Recommendations to better understand the origins of and factors for the emergence and re-emergence of mpox

Statement from the Scientific Advisory Group for the Origins of Novel Pathogens (SAGO)

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Purpose of the statement

The purpose of this statement is to outline the recommendations from the Scientific Advisory Group for the Origins of Novel Pathogens (SAGO) on studies that need to be conducted in order to better understand the origins of the virus that causes mpox (monkeypox virus) and the re-emergence of mpox in previously affected countries, as well as factors that drive this emergence and re-emergence.

Key Recommendations

A full list of recommended studies is provided at the end of this statement. Key recommendations include the following:

- Conduct **clinical and epidemiological retrospective studies** to better define the role of human-to-human transmission dynamics and drivers for spread in countries previously reporting cases of mpox and explore its potential spread to the first cases discovered in newly-affected countries in 2022.
- **Review clinical and laboratory records** in target settings in locations where Clade I, subclade IIa and early subclade IIb cases were detected to search for early cases presenting with similar rash that could have been missed.
- Sequence samples from historical cases of mpox, use metadata links to clinical histories, and perform **phylogenetic studies** to understand viral mutation patterns and the emergence of subclade IIb viruses with APOBEC3 changes and the effect of co-infections
- Conduct **infectiousness studies** to identify the reproductive number, duration of viral shedding and all possible transmission routes.
- Conduct multidisciplinary and multisectoral **zoonosis studies** to identify animal reservoirs or animal sources of infection in endemic and non-endemic regions to understand the role of animal-to-human transmission and any associated land use changes.
- Conduct **environmental, anthropological, behavioural and social science studies** around confirmed cases to better understand how mpox is transmitted between humans.

Background

The **Scientific Advisory Group for the origins of novel pathogens (SAGO)** was established to provide technical and scientific considerations regarding emerging and re-emerging pathogens and in this capacity to advise WHO on prioritizing studies and field investigations into the origins of such pathogens, as per their **terms of reference**. The sudden appearance of a **multi-country outbreak of mpox** (formerly known as monkeypox)\(^1\) in 2022 which reached over 110 countries, and the human-to-human spread of monkeypox virus (MPXV) through sexual and social networks around the world has highlighted the need to better understand the animal reservoir(s) of MPXV, animal-to-human transmission, human-to-human transmission and factors that contribute to the emergence and re-emergence of this virus over time.

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\(^1\) In 2022 WHO undertook a process under the International Classification of Diseases, 11\(^{th}\) Version, to rename the disease monkeypox as mpox. See the news release here: https://www.who.int/news/item/28-11-2022-who-recommends-new-name-for-monkeypox-disease
The purpose of this document is to outline recommendations by the SAGO on critical studies needed to better understand the origins of mpox, re-emergence of mpox and factors that drive emergence/re-emergence of the virus. The recommendations provided in this report should be read in connection with recent reports from the WHO Research and Development (R&D) for Epidemic reports on monkeypox.

Overview of what is currently known about the origins of mpox

A brief non-encompassing history of mpox disease is listed in Annex 1.

Two clades of MPXV have been identified – Clade I, formerly known as the Congo Basin or Central African clade, and Clade II, formerly known as the West African clade. Clade II is divided into subclade IIa and subclade IIb, the latter of which is linked to the global outbreak of mpox in 2022. (WHO, 2022b). Unlike clade I and subclade IIa, this virus has been detected only in humans to date, and there are no known subclade IIb sequences derived from animal sequences (Happi et al., 2022).

Although understood to be zoonotic, the origin and animal reservoirs of MPXV are still not completely understood. While the virus has been present in Africa for decades at least, research conducted to understand its origins and factors for re-emergence has been limited. Much of the work was carried out in the 1980s shortly after the eradication of smallpox, or in follow up to subsequent identified outbreaks of human mpox. Thus, the scientific understanding of MPXV as a zoonotic pathogen is limited, requiring further investigation; understanding of patterns of human-to-human transmission has also been limited. During the 1980s, some efforts were made to better understand the disease and its origins. Active surveillance studies were set up in the Democratic Republic of the Congo (DRC) to understand and characterize human disease and its transmission. Ecologic efforts were also undertaken to understand potential zoonotic reservoirs for the disease. In those studies, a number of animals were trapped in the vicinity of where human cases had been identified, and a wide array of species had evidence in radioimmunoassay adsorption assays of orthopoxvirus seroreactivity, and potentially, MPXV seroreactivity. Only one squirrel – a moribund Funisciuris anerythrus – was identified as positive for the virus, in the Bumba zone. In 2018, a Sooty mangabee monkey was identified as being infected with MPXV in Côte d’Ivoire.

In 2003, an outbreak of mpox in captive prairie dogs occurred in the United States of America after some were co-housed with a shipment of small mammals from West Africa. Animals from that shipment (Gambian pouched rats, rope squirrels, and dormice) were found to be infected with MPXV. This led to 47 persons being infected with Clade IIa MPXV(Reed et al., 2004, CDC, 2003). It was the first time human mpox was reported outside Africa.

To date, it is understood that human-to-human transmission can occur through direct contact with infectious skin or mucocutaneous lesions, this includes face-to-face, skin-to-skin, mouth-to-mouth or mouth-to-skin contact and respiratory droplets (and possibly short-range aerosols requiring prolonged close contact) (Brown and Leggat, 2016, Reynolds et al., 2006a, Reed et al., 2004). The presence of lesions on scrotal tissue, groin or buttocks had previously been noted in reports from 1988 and 2005.
(Jezek and Fenner, 1988) (Huhn et al., 2005) raising the possibility that human infection from intimate sexual activity may have already been a mode of transmission in the past. The current global outbreak is strongly associated with sexual activity in some networks. Descriptions of disease in Nigeria in 2017-2018 also suggest that intimate sexual contact could have been associated with infection and transmission, although it was not recorded as a mode of transmission at the time (Ogoina et al., 2020) (Yinka-Ogunleye et al., 2019). While within Clade I infections historically reported from DRC, congenital infection during pregnancy was documented, the mode of transmission was presumed to be by direct contact. (Jezek and Fenner, 1988) More recently, researchers depicted a case series review of four pregnant women found to have mpox infection, among whom only one had a live birth following vertical transmission of MPXV, and of the rest, at least one of the stillborn foetuses had evidence of mpox lesions (Mbala et al., 2017).

Between 2018-2021, there were eight confirmed cases of mpox associated with travellers from Nigeria reported to WHO by four countries outside of Africa. In two cases, disease spread from to others in the country of importation (Adler et al., 2022), including a health worker in the United Kingdom through exposure to presumably contaminated bed linens (2018), and a cluster with a secondary and a tertiary case within the patient’s family (2021). In the United States of America, clean-up of the household environment of a hospitalized patient revealed infectious virus on a number of porous surfaces within the household (Morgan, 2022).

**Overview of the multi-country mpox outbreak in 2022**

Because the SAGO focuses on studies of origins and emergence/re-emergence of known and novel pathogens with epidemic and pandemic potential, it's important to contextualize the current situation and provide a short overview of the global mpox outbreak. Initial reports of mpox in May 2022 were not linked to any travellers coming from previously affected regions. The United Kingdom health authorities posted a bulletin reporting that mpox had been identified in two individuals from a family who had not travelled outside the United Kingdom and had no known contact with travellers from endemic countries (WHO, 2022a). The United Kingdom then reported four cases in men who indicated they had sexual activity with men (UKHSA, 2022). None had travelled outside the United Kingdom or had any other contact with travellers. Images from subsequently identified mpox patients of individual lesions at the early vesiculopustular stages of formation appeared to show that lesions were primary in genital areas (anogenital lesions) and that the size was smaller than what was historically reported in endemic countries (UKHSA, 2022). Various patterns of transmission suggest that intimate skin-to-skin contact, such as during sexual contact, was a route of transmission, which had not been described in previous outbreaks. This may explain that other cases of disease, previously thought to be attributed to other rash-associated sexually transmissible infections (such as herpes, gonorrhoea and syphilis), could potentially have been un-diagnosed mpox cases. During this 2022 global outbreak, mpox has primarily been reported in persons who self-identify as gay or bisexual men who have sex with men (MSM).

In May 2022, viral sequencing of samples from patients in Belgium, Portugal and the U.S. revealed that the majority of virus variants were tightly clustered in a group subsequently named subclade IIB lineage.
B.1 (Gigante et al., 2022) (Isidro et al., 2022). The B.1 lineage viruses are related to a virus isolated in the U.S. in 2021 from a Nigerian traveller who became ill in Maryland. Additionally, in the U.S., a separate lineage was introduced; and was named subclade IIb, lineage A.2. The two 2022 viruses reported by Gigante et al. are related to a virus isolated from a Nigerian traveller who became ill in Texas, U.S. in 2021 (Gigante et al., 2022); the 2022 infected individuals reported travel to the Middle East and West Africa. Additionally, the first two cases of mpox that were detected in India had a history of travel to the United Arab Emirates and the associated MPXV variants belonged to subclade IIb.A.2 (Yadav et al., 2022). All of these viruses share common ancestors with viruses circulating in Nigeria since 2017 and are characterized by a number of mutations associated with host APOBEC3 genome editing (Gigante et al., 2022).

The 2022 global spread of mpox has been substantial. WHO had documented 73,437 laboratory confirmed cases with 29 deaths from 109 countries as of 19 October 2022 (WHO, 2022c). Over 98% of these confirmed cases were from the WHO European and Americas Regions with the United States of America reporting the most cases, with over 14,000 cases. Worldwide, 98.2% of cases were in individuals with male gender, and 95.8% of all cases were among MSM. About a quarter of all cases reported HIV status; and among those, 45% were living with HIV. Studies to evaluate when virus introductions in different contexts first occurred are underway in a number of countries, examining archived specimens that may yield information on the presence of virus or serologic evidence of recent infection, however more research is needed in a large number of areas.
**SGO recommendations; studies that are needed to further investigate the emergence and re-emergence of mpox**

Understanding the origin and drivers of the emergence and re-emergence of mpox is pertinent for containing the outbreak at source, preventing new outbreaks and understanding evolution patterns of similar viruses with the potential to cause future outbreaks. Understanding the prior emergence of MPXV in African countries, and in newly affected countries in 2022 will be critical to reducing the public health impact of mpox in the most affected countries.

In keeping with its remit, the SAGO recommends the following studies be undertaken to better understand the origins of the recent mpox re-emergence and factors that drive emergence/re-emergence of the virus. These recommendations have been organized into technical elements consistent with the latest SAGO report, which will be expanded in an upcoming publication of the SAGO: *Global framework to study emerging and re-emerging high-threat zoonotic pathogens*.

**Early investigation studies**

- Surveillance case-finding efforts should review clinical records in target settings (e.g., health clinics, dermatology clinics, HIV/STI clinics) in locations where cases were detected in the earliest affected settings to better understand exposures in settings where zoonotic spillover is believed to be possible and/or where outbreaks have led to extended chains of human-to-human transmission. The medical record review should include a search for early cases presenting with a similar rash who could have been missed.
  - If possible, identify serologic or clinical lesions specimen remainders that can be used to look for serologic evidence of prior orthopoxvirus infection.
  - If possible, conduct laboratory tests for MPXV on stored lesion specimens using nucleic acid-based testing or pathologic analyses, if formalin-fixed material is available.
- Serologic studies should be undertaken in countries which have reported cases in order to review the re-emergence of Clade I, subclade IIa and subclade IIb viruses by testing for antibodies in stored serum (ideally with a monkeypox virus specific assay, see below) that predate disease (re)emergence in those regions or predate the detection of the first few cases in Europe (e.g., specimens from blood banks, STI or HIV clinics). However, these can be limited to samples from patients meeting the case definition in the target settings noted above.
- Efforts should be made to develop a monkeypox virus serospecific assay format to facilitate specific determination of past monkeypox virus infection, as opposed to prior smallpox vaccination, or other orthopoxvirus infections currently used for this purpose.

**Epidemiological and evolutionary biology studies:**

- Conduct quality epidemiologic, anthropological and social science studies to better understand and assess human-animal, environmental and human interactions related to mpox
- Conduct epidemiologic studies to characterize exposures that have led to infections, including:
  - Further defining the role of physical skin-to-skin contact, mucosal, fomites and respiratory routes of infectious exposures in mpox disease transmission and determine if transmission routes have changed over time and/or are different by Clade or lineage.
- Further defining human behaviours and interactions that increase the risk of infection to better define harm reduction measures
- Further quantifying the risks of occupational exposures (to be identified where outbreaks are detected, including hunting, mining, health care, social and cultural practices) and harm reduction from prevention measures.

- Review and characterize various exposure routes on disease transmission and clinical presentation by Clade, including e.g., incubation period, signs and symptoms, asymptomatic transmissions, clinical progression and outcome
  - Explore differences in disease transmission potentially associated with Clade I and Clade II virus variants.
- Perform virus history and transmission dynamic studies (e.g. genomic studies and contact analysis); and studies on the role of HIV or other co-infections in altering mpox disease pathogenesis. Explore the potential relation of such co-infections to mpox APOBEC3 genome changes.
- Conduct retrospective clinical/epidemiological studies to better define the transmission dynamics in endemic African countries with the current outbreak, including:
  - Better epidemiological characterization of current situation in previously affected African countries.
- Understand the role of prior immunity (vaccine provided or prior infection).
- Conduct seroprevalence studies in populations who are disproportionately affected whenever possible.
  - Develop standardized reference reagents to enable comparison of results from different laboratories in different regions.
- Compare infectiousness and persistence of the virus in the different body fluids, tissues, skin lesions and crusts. Infectiousness studies should include reproductive number, viral shedding, duration of infectivity; re-infection; and viral sanctuaries in different body fluids and tissues such as semen, saliva, the rectum, the vagina and skin crusts.
- Conduct social network analyses to better understand how mpox is transmitted in most-affected countries.
- Conduct phylogenetic studies to understand viral mutation patterns and trends along with extensive molecular epidemiological studies on mpox. Studies should seek to address the question of how the current clades of the virus evolved and what populations are at risk of the different clades.
- Conduct ethnographic studies to understand patterns of transmission and sociocultural and behavioural risk factors for spread in both endemic and non-endemic regions.
- Rigorous mobility studies of the first few cases in non-endemic areas (travel history, participation in large social gatherings/sex parties, etc.) should be completed.
- Conduct immunological studies to determine the immune response to infection with the various clades of MPXV in endemic and non-endemic regions.

**Animal, environmental and ecological studies**

Studies are urgently needed to identify animal reservoirs or animal sources of infection in endemic and non-endemic regions. In order to do this the following actions are recommended:

- Qualitative studies of human-animal and human-human interactions related to mpox, including studies of human behaviours leading to exposures from animals and subsequent MPXV infections.
• Establish active surveillance in susceptible animals in endemic countries to identify potential reservoir and amplification hosts.

• Studies should identify transmitting or amplifying hosts and behaviours that put humans at risk of infectious exposures.

• Screening of illegally and legally traded animals and products/bushmeat confiscated at borders or sold at markets in endemic countries but also in the sites of emergence of the current outbreak (Europe) to identify possible source of mpox other than travellers.

• Enhance molecular epidemiological investigation and genomic surveillance in susceptible animals as well as human cases in endemic countries to determine the origin of locally circulating strains.

• Develop and validate mpox sero-specific or cellular-specific immunodiagnostic approaches to identify potential hosts.

• Evaluate the role of reverse zoonosis through studies and surveillance designed to evaluate the possibility of transmission from humans to animals. This may include active surveillance in pet rodents or animals that may come into contact with infected individual both in endemic and newly infected countries. These studies should guide the priority listing of susceptible animals (such as squirrels, rats, mice, prairie dogs and other rodents).

• Conduct environmental contamination studies such as sewage testing and fomite studies should address the following unknowns:
  - Infectiousness of virus in different settings and surfaces
  - Products that may be contaminated with MPXV infected animal materials
  - Viability of MPXV in aerosols and the role of aerosol, droplet and airborne transmission at varying distances and in different settings

• Conduct studies assessing which human behaviours lead to exposures from animals and subsequent MPXV infections.

• Understand the implications and meaning of the APOBEC edits.

Conclusion

Understanding the factors leading to the emergence and spread of mpox in previously and newly affected countries in 2022 requires a complex multidisciplinary study. Although it has been present in many countries for many years, there is a need to conduct further and more detailed research to better understand the emergence into the human population; the various routes of disease transmission; whether there are any new routes, sexual networks, virus evolution; the role of human behaviours that have resulted in disease acquisition and transmission; the role of prior immunity (with other orthopoxviruses) and the animal reservoirs in which the virus circulates in previously as well as newly affected countries.

SAGO outlines several studies that are urgently needed to understand mpox emergence, re-emergence and transmission dynamics. Consequently, many of these studies are also intertwined with disease control efforts and are urgently needed to guide control efforts and contribute to the control or elimination strategy in countries currently experiencing active outbreaks.

The WHO Research and Development Blueprint has organized several consultations of experts in 2022 to identify knowledge gaps and outline research priorities on mpox, and other WHO global outbreak
response team units are together with partners developing detailed research roadmaps in specific areas such as diagnostics, sexual health or One Health. The recommendations outlined by the SAGO are complementary to those outlined in the discussions in these different fora and should help guide research agendas and funders towards the key priority areas that are needed to explore the origins of this disease outbreak.
Annexes and References
Annex 1. History of mpox

The monkeypox virus (MPXV; species *Monkeypox virus*, genus *Orthopoxvirus*) was first identified in captive primates in 1958 at the Serum Institute in Copenhagen. Cynomolgus macaques and rhesus macaques were noted to have vesiculopustular lesions on their faces and extremities. The similarity of the rash to that of smallpox raised an alarm. After rash specimens were sent to a number of reference laboratories, biologic and subsequent genomic studies led to the description of a new orthopoxvirus. Because it was identified in monkeys and caused symptomatic rash illness, the virus was named monkeypox (Jezek and Fenner, 1988). Surveys of humans involved in handling the animals did not identify any cases of human rash illness.

Over the next 10 years, additional outbreaks of mpox occurred in a variety of non-human primates in holding colonies. The majority of animals were initially captured in Asian countries. Subsequent serosurveys of animals in the areas where animals had been captured did not reveal evidence of anti-orthopoxvirus reactivity by older serologic methodologies (RIAA). It was inferred that the unhygienic conditions during animal transport may have led to mixing of animals to allow infectious exposure to MPXV. No source, however, was ever identified.

**Human studies Democratic Republic of Congo (then Zaire) 1981-1986**

Human illness was first identified between 1970 and 1971 as part of the intensification of smallpox eradication and specific investigation of surveillance of sporadic cases of rash illness suspected to be smallpox with the aim of certifying eradication of smallpox. A number of cases of rash illness were identified in individual humans from Liberia, Nigeria and Zaire. Specimens were rushed to reference centre laboratories, and MPXV was detected in these rash specimens. By 1979, 54 cases of mpox had been identified in Liberia, Côte d’Ivoire, Sierra Leone, Nigeria, Cameroon and Zaire. Most of these were sporadic cases, or co-primary cases without secondary (human-to-human-transmission) cases. Four cases were identified as cases from associated human-to-human secondary transmission. From two of these, distinct one-time exposures were identified, and the time from exposure to symptom onset was established as ~10 days, and exposure to rash onset ~12 days. Transmission was presumed to be respiratory, but bed sharing was also involved in one instance.

Decisions were being made at this time on recommendations for smallpox vaccination in the context of smallpox eradication. Because there was greater awareness of the adverse events that could be associated with use of replication-competent vaccinia virus in smallpox vaccine, it was decided that smallpox vaccination would not be recommended to prevent mpox. Further studies were needed, however, to evaluate those recommendations and to better understand the disease and the virus. Because surveillance systems for smallpox were more robust in the Democratic Republic of the Congo (DRC, formerly Zaire) than in other countries, from 1981-1986, WHO focused efforts to evaluate mpox disease incidence and prevalence in the DRC. These studies encompassed clinical descriptions of disease, human disease epidemiology, serosurveys to understand exposure prevalence in a number of species, ecological (animal trapping and virus persistence) and anthropological studies to better understand what occurs at the human-animal interface.

In a five-year case series, representing 338 individuals, 58% of primary cases were male and 42% female. Among secondary cases, 57% were female, which may have been related to their role as care
providers. Secondary transmission was largely linked to household or healthcare exposures. Vaccination with smallpox vaccine, 3-19 years previously, appeared to be protective in household studies. The 85% smallpox vaccine effectiveness (VE) estimate for prevention of mpox comes from these observational studies. Genetic characterization, using hybridization and restriction enzyme genome profiling became adopted to further characterize the mpox viruses from other related orthopoxviruses.

These WHO and DRC Ministry of Health-supported active surveillance efforts are summarized in the monograph “Human Monkeypox” (Jezek and Fenner, 1988). The conclusion, from land use and human animal interaction investigations, was that forest clearing for agricultural land use may have led to increased squirrel populations coming into contact with humans, potentially increasing the risk of exposure. Because animal husbandry was also expected to increase as a route for protein sources, decreased potential exposures of humans to wild animals leading to infection was anticipated. In the 1986 monograph, mpox was referred to as a “disappearing disease” (Jezek and Fenner, 1988). Vaccination programmes were not reinstated. Rare occurrences of human disease were reported through 1996. Three outbreaks in the central part of the Democratic Republic of Congo (DRC) were investigated by Ministry of Health and international teams between 1996 and 1999 (the country’s name was changed in 1997).

**Animal investigations – reservoirs or transmitting hosts – 1981-1999**

Animal investigations to understand potential reservoirs – included seroprevalence studies from 1979-1999 and were largely undertaken in DRC. As part of the 1980s efforts, and also as investigations into the source of human exposures in the late 1990s outbreak investigations, a number of efforts to understand primary animal exposure possibly leading to infection and animals that may serve as reservoirs were undertaken. During these investigations, live virus was found from only one animal, a moribund rope squirrel (*Funisciurus anerythrus*). A number of other species, reported as potential contacts, or sources of infectious exposures, through trapping, skinning, food preparation or playing were identified as having potential MPXV seropositivity. These included terrestrial and arboreal rodents and non-human primates. Animal collections with orthopoxvirus seropositivity were largely from rain forested areas and included squirrels, rope squirrels (*Funisciurus* species) and sun squirrels (*Heliosciurus* species); and later, pouched rats (*Cricetomys* species). Additionally, a number of non-human primates (*Cercocebus, Cercopithecus, Colobus, Allenopithecus spp*) were found to be seropositive. Notably, the *Rattus* species were not found to be seropositive (Jezek and Fenner, 1988, Hutin et al., 2001).

**Two clades of virus**

In 2003, a consignment of rodents from Ghana that were destined for exotic pet trade arrived in the United States of America. Within the shipment, a number of animals died on arrival or after shipment to their destinations. Of the carcasses which had been stored, MPXV was identified in the Gambian pouched rats, dormice, and rope squirrels. Housing and storage of the remaining live animals led to onward transmission to domesticated North American prairie dogs, which later proved to be effective animal transmitters of the illness to humans (Reed et al., 2004).

Further characterization of the viruses identified in the United States from humans, prairie dogs and West African rodents identified them as tightly clustered (no more than 3-4 SNP differences across the ~190 kb genome). The virus genome clustered with viruses that had been sequenced from West
Africa and from primates infected with mpox between 1958 and 1970. There were a number of distinct differences between open reading frames between these viruses, and viruses sequenced from DRC between 1997 and 2000, which were noted and annotated (Jezek and Fenner, 1988). Disease in patients with virologically confirmed disease in the 2003 outbreak was less severe (no deaths, less rash) than what had been described in 338 confirmed cases in DRC in the 1980 studies (~10% case fatality). In the United States, no human-to-human transmission was documented at that time; and all potential exposures also had prairie dog exposures (handling, bites, scratches, cage cleaning or being in the vicinity). This led to a description of “two clades” of MPXV, now named Clade I (formerly known as the Congo Basin clade, inclusive of the viruses from the Central African Republic, the DRC, and some from Cameroon), and Clade II (formerly known as the West African clade, inclusive of viruses from Nigeria, Liberia, Sierra Leone, Côte d’Ivoire, (Likos et al., 2005). All cases in the United States were caused by Clade II MPXV. In understanding the reason for the divergence of the two clades, phylogeographic studies identify geographic boundaries important in the differentiation of the two clades. The Cameroon Highlands are the primary presumed barrier since rodents (the presumed reservoir sources) are unable to traverse the Highlands. Thus, it has been proposed that a rodent reservoir, or rodent reservoirs, maintain the separate clades (Nakazawa et al., 2015).

In human mpox as previously described, especially when caused by the Clade I virus, lesions were prominent in the extremities – palms and soles, face, throat, and in males, the scrotum. In the U.S. outbreak (Clade II virus) there was one individual who had only a single skin lesion – on the scrotum (Jezek and Fenner, 1988) (Reynolds et al., 2006b). Between 2017 and 2019, mpox re-emerged in Nigeria, although there had been no cases reported since 1978. In the first report, among cases identified between September 2017 and September 2018, 69% of 122 probable or confirmed cases were in males in whom illness included genital lesions. Seven deaths (CFR 6%) were reported, with four of them occurring in adults with newly diagnosed or unmanaged HIV infection. Human-to-human transmission likely occurred in healthcare areas, prisons and households. (Yinka-Ogunleye et al., 2019) Genome sequencing identified non-monophyletic viruses from 17 Nigerian states. All viruses from this cluster were within the Clade II grouping, and subsequent analyses suggest the virus in Nigeria may be a subset of the Clade II viruses, to be called subclade IIb. (Mauldin et al., 2022) (Gigante et al., 2022)
References:


