



Review

Emergence of mpox in the post-smallpox era—a narrative review on mpox epidemiology

Christophe Van Dijck¹, Nicole A. Hoff², Placide Mbala-Kingebeni^{3,4}, Nicola Low⁵, Muge Cevik⁶, Anne W. Rimoin², Jason Kindrachuk^{7,†}, Laurens Liesenborghs^{1,*}

¹ Department of Clinical Sciences, Institute of Tropical Medicine Antwerp, Antwerp, Belgium

² Department of Epidemiology, University of California, Los Angeles, CA, USA

³ Institut National de Recherche Biomédicale, Kinshasa, Democratic Republic of Congo

⁴ Université de Kinshasa, Democratic Republic of Congo

⁵ Institute of Social and Preventive Medicine, University of Bern, Bern, Switzerland

⁶ Division of Infection and Global Health, University of St Andrews, St Andrews, Scotland

⁷ Department of Medical Microbiology and Infectious Diseases, University of Manitoba, Winnipeg, Canada

ARTICLE INFO

Article history:

Received 11 March 2023

Received in revised form

9 July 2023

Accepted 8 August 2023

Available online 11 August 2023

Editor: R. Chelaly

Keywords:

Epidemiology

Monkeypox-mpox

Orthopoxvirus

Outbreak

Transmission

ABSTRACT

Background: The 2022 mpox outbreak drew global attention to this neglected pathogen. While most of the world was taken by surprise, some countries have seen this pathogen emerge and become endemic several decades prior to this epidemic.

Objectives: This narrative review provides an overview of mpox epidemiology since its discovery through the 2022 global outbreak.

Sources: We searched PubMed for relevant literature about mpox epidemiology and transmission through 28 February 2023.

Content: The emergence of human mpox is intertwined with the eradication of smallpox and the cessation of the global smallpox vaccination campaign. The first human clade I and II monkeypox virus (MPXV) infections were reported as zoonoses in Central and West Africa, respectively, around 1970 with sporadic infections reported throughout the rest of the decade. Over the next five decades, Clade I MPXV was more common and caused outbreaks of increasing size and frequency, mainly in the Democratic Republic of the Congo. Clade II MPXV was rarely observed, until its re-emergence and ongoing transmission in Nigeria, since 2017. Both clades showed a shift from zoonotic to human-to-human transmission, with potential transmission through sexual contact being observed in Nigeria. In 2022, clade II MPXV caused a large human outbreak which to date has caused over 86,000 cases in 110 countries, with strong evidence of transmission during sexual contact. By February 2023, the global epidemic has waned in most countries, but endemic regions continue to suffer from mpox.

Implications: The changing epidemiology of mpox demonstrates how neglected zoonosis turned into a global health threat within a few decades. Thus, mpox pathophysiology and transmission dynamics need to be further investigated, and preventive and therapeutic interventions need to be evaluated. Outbreak response systems need to be strengthened and sustained in endemic regions to reduce the global threat of mpox. **Christophe Van Dijck, Clin Microbiol Infect 2023;29:1487**

© 2023 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Introduction

Mpox (formerly monkeypox) is caused by the monkeypox virus (MPXV), which is a zoonotic orthopoxvirus in the poxvirus family [1]. MPXV was first discovered in 1958 following an outbreak among captive primates in Copenhagen [2]. The zoonotic reservoir for MPXV probably includes small rodents such as squirrels, and it

* Corresponding author. Laurens Liesenborghs, Department of Clinical Sciences, Institute of Tropical Medicine Antwerp, Nationalestraat 155, 2000 Antwerp, Belgium.

E-mail address: lliesenborghs@itg.be (L. Liesenborghs).

† Jason Kindrachuk and Laurens Liesenborghs contributed equally / supervised the work jointly.

is likely that many other mammalian species are involved [3]. There are two known clades of human MPXV, which originated from geographically distinct areas in Africa (Fig. 1). Both clades cause a smallpox-like disease, but clade I MPXV, which is endemic in Central Africa, appears to cause more severe disease than clade II MPXV, which is endemic in West Africa [4,5]. Based on genetic

differences, clade II MPXV is further subdivided into two subclades that are each endemic in specific regions in West Africa: clade IIa located to the west and clade IIb to the east of a savanna region called the Dahomey Gap. Clade IIa and IIb MPXV have evolved separately from a common ancestor dating back centuries [6]. Before 2022, clade I MPXV infections predominated, with most

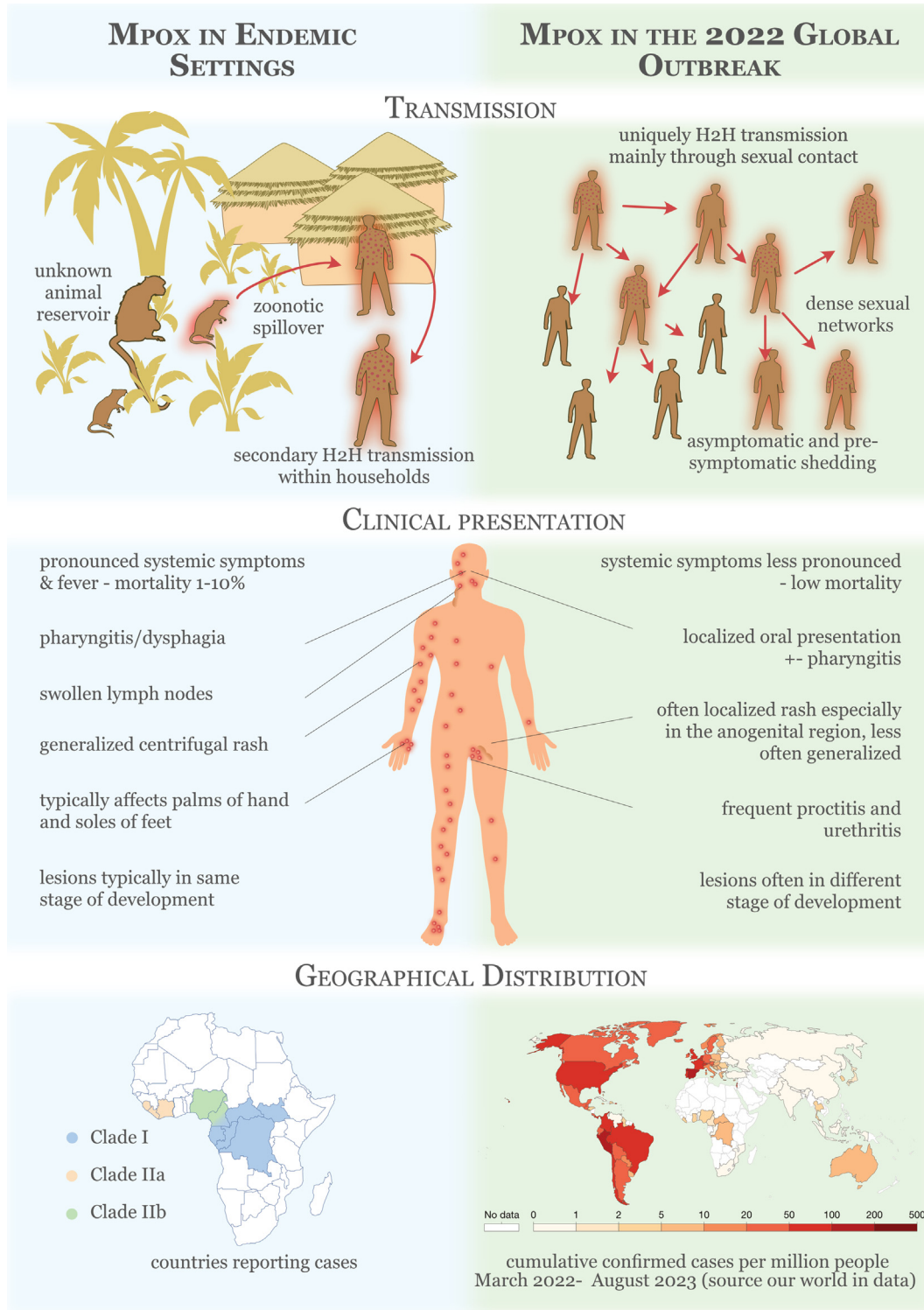


Fig. 1. Overview of transmission, clinical presentation and geographical distribution of mpox in endemic countries during the 2022 global outbreak. The map of cumulative confirmed cases for the 2022 global outbreak is adapted from <https://ourworldindata.org> (Mathieu Edouard, Spooner Fiona, Dattani Saloni, Ritchie Hannah, Roser Max. 'Mpox (monkeypox)'. Available at <https://ourworldindata.org/monkeypox>. Accessed August 30, 2023.). H2H = human-to-human.

mpox cases being detected in Central Africa. While countries such as the Central African Republic, Cameroon, the Republic of the Congo and Gabon regularly report cases, the Democratic Republic of the Congo (DRC) has historically reported most cases of clade I mpox, accounting for the overwhelming majority of cases worldwide. In contrast, clade II MPXV infections were considered rare, until an outbreak of clade IIb mpox occurred in Nigeria in 2017, which was eventually followed by a global outbreak in 2022.

This review will discuss the epidemiological aspects of mpox. We will describe the history and rise of clade I MPXV in Central Africa, followed by the emergence of clade II MPXV in West Africa, and finally, its spread to the rest of the world.

The Democratic Republic of the Congo: at the heart of the clade I mpox epidemic

Although the virus was discovered in the fifties [2], human mpox infections were not recognized until 1970 when a 9-year-old boy was diagnosed with mpox in the DRC [7]. This long interval between the initial discovery of mpox and the first confirmed human case might be explained by the intertwined histories of mpox and smallpox. First, before the WHO started its intensified global smallpox eradication programme in the late 1960s, smallpox was endemic in many countries in Central and West Africa. MPXV infections that occurred during this time may have been misdiagnosed as smallpox, especially as molecular diagnosis was not yet available. Second, the spread of MPXV was likely kept in check by smallpox vaccination campaigns. As there is a substantial antigenic similarity among orthopoxviruses, first-generation smallpox vaccines were believed to induce considerable cross-protection against MPXV [1]. As a result, MPXV did not cause large outbreaks and mathematical models based on pre-1980s epidemiological data estimated that the reproductive number of mpox in the population at the time was <1 , indicating a tendency to go extinct [3].

However, the gradual eradication of smallpox – the last smallpox case in the DRC was reported in 1971 and the last case worldwide in 1977 [8]—marked the beginning of the mpox era [9]. Smallpox was declared eradicated in 1980, which resulted in the subsequent end of most smallpox vaccination campaigns, including in the DRC [8]. As a result, the population of individuals susceptible to mpox grew year after year [10]. After the eradication of smallpox, the Global Commission for the Certification of Smallpox Eradication designated MPXV the most important orthopoxvirus and a WHO-led surveillance programme was started in the DRC. This programme detected 338 mpox cases between 1981 and 1986, contrasting with the 59 cases identified throughout the previous decade [10]. Most infected individuals were unvaccinated children and there was very little evidence of onward secondary transmission except in unvaccinated family members [1,11]. These initial surveillance efforts also indicated that mortality from mpox was lower (13%) than from variola major (around 30%), the most common form of smallpox. As a result, WHO determined that mpox did not pose a public health threat and that continued mass vaccination with smallpox vaccination was not warranted to prevent mpox infection [1,12]. In 1986, the mpox surveillance programme was abandoned and interest in the disease waned [10].

Increasing clade I MPXV transmission in the post-smallpox era

Between 1986 and 1996, relatively few MPXV infections were detected until the first large documented mpox outbreak occurred in the Sankuru province of central DRC, in 1996. Over a two-year time period, the 1996 outbreak affected more than 400 patients

[13]. Observations during this and subsequent outbreaks included a trend towards a higher age of affected individuals, which could be explained by the ageing of the vaccine-naïve population [10,14].

In 2000, the DRC initiated the Integrated Disease and Surveillance Response system, based on guidance from WHO. This system focused on the detection of diseases with epidemic potential identified by WHO. Countries were allowed to include additional diseases if they were of concern in their particular setting. In the DRC as well as in the Central African Republic, mpox was included in the passive surveillance efforts, since 2001 [9]. In the next 13 years, mpox incidence increased steadily in the DRC, and an incidence of 2.84 mpox cases per 100,000 population was reported in 2013 [9]. In the early 2000s, a number of projects focused on improving surveillance efforts for mpox. From 2002 to 2010, an active surveillance programme in the Sankuru province of DRC found a 20-fold increase in incidence between 2005 and 2007 compared to the 1980's WHO active surveillance programme [14]. Additionally, from 2007 to 2011, a clinical study in the same sites as the active surveillance programme in Sankuru province contributed data on the natural history of disease and also observed potential mother-to-fetal transmission of mpox – which had not been described previously [15].

Since restarting surveillance in 2001, the number of suspected cases in the DRC has continued to increase, leading to 6216 reported suspected cases in 2020 [16]. In addition, whereas mpox had previously been reported predominantly in highly forested regions, country-wide surveillance data indicate that the virus is spreading to new geographical areas [9]. The most recent example was a large outbreak with over 500 reported cases that started in 2021 in Maniema province, a region that is savannah rather than rainforest (unpublished observations).

Unfortunately, due to gaps in the surveillance system and diagnostic capacity, estimating the true burden of mpox in the DRC is challenging. In many regions, clinically suspected cases may remain unreported. In other regions, overreporting of mpox cases may occur due to a lack of confirmatory testing [17,18]. Overall, most researchers estimate that the real disease burden is underestimated, and some models indicate that true caseloads may be 5 to 15 times higher than those reported [19].

Parallel to the rise in cases in the DRC, an increase in human-to-human transmission was observed, especially within households and between neighbouring houses. Epidemiological assessment during the WHO surveillance efforts in DRC from 1980 to 1984 found that most cases (130/214 or 61%) were linked to zoonotic spillover [20], and that secondary attack rates were overall low ($<10\%$), but significantly higher for household contacts than other contacts [20]. An investigation in 1996 noted an increase in the proportion of cases who reported exposure to another case (73% compared to 28% in the 1980s), indicating a steady increase in human-to-human transmission from earlier studies [21]. Moreover, for the first time, prolonged community transmission was suggested [22]. Almost 20 years later, an outbreak investigation from 2013 in the DRC reported a secondary attack rate of 50% and prolonged transmission chains of up to six events [23]. Of note, variola major had a similar secondary attack rate in unvaccinated household members (37–88%, with an average of 58%) [11].

Despite observed increases in human-to-human transmission of mpox, the exact mechanisms of transmission remain poorly understood. Smallpox was thought to be transmitted predominantly by inhalation of virus-containing aerosols, but occasionally also by contact with pustules or crusted scabs [24]. There is less evidence for aerosol transmission of mpox and its transmission is thought to occur predominantly through direct contact with infectious saliva and/or respiratory secretions, skin lesions or scabs, and contaminated materials [25]. Factors associated with an increased risk of

mpox within households include sharing of a bed/bedroom or plates or cups with the index cases [26].

Meanwhile, in West Africa: the emergence of clade II MPXV

Similar to clade I MPXV, outbreaks of clade II MPXV were first reported in the 1970s. Between 1970 and 1979, a small number of cases were detected in rainforest areas of Liberia, Sierra Leone and Nigeria [27]. One epidemiological study reported 47 mpox cases from West ($n = 9$) and Central Africa ($n = 38$) from 1970 to 1979 [27]. Patients were primarily young (mean age 8 years) and male (55.3%). Household transmission was reported infrequently with similar or milder disease in secondary cases. In contrast to clade I MPXV endemicity in the DRC, these initial clade II MPXV outbreaks were followed by several decades of apparent absence of reported infections. However, despite the lack of reported cases in West Africa, an outbreak of clade IIa MPXV occurred in the US in 2002 following importation of clade IIa-MPXV-infected rodents imported to the US from Ghana which resulted in an outbreak of 47 reported cases [28]. Of those, 25.4% were hospitalized including two children with severe illness [28]. All infections during this outbreak were associated with zoonotic transmission from direct contact with or proximity to, infected prairie dogs [28]. No secondary transmission of MPXV was noted [28].

The absence of reported clade II cases changed abruptly in 2017 when Nigeria faced its first reported large nationwide outbreak [29]. The detection of MPXV in an 11-year-old boy triggered a national outbreak response, which eventually identified 122 cases over 17 states within the subsequent year [29]. Since then, sporadic cases have been reported throughout the country, often without reported wildlife contact [29]. Studies estimate that the true number of cases in Nigeria may be much higher than what was reported [30].

The 2017 outbreak in Nigeria was different from large outbreaks of clade I MPXV in Central Africa for several reasons. First, this outbreak occurred in a densely populated area, a minority (<10%) of patients reported contact with wildlife and patients clustered within households. These aspects suggest that most infections were attributable to human-to-human transmission rather than zoonotic spillover. Second, 69% of cases were men (mostly in their twenties or thirties) and 68% of investigated cases had genital ulcers [29]. Even though these findings did not receive much attention at the time, transmission during sexual contact had been suggested [31]. Last, Nigeria's higher connectivity through international air travel compared to remote forest areas in Central Africa may have contributed to the increased potential for MPXV to spread across the globe.

From West Africa to the rest of the world: the 2022 global epidemic

To date, despite the incidence of several thousands of yearly cases in some regions in Central Africa, no infections with clade I MPXV have been reported outside the continent. In contrast, following the resurgence of clade IIb MPXV in Nigeria, several travel-related clade IIb MPXV infections have been reported internationally, including in the UK ($n = 4$ in 2018, 2019, 2021), Israel ($n = 1$ in 2018), Singapore ($n = 1$ in 2019) and the USA ($n = 2$ in 2021) [3]. These cases caused no more than a handful of secondary infections, possibly thanks to their rapid recognition and isolation of cases.

On 7 May 2022, a report of a travel-related MPXV infection from Nigeria was quickly followed by a report of two additional infections and one probably infected but already recovered case in the UK on 12 May. The 12 May patients were not linked to the 7 May

case and had no history of recent travel or contact with travellers [32,33]. On 16 May, 4 new confirmed mpox patients were reported in the UK, all of whom were adult men and two were linked as sexual partners [33]. In the months that followed, this would appear to be a massive global outbreak of mpox, mainly transmitted through sexual contact among men who have sex with men, which to date, has caused more than 87,000 confirmed cases in 112 different countries [34]. Europe and the Americas have accounted for the majority of cases and the ten most affected countries worldwide accounted for almost 85% of reported cases [34]. The epidemic reached a peak in Europe and the Americas in August 2022, and since the beginning of 2023, only sporadic cases or case clusters have been reported from these regions [34]. Some countries in Asia observed almost no cases in 2022, but have reported a surge in cases since February–March 2023, including China, the Republic of Korea, Japan, and Thailand [34].

Phylogenetic studies indicate that almost all isolates from the 2022 global outbreak were caused by a monophyletic group of viruses designated as a new lineage B1 of clade IIb MPXV [35–37]. This lineage is genetically related to sequences from the outbreak in Nigeria in 2017 to 2018, travel-related cases in the UK, Israel and Singapore from 2018 to 2019, and a travel-related case in the USA in 2021, but diverged from them by a range of single nucleotide polymorphisms [36,37]. The exact course of events between 2017 and 2022 is elusive, but these findings are indicative for host adaptation during prolonged cryptic human-to-human transmission of clade IIb MPXV prior to its detection in the 2022 global outbreak [35–37].

A new side of mpox: sustained human-to-human transmission

During the 2022 global outbreak, mpox patients presented clinically with symptoms that were previously not considered common for mpox. Most patients lacked the typically reported generalized rash observed with mpox in endemic regions, but presented with one or more mucocutaneous lesions and relatively limited subsequent dissemination throughout the body [38]. The most common complications requiring medical treatment, and not commonly reported with clade I mpox, were severe rectal pain, anorectal abscesses, penile oedema, and odynophagia [38]. A minority of cases required hospitalization for treatment or isolation, the case-fatality rate was very low (<0.1%), and lethality was primarily observed in severely immunocompromised patients [38,39].

Unlike previous epidemics in Central and West Africa, the 2022 global outbreak was uniquely driven by human-to-human transmission and patients were linked through sexual contact rather than household or wildlife contacts. More than 95% of patients were men with a median age of 34 years and, where recorded, over 80% identified as gay, bisexual, or other men who have sex with men [34]. Most patients reported having had multiple sexual partners in the previous weeks or months and about one in four presented with a concomitant sexually transmitted infection [40]. The exact mechanism of transmission during sexual contact remains incompletely understood. Possible routes include transmission through respiratory droplets, shared fomites, and contact with infectious skin lesions, semen or mucosa. Indeed, MPXV has been cultured from saliva, other upper respiratory tract samples, anorectal swabs and semen of mpox patients [41]. Viable MPXV was also found in the anorectum of asymptomatic and presymptomatic patients [42–44]. These observations combined with the findings of a contact tracing study linking data on case-contact pairs in the UK indicate that asymptomatic and presymptomatic transmission may have contributed considerably to the rapid spread of mpox through sexual networks around the world [45]. In

response, several countries approved the use of smallpox vaccines and initiated vaccination campaigns among the populations at highest risk of infection. Yet in most of these countries, vaccination campaigns have started after the peak of the epidemic, when reported cases had already begun declining [46]. Thus, the reasons for the decline in cases are not fully clear [46]. Infection-induced immunity among individuals at the centre of the network, heightened awareness and early symptom recognition, diagnosis and self-isolation, scattering of sexual networks due to a change in behaviour, and swift response of a healthcare system experienced with contagious diseases since the COVID-19 pandemic may all have played a role. However, the relative contributions of each of these factors are uncertain [46]. Whether new waves of mpox are to be expected in the near or further away future remains unknown.

Conclusions and future prospects

The recent global mpox outbreak has highlighted the threat of a neglected emerging virus to global health. Although interest in mpox may fade due to the waning of the global epidemic, outbreaks of increasing size and frequency continue to occur in endemic countries in Central and West Africa. There is a need for concerted efforts to control mpox outbreaks, which include increasing our understanding of mpox pathophysiology and transmission dynamics, vaccinating populations at risk, and conducting clinical trials for preventive and therapeutic interventions. We need to prioritize collaborative research and clinical partnerships with endemic countries [47]. We also need to enhance surveillance and response capacities in vulnerable regions. It is important to note that concerns regarding MPXV have been raised for many years, but that there has been limited international investment in sustainable preparedness and response efforts despite the well-documented health and economic impacts of human mpox in endemic regions of West and Central Africa. Therefore, it is essential to prioritize concerted efforts for control in endemic regions to reduce the threat of MPXV outbreaks worldwide.

Author contributions

LL, CVD, and JK conceptualized the scope of the review. All authors contributed to the final version of the manuscript and approved it for publication.

Transparency declaration

JK was supported by the Canadian Institutes of Health Research (Grant Nos. 202209MRR-489062-MPX-CDAA-168421 and 202209PPE-491319-VVP-CDAA-168421). LL and CVD were supported by the Research Foundation Flanders (grant number G096222 N to LL).

References

- [1] Fine PE, Jezek Z, Grab B, Dixon H. The transmission potential of monkeypox virus in human populations. *Int J Epidemiol* 1988;17:643–50. <https://doi.org/10.1093/ije/17.3.643>.
- [2] Parker S, Buller RM. A review of experimental and natural infections of animals with monkeypox virus between 1958 and 2012. *Future Virol* 2013;8:129–57. <https://doi.org/10.2217/fvl.12.130>.
- [3] Haider N, Guitian J, Simons D, Asogun D, Ansumana R, Honeyborne I, et al. Increased outbreaks of monkeypox highlight gaps in actual disease burden in Sub-Saharan Africa and in animal reservoirs. *Int J Infect Dis* 2022;122:107–11. <https://doi.org/10.1016/j.ijid.2022.05.058>.
- [4] Happi C, Adetifa I, Mbala P, Njouom R, Nakoune E, Happi A, et al. Urgent need for a non-discriminatory and non-stigmatizing nomenclature for monkeypox virus. *PLOS Biol* 2022;20:e3001769. <https://doi.org/10.1371/journal.pbio.3001769>.
- [5] Rimoin AW, Kisalu N, Kebela-Ilunga B, Mukaba T, Wright LL, Formenty P, et al. Endemic human monkeypox, Democratic Republic of Congo, 2001–2004. *Emerg Infect Dis* 2007;13:934–7. <https://doi.org/10.3201/eid1306.061540>.
- [6] Likos AM, Sammons SA, Olson VA, Frace AM, Li Y, Olsen-Rasmussen M, et al. A tale of two clades: monkeypox viruses. *J Gen Virol* 2005;86:2661–72. <https://doi.org/10.1099/vir.0.81215-0>.
- [7] Ladnyj ID, Ziegler P, Kima E. A human infection caused by monkeypox virus in Basankusu Territory, Democratic Republic of the Congo. *Bull World Health Organ* 1972;46:593–7.
- [8] Muyembe-Tamfum JJ, Mulembakani P, Lekie RB, Szczeniowski M, Jeżek Z, Doshi R, et al. Smallpox and its eradication in the Democratic Republic of Congo: lessons learned. *Vaccine* 2011;29:D13–8. <https://doi.org/10.1016/j.vaccine.2011.10.049>.
- [9] Hoff N, Doshi R, Colwell B, Kebela-Ilunga B, Mukadi P, Mossoko M, et al. Evolution of a disease surveillance system: an increase in reporting of human monkeypox disease in the Democratic Republic of the Congo, 2001–2013. *Int J Trop Dis Heal* 2017;25:1–10. <https://doi.org/10.9734/ijtdh/2017/35885>.
- [10] Heymann DL, Simpson K. The evolving epidemiology of human monkeypox: questions still to be answered. *J Infect Dis* 2021;223:1839–41. <https://doi.org/10.1093/infdis/jiab135>.
- [11] Moore ZS, Seward JF, Lane JM. Smallpox *Lancet* 2006;367:425–35. [https://doi.org/10.1016/S0140-6736\(06\)68143-9](https://doi.org/10.1016/S0140-6736(06)68143-9).
- [12] Jezek Z, Grab B, Dixon H. Stochastic model for interhuman spread of monkeypox. *Am J Epidemiol* 1987;126:1082–92. <https://doi.org/10.1093/oxfordjournals.aje.a114747>.
- [13] Pebody R. Human monkeypox in Kasai Oriental, Democratic Republic of the Congo, February 1996 – October 1997: preliminary report. *Euro Surveill* 1997;1.
- [14] Rimoin AW, Mulembakani PM, Johnston SC, Lloyd Smith JO, Kisalu NK, Kinkela TL, et al. Major increase in human monkeypox incidence 30 years after smallpox vaccination campaigns cease in the Democratic Republic of Congo. *Proc Natl Acad Sci USA* 2010;107:16262–7. <https://doi.org/10.1073/pnas.1005769107>.
- [15] Mbala PK, Huggins JW, Riu-Rovira T, Ahuka SM, Mulembakani P, Rimoin AW, et al. Maternal and fetal outcomes among pregnant women with human monkeypox infection in the Democratic Republic of Congo. *J Infect Dis* 2017;216:824–8. <https://doi.org/10.1093/infdis/jix260>.
- [16] McCollum AM, Shelus V, Hill A, Traore T, Onoja B, Nakazawa Y, et al. Epidemiology of human mpox — worldwide, 2018–2021. *MMWR* 2023;72:68–72. <https://doi.org/10.15585/mmwr.mm7203a4>.
- [17] Whitehouse ER, Bonwitt J, Hughes CM, Lushima RS, Likafi T, Nguete B, et al. Clinical and epidemiological findings from enhanced monkeypox surveillance in Tshuapa Province, Democratic Republic of the Congo during 2011–2015. *J Infect Dis* 2021;223:1870. <https://doi.org/10.1093/infdis/jiab133>.
- [18] Mande G, Akonda I, De Weggheleire A, Brosius J, Liesenborghs L, Bottieau E, et al. Enhanced surveillance of monkeypox in Bas-Uélé, Democratic Republic of Congo: the limitations of symptom-based case definitions. *Int J Infect Dis* 2022;122:647–55. <https://doi.org/10.1016/j.ijid.2022.06.060>.
- [19] Beer EM, Bhargavi Rao V. A systematic review of the epidemiology of human monkeypox outbreaks and implications for outbreak strategy. *PLoS Negl Trop Dis* 2019;13:e0007791. <https://doi.org/10.1371/journal.pntd.0007791>.
- [20] Jezek Z, Marennikova SS, Mutumbo M, Nakano JH, Paluku KM, Szczeniowski M, et al. Human monkeypox: a study of 2,510 contacts of 214 patients. *J Infect Dis* 1986;154:551–5. <https://doi.org/10.1093/infdis/154.4.551>.
- [21] Hutin YJ, Williams RJ, Malfait P, Pebody R, Loparev VN, Ropp SL, et al. Outbreak of human monkeypox, Democratic Republic of Congo, 1996 to 1997. *Emerg Infect Dis* 2001;7:434–8. <https://doi.org/10.3201/eid0703.017311>.
- [22] Mukinda VB, Mwema G, Kilundu M, Heymann DL, Khan AS, Esposito JJ. Re-Emergence of human monkeypox in Zaire in 1996. monkeypox epidemiologic working group. *Lancet* (London, England) 1997;349:1449–50. [https://doi.org/10.1016/S0140-6736\(05\)63725-7](https://doi.org/10.1016/S0140-6736(05)63725-7).
- [23] Nolen LD, Osadebe L, Katomba J, Likofata J, Mukadi D, Monroe B, et al. Extended human-to-human transmission during a monkeypox outbreak in the Democratic Republic of the Congo. *Emerg Infect Dis* 2016;22:1014–21. <https://doi.org/10.3201/eid2206.150579>.
- [24] Milton DK. What was the primary mode of smallpox transmission? Implications for biodefense. *Front Cell Infect Microbiol* 2012;2:150. <https://doi.org/10.3389/fcimb.2012.00150>.
- [25] Reynolds MG, Yorita KL, Kuehnert MJ, Davidson WB, Huhn GD, Holman RC, et al. Clinical manifestations of human monkeypox influenced by route of infection. *J Infect Dis* 2006;194:773–80. <https://doi.org/10.1086/505880>.
- [26] Jezek Z, Grab B, Szczeniowski MV, Paluku KM, Mutumbo M. Human monkeypox: secondary attack rates. *Bull World Health Organ* 1988;66:465–70.
- [27] Breman JG, Ruti K, Steniowski MV. Human monkeypox, 1970–79. *Bull World Health Organ* 1980;58:165–82.
- [28] Centers for Disease Control and Prevention (CDC). Update: multistate outbreak of monkeypox - Illinois, Indiana, Kansas, Missouri, Ohio, and Wisconsin. *MMWR* 2003;52:561–4. <https://doi.org/10.1001/archderm.139.9.1229>.
- [29] Yinka-Ogunleye A, Aruna O, Dalhat M, Ogoina D, McCollum A, Disu Y, et al. Outbreak of human monkeypox in Nigeria in 2017–18: a clinical and epidemiological report. *Lancet Infect Dis* 2019;19:872–9. [https://doi.org/10.1016/S1473-3099\(19\)30294-4](https://doi.org/10.1016/S1473-3099(19)30294-4).
- [30] Marwah A, Ogoina D, Au NH, Gibb NP, Portillo MT, Thomas-Bachli A, et al. Estimating the size of the monkeypox virus outbreak in Nigeria and

- implications for global control. *J Travel Med* 2022;29:1–5. <https://doi.org/10.1093/jtm/taac149>.
- [31] Ogoina D, Yinka-Ogunleye A. Sexual history of human monkeypox patients seen at a tertiary hospital in Bayelsa, Nigeria. *Int J STD AIDS* 2022;33:928–32. <https://doi.org/10.1177/09564624221119335>.
- [32] World Health Organization (18 May 2022). Monkeypox - United Kingdom of Great Britain and Northern Ireland n.d. <https://www.who.int/emergencies/disease-outbreak-news/item/2022-DON383>. [Accessed 21 February 2023].
- [33] Vivancos R, Anderson C, Blomquist P, Balasegaram S, Bell A, Bishop L, et al. Community transmission of monkeypox in the United Kingdom, April to May 2022. *Eurosurveillance* 2022;27:1–4. <https://doi.org/10.2807/1560-7917.ES.2022.27.22.2200422>.
- [34] 2022–23 Mpox outbreak: global trends. Geneva: World Health Organization; 2023. n.d. https://worldhealthorg.shinyapps.io/mpox_global. [Accessed 27 June 2023].
- [35] Gigante CM, Korber B, Seabolt MH, Wilkins K, Davidson W, Rao AK, et al. Multiple lineages of monkeypox virus detected in the United States, 2021–2022. *Science* 2022;378:560–5. <https://doi.org/10.1126/science.add4153>.
- [36] Isidro J, Borges V, Pinto M, Sobral D, Santos JD, Nunes A, et al. Phylogenomic characterization and signs of microevolution in the 2022 multi-country outbreak of monkeypox virus. *Nat Med* 2022;28:1569–72. <https://doi.org/10.1038/s41591-022-01907-y>.
- [37] Dumonteil E, Herrera C, Sabino-Santos G. Monkeypox virus Evolution before 2022 outbreak. *Emerg Infect Dis* 2023;29:451–3. <https://doi.org/10.3201/eid2902.220962>.
- [38] Mitjà O, Ogoina D, Titanji BK, Galvan C, Muyembe J, Marks M, et al. Monkeypox *Lancet* (London, England) 2022;6736:1–15. [https://doi.org/10.1016/S0140-6736\(22\)02075-X](https://doi.org/10.1016/S0140-6736(22)02075-X).
- [39] Mitjà O, Alemany A, Marks M, Lezama Mora JI, Rodríguez-Aldama JC, Torres Silva MS, et al. Mpox in people with advanced HIV infection: a global case series. *Lancet* 2023;401:939–49. [https://doi.org/10.1016/s0140-6736\(23\)00273-8](https://doi.org/10.1016/s0140-6736(23)00273-8).
- [40] Thornhill JP, Barkati S, Walmsley S, Rockstroh J, Antinori A, Harrison LB, et al. Monkeypox virus infection in humans across 16 countries — April–June 2022. *N Engl J Med* 2022;387:679–91. <https://doi.org/10.1056/nejmoa2207323>.
- [41] Pan D, Nazareth J, Sze S, Martin CA, Decker J, Fletcher E, et al. Transmission of Mpox: a narrative review of environmental, viral, host and population factors in relation to the 2022 international outbreak. *J Med Virol* 2023;95:e28534. <https://doi.org/10.1002/jmv.28534>.
- [42] De Baetselier I, Van Dijck C, Kenyon C, Coppens J, Michiels J, de Block T, et al. Retrospective detection of asymptomatic monkeypox virus infections among male sexual health clinic attendees in Belgium. *Nat Med* 2022;28:2288–92. <https://doi.org/10.1038/s41591-022-02004-w>.
- [43] Ferré VM, Bachelard A, Zaidi M, Armand-Lefevre L, Descamps D, Charpentier C, et al. Detection of monkeypox virus in anorectal swabs from asymptomatic men who have sex with men in a sexually transmitted infection screening program in Paris, France. *Ann Intern Med* 2022;175:1491–2. <https://doi.org/10.7326/M22-2183>.
- [44] Brosius I, Dijck C Van, Coppens J, Vandenhove L, Bangwen E, Vanroye F, et al. Presymptomatic viral shedding in high-risk mpox contacts: a prospective cohort study. *J Med Virol* 2023;95:e28769. <https://doi.org/10.1002/jmv.28769>.
- [45] Ward T, Christie R, Paton RS, Cumming F, Overton CE. Transmission dynamics of monkeypox in the United Kingdom: contact tracing study. *BMJ* 2022;379:e073153. <https://doi.org/10.1136/bmj-2022-073153>.
- [46] Kupferschmidt K. Monkeypox outbreak is ebbing-but why exactly? *Science* 2022;378:343. <https://doi.org/10.1126/science.adf4961>.
- [47] Low N, Bachmann LH, Ogoina D, McDonald R, Ipekci AM, Quilter IAS, et al. Mpox virus and transmission through sexual contact: defining the research agenda. *PLOS Med* 2023;20:e1004163. <https://doi.org/10.1371/journal.pmed.1004163>.