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Original Article

Mpox virus genomic surveillance and typing in Sri Lanka, 2022-2025

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Abstract

Introduction: Mpox, a rare viral zoonotic disease attracted global attention in year 2022, with the global epidemic that occurred across non-endemic regions. This study aimed to determine the Mpox situation in Sri Lanka, with viral characterization, transmission dynamics and clinical profiles, within the context of the recent global epidemic.

Methods: This retrospective study utilized all samples of swabs from the lesions of suspected patients with mpox infection received by the National mpox laboratory, from May, 2022 to May, 2025. Commercially validated real time polymerase chain reaction was utilized to detect the mpox virus, followed by Oxford nanopore based whole genome sequencing for clade identification and phylogenetic analysis. Socio demographic and clinical characteristics were extracted from accompanied request forms.

Results: Five (11.36%) out of 44 samples tested detected the mpox virus. Four out of five positive samples were from patients aged between 15 to 45 years and male gender. One case was detected in a neonate. Four cases exhibited vesicular/pustular skin lesions and myalgia, while three and two cases experienced fever and lymphadenopathy respectively. Complicated disease with bronchopneumonia was present in the neonate. All cases reported a history of recent overseas travel. Genetic sequencing identified mpox clade IIb in all positive samples.

Conclusion: The study revealed all cases of mpox detected in Sri Lanka to be of clade IIb, on a par with the global outbreak which was primarily driven by the same. Chain transmission of Mpox infection was not observed within the country, with zero endogenous cases.

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Key words: Mpox virus, Sri Lanka, Genomic surveillance, Mpox typing

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Introduction

Mpox is a rare viral zoonotic disease which has been endemic in African countries for more than 50 years (1). It received global attention with the worldwide epidemic that occurred across non-endemic regions including in Asia, in year 2022, with the World Health Organization (WHO) declaring mpox as a public health emergency of international concern (1,2).

Mpox infection is caused by the mpox virus, an enveloped, double-stranded DNA virus belonging to genus Orthopoxvirus and family Poxviridae, the same family to which the variola virus belongs to. The virus is thought to be harboured in African rodents and non-human primates (2).

Two distinct clades of the virus, clade I and II have been identified (3). Mpox clade I has been predominantly associated with 95% of the cases historically in African countries. Interestingly, in the present context, clade II gained importance with the recent global epidemic led by clade IIb, lineage-B.1. The clade IIb still continues to transmit across countries in low intensity. Moreover, the Democratic Republic of the Congo reported an outbreak with clade Ib in 2023, with ongoing human to human transmission in several countries to date (4,5). A total of 137,892 confirmed cases of mpox have been reported from the 1st of January 2022 to 31st of March 2025 from 132 countries, with 317 confirmed deaths (6).

Although a zoonotic infection, human to human transmission via close contact with lesions, body fluids and infectious respiratory particles of infected individuals has largely determined the recent upsurge of the mpox infection. A high incidence of cases has been reported among individuals with multiple sexual partners, particularly during the recent global epidemic (1). Additionally, transmission through indirect contact, transplacental and perinatal mother to child transmission, as well as percutaneous transmission via needle stick injuries have been documented (1,7).

The typical presenting features of mpox infection include a vesiculo-pustular rash involving the skin and/or mucous membranes, fever and lymphadenopathy, which may be complicated with secondary bacterial skin infections, pneumonia, corneal infection with loss of vision, encephalitis, myocarditis and sepsis, which are predominantly seen in children, pregnant mothers and immunocompromized individuals. The infecting clade of the virus may also determine the severity of the disease, with surpassing disease severity and mortality rates associated with clade I(3,8).

Thus, this retrospective study aimed to determine the Mpox situation in Sri Lanka emphasizing the viral characterization, transmission dynamics and clinical profiles, within the context of the recent global outbreak.

Methods

This laboratory based retrospective study utilized all samples of swabs from the lesions of patients with suspected mpox infection, received at the National mpox laboratory, Medical Research Institute, Sri Lanka, from May, 2022 to May, 2025. Nucleic acid extraction from the samples was performed using the SpinStar viral nucleic acid extraction kit (ADT Biotech, Malaysia) according to the manufacturer's instructions. A commercially validated real time polymerase chain reaction (PCR), the LightMix Modular Mpox virus (MPXV) qPCR (TIB Molbiol,Germany) assay was utilized to detect the mpox virus specific nucleic acid. All samples positive for the mpox virus were incorporated into the Oxford nanopore based whole genome sequencing using a multiplex amplicon sequencing ARTIC protocol, and data analysis was carried out using the EPI2ME software, for identification of the mpox virus clades and phylogenetic analysis. Socio demographic and clinical characteristics were extracted from the request forms which accompanied the samples.

Results

A total of 44 samples of swabs were included for mpox virus specific nucleic acid testing. Five (11.36%) out of these samples detected the mpox virus specific nucleic acid confirming mpox infection.

Four of these cases belonged to ages between 15 to 45 years, while one case was detected in a neonate. Four out of those five patients were males. Of the positive cases, four exhibited vescicular/pustular skin lesions whereas, genital lesions were observed in two cases and the rest had lesions elsewhere. Four cases experienced myalgia while three cases developed fever and two cases developed lymphadenopathy. The infection was complicated with bronchopneumonia in one case while none of the other cases developed complications. All cases reported a history of recent overseas travel, of which four have travelled to Dubai and one patient to Thailand. Four of the cases gave a positive contact history with patients with mpox infection.

The first laboratory confirmed case of mpox was identified in Sri Lanka in November 2022 in a young adult male who had recently travelled to Dubai, with a history of close contact with a patient confirmed with mpox infection. The second case was detected in Sri Lanka during the same month.

The first neonatal mpox case was identified in Sri Lanka in 2023 in an 8-day old infant who had recently returned from Dubai, presenting with fever and a generalized maculopapular rash involving the face, chest, palms and soles. The neonate's mother gave a similar history of two days duration and was laboratory confirmed as the fourth case of mpox infection in Sri Lanka. The infection was complicated in the neonate and was treated with the antivirals accordingly.

Mpox virus clade IIb was identified in all five positive cases through genomic sequencing.

Discussion

With the global epidemic of mpox, mpox identification in Sri Lanka was established by the National mpox laboratory, Medical Research Institute, Sri Lanka, in year 2022, utilizing molecular diagnostics. The diagnostics were further armed with genetic sequencing of the virus subsequently. Currently, the National mpox laboratory is the sole centre in Sri Lanka which provides facilities for identification of the mpox virus.

To date, a total of five cases of laboratory confirmed mpox infection have been detected in Sri Lanka. Similarly, as of worldwide, male adolescents and young adults dominated the positive cases (9). The clinical presentations of the cases were similar to global evidence with majority presenting with fever, vesiculo-pustular rash and lymphadenopathy. Non-complicated disease was observed predominantly whereas complicated disease was only detected in the neonate, requiring antiviral treatment. Thus, the findings agreed with past evidence of more complicated disease associated with children and pregnancy (10).

All five cases of mpox infection reported a history of recent travel to countries reporting cases of mpox, while agreeing with the incubation period of the infection (11). Thus, Sri Lanka confirms zero endogenous cases of mpox with chain transmission within the country, to date.

Genome sequencing confirmed all mpox cases detected in Sri Lanka to belong to clade IIb, which complied with the clade of the global outbreak commenced in 2022 [4,5,6]. Further, cases related to clade I have not been detected within the country.

Conclusion

The study revealed five laboratory confirmed cases of mpox within Sri Lanka with clade IIb, on a par with the global outbreak which was primarily driven by the same. Chain transmission of mpox infection was not observed within the country to date. Majority of the confirmed cases unveiled mpox ulcers with non-complicated disease, adhering with the already established prevalent clinical manifestations of mpox infection.

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