Outbreak Reports

Imported Cases of Monkeypox Virus Clade Ⅰa — China, 2025

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Summary

What is already known about this topic?

Monkeypox virus (MPXV) is an orthopoxvirus comprising two major genetic clades: clade Ⅰ (subclades Ⅰa and Ⅰb) and clade Ⅱ (subclades Ⅱa and Ⅱb). The 2022–2023 global outbreak was predominantly driven by clade Ⅱb. Clade Ⅰ viruses remain endemic in Central Africa, particularly Democratic Republic of the Congo (DRC), and are historically associated with higher virulence and fatality rates.

What is added by this report?

Two imported MPXV cases were detected in Shanghai via real-time polymerase chain reaction (PCR) in 2025, both originating from DRC. Clade-specific PCR and whole-genome sequencing identified clade Ⅰa.

What are the implications for public health practice?

These cases underscore the ongoing risk of MPXV importation through international travel. The successful detection and management of these clade Ⅰa infections demonstrate the critical importance of port entry screening, enhanced surveillance systems, and coordinated multi-agency prevention and control strategies.

ABSTRACT

Introduction: Monkeypox virus (MPXV), an emerging zoonotic pathogen, comprises two main clades with distinct epidemiological and clinical characteristics. This study reports the epidemiological investigation and genomic characterization of imported MPXV clade Ⅰa cases detected in China during 2025.

Methods: During March and April 2025, two travelers arriving at Shanghai Pudong International Airport from the Democratic Republic of the Congo (DRC) underwent screening for MPXV infection. Clinical specimens were analyzed using real-time polymerase chain reaction (PCR), clade-specific PCR, and whole-genome sequencing to characterize the viral genomes.

Results: Both cases tested positive for MPXV infection. Clade-specific PCR and whole-genome sequencing confirmed infection with MPXV clade Ⅰa. The first case yielded partial viral genome data (approximately 7.2 kb; 3.64% genome coverage), whereas the second case produced near-complete genome sequences (196.7 kb; >99% coverage) through combined second- and third-generation sequencing platforms. Phylogenetic analysis revealed that these sequences clustered closely with clade Ⅰa strains currently circulating in the DRC.

Conclusions: These findings demonstrate the effectiveness of port-based infectious disease surveillance and multi-agency joint prevention and control mechanisms in identifying and managing imported MPXV cases. Enhanced surveillance capacity, rapid laboratory confirmation, and robust multi-agency collaboration are essential for preventing cross-border transmission of emerging infectious diseases.

Monkeypox virus (MPXV), a zoonotic pathogen belonging to the genus *Orthopoxvirus*, has emerged as a significant global public health threat following its unprecedented multi-country outbreak (*1*). Genetically, MPXV comprises two major clades: clade I (Central African clade), encompassing subclades Ia and Ib, and clade Ⅱ (West African clade), comprising subclades Ⅱa and Ⅱb (*2*). The 2022–2023 global outbreak, driven predominantly by clade Ⅱb, disseminated to over 100 countries and prompted the World Health Organization (WHO) to declare a Public Health Emergency of International Concern (PHEIC) (*3*).

Prior to 2024, all confirmed MPXV cases in China were attributed to clade Ⅱb, consistent with the global transmission pattern of the 2022 outbreak (*4*–*5*). In late 2024, China reported its first clade Ib outbreak event, originating from the Democratic Republic of the Congo (DRC), which underscored the potential for introduction of clade I viruses from endemic regions (*6*). Given the increasing volume of international travel between China and African

countries, the risk of importing clade I strains (including Ⅰa) has become increasingly significant.

Herein, we report two imported cases of MPXV clade Ⅰa detected in travelers returning from the DRC in 2025. This report characterizes the epidemiological features, laboratory findings, and genomic profiles of these cases, with the primary objective of demonstrating the critical role of port health surveillance and multi-agency joint prevention and control mechanisms in enabling timely detection and response to imported emerging infectious diseases.

INVESTIGATION AND RESULTS

Epidemiological Investigation

Case 1: A 33-year-old Chinese male arrived at Shanghai Pudong International Airport on March 28, 2025, aboard Flight ET684 from Addis Ababa, Ethiopia, after departing from Kinshasa, DRC. Upon arrival, he wore a mask and presented without fever or other apparent symptoms. The patient reported employment as a security guard in Africa, where his duties involved direct contact with multiple animal species, including vipers, baboons, caracals, raptors, pangolins, and crocodiles. He denied human immunodeficiency virus (HIV) infection, sexual contact with men, or exposure to known or suspected MPXV cases.

Case 2: A 39-year-old Chinese male arrived at Shanghai Pudong International Airport on April 13, 2025, aboard Flight ET684 from Addis Ababa after departing from Kinshasa, DRC. Upon arrival, he presented with papular rash-like lesions distributed across the face, arms, fingers, and chest, accompanied by dry cough and sore throat. Epidemiological investigation identified him as a close contact and workplace colleague of Case 1, whose MPXV clade Ⅰa infection had been laboratory-confirmed by Shandong CDC on March 31, 2025 (*7*).

Laboratory Testing

Clinical specimens, including throat swabs, vesicular fluid, whole blood, and serum samples, were collected from both cases and tested for MPXV using quantitative PCR detection kits (DaanGene Co., Ltd. and BioGerm Co., Ltd.). In Case 1, MPXV DNA was detected in serum (cycle threshold [Ct] values: 36, 34) and whole blood (Ct values: 38, 35), whereas the throat swab, which was the sole specimen type subjected to testing at the time of entry, tested negative. In Case 2, MPXV DNA was detected in vesicular fluid samples (vesicular fluid 1: Ct values 22, 20; vesicular fluid 2: Ct values 33, 36) and throat swab samples (Ct values 30, 30), while whole blood and serum samples tested negative. Subsequent clade-specific PCR assays performed on Case 2 specimens identified MPXV clade Ⅰa in vesicular fluid (Ct values: 22 and 33) and throat swab (Ct value: 31) samples; whole blood and serum samples remained negative.

Whole-genome sequencing of MPXV was performed using a multiplex PCR amplification strategy combined with high-throughput sequencing (*8*). Viral nucleic acids extracted from clinical specimens were amplified using multiplex PCR targeting overlapping genomic regions spanning the entire MPXV genome (approximately 197 kb). The resulting amplicons were prepared for sequencing using two distinct platforms: Illumina (second-generation sequencing) and QITAN-Gene (third-generation sequencing). Genome assembly quality was evaluated based on coverage depth (mean sequencing depth) and genome completeness (percentage of the reference genome covered). Clade assignment and phylogenetic analysis were conducted using the Nextclade platform. For Case 1, Illumina sequencing produced a partial MPXV genome of approximately 7.2 kb, representing 3.64% of the 197 kb reference genome, with a mean sequencing depth of 1,533×. For Case 2, Illumina sequencing yielded a near-complete MPXV genome of 196.6 kb (99.6% coverage, mean depth about 18,320×), while QITAN-Gene sequencing independently generated a 196.6 kb genome (99.6% coverage, approximately 3,885× depth).

Phylogenetic analysis was performed using Nextclade (https://clades.nextstrain.org). The resulting maximum-likelihood tree positioned the Case 2 sequence in close proximity to recent clade Ⅰa strains circulating in the DRC, clearly distinguishing it from clade Ⅱb strains that have dominated global outbreaks since 2022 (Figure 1A). The high-quality near-complete genome from Case 2 shared 99.8% nucleotide identity with an MPXV clade Ⅰa isolate from the DRC (DRC/PP_0012WRG/2024-09-10) (Figure 1B), while demonstrating 96.2% similarity to a clade Ⅰb sequence associated with the concurrent outbreak in Kinshasa, DRC (DRC/PP_004B9Y2.1/2025-04-05).

PUBLIC HEALTH RESPONSE

Shanghai Port maintained rigorous health

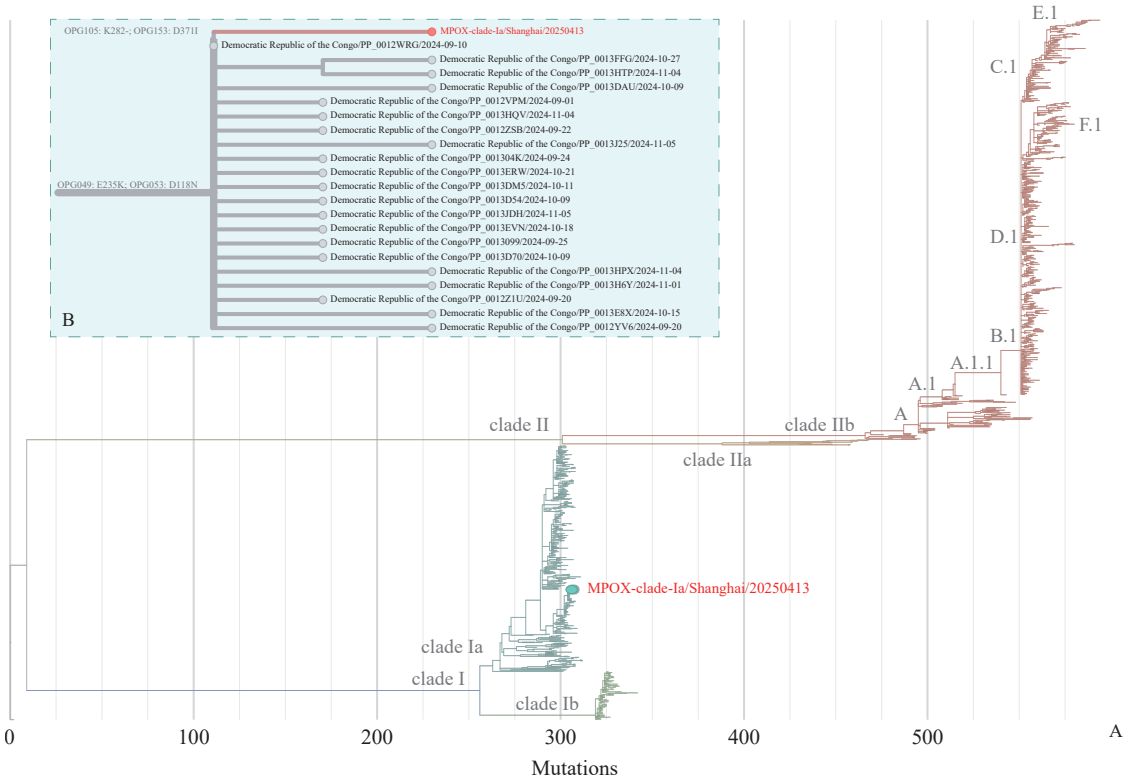

FIGURE 1. Maximum-likelihood phylogenetic tree generated using Nextclade.
Note: The viral sequences from Case 2 (highlighted in red) cluster within clade I (Central African clade) and exhibit closest genetic similarity to an MPXV strain isolated in the DRC (PP_0012WRG, GenBank accession: OZ254474, collection date: September 10, 2024).
Abbreviation: MPXV=monkeypox virus; DRC=Democratic Republic of the Congo.

surveillance protocols for arriving international travelers, encompassing temperature monitoring, symptom assessment, and detailed epidemiological interviews. Although Case 1 presented with normal body temperature and declared no symptoms upon arrival, the individual subsequently sought medical care in Shandong Province, where MPXV infection was laboratory-confirmed by Shandong CDC (*7*). Following notification from Shandong CDC, Shanghai Customs immediately initiated comprehensive contact tracing, identifying and monitoring all passengers seated within three rows of the confirmed case during the inbound flight. All identified close contacts underwent specimen collection and medical observation according to established protocols.

Case 2 was detected during routine entry screening when port health officers observed characteristic skin lesions. Subsequent epidemiological investigation established the epidemiological link to Case 1. Upon laboratory confirmation of both cases, Shanghai Customs promptly notified the Shanghai Municipal Health Commission and Shanghai CDC, triggering a coordinated multi-agency response. A comprehensive joint risk assessment was conducted to evaluate potential community transmission risks, laboratory diagnostic capacity, and emergency response preparedness.

In response to these imported cases, Shanghai Port enhanced surveillance measures for travelers arriving from high-risk countries, intensified epidemiological screening of returning residents with potential exposure histories, and strengthened quarantine inspection procedures. Medical patrols and targeted health education campaigns were implemented for high-risk flights. All suspected cases underwent immediate specimen collection and laboratory testing, establishing a robust frontline defense system against cross-border pathogen introduction.

DISCUSSION

MPXV, an emerging zoonotic orthopoxvirus, has attracted sustained global attention as outbreaks have occurred in both endemic and non-endemic regions. Historically confined to Central and West Africa, MPXV infections are now increasingly detected among international travelers, underscoring the persistent risk

of cross-border transmission in an era of global mobility (*1*). This report documents two imported MPXV clade Ia infections detected in China, representing a Central African lineage historically associated with higher virulence and elevated case fatality rates (*2*,*9*). These findings reinforce the critical need for sustained vigilance at international points of entry to intercept pathogens originating from endemic regions.

Given the increasing volume of international travel between China and MPXV-endemic regions, maintaining and strengthening port health surveillance remains essential (*9*). The primary public health significance of these cases extends beyond the rarity of the viral lineage to demonstrate the effectiveness of coordinated multi-agency response systems (*10*). Through collaboration among customs authorities, health commissions, and CDCs, this integrated approach plays a pivotal role in coordinating resources, ensuring rapid response, and achieving closed-loop management of cases and their contacts.

Laboratory assays of these cases showed that pathogen-detectable sample types vary depending on the infection stage and further underscored the critical importance of integrated laboratory capacity and genomic characterization within port health surveillance systems. The application of clade-specific PCR and whole-genome sequencing enabled precise lineage identification and comprehensive risk assessment, directly supporting evidence-based decision-making for public health interventions. Notably, genomic analysis provided essential context for distinguishing imported high-virulence lineages from strains associated with ongoing global outbreaks, thereby enhancing situational awareness and improving response precision.

In conclusion, these imported MPXV clade Ia cases provide compelling evidence that well-functioning port health quarantine systems, supported by robust laboratory and genomic surveillance coupled with multi-agency coordination, effectively mitigate the risk of cross-border transmission of emerging infectious diseases. Continued investment in port biosecurity infrastructure and diagnostic capacity will be essential for safeguarding public health security. Such investments are particularly critical amid increasing global population mobility and the ongoing threat of pathogen importation from endemic regions.

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