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Nima Rezaei *Editor*

Poxviruses

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Preface

Monkeypox (Mpox) is an infectious disease, caused by the monkeypox virus, which led to an outbreak in non-endemic region in 2022, after about 80 years of its identification in endemic regions. It shows the importance of being updated on poxviruses, not only the pathogenesis and characteristics, but also the diagnosis and treatment.

Poxviruses are oval-shaped viruses with large double-stranded DNA genomes, which could lead to infections in humans and mainly present with skin lesions and nodules, or disseminated rash.

Orthopoxvirus (smallpox virus, vaccinia virus, cowpox virus, and monkeypox virus), Parapoxvirus (orf virus, pseudocowpox, bovine papular stomatitis virus), Yatapoxvirus (tanapox virus, yaba monkey tumor virus), and Molluscipoxvirus (molluscum contagiosum virus) are four genera of poxviruses that can infect humans.

As of importance of Mpox, the book starts with a chapter on history of Monkeypox from the past to the future. Chapter 2 explains the concept of One Health in poxviruses. Evolution and characterization of poxviruses are discussed in Chaps. 3 and 4. Zoonotic and Zooanthroponotic potential of Mpox is the subject of Chap. 5. Molecular immunobiology of Mpox, vaiola, molluscum contagiosum, and orf are explained in Chaps. 6–11. Chapter 12 is focused on poxviridae pneumonia, while Chap. 13 is about poxviruses in children. Laboratory diagnosis and potential challenges is the subjects of Chaps. 14–16. Poxvirus (Mpox) Vaccines are explained in details in Chaps. 17–20. Potential antiviral bioactive compounds and complementary therapy for poxviruses are discussed in Chaps. 21 and 22, respectively. Chapters 23 and 24 are discussed the case of Mpox outbreak 2023 for travellers and in cancer therapy, respectively. Finally, stigma, and the importance of ethical standards for research on poxviruses are discussed on the final Chaps. 25 and 26.

I hope that this on time book will be cogent and of special value for researchers and clinicians, especially for virologists, immunologists, infectious disease specialists as well as those who are working in public health who wish to extend their knowledge on poxviruses.

Stockholm, Sweden — Nima Rezaei, MD, Ph.D.

Acknowledgment I would like to express my gratitude to the Editorial Assistant of this book series, Dr. Amene Saghazadeh.

Contents

1 **Monkeypox: Past, Present, and Future** 1
Gulfaraz Khan and Nighat Perveen

2 **Poxviruses from the Concept of One Health** 21
Laith AL-Eitan, Mountaser Haddad and Ahmad Mihyar

3 **Assembly and Evolution of Poxviruses** 35
Tanvi Aggarwal and Kiran Kondabagil

4 **Characterization of Fowlpox Virus** 55
Rajesh Kumar Verma and A. K. Gangwar

5 **Zoonotic and Zooanthroponotic Potential of Monkeypox** 75
Mustafa O. Atasoy, Rania F. El Naggar, Mohammed A. Rohaim and Muhammad Munir

6 **Biological Characteristics and Pathogenesis of Monkeypox Virus: An Overview** 91
Mohamed H. Kalaba, Gamal M. EL-Sherbiny, Mohammed H. Sharaf and Eman E. Farghal

7 **Molecular Virology of Orthopoxviruses with Special Reference to Monkeypox Virus** 111
Mohammed A. Rohaim, Rania F.El Naggar, Mustafa O. Atasoy and Muhammad Munir

8 **Type I Interferon: Monkeypox/Mpox Viruses Achilles Heel?** . . . 125
Jacqueline Williams, James Bonner, Karen Kibler and Bertram L. Jacobs

9 **Biology of Variola Virus** 139
Poornima Gopi, Gayathri Krishna and Mohanan Valiya Veettil

10 **Molluscum Contagiosum Virus: Biology and Immune Response** 151
Luigi Santacroce and Thea Magrone

11 **Orf, a Human Parapoxvirus Infection** 171
Rujittika Mungmunpuntipantip and Viroj Wiwanitkit

12 Poxviridae Pneumonia 183
Francesco Nucera, Letterio Bonina, Antonino Cipolla, Pietro Pirina, Philip M. Hansbro, Ian M. Adcock and Gaetano Caramori

13 Poxviruses in Children 205
Katarzyna Mazur-Melewska

14 Human Monkeypox Virus and Host Immunity: New Challenges in Diagnostics and Treatment Strategies 219
Shailendra Dwivedi, Vijay Singh, Ruchika Agrawal, Radhieka Misra, Sadashiv, Ghizal Fatima, Afroz Abidi and Sanjeev Misra

15 Role of the Laboratory in the Diagnosis of Poxvirus Infections 239
Pragya Agarwala and Archa Sharma

16 Monkeypox Diagnosis in Clinical Settings: A Comprehensive Review of Best Laboratory Practices 253
Nityanand Jain, Tungki Pratama Umar, Reem Sayad, Muhammed Edib Mokresh, Kevin Tandarto, Reynold Siburian, Phey Liana, Sniedze Laivacuma and Aigars Reinis

17 Poxvirus Vaccines: Past, Present, and Future 273
Malay Jhancy

18 Current Status of Vaccine Development for Monkeypox Virus 289
Amber Rastogi and Manoj Kumar

19 Treatment and Vaccination for Smallpox and Monkeypox 301
Klaus P. Saalbach

20 A Multi-pronged Approach to Addressing Global Poxviruses Vaccine Inequity: A Case of Monkeypox 317
Barbara W. K. Son, Otioli W. Wambalaba and Wamukota Francis Wambalaba

21 The Overview of Potential Antiviral Bioactive Compounds in Poxviruses 331
Sunil Kumar

22 Natural Immunomodulatory Agents as a Complementary Therapy for Poxviruses 337
Sami I. Ali and Abeer Salama

23 Monkeypox Outbreak 2022, from a Rare Disease to Global Health Emergence: Implications for Travellers 355
Oyelola Adegboye, Faith Alele, Anton Pak, Emmanuel Alakunle, Theophilus Emeto, Peter Leggat and Malachy Okeke

24 Application of Oncolytic Poxviruses: An Emerging Paradigm in Cancer Therapy 369
Prasenjit Chakraborty, Randhir Kumar, Sanjay Karn, Dharmiben D. Raviya and Priya Mondal

25 Overcoming Stigma: The Human Side of Monkeypox Virus 383
Tungki Pratama Umar, Nityanand Jain, Reem Sayad, Kevin Tandarto, Shivani Jain and Aigars Reinis

26 Poxviruses as Agents of Biological Warfare: The Importance of Ensuring Ethical Standards for Research with Viruses 399
Prasenjit Chakraborty, Randhir Kumar, Sanjay Karn, Dharmiben D. Raviya and Priya Mondal

Subject Index 413

Author Index 421

About the Editor

Prof. Nima Rezaei, MD, Ph.D. gained his medical degree (MD) from Tehran University of Medical Sciences and subsequently obtained an M.Sc. in Molecular and Genetic Medicine and a Ph.D. in Clinical Immunology and Human Genetics from the University of Sheffield, UK. He also spent a short-term fellowship of Pediatric Clinical Immunology and Bone Marrow Transplantation in the Newcastle General Hospital. Professor Rezaei is now the Full Professor of Immunology and Vice Dean of Research and Technologies, School of Medicine, Tehran University of Medical Sciences, and the co-founder and Head of the Research Center for Immunodeficiencies. He is also the Founder of Universal Scientific Education and Research Network (USERN). Professor Rezaei has already been the Director of more than 100 research projects and has designed and participated in several international collaborative projects. Professor Rezaei is the editor, editorial assistant, or editorial board member of more than 40 international journals. He has edited more than 50 international books, has presented more than 500 lectures/posters in congresses/meetings, and has published more than 1200 scientific papers in the international journals.

Monkeypox: Past, Present, and Future

1

Gulfaraz Khan and Nighat Perveen

Abstract

Monkeypox (Mpox) is a zoonotic disease caused by a virus (monkeypox virus-MPV) belonging to the Poxviridae family. In humans, the disease has an incubation period of 5–21 days and then progresses in two phases, the prodromal phase and the rash phase. The prodromal phase is characterized by non-specific symptoms such as fever, muscle pain, malaise, lymphadenopathy, headache, and chills. Skin lesions appear in the rash phase of the disease. These lesions progress through different stages (macules, papules, vesicles, and pustules). In May 2022, WHO reported an outbreak of human Mpox in several countries which were previously Mpox-free. As per the CDC report of March 01, 2023, a total of 86,231 confirmed cases of Mpox and 105 deaths have been reported from 110 countries and territories across the globe. Notably, more than 90% of these countries were reporting Mpox for the first time. The phylogenetic analysis revealed that this outbreak was associated with the virus from the West African clade. However, most of the cases in this outbreak had no evidence of travel histories to MPV-endemic countries in Central or West Africa. This outbreak was primarily driven by the transmission of the virus via intimate contact in men who have sex with men (MSM). The changing epidemiology of Mpox raised concerns about the increasing spread of the disease in non-endemic countries and the urgent need to control and prevent it. In this chapter, we present all the documented cases of Mpox from 1970 to 2023 and discuss the past, present, and future of MPV.

Keywords

Monkeypox · Monkeypox virus · Prevalence · Distribution · Epidemiology · Transmission · MPV strains

1.1 Introduction

Remarkable success in the development of antibiotics and vaccines in the mid-twentieth century gave the impression that we could control

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and eventually eliminate infectious diseases (Jos and van der 2013; Morse 1991). However, the emergence and re-emergence of various infectious diseases over the last few decades have proved that controlling or eliminating infectious diseases is a much bigger challenge than we assumed (Morens et al. 2004; Perveen and Khan 2022; Reperant and Osterhaus 2017). We live in a world in which we interact with not only ourselves but also with animals and the environment. Additional factors such as widespread travel, pathogens mutating, civil unrest and wars, and changing human behaviors, provide ample opportunity for the emergence and re-emergence of infectious diseases (Church 2004; Costello et al. 2022; Morens et al. 2004; Reperant and Osterhaus 2017). The recent pandemic of the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) is an example of the devasting impact emerging pathogens can have on all aspects of a society. As the world was battling to control SARS-CoV2, another viral disease reemerged, monkeypox (Mpox). On 23rd July 2022, the WHO declared its highest-level alert for the Mpox outbreak.

The re-emergence of monkeypox virus (MPV) raised serious global health concerns. Mpox is related to smallpox, one of the most feared human diseases with a 30% case fatality rate and high virulence (Xiang and White 2022). After the eradication of smallpox in 1980, routine smallpox vaccination was stopped and vaccine-derived immunity waned. Since smallpox vaccine also provided approximately 85% protection against MPV infection or/and reduction in disease severity (Di-Giulio and Eckburg 2004; Jezek et al. 1988a), waning immunity to smallpox, increased the proportion of people living in the endemic areas in Central and West Africa susceptible to Mpox (Arita et al. 1985; Brown and Leggat 2016; Fine et al. 1988). The first MPV outbreak outside of Africa occurred in 2003 in the USA when small mammals, such as rope squirrels, giant pouched rats, and dormice, were shipped from Ghana to Texas (Hutson et al. 2015; Sale et al. 2006). Infected rodents were kept with native prairie dogs and the latter became the source of the monkeypox outbreak in the different states (Sale et al. 2006).

In contrast to the 2003 outbreak, the characteristics of the 2022 multi-country Mpox outbreak were very different. The outbreak was first recognized in May 2022 when Mpox cases were reported to WHO from almost 12 non-endemic countries (WHO 2022c). On June 23, 2022, the Committee for International Health Regulations (IHR) held an emergency meeting to discuss the outbreak. The WHO Secretariat discussed the global epidemiological situation and reported 3040 cases from 47 countries since the beginning of the outbreak. The number of cases continued to rise rapidly and by 14 July, 66 countries reported confirmed cases, totaling 11,188, with two deaths, one in Nigeria and one in the Central African Republic (WHO 2022d). Notably, 80% of the cases were reported from the European Region, followed by 18% from the America Region. African, Eastern Mediterranean, and the Western Pacific Regions reported less than 2% of the cases (WHO 2022d). Virtually all (99%) of the confirmed cases were in males, 79% of whom were in the age group 25–45 years. Furthermore, the cases in Western countries had no epidemiological links to the areas where Mpox was endemic. Moreover, most of the cases were among gay, bisexual, and men who have sex with men (MSM) living in urban areas in clustered social and sexual networks (WHO 2022a). However, after the second committee meeting, on July 23, 2022, the Director-General (WHO) declared Mpox a Public Health Emergency of International Concern (PHEIC).

In this chapter, we discuss the past and present multi-country Mpox outbreak, with emphasis on epidemiology, classification, natural reservoirs, transmission route, clinical features, diagnosis, vaccines and drugs, and prevention and control strategies to circumvent future human infections. Furthermore, monkeypox viruses, group into two clades, the Congo Basin and the West African clade. We retrieved MPV genome data from the GenBank and performed the phylogenetic analyses of genome sequences from the 2022 outbreak and found that this outbreak was associated with the spread of the West African clade. This clade is associated

with milder disease with known human-to-human spread. We also document all human cases of Mpox from 1970 to 2023 country-wise (Table 1.1) and also in various regions.

1.2 Past

1.2.1 Epidemiology of Monkeypox Virus

The last human case of smallpox occurred in 1977 in Somalia (Deria et al. 1980). However, total eradication was not confirmed until 1980. With the subsequent ending of smallpox vaccination, monkeypox emerged as an important *Orthopoxvirus* pathogenic to humans. The first human Mpox case was reported in August 1970 in the Democratic Republic of Congo (DRC) in a 9-month-old child admitted to hospital on suspicion of smallpox (Ladnyj et al. 1972). WHO Smallpox Reference Centre, Moscow, confirmed the causative agent to be monkeypox and not smallpox virus (Marennikova et al. 1972). The child's family members denied contact with any person who had a pox-like rash and there were no other cases reported in the area. The patient's father however revealed that monkeys were eaten by the family from time to time. The MPV was first identified in monkeys from Asia in a laboratory in Copenhagen, Denmark, in 1958 (Von Magnus et al. 1959). It was believed that primates caught the virus from an African source. The virus was detected in numerous animals in Africa, including Gambian rat, shrew, sooty mangabey monkey, and rope squirrel. However, antibodies to the virus were most prevalent in African squirrels (Falendysz et al. 2015; Hutin et al. 2001; Khodakevich et al. 1986; Radonić et al. 2014; Reynolds et al. 2019). In 1964, an outbreak of MPV occurred in a Zoo in Rotterdam, Netherlands. During this outbreak, the virus infected several different types of animals, including, gorillas, chimpanzees, gibbons, giant anteaters, orangutans, and marmosets (Wachtman and Mansfield 2012). However, not all animals are susceptible to MPV. For example, chickens, rabbits, hamsters, and guinea pigs showed no detectable infection when these animals were intentionally infected in the lab (Crandell 1969).

Until the 2022 outbreak, Mpox in humans was fairly uncommon, only sporadic cases were reported in tropical rainforest regions of Central and Western Africa, most often as a result of animal-to-human transmission. Secondary human-to-human spread accounted for only about 28% of the cases (Shchelkunov et al. 2001). Furthermore, in DRC, during the surveillance for human Mpox from 1981 to 1986, the virus was identified in 338 cases. The case fatality rate was around 10% in individuals not vaccinated with vaccinia (the smallpox vaccine virus) (Hutin et al. 2001).

The first case of Mpox outside of Africa was reported in 2003 in the USA when a 3-year-old girl was diagnosed with the disease after being bitten by her pet, prairie dog (Reed et al. 2004). The prairie dog contracted the infection when housed together with rodents imported from Ghana. This outbreak resulted in the girl's parents and 69 others contracting the infection. However, survey of wild animals in USA, especially in Wisconsin and Illinois, indicated that there was no spillover of the virus into wild animals (Cohen 2022a). Furthermore, infected humans did not pass on the disease to others. Therefore, the disease was contained and the fear of a major outbreak quickly disappeared.

1.2.2 Natural Reservoirs of MPV

Mpox is a zoonotic disease. However, the natural reservoir remains unknown. Assessment of MPV prevalence in small mammals at the human–animal interface in the DRC, indicated that several animal species were positive for anti-orthopoxvirus IgG antibodies, including *Funisciurus spp*. (African-striped squirrel), *Graphiurus lorraineus* (Lorrain dormouse), *Cricetomys emini* (Emin's pouched rat), *Heliosciurus rufobrachium* (Red-legged sun squirrel), *Oenomys hypoxanthus* (Rufous-nosed

rat), and *Petrodromus tetradactylus* (Four-toed elephant shrew) (Doty et al. 2017; Hutson et al. 2007). Rodents are considered to be the most likely host reservoir (Doty et al. 2017). Similarly, other species of African-striped squirrel, redless tree squirrel (*Funisciurus anerythrus*), Congo rope squirrel (*Funisciurus congicus*), and wild boar (*Sus scrofa*), were also found to be positive for anti-orthopoxvirus antibodies in the DRC during epidemiologic and clinical studies of MPV (Hutin et al. 2001; Khodakevich et al. 1986). Although several different species of non-human primates have also been shown to be seropositive for MPV, they are unlikely to be the natural reservoir because the seroprevalence in these animals is fairly low. The MPV has also been isolated from Ivory Coast from sooty mangabey (*Cercocebus atys*) (Radonić et al. 2014).

1.2.3 What Is MPV?

Poxviruses cause infections in both vertebrates and invertebrates. MPV belongs to the genus *Orthopoxvirus* in the family Poxviridae. The Poxviridae family is divided into two subfamilies, Chordopoxvirinae and Entomopoxvirinae. Poxviruses of the subfamily Chordopoxvirinae cause infections in vertebrates, whereas the Entomopoxvirinae cause infections in insects (Sklenovská 2020). The Chordopoxvirinae subfamily consists of 11 genera, and *Orthopoxvirus* is one of them. Most of *Orthopoxviruses* are zoonotic pathogens and are sustained in nature in animal reservoirs (Sklenovská 2020). MPV is one of the five species of *Orthopoxvirus*. Members pathogenic to humans include variola virus (the causative agent of smallpox), cowpox virus, camelpox virus, and vaccinia virus (Marennikova and Moyer 2005). The Orthopoxvirion comprises four main components, namely the core, the lateral bodies, the inner membrane, and the outer protein cover. The central core contains the viral double-stranded DNA (dsDNA) and associated enzymes. The central core and the lateral bodies are surrounded by the outer membrane that is composed of surface tubules (Sklenovská 2020) (Fig. 1.1). For binding to receptors on its target cells, the virus uses proteins on its surface. The MPV genome is a large (197 kbp) single linear molecule of dsDNA, which is among the largest of all viral genomes (Moss and Damon 2013). However, unlike other DNA viruses, MPV is unique in that it replicates in the cytoplasm instead of the nucleus. Moreover, MPV does not require a particular host receptor, and hence, it can infect a number of different types of mammalian cells (Sklenovská 2020).

1.2.4 Transmission Route of MPV to Humans

MPV is a zoonotic infection, usually transmitted from animals to humans. Human-to-human spread can be due to nosocomial (Adler et al. 2022) and household transmission (Nolen et al. 2015). Humans become infected when there is direct physical contact with an infected animal or person or their body fluid (Bernard and Anderson 2006; Jezek et al. 1988a). Infected surfaces, tools, or bedding/clothing in hospitals and houses can also be the source of transmission (Nakoune et al. 2017; Nolen et al. 2015) (Fig. 1.2). Another source of transmission can be the virus shed in urine and feces (Hutson et al. 2015).

Animal hosts of MPV include rodents and primates, and the risk of the virus transmission from animals can be prevented by avoiding contact with sick or dead animals, especially in endemic countries. MPV can also spread by handling or consuming bush meat from infected animals or monkeys (Alakunle et al. 2020; Brown and Leggat 2016). Furthermore, MPV-infected individuals should avoid touching their pets, livestock, and wildlife. The natural route of transmission of MPV in animals can include ingestion of viral particles or via respiratory transmissions when healthy animals are caged together. MPV infections in children have been associated with severe disease and a high mortality compared to adults (Mbala et al. 2017; Yinka-Ogunleye et al. 2019). Vertical

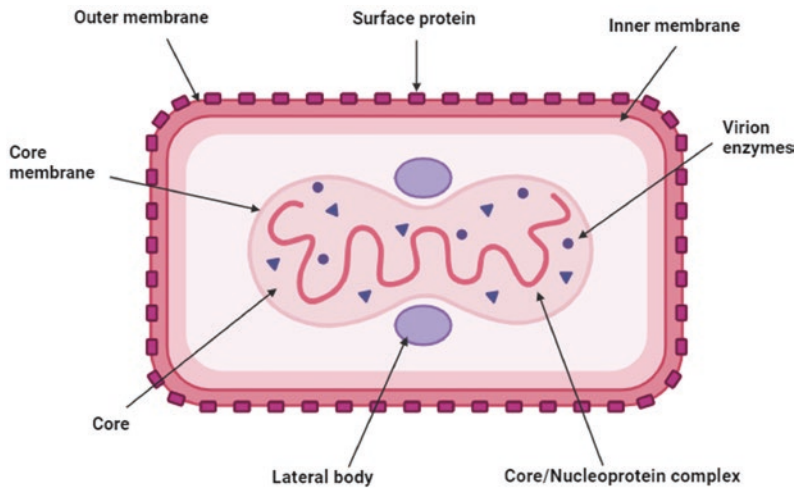

Fig. 1.1 The structure of poxvirus. The figure was created with BioRender (https://Biorender.Com/)

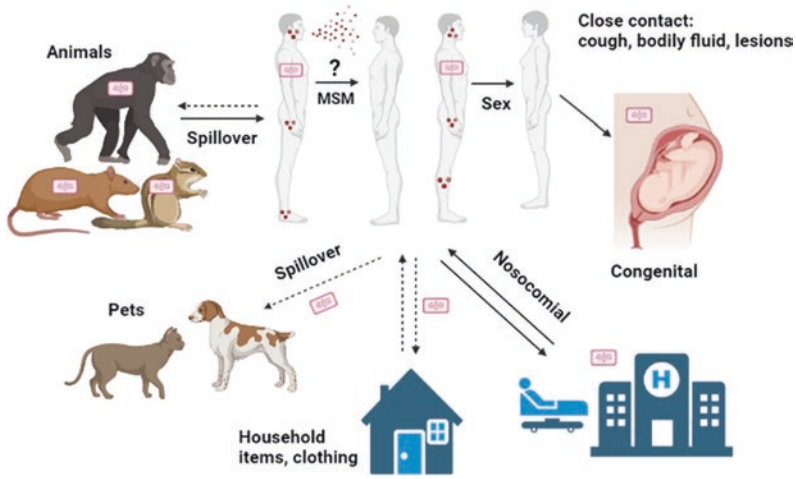

Fig. 1.2 Transmission routes of monkeypox virus. The figure was created with BioRender (https://Biorender.Com/)

transmission of MPV from infected mother to her fetus has also been reported during Mpox outbreak in the DRC (Mbala et al. 2017).

A few decades after the cessation of smallpox vaccination, the number of human Mpox cases in DRC was observed to have increased significantly (Breman et al. 1980; Rimoin et al. 2010). It was believed that this surge was due to a number of contributing factors, such as increasing proportion of people unvaccinated for smallpox and waning immunity (Breman et al. 1980; Rimoin et al. 2010). Moreover, increased contact between humans and animals or their body fluids, brought about by deforestation, urbanization, destruction of natural habitats, changes in farming practices, and consumption of wild animals, are also believed to facilitate spillover events (Magouras et al. 2020; Zhang et al. 2008). However, the 2022 multi-country Mpox outbreak had a different pattern; Mpox clusters were reported primarily in men who have sex with men (MSM).

1.2.5 Clinical Picture of Mpox

Symptoms of Mpox can include fever, headache, muscle aches, backache, and lymphadenopathy (Sklenovská 2020; Tack and Reynolds 2011). However, symptoms vary from person to person. The disease appears with the development of a characteristic rash of varying severity, with an incubation period ranging from 5 to 21 days (Al-Tammemi et al. 2022). MPV lesions progresses through different stages, from macules to papules, to vesicles and pustules, and finally to scabs, before falling off. The illness persists for 2–4 weeks (Al-Tammemi et al. 2022). In the 2022 outbreak, most patients presented with lesions less than 100 in number, often localized to a few regions of the body (Mitjà et al. 2023b). The clinical presentation has some resemblance to several other viral exanthems, such as smallpox, bacterial skin infections, scabies, measles, syphilis, and most notably, chickenpox (Moore et al. 2023). However, patients with advanced HIV infection, having CD4 counts less than 100 cells per μl, tend to present with more severe, disseminated, necrotizing skin lesions, as well as involvement of lungs, secondary infections, and sepsis (Mitjà et al. 2023a). These individuals have a poor prognosis compared to non-immunosuppressed individuals. Due to the similarities in the clinical presentation between chickenpox and Mpox in healthy immunocompetent individuals, without laboratory testing, the two diseases can be misdiagnosed (Jezek et al. 1988b; Sklenovská 2020). Early detection of MPV infection and the application of appropriate preventive measures are important in reducing the transmission of virus. Delays in confirming the infection can lead to inappropriate treatment and prolonged recovery (Tack and Reynolds 2011).

1.3 Present

1.3.1 The 2022 MPV Outbreak

In the 2022 outbreak, most of the infected cases were outside of Africa. The demographics of this outbreak were very different from the previous outbreaks that occurred in Africa; more than 95% of the cases in the 2022 outbreak were in MSM with a median age of 37 years (Angelo et al. 2023). By contrast, the outbreaks in Africa were sporadic, usually restricted to one location, and often seen in children less than 15 years of age (Ježek et al. 1987). Moreover, in the 2022 outbreak, the virus spread very quickly and to multiple countries. By 20th July, 2022 (less than 3 months into the outbreak), a total of 16,836 cases were reported worldwide; 99% of which were in countries that did not previously have MPV. This led to the Director-General of WHO to declare the Mpox outbreak a Public Health Emergency of International Concern (PHEIC) (WHO 2022e). According to the most recent figures, by March 1, 2023, a total of 86,231 cases had been reported from 110 locations worldwide, 103 of which were reporting MPV for the first time (CDC 2023). In terms of mortality, a total of 105 deaths had been reported from 18 areas, and 89/105 deaths were in 14 locations with no previous evidence of MPV infection in the population. The highest number of cases (30,225) were reported from the USA, followed by Brazil (10,846 cases) and Spain (7543 cases). The highest number of deaths was also from the USA (38 deaths), followed by Brazil (15 deaths) and Peru (15 deaths) (CDC 2023).

1.3.2 MPV Reservoirs and Zoonosis

MPV was first reported in 1958 in a monkey, but it became clear that the virus could infect many different kinds of animals, including gorillas, chimpanzees, marmoset, squirrels, and Gambian rats. Although no wild animal reservoir has been reported outside of Africa, the 2022 MPV outbreak raised the possibility that wildlife outside the African continent could in future serve as a reservoir for MPV. Our direct and indirect contact with animals increases the risk of spillovers from animals to humans, and occasionally from humans to animals. This can lead to the establishment of new reservoirs and potentially pave the way for the evolution of new variants with higher virulence. Indeed, the SARS-CoV-2,

the cause of COVID-19 pandemic which killed nearly 7 million people within its first 3 years, is believed to be the result of a spillover of the virus from bats (Perveen et al. 2021; Ye et al. 2020). Moreover, reverse zoonoses for SARS-CoV-2 have also been reported in a number of different animals, including cats, dogs, and minks (Prince et al. 2021). Based on such observations, with the 2022 Mpox outbreak, public health officials in several countries instructed people to avoid contact with their pets if they had contracted MPV infection. At the time of writing this chapter, only one case of reverse zoonosis for MPV was reported (Seang et al. 2022). The spillover was reported to have occurred between two MSM and their 4-year-old dog who shared their bed. These reports, albeit anecdotal, clearly indicate that human-to-animal transmission can occur, and such spillovers could potentially lead to the establishment of new animal reservoirs (Cohen 2022b). Thus, surveillance, monitoring, and close collaboration between human and veterinary public health authorities is essential in controlling such outbreaks (Yuan et al. 2023).

1.3.3 Phylogenetic Analysis

Following the isolation and characterization of MPV in humans, efforts continued in an attempt to eradicate Mpox by vaccination and control strategies. Advances in biotechnology and the development of new techniques such as whole genome sequencing (WGS), allowed researchers to compare different strains of the virus circulating in different regions of the world and identify causes of virulence. However, the use of these novel technologies in molecular epidemiology studies is costly. In this context, the availability of viral genome data in open-access GenBanks has allowed more researchers to study the evolution and molecular epidemiology of emerging viruses, such as SARS-CoV-2 and MPV. By analyzing the phylogenetic tree, the origin of MPV was identified to the Central African Republic (CAR) and the Democratic Republic of the Congo (DRC) (Fig. 1.3). Based on the 2022 WHO recommendations, the Cong Basin (Central African) variant of the virus is now referred to as Clade I and the West African clade as Clade II (WHO 2022f). The latter consists of two subclades referred to as IIa and IIb. The 2022 MPV outbreak, which spread across the globe, was associated with the West African Clade IIb (Fig. 1.3). A recent study assessing the virulence differences of the MPV clades using a mouse animal, indicated that Clade I was the most virulent and Clade IIb the least (Americo et al. 2023). Thus, it appears that as MPV was spreading across the globe, it was adapting and becoming less virulent. Almost all MPV genomes submitted to the GenBank were from the 2022 outbreak (isolated from May–June 2022). The exceptions were the isolates from Nigeria (KJ642615.1; 2014), Russia (AF380138.1; 2001), CAR (MN702453.1; 2001 and MN702445.1; 2017), and DRC (JX878408.1; 2006 and JX878420.1; 2007) which were submitted prior to 2022. The cladogram revealed that there was a close relationship between the West African Clade (from Nigeria), and the variants reported from the American Region, European Region, and Western Pacific Region. However, the MPV from Russia grouped with virus from CAR and DRC (Clade I).

1.3.4 Comparing MPV with SARS-CoV-2 Outbreak

MPV is not like SARS-CoV-2 (Table 1.2). SARS-CoV-2 is a ssRNA virus while MPV is a dsDNA virus. Due to the low fidelity of the RNA polymerase required for viral replication, RNA viruses have a high propensity to mutate and give rise to new variants. Such variants can escape immune surveillance and limit the effectiveness of vaccines. Indeed, this is what was observed with SARS-CoV-2 outbreak. Within a short period of two years, numerous variants emerged with varying characteristics, both in terms of biology and disease pathogenesis (Barouch 2022). By contrast, DNA viruses use DNA polymerase for the

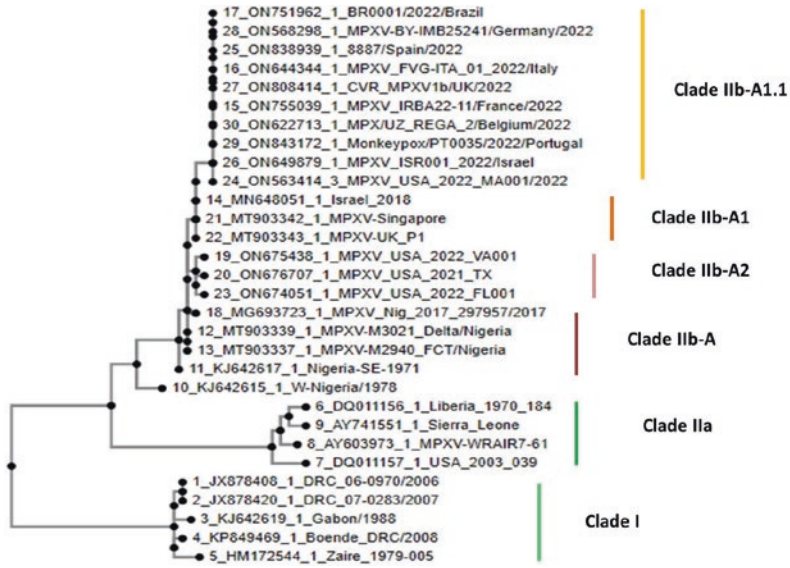

Fig. 1.3 Phylogenetic tree of monkeypox virus (MPV). Representative MPV genomes were selected from both the Congo basin and the West African clades. The sequence dataset ($n = 30$ sequences) containing all MPV genomes from *Homo sapiens* in different countries was downloaded from the GenBank database (http://www.ncbi.nlm.nih.gov/ accessed on March 10, 2023). Unique sequences in 2022 outbreak were obtained by filtration according to (De la Cruz et al. 2020) and information including year of virus collection/isolation, country, and host was also extracted. Multiple Sequence Alignment (MSA) was performed using CLUSTAL format alignment by Multiple Alignment Fast Fourier Transform (MAFFT) software (FFT-NS-2, v7.505) (Katoh et al. 2019; Kuraku et al. 2013). The online version is freely available at https://mafft.cbrc.jp/alignment/server/ (accessed on March 15, 2023). A Neighbor-Joining (NJ) phylogenetic tree was computed using Jukes–Cantor method to calculate distances from conserved sites in sequence alignment by selecting 1000 replicates of bootstrap in the MAFFT program

replication of their genome. This enzyme has high fidelity, and hence, DNA viruses are relatively more stable and less likely to result in the emergence of new variants (Kozlov 2022). In terms of clinical presentation of primary infection, SARS-CoV-2 is associated with respiratory infection, with or without symptoms, while MPV infection is associated with visible skin lesions. MPV is much less contagious than SARS-CoV-2. SARS-CoV-2 can efficiently spread through small respiratory droplets. By contrast, MPV is predominantly transmitted by close or intimate contact with actively infected persons. This includes oral, anal or vaginal sex, and kissing or touching lesions, and sharing contaminated material such as bedding. MPV infection typically presents with fever, lymphadenopathy, and the development of distinct fluid-filled lesions, most often appearing on the face and genitalia (Angelo et al. 2023; Bragazzi et al. 2022). Preliminary analysis of the genetic sequence of MPV indicated that the strain in the 2022 outbreak was related to the strain previously detected in West Africa and associated with milder disease and lower mortality rate. However, the epidemiological pattern of the 2022 virus differed from the West African isolate in that the 2022 virus was primarily transmitted via close contact in MSM community and mainly affected men in the age group 20–50 years (Kozlov 2022).

1.4 Future

1.4.1 Vaccines and Drugs

Vaccination against smallpox provides cross-protection against other poxviruses. According to the currently available statistics, about 90%

Table 1.1 Number of confirmed cases of human monkeypox from 1970 to 2023

Continent/ region	Country	Year	No. of confirmed cases	References
African Region	Democratic Republic of the Congo	1970–1986	386	Ježek and Fenner (1988)
		1997	181	WHO (1997b, c)
		1997	511?	WHO (1997a)
		2019	1739 (37 deaths)	WHO (2019b)
		2020	4594	WHO (2020)
		2022–2023	395	CDC (2023)
	Central African Republic	1984	6	Durski et al. (2018) and Khodakevich et al. (1985)
		2001	4	Durski et al. (2018)
		2010	2	Berthet et al. (2011) and Durski et al. (2018)
		2015	12	Durski et al. (2018)
		2016	11	Durski et al. (2018) and WHO (2016)
		2017	8	Durski et al. (2018)
		2018	6	Besombes et al. (2019)
		2019	25	WHO (2019b)
		2022–2023	27 (1 death)	CDC (2023)
	Cameroon	1979	1	Durski et al. (2018) and Sadeuh-Mba et al. (2019)
		1989	1	Durski et al. (2018) and Tchokoteu et al. (1991)
		2018	1	Sadeuh-Mba et al. (2019)
		2018	16	WHO (2018a)
		2022–2023	18 (3 deaths)	CDC (2023)
	Egypt	2022–2023	3	CDC (2023)
	Ghana	2022–2023	121 (4 deaths)	CDC (2023)
	Nigeria	1971	2	Breman et al. (1980)
		1978	1	Durski et al. (2018)
		2017–2018	122	Yinka-Ogunleye et al. (2019)
		2022–2023	800 (8 deaths)	CDC (2023)
	Ivory Coast	1971	1	Breman et al. (1980)
		1981	1	Merouze and Lesoin (1983)
	Liberia	1970	4	Durski et al. (2018) and Lourie et al. (1972)
		2017–2018	2 (2 deaths)	WHO (2018b)
	Liberia	2022–2023	7	CDC (2023)
	Mozambique	2022–2023	1 (1 death)	CDC (2023)
	Sierra Leone	1970	1	Durski et al. (2018) and Lourie et al. (1972)
		2014	1	Durski et al. (2018) and Reynolds et al. (2022)
		2017	1	Durski et al. (2018) and Ye et al. (2019)
	Gabon	1987	5	Durski et al. (2018)
	Benin	1978	1	Breman et al. (1980)
		2022	3	WHO (2022b)

(continued)

Table 1.1 (continued)

Continent/ region	Country	Year	No. of confirmed cases	References
	Republic of Congo	2003	3	Learned et al. (2005)
		2009	2	Reynolds et al. (2013)
		2017	6	Doshi et al. (2018)
		2019	2	WHO (2019b)
		2022–2023	5	CDC (2023)
	South Africa	2022–2023	5	CDC (2023)
	South Sudan	2005	10	Formenty et al. (2010)
	Sudan	2022–2023	18 (1 death)	CDC (2023)
Regional total		1970–2023	9072 (57 deaths)	
American Region	USA	2003	37	Reed et al. (2004)
		2022–2023	30,225 (38 deaths)	CDC (2023)
	Canada	2022–2023	1460	CDC (2023)
	Argentina	2022–2023	1099 (2 deaths)	CDC (2023)
	Aruba	2022–2023	3	CDC (2023)
	Bahamas	2022–2023	2	CDC (2023)
	Barbados	2022	1	CDC (2022)
	Bermuda	2022–2023	1	CDC (2023)
	Bolivia	2022–2023	265	CDC (2023)
	Brazil	2022–2023	10,846 (15 deaths)	CDC (2023)
	Chile	2022–2023	1431 (2 deaths)	CDC (2023)
	Costa Rica	2022–2023	188	CDC (2023)
	Colombia	2022–2023	4081	CDC (2023)
	Cuba	2022–2023	8 (1 death)	CDC (2023)
	Curacao	2022–2023	3	CDC (2023)
	Dominican Republic	2022	3	CDC (2022)
	Ecuador	2022–2023	512 (3 deaths)	CDC (2023)
	El Salvador	2022–2023	96	CDC (2023)
	Guatemala	2022–2023	390	CDC (2023)
	Guyana	2022–2023	2	CDC (2023)
	Honduras	2022–2023	18	CDC (2023)
	Jamaica	2022–2023	18	CDC (2023)
	Mexico	2022–2023	3877	CDC (2023)
	Martinique	2022–2023	7	CDC (2023)
	Panama	2022–2023	160	CDC (2023)
	Paraguay	2022–2023	109	CDC (2023)
	Peru	2022–2023	3752 (15 deaths)	CDC (2023)
	Puerto Rico	2022	4	PAHO (2022)
	Uruguay	2022–2023	19	CDC (2023)
	Venezuela	2022–2023	12	CDC (2023)

(continued)

Table 1.1 (continued)

Continent/ region	Country	Year	No. of confirmed cases	References
Regional total		2003–2023	58,629 (76)	
European Region	The UK	2018	2	Vaughan et al. (2018)
		2019	3	WHO (2021a, b)
		2022–2023	3735	CDC (2023)
	Andorra	2022–2023	4	CDC (2023)
	Austria	2022	327	CDC (2022)
	Bosnia and Herzegovina	2022–2023	9	CDC (2023)
	Belgium	2022	793 (2 death)	CDC (2023)
	Bulgaria	2022–2023	6	CDC (2023)
	Croatia	2022–2023	33	CDC (2023)
	Czechia	2022–2023	71 (1 death)	CDC (2023)
	Estonia	2022	11	ECDC (2022)
	Denmark	2022–2023	196	CDC (2023)
	Dominican Republic	2022–2023	52	CDC (2023)
	Finland	2022–2023	42	CDC (2023)
	France	2022–2023	4128	CDC (2023)
	Germany	2022–2023	3692	CDC (2023)
	Gibraltar	2022–2023	6	CDC (2023)
	Greece	2022–2023	86	CDC (2023)
	Georgia	2022–2023	2	CDC (2023)
	Greenland	2022–2023	2	CDC (2023)
	Guadeloupe	2022–2023	1	CDC (2023)
	Hungary	2022–2023	80	CDC (2023)
	Iceland	2022–2023	16	CDC (2023)
	Ireland	2022–2023	228	CDC (2023)
	Italy	2022–2023	957	CDC (2023)
	Latvia	2022–2023	6	CDC (2023)
	Lithuania	2022–2023	5	CDC (2023)
	Luxembourg	2022–2023	57	CDC (2023)
	Malta	2022–2023	33	CDC (2023)
	Moldova	2022–2023	2	CDC (2023)
	Monaco	2022–2023	3	CDC (2023)
	Montenegro	2022–2023	2	CDC (2023)
	Netherlands	2022–2023	1261	CDC (2023)
	Norway	2022–2023	95	CDC (2023)
	Poland	2022–2023	215	CDC (2023)
	Portugal	2022–2023	951	CDC (2023)

(continued)

Table 1.1 (continued)

Continent/ region	Country	Year	No. of confirmed cases	References
	Romania	2022–2023	47	CDC (2023)
	San Marino	2022–2023	1	CDC (2023)
	Serbia	2022–2023	40	CDC (2023)
	Slovenia	2022–2023	47	CDC (2023)
	Slovakia	2022–2023	14	ECDC (2022) and CDC (2023)
	Spain	2022–2023	7543 (3 deaths)	CDC (2023)
	Sweden	2022–2023	260	CDC (2023)
	Switzerland	2022–2023	551	CDC (2023)
	Ukraine	2022–2023	5	CDC (2023)
	Israel	2018	1	Erez et al. (2019)
		2022–2023	262	CDC (2023)
	Turkey	2022–2023	12	CDC (2023)
	Russia	2022–2023	2	CDC (2023)
Regional total		2018–2023	25,897 (6 deaths)	
Western Pacific Region	Singapore	2019	1	WHO (2019a)
		2022–2023	21	Akhmetzhanov et al. (2022) and CDC (2023)
	New Zealand	2022–2023	41	Akhmetzhanov et al. (2022) and CDC (2023)
	South Korea	2022–2023	4	Akhmetzhanov et al. (2022) and CDC (2023)
	Taiwan	2022–2023	4	Akhmetzhanov et al. (2022) and CDC (2023)
	Australia	2022–2023	144	CDC (2023)
	New Caledonia	2022	1	CDC (2022)
Regional total		2019–2023	216 (0 deaths)	
Eastern Mediterranean Region	Bahrain	2022–2023	1	CDC (2023)
	Cyprus	2022–2023	5	CDC (2023)
	Iran	2022–2023	1	CDC (2023)
	Jordan	2022–2023	1	CDC (2023)
	Lebanon	2022–2023	26	CDC (2023)
	Morocco	2022–2023	3	CDC (2023)
	Qatar	2022–2023	5	CDC (2023)
	Saudi Arabia	2022–2023	8	ArabNews (2022), Reuters (2022) and CDC (2023)
	United Arab Emirates	2022–2023	16	CDC (2023)

Table 1.1 (continued)

Continent/ region	Country	Year	No. of confirmed cases	References
Regional total		2022–2023	66 (0 deaths)	
South-East Asian Region (SEAR)	China	2022–2023	1	CDC (2023)
	Hong Kong	2022–2023	1	CDC (2023)
	India	2022–2023	22 (1 death)	Dutt (2022) and CDC (2023)
	Indonesia	2022–2023	1	CDC (2023)
	Japan	2022–2023	22	CDC (2023)
	Philippines	2022–2023	4	CDC (2023)
	Sri Lanka	2022–2023	2	CDC (2023)
	Thailand	2022–2023	15	CDC (2023)
	Vietnam	2022–2023	2	CDC (2023)
Regional total		2022–2023	70 (1 deaths)	
World total			93,950 (140 deaths)	

We retrieved literature published from 1970 to January 2023 on Mpox or MPV across the world to document confirmed human cases of Mpox. We used various search engines such as Google Scholar, Web of Science, PubMed, Scopus, and Science Direct to retrieve the data. Additionally, we searched information on the virus transmission route, clinical diagnosis, vaccines, and treatment. Keywords for retrieving and screening the data were "monkeypox", "monkeypox virus", "country name", "monkeypox update", "monkeypox transmission route", "natural host reservoir of monkeypox", "monkeypox and wild mammals", "monkeypox symptoms", "monkeypox structure", etc. For updates on Mpox case reports, we also searched the WHO website, the Centers for Disease Control and Prevention (CDC) website, African CDC, the Pan American Health Organization (PAHO) website, the European Centre for Disease Prevention and Control (ECDC), and various news web pages continuously

of the identified cases have been in individuals who have not received the smallpox vaccine and were naive to poxviruses (Alakunle et al. 2020; Brown and Leggat 2016). Interestingly, individuals vaccinated for smallpox, had 85% protection against MPV. Although the original first-generation smallpox vaccines are no longer available for the general population, second- and third-generation vaccines have been developed and approved (Brown and Leggat 2016). However, the degree of efficacy of these vaccines to protect against MPV infection remains to be fully evaluated (Alakunle et al. 2020). In the 2022 MPV outbreak, public health authorities suggested ring vaccination, that is vaccinating close contacts of the infected person to limit and control the outbreak. Since MPV infections were primarily seen in MSM population, this strategy had merits. There is currently no universally approved antiviral for the treatment of Mpox (Adler et al. 2022). Two drugs, brincidofovir and tecovirimat, approved by the US FDA for the treatment of smallpox (in preparation for any potential bioterrorism event), have been investigated for their activity against MPV (Chittick et al. 2017; Grosenbach et al. 2018; Siegrist and Sassine 2023). However, these drugs have not been studied in human efficacy trials, and their effectiveness in preventing MPV remains to be verified. The compassionate use of tecovirimat against monkeypox has been reported without any complications (Adler et al. 2022).

Table 1.2 Comparison of some of the features of MPV and SARS-CoV2

	Monkeypox virus	SARS-CoV2	References
Year/place of initial outbreak	1970/Democratic Republic of the Congo	2019/China	Heymann et al. (1998) and Jiang et al. (2020)
Suspected natural host	Monkeys/rodents	Bats	Aghajani et al. (2020), Heymann et al. (1998), Hutson et al. (2007, 2015) and Perveen et al. (2021)
Case mortality rate (%)	< 1	< 1	Vogel (2022)
Classification	Orthopoxvirus/Poxviridae	Coronavirus/Coronaviridae	Al-Tammemi et al. (2022) and Fehr and Perlman (2015)
Type of virus	Double-stranded DNA (dsDNA)	Single-stranded RNA genome	Fehr and Perlman (2015) and Sklenovská (2020)
Main mode of transmission	Close/intimate contact: sex, kissing, touching infected lesions	Respiratory droplets: direct/indirect	Al-Tammemi et al. (2022) and Fehr and Perlman (2015)
Incubation period (days)	5–21	2–7	Al-Tammemi et al. (2022) and Cortés Martínez et al. (2022)
Genome size (kb)	197	30	Fehr and Perlman (2015), Haller et al. (2014) and Shchelkunov et al. (2001)
Typical symptoms	Fever, headache, muscle aches, back pain, low energy, and swollen lymph nodes, rash	Fever, cough, tiredness, loss of taste/smell, sore throat, headache, aches and pains, diarrhea, shortness of breath, chest pain	Al-Tammemi et al. (2022), Bragazzi et al. (2022), Chen et al. (2020), Hui et al. (2020) and Jiang et al. (2020)

1.4.2 One Health Perspective

In Africa, especially in disease endemic area such as the DRC, several wild animals have been recognized as susceptible to MPV infection (Doty et al. 2017). Some animals may have asymptomatic infection, while others such as non-human primates, show skin rashes similar to what is seen in humans. Poxviruses have been documented in domestic cats, sheep, goats, and cattle (Tack and Reynolds 2011). In the 2022 MPV outbreak, human-to-human transmission was the main driving force for the global spread of the virus. As with many zoonotic infections, there is an intricate connection between humans, animals, and the environment. Thus, the One Health approach is crucial for control strategies (Hassani and Khan 2020; Reynolds et al. 2019). There is a need for joint investigations of human and animal health teams to study the sources of infection, risk factors, and modes of transmission (Eteng et al. 2018). The role of environmental factors is yet to be explored. Institutional collaboration for information sharing with regard to wider scientific research interest would also help in identifying the origin of zoonosis and causes of an outbreak. Moreover, there are massive gaps in our understanding of the dynamics MPV emergence, epidemiology, and ecology. Without information sharing, it is hard to verify data to support active surveillance programs (Sklenovská and Van Ranst 2018). The communication teams can alleviate public fear and anxiety by providing correct and timely information and curtail misinformation. Human, animals, and environmental health experts should address health advisories, key messages, press releases, and frequently asked questions to

guide public to best practices in reducing transmission and spread of infection (Eteng et al. 2018).

1.4.3 Control Strategies

For developing and implementing control strategies for human Mpox, it is crucial to understand the epidemiology of virus, natural reservoirs, modes of transmission, and best methods for rapid and accurate diagnosis. In African countries where MPV is endemic in the animal population, sporadic spillovers occur from time to time, resulting in clusters of infections in human (Table 1.1). Such infections could be prevented by focusing on surveillance of MPV in the animal population, better public awareness of the disease and its mode of transmission, and vaccinating individuals working with livestock and wild animals (Bernard and Anderson 2006). By contrast, the pattern of spread of MPV in the global 2022 outbreak which resulted in over 80,000 cases within 6 months of the outbreak was driven by a sustained human-to-human transmission. The infection was primarily seen in the MSM community. The risk to the general population was minimum. Control and prevention of this pattern of spread requires a focus on adopting and implementing different sets of strategies. These include raising awareness among healthcare professionals, availability and access to sexual health services, early detection, testing, contact tracing and management of confirmed cases. Educational campaigns aimed at high-risk groups and focusing on addressing risky behaviors are also necessary.

1.5 Conclusion

The threat of emerging and re-emerging viral infections with pandemic potential is real. The 1918 Flu pandemic, famously known as the "Spanish Flu", claimed an estimated 17–50 million deaths worldwide (Spreeuwenberg et al. 2018; Taubenberger and Morens 2006), and the recent COVID-19 pandemic which has claimed nearly 7 million deaths within 3 years, are stark reminders. Thus, it is not a question of whether we are going to have another pandemic or not, but rather when this will happen next. Viruses, such MPV and H5N1 (bird flu) which are currently prevalent in certain high-risk groups, could mutate and become highly transmittable in the general population and lead to large-scale outbreaks. The world needs to be better prepared for such events. More investment in pandemic preparedness and building health capacity, better international cooperation and data sharing, continued surveillance and monitoring of pathogen dynamics, understanding human–animal interactions, rapid diagnosis and containment, and developing effective antivirals and vaccines, are all key tools for preventing and controlling future outbreaks.

References

Adler H, Gould S, Hine P, Snell LB, Wong W, Houlihan CF et al (2022) Clinical features and management of human monkeypox: a retrospective observational study in the UK. Lancet Infect Dis 3099(22):1–10. https://doi.org/10.1016/s1473-3099(22)00228-6

Aghajani J, Farnia P, Ayoubi S, Farnia P, Ghanavi J, Velayati A (2020) Can animals like bats, pangolins, and ticks would be considered as long-term reservoirs of severe acute respiratory syndrome coronavirus 2. Biomed Biotechnol Res J 4(5):S3–S12. https://doi.org/10.4103/bbrj.bbrj_120_20

Akhmetzhanov AR, Ponce L, Thompson RN (2022) Emergence potential of monkeypox in the Western Pacific Region, July 2022. Int J Infect Dis 1–8. https://doi.org/10.1016/j.ijid.2022.07.044

Al-Tammemi AB, Albakri R, Alabsi S (2022) The outbreak of human monkeypox in 2022: a changing epidemiology or an impending aftereffect of smallpox eradication? Front Trop Dis 3:1–5. https://doi.org/10.3389/fitd.2022.951380

Alakunle E, Moens U, Nchinda G, Okeke MI (2020) Monkeypox virus in Nigeria: infection biology, epidemiology, and evolution. Viruses 12:1–29. http://www.ncbi.nlm.nih.gov/pubmed/21413273

Americo JL, Earl PL, Moss B (2023) Virulence differences of mpox (monkeypox) virus clades I, IIa, and IIb.1 in a small animal model. Proc Natl Acad Sci USA 120(8):e2220415120. https://doi.org/10.1073/pnas.2220415120

Angelo KM, Smith T, Camprubí-Ferrer D, Balerdi-Sarasola L, Díaz Menéndez M, Servera-Negre G et al (2023) Epidemiological and clinical characteristics of

patients with monkeypox in the GeoSentinel Network: a cross-sectional study. Lancet Infect Dis 23(2):196–206. https://doi.org/10.1016/s1473-3099(22)00651-x

ArabNews (2022) Saudi Health Ministry announces first monkeypox case in Kingdom. https://www.Arabnews.Com/Node/2122491/Saudi-Arabia. Accessed 25 July 2022

Arita I, Jezek Z, Khodakevich L, Ruti K (1985) Human monkeypox: a newly emerged ortbopox virus zoonotij in the tropical rain forestt of Africa. Am J Trop Med Hyg 34:781–789

Barouch DH (2022) Covid-19 vaccines—immunity, variants, boosters. N Engl J Med 387(11):1011–1020. https://doi.org/10.1056/nejmra2206573

Bernard SM, Anderson SA (2006) Qualitative assessment of risk for monkeypox associated with domestic trade in certain animal species, United States. Emerg Infect Dis 12(12):1827–1833. https://doi.org/10.3201/eid1212.060454

Berthet N, Nakoune E, Whist E, Selekon B, Burguiere AM, Manuguerra JC, Kazanji M (2011) Maculopapular lesions in the Central African Republic. Lancet 378(9799):1354. https://doi.org/10.1016/s0140-6736(11)61142-2

Besombes C, Gonofio E, Konamna X, Selekon B, Gessain A, Berthet N et al (2019) Intrafamily transmission of monkeypox virus, Central African Republic, 2018. Emerg Infect Dis 25(8):1602–1604. https://doi.org/10.3201/eid2508.190112

Bragazzi NL, Kong JD, Mahroum N, Tsigalou C, Khamisy-Farah R, Converti M, Wu J (2022) Epidemiological trends and clinical features of the ongoing monkeypox epidemic: a preliminary pooled data analysis and literature review. J Med Virol. https://doi.org/10.1002/jmv.27931

Breman JG, Ruti K, Steniowski MV (1980) Human monkeypox, 1970–79. Bull World Health Organ 58(2):165–182

Brown K, Leggat PA (2016) Human monkeypox: current state of knowledge and implications for the future. Trop Med Infect Dis 1(1):1–13. https://doi.org/10.3390/tropicalmed1010008

CDC (2022) 2022 monkeypox outbreak global map. https://www.Cdc.Gov/Poxvirus/Monkeypox/Response/2022/World-Map.Html. Accessed 25 July 2022

CDC (2023) 2022 monkeypox outbreak global map. https://www.Cdc.Gov/Poxvirus/Monkeypox/Response/2022/World-Map.Html. Accessed 08 Mar 2023

Chen N, Zhou M, Dong X, Qu J, Gong F, Han Y et al (2020) Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study. Lancet (London, England) 6736(20):1–7. https://doi.org/10.1016/S0140-6736(20)30211-7

Chittick G, Morrison M, Brundage T, Nichols WG (2017) Short-term clinical safety profile of brincidofovir: a favorable benefit–risk proposition in the treatment of smallpox. Antiviral Res 143:269–277. https://doi.org/10.1016/j.antiviral.2017.01.009

Church DL (2004) Major factors affecting the emergence and re-emergence of infectious diseases. Clin Lab Med 24(3):559–586. https://doi.org/10.1016/j.cll.2004.05.008

Cohen J (2022a) Concern grows that human monkeypox outbreak will establish virus in animals outside Africa. Science 376(6599). https://doi.org/10.1126/science.add3947. https://www.Science.Org/Content/Article/Concern-Grows-Human-Monkeypox-Outbreak-Will-Establish-Virus-Animals-Outside-Africa

Cohen J (2022b) Monkeypox could establish new reservoirs in animals. Science 376(6599):1258–1259. https://doi.org/10.1126/science.add4868

Cortés Martínez J, Pak D, Abelenda-Alonso G, Langohr K, Ning J, Rombauts A et al (2022) SARS-Cov-2 incubation period according to vaccination status during the fifth COVID-19 wave in a tertiary-care center in Spain: a cohort study. BMC Infect Dis 22(1):1–7. https://doi.org/10.1186/s12879-022-07822-4

Costello V, Sowash M, Gaur A, Cardis M, Pasieka H, Wortmann G, Ramdeen S (2022) Imported monkeypox from international traveler, Maryland, USA, 2021. Emerg Infect Dis 28(5):5–8

Crandell RA, Casey HW, Brumlow WB (1969) Studies of a newly recognized poxvirus of monkeys. J Infect Dis 119:80–88

De la Cruz L, Barrera M, Rios L, Corona-González B, Bulnes CA, Díaz-Sánchez AA et al (2020) Unraveling the global phylodynamic and phylogeographic expansion of *Mycoplasma gallisepticum*: understanding the origin and expansion of this pathogen in Ecuador. Pathogens 9(9):1–18. https://doi.org/10.3390/pathogens9090674

Deria A, Jezek Z, Markvart K, Carrasco P, Weisfeld J (1980) The world's last endemic case of smallpox: surveillance and containment measures. Bull World Health Organ 58(2):279–283

Di-Giulio DB, Eckburg PB (2004) Human monkeypox: an emerging zoonosis. Lancet Infect Dis 4:15–25

Doshi RH, Guagliardo SAJ, Dzabatou-Babeaux A, Likouayoulou C, Ndakala N, Moses C et al (2018) Strengthening of surveillance during monkeypox outbreak, Republic of the Congo, 2017. Emerg Infect Dis 24(6):1158–1160. https://doi.org/10.3201/eid2406.180248

Doty JB, Malekani JM, Kalemba LN, Stanley WT, Monroe BP, Nakazawa YU et al (2017) Assessing monkeypox virus prevalence in small mammals at the human–animal interface in the Democratic Republic of the Congo. Viruses 9(10). https://doi.org/10.3390/v9100283

Durski KN, Mccollum AM, Nakazawa Y, Petersen BW, Reynolds MG (2018) Emergence of monkeypox—West and Central Africa, 1970–2017. Morb Mortal Wkly Rep 67(10):306–310

Dutt A (2022) India's fourth monkeypox case in Delhi; patient went to Himachal, no history of foreign travel. https://Indianexpress.Com/Article/Cities/Delhi/Delhi-Man-Tests-Positive-for-Monkeypox-8048431/. Accessed 25 July 2022

ECDC (2022) Monkeypox multi-country outbreak—situation update, 21 July 2022. https://www.Ecdc.Europa.Eu/En/Monkeypox-Outbreak. Accessed 25 July 2022

Erez N, Achdout H, Milrot E, Schwartz Y, Wiener-Well Y, Paran N et al (2019) Diagnosis of imported monkeypox, Israel, 2018. Emerg Infect Dis 25(5):980–983. https://doi.org/10.3201/eid2505.190076

Eteng W, Mandra A, Doty J, Aruna S, Reynolds MG, Mccollum AM et al (2018) Notes from the field: responding to an outbreak of monkeypox using the One Health approach—Nigeria, 2017–2018. Morb Mortal Wkly Rep 67(37):1040

Falendysz EA, Lopera JG, Lorenzsonn F, Salzer JS, Hutson CL, Doty J et al (2015) Further assessment of monkeypox virus infection in Gambian pouched rats (*Cricetomys gambianus*) using in vivo bioluminescent imaging. PLoS Negl Trop Dis 9(10):1–19. https://doi.org/10.1371/journal.pntd.0004130

Fehr AR, Perlman S (2015) Coronaviruses: an overview of their replication and pathogenesis. In: Coronaviruses, vol 1282. Humana Press, New York, NY, pp 1–23. https://doi.org/10.1007/978-1-4939-2438-7

Fine PEM, Jezek Z, Grab B, Dixon H (1988) The transmission potential of monkeypox virus in human populations. Int J Epidemiol 17(3):643–650. https://doi.org/10.1093/ije/17.3.643

Formenty P, Muntasir MO, Damon I, Chowdhary V, Opoka ML, Monimart C et al (2010) Human monkeypox outbreak caused by novel virus belonging to Congo Basin clade, Sudan, 2005. Emerg Infect Dis 16(10):1539–1545. https://doi.org/10.3201/EID1610.100713

Grosenbach DW, Honeychurch K, Rose EA, Chinsangaram J, Frimm A, Maiti B et al (2018) Oral tecovirimat for the treatment of smallpox. N Engl J Med 379(1):44–53. https://doi.org/10.1056/nejmoa1705688

Haller SL, Peng C, McFadden G, Rothenburg S (2014) Poxviruses and the evolution of host range and virulence. Infect Genet Evol 21:15–40. https://doi.org/10.1016/j.meegid.2013.10.014

Hassani A, Khan G (2020) Human-animal interaction and the emergence of SARS-CoV-2. JMIR Public Health Surveill 6(4):4–10. https://doi.org/10.2196/22117

Heymann DL, Szczeniowski M, Esteves K (1998) Re-emergence of monkeypox in Africa: a review of the past six years. Br Med Bull 54(3):693–702. https://doi.org/10.1093/oxfordjournals.bmb.a011720

Hui DS, Azhar EI, Madani TA, Ntoumi F, Kock R, Dar O et al (2020) The continuing 2019-nCoV epidemic threat of novel coronaviruses to global health—the latest 2019 novel coronavirus outbreak in Wuhan, China. Int J Infect Dis. https://doi.org/10.1016/j.ijid.2020.01.009

Hutin YJ, Williams RJ, Malfait P, Pebody R, Loparev VN, Ropp SL et al (2001) Outbreak of human monkeypox, Democratic Republic of Congo, 1996 to 1997. Emerg Infect Dis 7(3):434–438. https://doi.org/10.3201/eid0703.017311

Hutson CL, Lee KN, Abel J, Carroll DS, Montgomery JM, Olson VA, Regnery RL (2007) Monkeypox zoonotic associations: insights from laboratory evaluation of animals associated with the multi-state US outbreak. Am J Trop Med Hyg 76(4):757–768

Hutson CL, Nakazawa YJ, Self J, Olson VA, Regnery RL, Braden Z et al (2015) Laboratory investigations of African pouched rats (*Cricetomys gambianus*) as a potential reservoir host species for monkeypox virus. PLoS Negl Trop Dis 9(10):1–20. https://doi.org/10.1371/journal.pntd.0004013

Jezek Z, Grab B, Szczeniowski MV, Paluku KM, Mutombo M (1988a) Human monkeypox: secondary attack rates. Bull World Health Organ 66(4):465–470

Jezek Z, Szczeniowski M, Paluku KM, Mutombo M, Grab B (1988b) Human monkeypox: confusion with chickenpox. Acta Trop 45(4):297–307

Ježek Z, Fenner F (1988) Human monkeypox. In: Monographs in virology, vol 17. S. Karger Ag, Basel, Switzerland, p 140

Ježek Z, Szczeniowski M, Paluku KM, Mutombo M (1987) Human monkeypox: clinical features of 282 patients. J Infect Dis 156(2):293–298. https://doi.org/10.1093/infdis/156.2.293

Jiang F, Deng L, Zhang L, Cai Y, Cheung CW (2020) Review of the clinical characteristics of coronavirus disease 2019 (COVID-19). J Gen Intern Med 04:1–5. https://doi.org/10.1007/s11606-020-05762-w

Jos WM, van der M (2013) The infectious disease challenges of our time. Front Public Health 4:1–2. https://doi.org/10.1038/ncomms2343

Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Brief Bioinform 20(4):1160–1166. https://doi.org/10.1093/bib/bbx108

Khodakevich L, Widy-Wirsk IR, Arita I, Marennikova SS, Nakano J, Meunier D (1985) Orthopoxvirose simienne de l'home en république centrafricaine. Bull Soc Pathol Exot 78:311–320

Khodakevich L, Jezek Z, Kinzanzka K (1986) Isolation of monkeypox virus from wild squirrel infected in nature. Lancet 1:98–99

Kozlov M (2022) Monkeypox goes global: why scientists are on alert. Nature 606(7912):15–16. https://doi.org/10.1038/d41586-022-01421-8

Kuraku S, Zmasek CM, Nishimura O, Katoh K (2013) aLeaves facilitates on-demand exploration of metazoan gene family trees on MAFFT sequence alignment server with enhanced interactivity. Nucleic Acids Res 41:22–28. https://doi.org/10.1093/nar/gkt389

Ladnyj ID, Ziegler P, Kima E (1972) A human infection caused by monkeypox virus in Basankusu Territory,

Democratic Republic of the Congo. Bull World Health Organ 46(5):593–597
Learned LA, Reynolds MG, Wassa DW, Li Y, Olson VA, Karem K, Damon IK (2005) Extended interhuman transmission of monkeypox in a hospital community in the Republic of the Congo, 2003. Am J Trop Med Hyg 73(2):428–434
Lourie B, Bingham PG, Evans HH, Foster SO, Nakano JH, Herrmann KL (1972) Human infection with monkeypox virus: laboratory investigation of six cases in West Africa. Bull World Health Organ 46(5):633–639
Magouras I, Brookes VJ, Jori F, Martin A, Pfeiffer DU, Dürr S (2020) Emerging zoonotic diseases: should we rethink the animal-human interface? Front Vet Sci 7:1–6. https://doi.org/10.3389/fvets.2020.582743
Marennikova SS, Moyer RW (2005) Classification of poxviruses and brief characterization of the genus Orthopoxvirus. In: Orthopoxviruses pathogenic for humans. Springer, Boston, MA, pp 11–18
Marennikova SS, Climiskjan KL, Senkman LS, Macevic GR (1972) Some factors determining differences in the antigenicity of vaccinia virus strains. Bull World Health Organ 46(2):159–163
Mbala PK, Huggins JW, Riu-Rovira T, Ahuka SM, Mulembakani P, Rimoin AW et al (2017) Maternal and fetal outcomes among pregnant women with human monkeypox infection in the Democratic Republic of Congo. J Infect Dis 216(7):824–828. https://doi.org/10.1093/infdis/jix260
Merouze F, Lesoin JJ (1983) Monkeypox: second cas humain observe en Cote D'Ivoire. Méd Trop 43(2):145–147
Mitjà O, Alemany A, Marks M, Mora JIL, Rodríguez-Aldama JC, Secco M et al (2023a) Mpox in people with advanced HIV infection: a global case series. Lancet 6736(23):14–16. https://doi.org/10.1016/S0140-6736(23)00273-8
Mitjà O, Ogoina D, Titanji BK, Galvan C, Muyembe J-J, Marks M, Orkin CM (2023b) Monkeypox. Lancet 401:60–74
Moore MJ, Rathish B, Zahra F (2023) Mpox (monkeypox). In: StatPearls [Internet]. StatPearls Publishing, Treasure Island (FL). PMID: 34662033
Morens DM, Folkers GK, Fauci AS (2004) The challenge of emerging and re-emerging infectious diseases. Nature 430:242–249. www.nature.com/nature
Morse SS (1991) Emerging viruses: defining the rules for viral traffic. Perspect Biol Med 34(3):387–409
Moss B, Damon I (2013) Poxviridae. In: Knipe DM, Howley PM (eds) Fields virology, 6th edn. Wolters Kluwer Health/Lippincott Williams & Wilkins, Philadelphia
Nakoune E, Lampaert E, Ndjapou SG, Janssens C, Zuniga I, Van Herp M et al (2017) A nosocomial outbreak of human monkeypox in the Central African Republic. Open Forum Infect Dis 4(4):1–4. https://doi.org/10.1093/ofid/ofx168
Nolen LD, Osadebe L, Katomba J, Likofata J, Mukadi D, Monroe B et al (2015) Introduction of monkeypox into a community and household: risk factors and zoonotic reservoirs in the Democratic Republic of the Congo. Am J Trop Med Hyg 93(2):410–415. https://doi.org/10.4269/ajtmh.15-0168
PAHO (2022) Monkeypox situation reports. https://www.Paho.Org/En/Monkeypox-Situation-Reports. Accessed 21 July 2022
Perveen N, Khan G (2022) Crimean—Congo hemorrhagic fever in the Arab world: a systematic review. Front Vet Sci 9(938601):1–16. https://doi.org/10.3389/fvets.2022.938601
Perveen N, Muzaffar SB, Al-Deeb MA (2021) Exploring human-animal host interactions and emergence of COVID-19: evolutionary and ecological dynamics. Saudi J Biol Sci. https://doi.org/10.1016/j.sjbs.2020.11.077
Prince T, Smith SL, Radford AD, Solomon T, Hughes GL, Patterson EI (2021) SARS-CoV-2 infections in animals: reservoirs for reverse zoonosis and models for study. Viruses 13(3):1–14. https://doi.org/10.3390/v13030494
Radonić A, Metzger S, Dabrowski PW, Couacy-Hymann E, Schuenadel L, Kurth A et al (2014) Fatal monkeypox in wild-living sooty mangabey, Côte d'Ivoire, 2012. Emerg Infect Dis. https://doi.org/10.3201/eid2006.131329
Reed KD, Melski JW, Graham MB, Regnery RL, Sotir MJ, Wegner MV et al (2004) The detection of monkeypox in humans in the western hemisphere. N Engl J Med 350(4):342–350. https://doi.org/10.1097/01.idc.0000130890.12611.f3
Reperant LA, Osterhaus ADME (2017) AIDS, Avian flu, SARS, MERS, Ebola, Zika… what next? Vaccine 35(35):4470–4474. https://doi.org/10.1016/j.vaccine.2017.04.082
Reuters (2022) Saudi Arabia detects its first monkeypox case—SPA. https://www.Reuters.Com/Business/Healthcare-Pharmaceuticals/Saudi-Arabia-Detects-Its-First-Monkeypox-Case-Spa-2022-07-14/. Accessed 25 July 2022
Reynolds MG, Emerson GL, Pukuta E, Karhemere S, Muyembe JJ, Bikindou A et al (2013) Short report: detection of human monkeypox in the Republic of the Congo following intensive community education. Am J Trop Med Hyg 88(5):982–985. https://doi.org/10.4269/ajtmh.12-0758
Reynolds MG, Doty JB, McCollum AM, Olson VA, Nakazawa Y (2019) Monkeypox re-emergence in Africa: a call to expand the concept and practice of One Health. Expert Rev Anti Infect Ther 17(2):129–139. https://doi.org/10.1080/14787210.2019.1567330
Reynolds MG, Wauquier N, Li Y, Satheshkumar PS, Kanneh LD, Monroe B et al (2022) Human monkeypox in Sierra Leone after 44-year absence of reported cases. Emerg Infect Dis 18(5):31–44. https://doi.org/10.1007/978-3-030-91491-2_3
Rimoin AW, Mulembakani PM, Johnston SC, Lloyd Smith JO, Kisalu NK, Kinkela TL et al (2010) Major increase in human monkeypox incidence 30 years

after smallpox vaccination campaigns cease in the Democratic Republic of Congo. Proc Natl Acad Sci USA 107(37):16262–16267. https://doi.org/10.1073/pnas.1005769107

Sadeuh-Mba SA, Yonga MG, Els M, Batejat C, Eyangoh S, Caro V et al (2019) Monkeypox virus phylogenetic similarities between a human case detected in Cameroon in 2018 and the 2017–2018 outbreak in Nigeria. Infect Genet Evol 69:8–11. https://doi.org/10.1016/j.meegid.2019.01.006

Sale TA, Melski JW, Stratman EJ (2006) Monkeypox: an epidemiologic and clinical comparison of African and US disease. J Am Acad Dermatol 55(3):478–481. https://doi.org/10.1016/j.jaad.2006.05.061

Seang S, Burrel S, Todesco E, Leducq V, Monsel G, Le Pluart D et al (2022) Evidence of human-to-dog transmission of monkeypox virus. Lancet 400(10353):658–659. https://doi.org/10.1016/S0140-6736(22)01487-8

Shchelkunov SN, Totmenin AV, Babkin IV, Safronov PF, Ryazankina OI, Petrov NA et al (2001) Human monkeypox and smallpox viruses: genomic comparison. FEBS Lett 509(1):66–70. https://doi.org/10.1016/S0014-5793(01)03144-1

Siegrist EA, Sassine J (2023) Antivirals with activity against Mpox: a clinically oriented review. Clin Infect Dis 76(1):155–164. https://doi.org/10.1093/cid/ciac622

Sklenovská N (2020) Monkeypox virus. In: Malik YS, Singh RK, Dhama K (eds) Livestock diseases and management. Springer Nature Singapore Pte Ltd., Singapore, pp 39–68. https://doi.org/10.3126/mjsbh.v4i0.21403

Sklenovská N, Van Ranst M (2018) Emergence of monkeypox as the most important orthopoxvirus infection in humans. Front Public Health 6:1–12. https://doi.org/10.3389/fpubh.2018.00241

Spreeuwenberg P, Kroneman M, Paget J (2018) Reassessing the global mortality burden of the 1918 influenza pandemic. Am J Epidemiol 187(12):2561–2567. https://doi.org/10.1093/aje/kwy191

Tack DM, Reynolds MG (2011) Zoonotic poxviruses associated with companion animals. Animals 1(4):377–395. https://doi.org/10.3390/ani1040377

Taubenberger JK, Morens DM (2006) 1918 influenza: the mother of all pandemics. Emerg Infect Dis 12(1):15–22. https://doi.org/10.3201/eid1209.050979

Tchokoteu PF, Kago I, Tetanye E, Ndoumbe P, Pignon D, Mbede J (1991) Variole ou varicelle grave? Un cas de variole humaine a monkeypox virus chez un enfant camerounais. Ann Soc Belge Méd Trop 71:123–128

Vaughan A, Aarons E, Astbury J, Balasegaram S, Beadsworth M, Beck CR et al (2018) Two cases of monkeypox imported to the United Kingdom, September 2018. Eurosurveillance 23(38). https://doi.org/10.2807/1560-7917.ES.2018.23.38.1800509

Vogel L (2022) Making sense of monkeypox death rates. CMAJ Can Med Assoc J 194(31):E1097. https://doi.org/10.1503/cmaj.1096012

Von Magnus P, Andersen EK, Petersen KB, Birch-Andersen AA (1959) A pox-like disease in cynomolgus monkeys. Acta Pathol Microbiol Immunol 46:156–176

Wachtman L, Mansfield K (2012) Viral diseases of nonhuman primates. Nonhuman Primates Biomed Res. https://doi.org/10.1016/B978-0-12-381366-4.00001-8

WHO (1997a) Monkeypox—Democratic Republic of the Congo, 14 Nov 1997. https://www.Who.Int/Emergencies/Disease-Outbreak-News/Item/1997_11_14b-En. Accessed 22 July 2022

WHO (1997b) Monkeypox—Democratic Republic of the Congo, 21 Mar 1997. https://www.Who.Int/Emergencies/Disease-Outbreak-News/Item/1997_03_21c-En. Accessed 22 July 2022

WHO (1997c) Monkeypox—Democratic Republic of the Congo, 31 July 1997. https://www.Who.Int/Emergencies/Disease-Outbreak-News/Item/1997_07_31b-En. Accessed 22 July 2022

WHO (2016) Monkeypox—Central African Republic, 13 Oct 2016. https://www.Who.Int/Emergencies/Disease-Outbreak-News/Item/13-October-2016-Monkeypox-Caf-En. Accessed 22 July 2022

WHO (2018a) Monkeypox—Cameroon, 5 June 2018. https://www.Who.Int/Emergencies/Disease-Outbreak-News/Item/05-June-2018-Monkeypox-Cameroon-En. Accessed 22 July 2022

WHO (2018b) Weekly bulletin on outbreaks and other emergencies, pp 1–19. https://Apps.Who.Int/Iris/Bitstream/Handle/10665/260335/OEW8-1723022018.Pdf?Sequence=1. Accessed 25 July 2022

WHO (2019a) Monkeypox—Singapore, 16 May 2019. https://www.Who.Int/Emergencies/Disease-Outbreak-News/Item/16-May-2019-Monkeypox-Singapore-En. Accessed 22 July 2022

WHO (2019b) Weekly bulletin on outbreaks and other emergencies, pp 1–25. https://Apps.Who.Int/Iris/Bitstream/Handle/10665/324819/OEW20-1319052019.Pdf?Sequence=1&isAllowed=y. Accessed 25 July 2022

WHO (2020) Monkeypox—Democratic Republic of the Congo, 1 Oct 2020. https://www.Who.Int/Emergencies/Disease-Outbreak-News/Item/Monkeypox-Democratic-Republic-of-the-Congo. Accessed 22 July 2022

WHO (2021a) Monkeypox—United Kingdom of Great Britain and Northern Ireland, July 2021. https://www.Who.Int/Emergencies/Disease-Outbreak-News/Item/Monkeypox---United-Kingdom-of-Great-Britain-and-Northern-Ireland. Accessed 24 July 2022

WHO (2021b) Monkeypox—United Kingdom of Great Britain and Northern Ireland, June 2021. https://www.Who.Int/Emergencies/Disease-Outbreak-News/Item/Monkeypox---United-Kingdom-of-Great-Britain-and-Northern-Ireland-Ex-Nigeria. Accessed 24 July 2022

WHO (2022a) Meeting of the International Health Regulations (2005) Emergency Committee regarding the multi-country monkeypox outbreak

WHO (2022b) Multi-country monkeypox outbreak: situation update, 27 June 2022. https://www.Who.Int/Emergencies/Disease-Outbreak-News/Item/2022-DON396. Accessed 22 July 2022

WHO (2022c) Multi-country monkeypox outbreak in non-endemic countries

WHO (2022d) Weekly situation report on monkeypox multi-country outbreak response—region of the Americas. https://www.Paho.Org/En/Documents/Weekly-Situation-Report-Monkeypox-Multi-Country-Outbreak-Response-Region-Americas-15-July#:~:Text=As%20of%2014%20July%202022,In%20the%20Western%20Pacific%20Region. Accessed 21 July 2022

WHO (2022e) WHO Director-General declares the ongoing monkeypox outbreak a Public Health Emergency of International Concern. https://www.Who.Int/Europe/News/Item/23-07-2022-Who-Director-General-Declares-the-Ongoing-Monkeypox-Outbreak-a-Public-Health-Event-of-International-Concern. Accessed 24 July 2022

WHO (2022f) WHO recommends new name for monkeypox disease. https://www.Who.Int/News/Item/28-11-2022-Who-Recommends-New-Name-for-Monkeypox-Disease. Accessed 05 Mar 2023

Xiang Y, White A (2022) Monkeypox virus emerges from the shadow of its more infamous cousin: family biology matters. Emerg Microbes Infect 11(1):1768–1777. https://doi.org/10.1080/22221751.2022.2095309

Ye F, Song J, Zhao L, Zhang Y, Xia L, Zhu L et al (2019) Molecular evidence of human monkeypox virus infection, Sierra Leone. Emerg Infect Dis 25(6):1220–1222. https://doi.org/10.3201/eid2506.180296

Ye Z, Yuan S, Yuen K, Fung S, Chan C, Jin D (2020) Zoonotic origins of human coronaviruses. Int J Biol Sci 16:6–8. https://doi.org/10.7150/ijbs.45472

Yinka-Ogunleye A, Aruna O, Dalhat M, Ogoina D, McCollum A, Disu Y et al (2019) Outbreak of human monkeypox in Nigeria in 2017–18: a clinical and epidemiological report. Lancet Infect Dis 19(8):872–879. https://doi.org/10.1016/S1473-3099(19)30294-4

Yuan P, Tan Y, Yang L, Aruffo E, Ogden NH, Bélair J et al (2023) Assessing transmission risks and control strategy for monkeypox as an emerging zoonosis in a metropolitan area. J Med Virol 95(1). https://doi.org/10.1002/jmv.28137

Zhang L, Hua N, Sun S (2008) Wildlife trade, consumption and conservation awareness in southwest China. Biodivers Conserv 17(6):1493–1516. https://doi.org/10.1007/s10531-008-9358-8