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# A Review: The Impact of Viral Mutations on theTtransmission Dynamics of the Monkeypox Virus

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*P A P E R I N F O*

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*A B S T R A C T*

Monkeypox virus (MPXV) is an emerging zoonotic pathogen under the Orthopoxvirus genus, primarily found in Central and West Africa. It shares similarities with the variola virus, responsible for smallpox, and causes symptoms such as fever, rash, and swollen lymph nodes. The virus spreads through direct contact with infected animals, people, or contaminated objects. The recent rise in monkeypox cases beyond its usual regions has raised global health concerns. Understanding its epidemiology, clinical symptoms, and transmission is crucial for effective prevention and control. Research on vaccines and treatments is essential to mitigate future outbreaks.Viral mutations play a significant role in the evolution and behavior of MPXV, affecting transmission, virulence, and immune system interactions. This review examines how genetic changes influence the virus's spread, enhance its pathogenicity, and alter immune responses. Mutations in surface proteins may improve viral attachment to host cells, facilitating transmission. Additionally, changes in key viral genes can help evade immune detection, leading to more severe outcomes. These mutations pose public health challenges, potentially reducing vaccine and diagnostic effectiveness.Understanding the impact of viral mutations on monkeypox is crucial for effective surveillance, prevention, and treatment strategies. This analysis emphasizes the importance of continuous genomic monitoring to anticipate changes in monkeypox epidemiology and adapt public health responses accordingly.

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## 1. INTRODUCTION

Belonging to the Orthopoxvirus genus of the Poxviridae family, the Monkeypox virus (MPXV) was first discovered in 1970 in a 9-month-old infant in the Democratic Republic of the Congo. (Berche, 2022) (Huang et al., 2022) (Reed et al., 2004) Interest in MPXV resurged after the cessation of smallpox vaccinations in the 1970s, (Likos et al., 2005) leading to increased susceptibility (McCollum & Damon, 2014). The virus is zoonotic, mainly found in rodents and small mammals, with occasional spillovers to humans. Monkeypox manifests through Elevated body temperature, cephalalgia, and enlarged lymphatic glands (Letafati & Sakhavarz, 2023) (Stanford et al., 2007) and a rash that progresses to fluid-filled lesions (Moss, 2012) (Okyay et al., 2022) .Although it is usually milder than smallpox, it may result in complications such as pneumonia and sepsis (Petersen et al., 2019). There is no specific treatment, but smallpox vaccines provide partial protection (Moss, 2013) (Tolonen et al., 2001) (World Health Organization, 2022)

Monkeypox is the organism which is categorized into two genetic clades: the Central African clade, prevalent in the Congo Basin and known for its greater virulence, and the West African clade, which is correlated with a less severe disease presentation (Reynolds & Damon, 2012) (Simpson et al., 2020). The virus spreads via respiratory droplets, direct contact with
infected fluids, and contaminated surfaces. In the 2003 U.S (Bartlett, 2002) (Thornhill et al., 2022) outbreak, infected prairie dogs were the primary source of human infections, demonstrating its potential for transmission across species (Di Giulio & Eckburg, 2004) (Kieser et al., 2020) (Rao, 2022). The increasing human-to-human transmission highlights the need for effective monitoring and containment strategies (Vaccines, W.H.O., 2022) (Afshar et al., 2022) (Kmiec & Kirchhoff, 2022).

The purpose of this review is to evaluate and consolidate existing knowledge regarding the impact of genetic mutations in the monkeypox virus (MPXV) on its transmission dynamics. This involves investigating the

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molecular alterations noted in recent outbreaks, assessing their influence on viral fitness, transmissibility, and interactions with hosts, as well as considering the implications for public health responses and future surveillance initiatives.

## 2. GENOMIC CHARACTERIZATION OF MPXV

MPXV is a double-stranded DNA virus with a genome size of approximately 197 kilobases (Kmiec & Kirchhoff, 2022). It comprises a central region that is preserved, bordered by variable terminal regions that encode virulence factors. The genome contains inverted terminal repeats, open reading frames, and genes linked to immune evasion. Genetic diversity within MPXV enhances its adaptability to new hosts and environments (Beer & Rao, 2019) (Alakunle et al., 2020). The Central African clade exhibits mutations that suppress T-cell activation and inflammatory cytokine production, leading to higher virulence. Studies show that the West African clade has deletions in specific genes, correlating with lower pathogenicity (Kugelman et al., 2014).

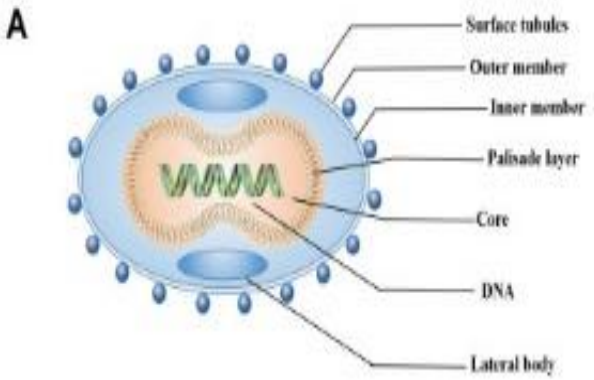


**Figure 1.** This illustration presents the structural and genomic attributes of the monkeypox virus (MPXV). (Kugelman et al., 2014) .(A) The composition of MPXV consists of five unique elements: Key elements consist of the core, the palisade layer, the outer and inner membranes, surface tubules, and nucleic acids, specifically DNA (Beer & Rao, 2019).

Electron microscopy reveals that MPXV particles are large, brick-shaped, and contain essential enzymes for transcription and replication. The virus exists in two forms: mature virions (MVs) with a single membrane, responsible for initial host attachment, and extracellular enveloped virions (EVs), which aid in viral spread. These structural characteristics impact the capability of a virus to infect host entities while successfully evading immune reactions. (Di Giulio & Eckburg, 2004) (Berthet et al., 2021)

## 3. PATHOGENESIS AND IMMUNE RESPONS

MPXV infects hosts via respiratory droplets, direct contact, or through skin lesions (Durski, 2018) (Doshi et al., 2019) (Smith & Kotwa, 2002) .The virus enters through mucosal surfaces, replicates in local tissues, and spreads to lymph nodes, leading to systemic infection (Alzhanova & Früh, 2010) (Realegeno et al., 2020) (Weinstein et al., 2005).The incubation period ranges from 7 to 21 days. During early infection, the virus remains non-transmissible (Stanford et al., 2007) (Cann et al., 2013) (Elwood, 1989)However, once symptoms appear, particularly skin lesions, transmission risk increases (Liu et al., 2005) (MacLeod et al., 2015).

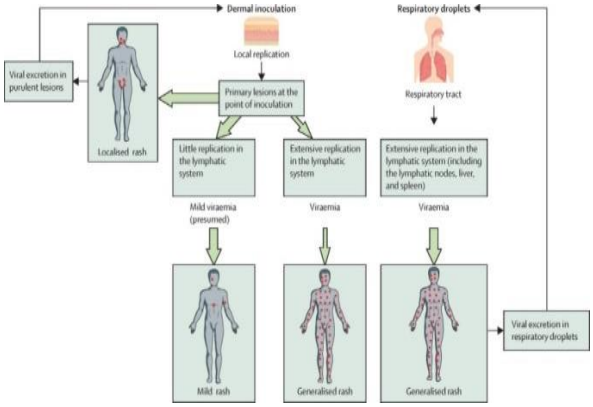


**Figure 2.** Recommended framework for understanding the distribution the spread of the monkeypox virus throughout the organism and its consequences. association with the modes of transmission.

The immune system responds to MPXV through humoral and cellular mechanisms (Realegeno et al., 2017) (Karem et al., 2007)Natural infection or vaccination induces IgM and IgG antibody production, promoting immunity (Shao et al., 2009) (Zaeck et al., 2023) (Verreault et al., 2013). CD4+ and CD8+ T cells also play a role in viral clearance. Some studies suggest that smallpox vaccination provides long-lasting immunity against MPXV, (Edghill-Smith et al., 2005) (Hammarlund et al., 2008) though vaccine-derived immunity has declined over time. Research indicates that the monkeypox virus can persist in antigen-presenting cells, allowing prolonged immune evasion (Hammarlund et al., 2003).

## 4. TRANSMISSION AND SYMPTOMS

Monkeypox is primarily zoonotic but can spread between humans. Transmission occurs through contact with infected animals (e.g., rodents, monkeys) or through contaminated materials. The occurrence of human-to-human transmission is relatively rare. It remains a possibility through respiratory secretions, skin-to-skin contact, and fomites (WHO, 2022)as shown in Figure (3) (Islam et al., 2022).

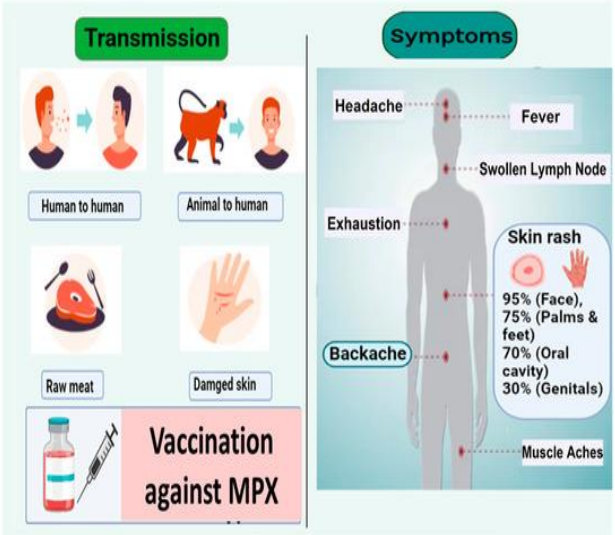


**Figure 3**. Symptoms resemble those of smallpox and include fever, swollen lymph nodes, muscle aches, and rashes (Reynolds et al., 2007). The rash develops in stages, starting with macules, advancing to papules, and subsequently forming Prior to this, the presence of vesicles, pustules, and scabs was noted. healing. Children and immunocompromised individuals are at higher risk of severe disease. (Reynolds et al., 2006) (Huhn et al., 2005).

## 5.THE IMPACT OF FEAR ON MPXV TRANSMISSION

Public perception and fear influence the spread of monkeypox (Islam et al., 2022) (Gross & Canteras, 2012) (Mobbs et al., 2010).Psychological responses to outbreaks can drive panic and misinformation (Davis et al., 2010) (Schmidt-Sane et al., 2022) .Studies from previous epidemics, such as COVID-19, show that fear disproportionately affects certain demographics, particularly healthcare workers and socially vulnerable populations (Nimbi et al., 2023) (Fitzpatrick et al., 2020). Media coverage plays a crucial role in shaping public attitudes and adherence to preventive measures. Effective risk communication, avoiding stigma, and promoting accurate information are essential in controlling the outbreak (Schmidt-Sane et al., 2022) (Nimbi et al., 2021).

## 6. FACTORS INFLUENCING MPXV TRANSMISSION

### 6.1 Ecological Sustainability

MPXV persists in the environment under specific conditions (Breman et al., 1980) (Titanji et al., 2022) .Studies indicate that the virus remains viable for weeks on contaminated surfaces, particularly in low-temperature, low-humidity settings (Pan et al., 2023) (Huq, 1976) .PCR analyses of household and hospital surfaces show MPXV DNA contamination (Verreault et al., 2013) underscoring the need for stringent disinfection practices (Pfeiffer, 2022).

### 6.2 Host and Viral Factors

MPXV is transmitted 1. Transmission occurs through direct contact with lesions, via respiratory droplets, and through other means.

2. The spread of infection can happen through direct interaction with lesions, through respiratory droplets, and by additional methods.

3. Infection can be transmitted through direct contact with lesions, through respiratory droplets, and by various other routes. contaminated surfaces (Nörz et al., 2022) (Morgan et al., 2022) (Gould et al., 2022). Studies suggest that the current outbreak strain exhibits higher transmission rates due to mutations affecting viral attachment and immune evasion (Chen et al., 2005) (Weaver & Isaacs, 2008). The 2022 outbreak primarily have affected individuals identified as men and they have sexual encounters with other men (MSM), (Mitjà et al., 2023) (Yinka-Ogunleye et al., 2019) (UK Health Security Agency, 2022) suggesting transmission through close physical contact, including sexual activity (Isidro et al., 2022) (Kaler et al., 2022) (Pan et al., 2022).

### 6.3 Cross-Species Transmission and Human-to-Human Transmission.

Animal reservoirs, including rodents and primates, play a key role in maintaining MPXV circulation. Evidence has emerged regarding the spread of illnesses from humans to animal populations (Jezek et al., 1986) (Vivancos et al., 2022)such as a case involving a dog in France, indicates that infected pets could contribute to viral spread (Hutson et al., 2009) (Ježek et al., 1988). Additionally, It has been observed that transmission occurs from the mother to the fetus. (Learned et al., 2005) with severe outcomes such as fetal demise (Cudmore et al., 1995) (Peiró-Mestres et al., 2022)

## 7. POPULATION DYNAMICS AND OUTBREAK PATTERNS

Mathematical models suggest that MPXV transmission is influenced by social and behavioral factors (Lapa et al., 2022) Studies on sexual networks indicate that a small group of highly connected individuals may drive outbreaks, explaining the rapid spread within specific communities (Lapa et al., 2022) (Parker & Buller, 2013). Differences in median age and transmission dynamics between outbreaks in Africa and recent global cases suggest evolutionary changes in MPXV (Seang et al., 2022).

## 8. CONCLUSION

Monkeypox continues to spread globally, presenting challenges similar to COVID-19. Viral mutations play a critical role in transmission, virulence, and immune evasion. The ability of MPXV to adapt to new hosts underscores the need for continuous genomic surveillance. Understanding these mutations is essential

for developing effective vaccines, treatments, and public health interventions. Future research should focus on monitoring viral evolution and improving outbreak response strategies.

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