent format to offer comprehensive protection against the divergent, epidemiologically significant clades currently in circulation. The proposed polyvalent prototype vaccine, if feasible, should be integrated into the National Programme on Immunization (NPI) in endemic countries as either a single-pathogen or multi-pathogen vaccine. Such integration would help reduce overhead costs and the discomfort associated with multiple injections [56]. While waiting for the production of accepted vaccine in sufficient quantity, other pillars of mitigation measures including effective IPC principles should be strengthened, implemented and sustained to minimise the risk and spread.

Given the ongoing PHECS and PHEIC with the accompanying global public health burden, several mitigating measures are urgently needed. These include: 1) Continental collaboration and policy commitment of Governments of endemic and neighbouring countries. Ministries of health, agriculture, veterinary agencies, pharmaceutical industries, and research institutions must adopt a one health strategy by mobilizing collective resources and political will to strengthen epidemiological surveillance and early disease detection. Additionally, implementing robust IPC measures at all levels, enforcing biosecurity measures to prevent zoonotic spillovers, and accelerating the development of antiviral drugs through research and innovation, as well as driving vaccine production and equitable distribution for both humans and livestock [13, 14]. 2) Public awareness and education programs focusing on Mpox transmission dynamics, as well as effective infection prevention and control (IPC) strategies, should be emphasized. Measures such as hand hygiene, improved personal and public hygiene practices, as well as public enlightenment programmes are crucial to bridging the knowledge gap [2, 3, 13]. 3) Enhanced surveillance and cross-border collaboration to strengthen cross-border information sharing and surveillance systems is key to tracking outbreaks and mitigating their spread. [13] 4) Genomic sequencing is a key tool in the detection of existing or emerging variants, tracking the spread, assessing their pathogenicity, vaccine development and treatment [60, 61].

Improved diagnostic capacity training of healthcare providers at the point of care, particularly in endemic regions, will bolster laboratory diagnostic capabilities and enhance the effectiveness of outbreak management efforts [2, 13].

However, this vision is far from reality due to the limited availability of currently licensed or approved Mpox vaccines and the scarcity of funds to support such an important initiative. While advocating for a vaccine intervention, which is obviously a medium- to long-term solution, the alarming rate of transmission, spread, and the resulting mortality and morbidity of the virulent new mutant clades demand urgent action. While awaiting the large-scale production of novel vaccines, it is crucial to strengthen, implement, and sustain other key mitigation strategies, to minimize the risk and spread of the disease. Therefore, endemic countries must strengthen preventive strategies and uphold the policies and recommendations of the Africa CDC and WHO. These efforts should build on capacities developed during the COVID-19 pandemic, focusing on human health, livestock, the pharmaceutical industry, community engagement, risk communication, and enhanced surveillance. Unfortunately, many of the valuable gains from the pandemic response have been neglected in several African nations. The pandemic highlighted the importance of infection prevention measures in curbing infectious threats, yet the progress made in this area has not been sustained. This decline in investment and preparedness across low- and middle-income countries (LMICs) has weakened outbreak response, leaving healthcare systems vulnerable to future public health threats [62].

Conflict and wars affecting DRC and neighbouring countries could also be a contributory driving force as people are internally displaced in their numbers leading to human and animal ecosystem disturbances, overcrowded in camps facing food and medical care insecurity with a higher risk of malnutrition and infectious diseases [63]. Worsening security situation has led to the reduction of the United Nations stabilization mission in some areas of the DRC [63]. This could be as a result of recent takes of M23 rebels in the city of Goma (North Kivu) and Bukavu (South Kivu), which are two MPXV clade Ib hot spots in Eastern DRC [64, 65].

Increased gender-based violence, increased rape [66], transactional sex activity with risky sexual behaviours [32, 66]. These disturbances were contributory to the exacerbation of the spread of the new MPXV clades [63].

If effective and sustained countermeasures are not urgently implemented, the unchecked spread of these emerging virulent clades beyond non-endemic African regions and globally could escalate into a devastating pandemic. The time for concerted action is now.

Conclusion

The genetically modified Clades Ia, Ib, and IIb are driving the current Mpox outbreaks and pose a significant global health threat. To mitigate the risks associated with these emerging and re-emerging divergent clades and sublineages of MPXV, it is essential to establish and sustain strong national-level coordination, enhance surveillance systems, expand diagnostic laboratory capacity, implement effective infection prevention and control (IPC) programs across all levels of healthcare and communities, and ensure robust case management strategies.

Additionally, the proposed polyvalent vaccine model as one of the mitigation measures, offers a cost-effective solution with broader coverage, making it a critical tool for addressing the ongoing Public Health Emergency of International Concern (PHEIC) and mitigating the global health security risks posed by circulating virulent clades.

For these efforts to succeed, a strong commitment from key stakeholders—including community leaders, ministries of health, the pharmaceutical industry, veterinary services, and the animal husbandry sector—is necessary. Heads of state must provide both financial and political support to drive these initiatives forward. Furthermore, international

organizations (Africa CDC, WHO) should facilitate interaction and collaboration with stake holders as well as sponsors at the global level to support one health and governance initiatives in the world / mpox affected countries. This approach is essential to effectively combat the resurgence of this viral threat and prevent future outbreaks.

Abbreviations

DRC	Democratic Republic of the Congo
MPXV	Monkeypox virus
WHO	World Health Organization
PHEIC	Public Health Emergency of International Concern
PHECS	Public Health Emergency of Continental Security
Africa CDC	Africa Centres for Disease Control and Prevention
CDC	Centres for Disease Control and Prevention
MSM	Men who have sex with men
IPC	Infection Prevention and Control
APOBEC	Apolipoprotein B mRNA editing enzyme catalytic polypeptide
PHEIC	Public health emergency of international concern
VZV	Varicella zoster virus

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