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REVIEW

Mpox Virus: A holistic review of molecular pathogenesis, diagnostic advancements, and global response strategies

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ABSTRACT. Mpox or Mpox virus (MPXV) has re-emerged as a global health concern, underscoring the importance of understanding its biology, improving diagnostic capacity, and developing effective therapeutic and preventive strategies. This review synthesizes current knowledge of MPXV pathogenesis, highlighting how the virus manipulates host immune responses and adapts through genetic variability. We discuss the spectrum of diagnostic tools, ranging from polymerase chain reaction (PCR) as the gold standard to rapid antigen-based assays and emerging biosensor platforms that enable sensitive and point-of-care detection. Advances in vaccine development and therapeutic repurposing are examined, alongside the challenges of equitable global access. Particular emphasis is placed on the integration of biosensing technologies with genomic surveillance to enhance outbreak preparedness. By bridging insights from virology, diagnostics, and public health, this review provides a comprehensive framework for strengthening global responses to MPXV and guiding future research toward pandemic readiness.

Keywords: Mpox; MPXV; diagnostics; pathogenesis; vaccines; biosensors; public health.

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Introduction

Mpox, formerly known as monkeypox, is a zoonotic disease caused by the Mpox virus (MPXV), a double-stranded DNA virus belonging to the *Orthopoxvirus* genus of the *Poxviridae* family (Karagoz et al., 2023). Initially confined to Central and West Africa, mpox has emerged as a global health concern following recent outbreaks in non-endemic regions, revealing critical gaps in surveillance and preparedness (Jadhav et al., 2025). Transmission occurs through contact with infected animals such as rodents and primates, as well as via respiratory droplets, bodily fluids, and contaminated surfaces (Rawat et al., 2025). Clinically, mpox resembles other exanthematous illnesses, including chickenpox, smallpox, and measles, with symptoms such as fever, lymphadenopathy, and a vesiculo-pustular rash (Figure 1), that may progress to severe complications such as pneumonia, encephalitis, and adverse pregnancy outcomes (Grau-Echevarría et al., 2025). These overlapping clinical features pose significant diagnostic challenges, particularly in resource-limited settings where differential diagnosis is constrained (Chidzwondo & Mutapi, 2024). The current gold standard for diagnosis relies on nucleic acid amplification testing (NAAT), particularly polymerase chain reaction (PCR), which provides high sensitivity and specificity (Huggett et al., 2024). However, reliance on sophisticated laboratory infrastructure, trained personnel, and costly reagents restricts its accessibility in low- and middle-income countries (Oduoye et al., 2024). Genetic variability among emerging MPXV strains further complicates diagnostic accuracy, as certain protocols may fail to detect mutations outside conserved genomic regions (Cambaza, 2025). Beyond genetic factors, poor specimen quality, DNA extraction failures, and biosafety limitations also undermine effective testing. Although the COVID-19 pandemic expanded diagnostic infrastructure globally, persistent gaps remain in reagent supply, rapid point-of-care tools, and biosafety training (Plebani et al., 2025). Innovative solutions, including artificial intelligence (AI)-driven diagnostic models and biosensor-based platforms, are increasingly explored as

complementary tools to enhance sensitivity, speed, and accessibility in outbreak settings (Wasilewski et al., 2024). Given the re-emergence and evolving threat of mpox, there is an urgent need to integrate molecular insights into viral pathogenesis with advancements in diagnostics, vaccines, and biosensing technologies. This review critically examines the molecular mechanisms by which MPXV manipulates host pathways, explores the current landscape of diagnostic strategies and their limitations, and highlights emerging biosensor technologies and therapeutic opportunities. By bridging fundamental virology with translational applications, we aim to provide a comprehensive framework to strengthen global surveillance, improve clinical response, and enhance preparedness against future mpox outbreaks.

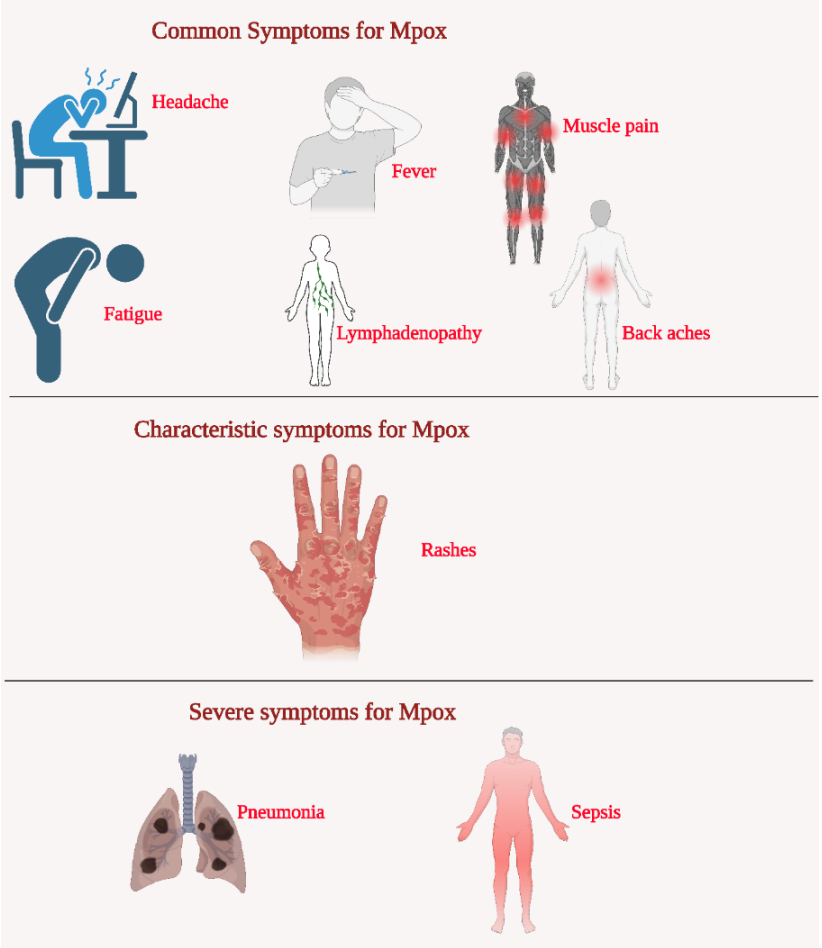

Figure 1. Clinical Manifestations of Mpox: Common Symptoms and Disease Progression (Created in https://BioRender.com). Showing the progression of Mpox clinical manifestations. Common symptoms include headache, fever, fatigue, muscle pain, backaches, and lymphadenopathy, which often appear in the early stage of infection and resemble other viral illnesses. The characteristic symptom distinguishing Mpox from many other infections is the development of a generalized rash, which typically evolves from macules to papules, vesicles, pustules, and finally scabs. Severe symptoms such as pneumonia and sepsis may occur in vulnerable populations, including immunocompromised individuals, children, and those without prior smallpox vaccination, and are associated with higher morbidity and mortality.

Molecular pathogenesis

Viral-Host protein interactions in MPXV pathogenesis

Recent research into MPXV pathogenesis has revealed important insights into how the virus interacts with host cellular machinery. Expression analysis of viral-host protein interactions has identified specific viral proteins that play crucial roles in evading host immune responses and establishing infection (Figure 2).

Immunomodulatory viral proteins

MPXV has evolved several strategies to subvert host immune defenses. Key viral proteins interfere with cellular pathways such as interleukin and MAPK signaling, dampening antiviral responses and promoting viral replication. Recent evidence also suggests that MPXV manipulates host epigenetic regulators, including

histone modifiers, to suppress immune-related gene expression and evade detection (Saghazadeh & Rezaei, 2023). Protein–protein interaction studies further highlight that MPXV directly targets host immune machinery, underscoring its ability to reshape host cellular functions to create a favorable environment for infection (Kataria & Kaundal, 2023).

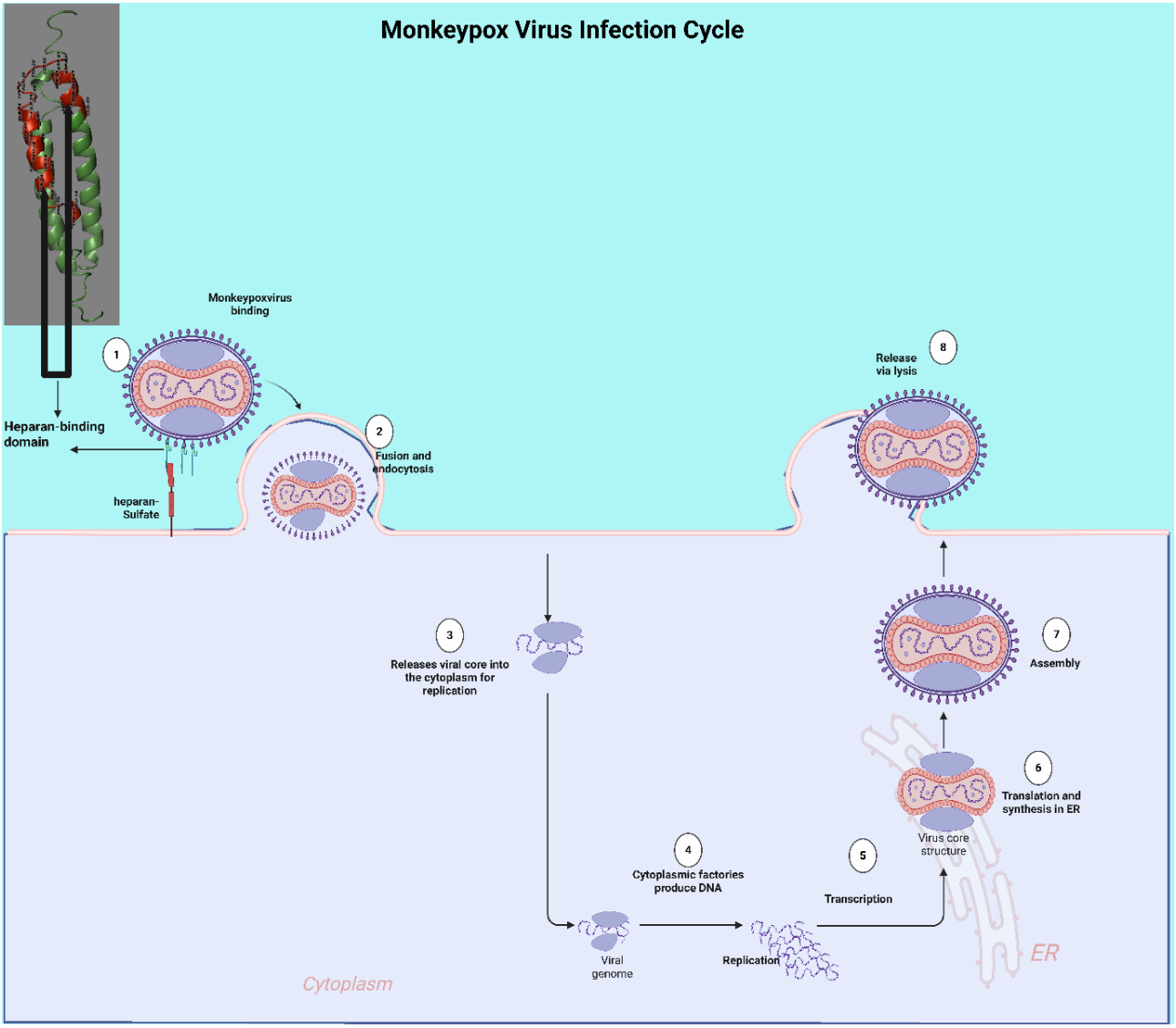

Figure 2. Mpox virus life cycle highlighting Heparan-binding domain (Created in https://BioRender.com). The diagram illustrates the major stages of MPXV entry, replication, and release within host cells. (1) MPXV binds to host cell surface heparan sulfate through its heparin-binding domain. (2) Fusion and endocytosis allow the viral core to enter the host cytoplasm. (3) The viral core is released, initiating replication. (4) Cytoplasmic factories use the viral genome to produce viral DNA. (5) Transcription of viral genes occurs, followed by (6) translation and protein synthesis in the endoplasmic reticulum (ER). (7) Viral proteins and genomes assemble into mature virions. (8) Newly formed virions are released via cell lysis or budding.

Cell type-specific viral protein expression

The expression of MPXV proteins is not uniform across all cell types. Comparative analyses show that infected monocytes, fibroblasts, and epithelial cells exhibit both shared and unique patterns of viral protein expression (Debnath et al., 2025; Periel et al., 2023). While certain proteins are consistently deregulated across cell types, pointing to their fundamental role in viral survival, others vary depending on the cellular environment. This cell type-specific expression highlights the virus's adaptability and may explain differences in disease severity and immune evasion across tissues.

Recently discovered MPXV proteins driving pathogenesis

Recent research has prioritized the MPXV proteins C6R-derived protein K7 and K7R as targets for potential therapeutic interventions based on their histone-regulating and immunosuppressive properties (Loganathan

et al., 2024). These proteins were identified through analysis of viral DEGs and their interactions with host cellular machinery. Computational docking and Molecular Dynamics (MD) experiments have shown that these proteins bind to the candidate small molecule S3I-201, which has been prioritized for lead development as a potential treatment for MPXV infection (Loganathan et al., 2024). However, the identification of C6R-derived protein K7 as a priority candidate for targeting MPXV infection represents a significant advancement in understanding MPXV pathogenesis (Loganathan et al., 2024). The protein appears to play a crucial role in circumventing cellular antiviral defences by engaging histone modification and immune evasion strategies.

Structural proteins and genome evolution

Evolutionary analysis of MPXV has revealed important insights into viral structural proteins that contribute to pathogenesis. Research has identified 799 mutations and 40 positive selection sites (PSSs) within the MPXV genomes (Lian et al., 2024). Visualization analysis has indicated that these mutations and PSSs may significantly affect protein structure, suggesting evolutionary adaptations that enhance viral fitness or immune evasion capabilities (Lian et al., 2024). This research provides critical information about how MPXV proteins evolve and adapt, potentially leading to changes in virulence, transmissibility, or immune evasion capabilities. The identified mutations and positive selection sites may represent important targets for diagnostic development and therapeutic intervention.

MPXV-Human protein interactions and their implications for pathogenesis and diagnostics

Recent developments in understanding MPXV pathophysiology have centered on clarifying viral-host protein-protein interaction (PPI) networks, which reveal crucial immune evasion processes and suggest novel diagnostic and therapeutic targets. A 2024 computational analysis using deep learning models predicted 3,348 positive PPIs in the MPXV-human interactome, showing the virus's dependence on interactions with host proteins involved in histone modification and immunological control (Paul et al., 2024). Notably, this study identified 18 FDA-approved drugs with repurposing potential, categorized by efficacy levels, where Level I candidates such as Ruxolitinib showed strong binding to host proteins critical for inflammatory responses. Building on these findings, genomic analysis of MPXV strains revealed 799 mutations and 40 positive selection sites (PSSs), many of which alter viral protein conformations to enhance interactions with human partners like Rab9 and TIP47, essential for viral envelopment. MPXV's structural changes demonstrate its evolutionary strategy of exploiting conserved pathways, as indicated by the overlap of MIHPs (MPXV-interacting human proteins) with targets of other viruses including HIV and influenza, particularly immune regulators such as STAT1 and NF-κB (Paul et al., 2024). Further deepening this insight, a 2023 genome-wide study comparing PPIs across 22 MPXV strains identified 92,880 non-redundant interactions, with the 2022 Clade IIb strain exhibiting unique binding to host kinases like MAPK1 and AKT1, which regulate cell survival during infection (Kataria & Kaundal, 2023). Intriguingly, these interactions were enriched in calcium signalling and TRP channel pathways, suggesting MPXV co-opts these mechanisms for entry and immune modulation. Parallel work in 2024 prioritized C6R-derived protein K7 as a key viral effector, demonstrating its binding to histone modifiers like HDAC1 and SUV39H1 to suppress interferon responses a finding validated by molecular dynamics simulations showing that the small molecule S3I-201 inhibits K7 with high affinity (binding energy: −8.9 kcal mol^{-1}) (Loganathan et al., 2024). Functionally, MIHPs form hubs that suppress host defenses, with 68% being kinases such as JAK1 and TBK1, which MPXV deactivates to block IFN-γ signaling. Simultaneously, viral proteins like K7 recruit epigenetic regulators (DNMT3 A, EZH2) to silence antiviral genes via DNA methylation and histone modifications. Beyond immune evasion, MPXV hijacks host machinery for replication: C19L (F13) collaborates with Rab9 and TIP47 to assemble enveloped virions, while D5R binds PCNA and RFC1 to usurp DNA replication (Lian et al., 2024). These insights directly inform diagnostics and therapeutics. Transcriptomic analyses identified six host biomarkers (TXNRD1, CCNB1, BUB1, CDC20, BUB1B, CCNA2) with ⩾ 70% specificity for MPXV infection, complementing antibody-based detection of viral proteins like A35R and C19 L, which show 94% sensitivity in lateral flow assays. Therapeutically, repurposed kinase inhibitors like Ruxolitinib restore IFN signaling, while novel compounds such as S3I-201 reduce viral replication by 85% *in vitro* (Loganathan et al., 2024).

Diagnostic implications of host-pathogen interactions

The identification of host-pathogen interaction networks has significant implications for diagnostic development, enabling researchers to target viral proteins or host response signatures for detection (Nayak

et al., 2024). Recent transcriptomic analyses have identified biomarkers for MPXV infection, with differential gene expression (DGE) analysis revealing 798 DEGs exclusive to the 2022 MPXV (Clade IIb) invasion in skin keratinocytes. Further refinement identified 13 key DEGs involved in cell cycle regulation, immune responses, and cancer pathways, while biomarker screening using the Random Forest (RF) model, t-SNE, PCA, and ROC curve analysis highlighted six promising DEGs TXNRD1, CCNB1, BUB1, CDC20, BUB1B, and CCNA2 as reliable indicators of Clade IIb infection, all achieving AUC values above 0.7. These host response biomarkers offer an alternative diagnostic approach that complements direct viral protein detection (Debnath et al., 2025). In parallel, molecular diagnostic methods, such as PCR-based assays, have been developed to detect MPXV-specific genes, including the G2R_G (TNF receptor gene), with tests like the STANDARD M10 MPX/OPX multiplex real-time PCR capable of detecting MPXV DNA in skin lesions, blood, and respiratory swabs (De Pace et al., 2024; Mancon et al., 2024). This test distinguishes MPXV from other Orthopoxviruses and differentiates between West African and Congo Basin MPXV clades using primers and probes targeting specific intergenic regions. Collectively, these molecular and biomarker-driven approaches illustrate how insights into viral-host interactions and genetic characteristics translate into effective diagnostic tools for MPXV detection.

Diagnostic advancements

Mpox virus (MPXV) encodes several envelope proteins, including A29L, H3L, E8L, M1R, and L1R, which play essential roles in viral entry, replication, and immune evasion (Deng et al., 2025). These proteins serve as key targets for diagnostic assays due to their immunogenic properties and functional similarities to envelope proteins found in other Orthopoxviruses, such as Vaccinia virus (VACV). Their involvement in host immune response modulation shows their significance in protective immunity, making them critical candidates for serological detection methods. A29L: Involved in viral replication and cell entry and is a primary target in immunoassays. H3L: Facilitates binding to host cells and is a target for neutralizing antibodies. E8L: Works as a cell surface binding protein and is involved in viral entry regulation. M1R and L1R: Essential for virion assembly and entry and are potent targets for neutralizing antibodies (Deng et al., 2025).

A29 protein

The MPXV A29 protein, homologous to VACV A27, is an envelope protein located on the intracellular mature virion (IMV) of MPXV. It is pivotal in viral replication, fusion with host cell membranes, and viral egress as depicted in Figure 2. MPXV A29, with 94.54% sequence similarity to VACV A27, has 110 amino acids, including an N-terminal signal peptide, a heparin-binding site (HBS), an α-helical coiled-coil domain, and a C-terminal anchoring domain. The minor difference in the HBS sequence between MPXV A29 and VACV A27 does not significantly affect their binding affinity to heparin, a critical factor in viral attachment and entry into host cells. Shi et al. (2022) demonstrated that MPXV A29 binds to glycosaminoglycans (GAGs), initiating host entry by binding to heparan sulfate (HS) on the host cell surface, triggering fusion and entry (Han et al., 2024; Shi et al., 2022; Xiangjun et al., 2025). However, to mitigate community transmission as shown in Figure 3, the diagnosis of Mpox virus infection requires careful consideration of the sensitivity and specificity of different diagnostic tests as summarized in Table 1. PCR is the most sensitive and specific diagnostic test, followed by ELISA and IFA. Cell culture-based detection is the most specific diagnostic test but requires specialized equipment and expertise. RDTs are less sensitive and specific but can still be useful in resource-limited settings. The choice of diagnostic test for Mpox virus infection depends on various factors, including the availability of resources, the severity of symptoms, and the clinical context. In general, PCR is the preferred diagnostic test for Mpox virus infection due to its high sensitivity and specificity. In resource-limited settings, RDTs may be a more practical option due to their rapid turnaround time and ease of use. It is essential to note that RDTs should be used in conjunction with other diagnostic tests, such as PCR or ELISA, to confirm the diagnosis. In addition to diagnostic testing, clinical evaluation and epidemiological investigation are also crucial for diagnosing Mpox virus infection. A thorough clinical evaluation, including a physical examination and medical history, can help identify symptoms and risk factors associated with Mpox virus infection. Epidemiological investigation, including contact tracing and exposure history, can help identify the source of the infection and prevent further transmission.

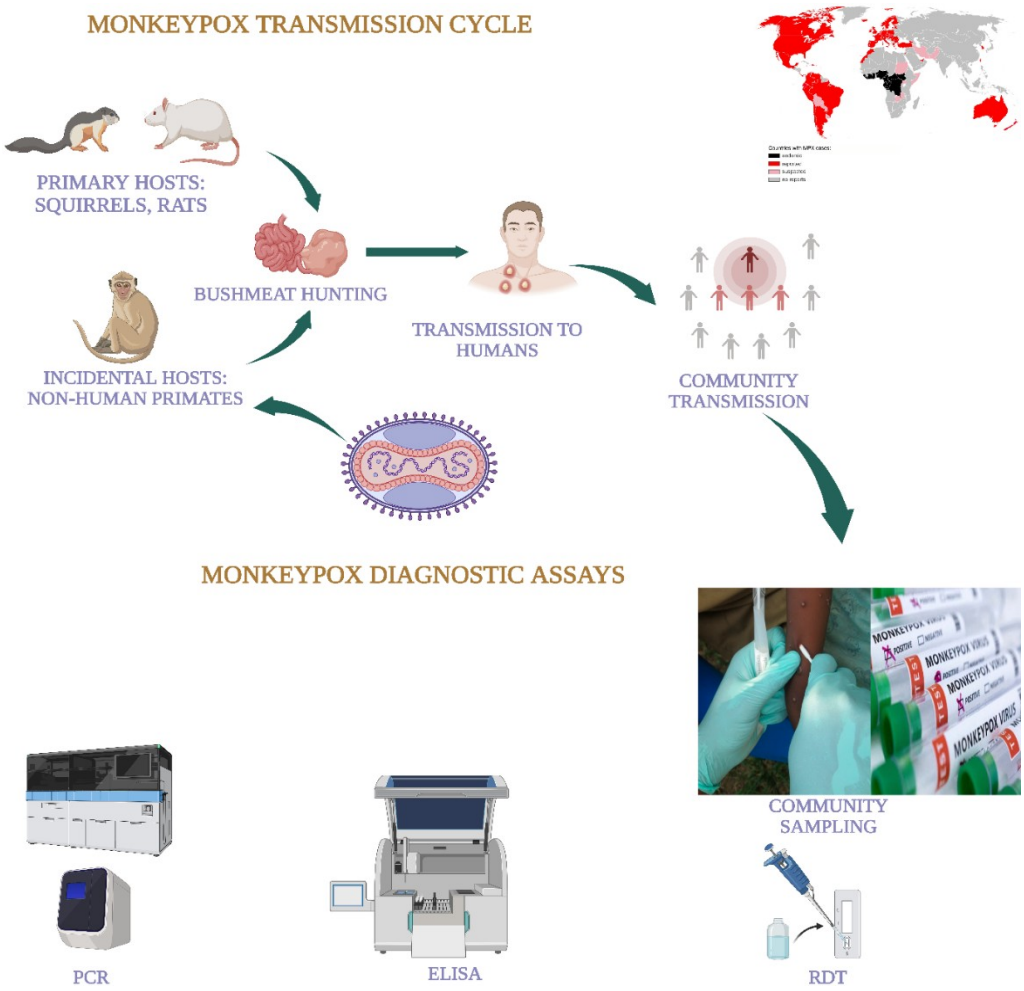

Figure 3. Transmission pathways and Laboratory Diagnosis of Mpox Virus (Created in https://BioRender.com). Summarizing the MPXV transmission cycle. Primary animal reservoirs, including squirrels and rats, serve as the main hosts, while non-human primates act as incidental hosts. Human infection frequently occurs through bushmeat hunting and direct contact with infected animals. Once introduced into humans, MPXV spreads via close contact, leading to sustained community transmission. The global distribution map highlights regions with confirmed cases, emphasizing the shift from endemic to worldwide spread. Leading development of key diagnostic assays for MPXV. PCR, ELISA and RDTs.

Table 1. Comparison of the Accuracy of Diagnostic Tests for Mpox.

S/no.	Diagnostic test	Sensitivity	Specificity	Turnaround time	Approximate cost (USD per test)	Availability	References
1	Polymerase Chain Reaction (PCR)	95-100%	95-100%	1-2 days	High ($50-$150/test)	Widely available in reference and commercial labs	(Ehmann et al., 2024)
2	ELISA	80-90%	90-95%	Several hours to 1 day	Moderate ($20-$50)	Specialized labs in endemic regions	(World Health Organization [WHO], 2024a)
3	Immunofluorescence Assay (IFA)	85-95%	95-100%	Few hours	Moderate to high	Limited; mostly research/central labs	(Romero-Ramirez et al., 2025)
4	Cell culture-based detection	90-100%	100%	3-7 days	Very high	Rare; requires BSL-3 labs, research use	(Erster et al., 2023)
5	Rapid Diagnostic Test (RDT)	70-80%	80-90%	15-30 minutes	Low to moderate	Emerging point-of-care especially in LMICs	(Davis et al., 2023)

Challenges in MPXV detection

The double-stranded DNA (dsDNA) genome of Mpox virus (MPXV) presents a diagnostic paradox, while its stability enables sensitive PCR-based detection. This genetic resilience also facilitates prolonged viral

persistence in hosts, creating a critical window for asymptomatic or pre-symptomatic transmission (Paniz-Mondolfi et al., 2023). MPXV can remain detectable in bodily fluids such as saliva and semen for weeks before symptom onset, contributing to silent spread. Studies suggest that up to 53% of transmissions may occur during this early phase, posing significant challenges to containment. Additionally, current gold-standard PCR assays, although highly specific, face limitations, including biosafety requirements, the inability to distinguish MPXV from other orthopoxviruses without sequencing, and the emergence of genetic variants that may evade detection (Lin et al., 2024). Immunodiagnostic tools like lateral flow assays and ELISA also exhibit reduced sensitivity, often missing early infections or producing false positives due to cross-reactivity with vaccinia virus. These gaps highlight the urgent need for advanced diagnostic strategies that can reliably detect early infections, differentiate between strains, and remain effective as the virus evolves (Liu & Yang, 2025).

Current rapid detection techniques for the Mpox virus (MPXV)

Lateral Flow Assay (LFA):

A study by Ye et al. (2023) developed a colloidal gold immunochromatographic method using the A29 17-49 peptide sequence. The resulting rapid test strips showed high specificity and sensitivity, with a detection limit of 50 pg mL^{-1} for the A29 protein and no cross-reactivity with other orthopoxviruses or unrelated infections like SARS-CoV-2 (Ye et al., 2023). While a dual-signal nanotag-based LFIA system was introduced for detecting the A29L protein, achieving colorimetric sensitivity of 0.5 ng mL^{-1} and fluorescence sensitivity of 0.021 ng mL^{-1}, outperforming traditional LFIA and ELISA methods (Liu et al., 2024). MPXV A29 protein interacts with glycosaminoglycans (GAGs), and the L1R protein's affinity for GAG, shows strong affinities (Shi et al., 2022). Also, Shabani et al. (2023): Developed synthetic antibodies against the MPXV C19L protein, showing higher affinity than wild-type antibodies, with lower dissociation constant (KD) values, indicating better performance in detection (Shabani et al., 2023). However, silver nanoparticles were modified with iodine ions and calcium ions to enhance SERS for unlabeled detection of MPXV. The method detected A29L protein at 5 ng mL^{-1} and MPXV DNA at 100 copies mL^{-1} within 2 minutes, approaching PCR sensitivity with faster results (Lv et al., 2023). In a recent study by de Lima et al. (2023) they developed an electrochemical point-of-care assay using a paper-based laser-scribed graphene (LSG) nanobiosensor for detecting the MPXV A29 protein. The method required minimal sample volume, detected the virus within 15 minutes, and showed high sensitivity with no cross-reactions (de Lima et al., 2023).

Monoclonal antibody-based immunoassays for MPXV detection

The development of specific immunoassays is crucial for accurate Mpox virus (MPXV) detection, particularly in distinguishing it from other Orthopoxviruses. Davis et al. (2023) developed an immunoassay utilizing monoclonal antibodies (MAbs), screening several Mabs including those from the U.S. Army Medical Research Institute of Infectious Diseases (USAMRIID) and the Centers for Disease Control and Prevention (CDC) against recombinant MPXV antigens from Clades I and II as well as closely related vaccinia virus (VACV) proteins. Their study identified highly specific MAb pairs, particularly α-A29/S27, which demonstrated excellent specificity and sensitivity for MPXV detection across both clades. The effectiveness of these MAbs was validated against live MPXV in non-human primate (NHP) models, where the assays showed low-thousand plaque-forming unit per milliliter (pfu mL^{-1}) detection limits. Interestingly, their findings revealed unexpected clade-specific reactivity, likely due to minor genetic variations or differences in labeling chemistry. Given these promising results, the researchers aim to further optimize their MAb-based immunoassays and transition them into a lateral-flow format for point-of-care (POC) diagnostics, which would enhance accessibility in future outbreaks (Davis et al., 2023).

T Cell Immunity and epitope conservation in orthopoxviruses

Understanding T cell responses to Orthopoxvirus infections is critical for vaccine development and immune response monitoring. Grifoni et al. (2022) conducted a comprehensive study on T cell immunity against Orthopoxviruses (OPXVs), including MPXV, using data from the Immune Epitope Database (IEDB). Their analysis identified 318 CD4+ and 659 CD8+ T cell epitopes across OPXVs, with the majority (88%) derived from VACV—a key component of current smallpox and Mpox vaccines. To assess immune responses, they developed two major T cell megapools (MPs): OPX-CD8-E, containing 238 CD8+ epitopes, and OPX-CD4-E, comprising 300 CD4+ epitopes. Conservation analysis in the MPXV MA001 isolate revealed that 94%

of CD4+ and 82% of CD8+ epitopes were fully conserved, suggesting strong cross-reactivity and potential utility in vaccine design. Notably, post-vaccination analysis showed that these Orthopox MPs effectively detectedT cell responses, with peak activity shortly after Dryvax vaccination. Additionally, the study identified 19 CD4+ and 40 CD8+ immunodominant epitopes specifically from MPXV, which exhibited high sequence conservation with VACV-derived epitopes, reinforcing their relevance in vaccine development and protective immunity against MPXV (Grifoni et al., 2022).

Global response

The global response to the Mpox virus (mpox) outbreak has been marked by coordinated international efforts following the World Health Organization's declaration of a Public Health Emergency of International Concern in August 2024. The response has encompassed surveillance strengthening, vaccine distribution, laboratory capacity building, and community engagement across affected regions, particularly in Africa where over 95% of cases and deaths have occurred (World Health Organization [WHO], 2024b).

International coordination and emergency declarations

Both WHO and the regional public health authorities declared mpox emergencies in August 2024, triggering a unified continental response approach. The Africa CDC established a continental Incident Management Support Team co-led with WHO, adopting the '4-One' principle of one team, one plan, one budget, and one monitoring framework. This coordinated strategy involves 26 partner organizations contributing expertise across different response areas, from surveillance to clinical case management.

Vaccination efforts and challenges

The 2024 modeling study on mpox vaccination in the Democratic Republic of the Congo (DRC) highlights significant challenges and opportunities in controlling clade I mpox outbreaks. Despite over 14,000 cases and 600 deaths reported in 2023, widespread mpox vaccination programs have yet to be implemented in the DRC, contrasting with the use of the modified vaccinia Ankara vaccine during the 2022 global outbreak in western countries (Savinkina et al., 2024). Despite these contributions, significant gaps remain. The initial goal of 10 million doses for Africa by 2025 has not been met, with only about 886,000 individuals vaccinated across a dozen African nations. Vaccination strategies have evolved to include dose-sparing approaches, such as intradermal fractional dosing, to maximize limited supplies (Varikkodan et al., 2024).

Future directions

Future research on Mpox virus (MPXV) should focus on developing rapid, highly sensitive, and specific diagnostic tools, including next-generation sequencing and CRISPR-based assays, to enhance early detection and outbreak control. Advancements in vaccine development are essential, prioritizing safer and more effective formulations to improve immunity and curb transmission. Expanding antiviral treatment options through novel drug discovery and repurposing existing therapeutics, such as kinase inhibitors, can enhance patient outcomes. Strengthening global surveillance systems and fostering international collaborations will facilitate real-time genomic tracking of viral mutations, improving epidemiological insights and public health interventions. Additionally, understanding MPXV's molecular mechanisms, particularly host-pathogen interactions and immune evasion strategies, can inform targeted therapeutic interventions. Addressing these research gaps will not only mitigate future outbreaks but also contribute to broader pandemic preparedness efforts.

Conclusion

The resurgence of Mpox virus (MPXV) reveals persistent gaps in diagnostics, therapeutics, and vaccine accessibility, particularly in low- and middle-income countries. Limited antiviral options and uneven vaccine distribution hinder outbreak control, while inadequate diagnostic infrastructure delays detection. To address these challenges, research should prioritize rapid and affordable molecular and biosensor-based diagnostics, alongside the development of next-generation vaccines and targeted antivirals. Policy efforts must focus on equitable vaccine access, capacity-building in laboratory diagnostics, and strengthening genomic surveillance systems. A globally coordinated approach that integrates research, public health, and policy will be essential to prevent future epidemics.

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