

Vital Surveillances

Genomic Surveillance and Phylogenetic Analysis of Monkeypox Virus Sampled from Clinical Monkeypox Cases and Sewage — Sichuan Province, China, 2023

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ABSTRACT

Introduction: Monkeypox (Mpox) has reemerged globally, with thousands of confirmed cases reported in China. However, limited data exist on the genomic variations and transmission patterns of monkeypox virus (MPXV) in southwestern China.

Methods: Clinical samples from Mpox cases and sewage samples from wastewater treatment plants were collected from Sichuan Province for whole-genome sequencing and MPXV analysis.

Results: In the second half of 2023, 96 clinical samples from Mpox patients were collected, yielding 58 full-length viral genomes. All sequenced viruses belonged to the Western African clade (IIB), comprising three C.1 and fifty-five C.1.1 sequences. This study determined that Mpox cases in Sichuan originated from both importation and subsequent local transmission, with evidence of at least six distinct transmission clusters. Additionally, 26 sewage samples were collected, and 3 complete MPXV genomes were constructed. Analysis of viral genomes from sewage samples demonstrated a 95% concordance in high-frequency mutation sites with those observed in clinical cases, suggesting that sewage surveillance effectively captures diagnosed cases and serves as a robust complement to conventional monitoring. The integration of newly sequenced genomes with published data revealed an increased mutation rate in MPXV, along with fluctuating patterns of expansion and contraction of the effective viral population size.

Conclusion: This study provides preliminary insights into MPXV transmission dynamics and genomic evolution in Sichuan and demonstrates the utility of sewage monitoring in tracking viral diversity.

infection with Monkeypox virus (MPXV), characterized by clinical symptoms including fever, rash, and lymphadenopathy (1). Since the first reported case of Mpox in the Democratic Republic of Congo in 1970 (2), it has primarily circulated in African countries. However, the number of Mpox cases has been increasing in Europe (3) and the Americas (4), and has attracted global attention since 2022. By January 2025, 130 countries had reported Mpox cases, with approximately 127,960 cases and 281 deaths (WHO). Recently, MPXV strains from Central Africa (including clades Ia and Ib) began to appear (5), prompting the WHO to reclassify Mpox as a Public Health Emergency of International Concern (PHEIC). In September 2022, China reported the first imported case of Mpox (6–7), with no further reports thereafter. However, in June 2023, Beijing provincial-level administrative division (PLAD) reported the first local case of Mpox, followed by reports from several other provinces such as Beijing, Guangdong (8), Zhejiang, and Jiangsu PLADs (9), leading to local transmission with a cumulative number of cases exceeding 1,000 (10).

The rapid global spread of MPXV may be attributed to factors such as the accelerated virus evolution rate (11) and changes in transmission routes (12); however, the genetic evolution characteristics and evolutionary trajectory of MPXV remain unclear. Therefore, continuous research on the variation and evolution of MPXV and its role in the transmission process is crucial for tracking the sources of infection, predicting transmission patterns, and monitoring epidemic warnings. However, there have been no reports of the long-term monitoring of Mpox transmission and virus evolution patterns within the scope of a province in China. Moreover, reports on the simultaneous monitoring of MPXV in Mpox cases and sewage samples are limited. The performance of sewage sample-based monitoring in detecting variants and

Monkeypox (Mpox) is a zoonotic disease caused by

mutations requires further investigation. Chengdu, the capital city of Sichuan Province, has a resident population of 21.4 million, making it the fourth largest city in the country. Despite consistently ranking high in the reported Mpox cases nationally, there have been relatively few reports on the genomic characteristics of locally circulating strains.

In this study, researchers conducted whole-genome sequencing of MPXV from confirmed Mpox cases and sewage samples from Sichuan, China. These findings expand China's genomic surveillance dataset of MPXV and enhance national understanding of Mpox transmission dynamics, evolutionary patterns, and containment strategies: offering critical insights for both national and global public health efforts.

METHODS

Sample Collection and Pretreatment

The definition of confirmed cases refers to the “Monkeypox Prevention and Control Plan” from China's Center for Disease Control and Prevention. A total of 96 clinical samples, including throat swabs and vesicle fluid swabs, were collected from confirmed cases of Mpox in Sichuan Province ([Supplementary Table S1](#), available at <https://weekly.chinacdc.cn/>). These samples were transported to the laboratory of the Sichuan Provincial Center for Disease Control and Prevention (SCDC) and stored at -80°C . Sewage samples (300 mL) were collected weekly from the Ninth Regenerated Water Plant in Chengdu City, Sichuan Province (a living sewage treatment facility in the core area of Chengdu City with an area of about 200 km^2) and transported to the SCDC laboratory. According to the “Method for enrichment and nucleic acid detection of SARS-CoV-2 in sewage” (WS/T 799-2022), the polyethylene glycol precipitation method was used to concentrate 105 mL of sewage to 0.6 mL for subsequent nucleic acid extraction.

Nucleic Acid Extraction and PCR Diagnosis

To determine the total viral nucleic acid content in clinical samples of Mpox cases, a magnetic bead virus DNA/RNA extraction kit (Xi'an Tianlong Technology Co., Ltd.) was used, and the extracted nucleic acid was stored at -80°C according to the operating instructions of the GeneRotex 96 Nucleic Acid Extractor (Xi'an Tianlong Technology Co., Ltd.). To

determine the total viral nucleic acid content in sewage samples, the Shuoshi nucleic acid extraction kit (Jiangsu Shuoshi Biological Technology Co., Ltd.) was used, and the extracted nucleic acid was stored at -80°C following the operating instructions. The MPXV nucleic acid detection reagent (Jiangsu Shuoshi Biological Technology Co., Ltd.) was used to detect nucleic acids in the sewage samples using a SLAN-96S fully automatic PCR medical analysis system (Shanghai Hongshi Medical Technology Co., Ltd.).

Whole Genome Amplification and Sequencing

All samples meeting the criteria of monkeypox virus nucleic acid detection with Ct values ≤ 32 were subjected to subsequent viral genome sequencing. Detailed experimental procedures for MPXV genome amplification, library construction, and sequencing were as described in this study's authors' recent studies ([7,13](#)). Briefly, the MPXV whole-genome sequencing kit (Hangzhou Baiyi Technology Co., Ltd.) was used to specifically amplify the whole genome of MPXV in clinical samples of cases and sewage samples. The amplification products were purified using the AMPure XP purification kit (Beckman Coulter, USA). Subsequently, sequencing was performed on the Illumina Nextseq2000, QNOME-3841, and Oxford Nanopore GridION platforms. The sequencing platform had no significant impact on the accuracy of the monkeypox virus genomic variant identification ([7](#)). Therefore, only one sequencing platform was used for the genomic sequencing of each sample.

Genome Assembly

The viral genomes were assembled and analyzed using the MPXV genome analysis workbench developed by Hangzhou Baiyi Technology Co., Ltd. Initially, primers were eliminated using Porechop (v0.2.4) and Fastp (v0.23.2) ([14](#)). The clean reads were aligned to MPXV-M5312_HM12_Rivers (NC_063383.1) using Minimap2 (v2.24-r1122) ([15](#)). For second- and third-generation sequencing data, the minimum depth thresholds were set at $10\times$ and $40\times$, respectively. Variants were identified using Freebayes (v1.3.2) ([16](#)), with low-quality variations filtered using bcftools (v1.15.1) ([17](#)). The definitive consensus sequence was then derived based on high-confidence mutations (allele frequency $\geq 50\%$) employing the bcftools consensus command. Alignment visualization was performed using IGV (v2.12). To minimize false-

positive mutations caused by low-quality sequencing data, this study retained 49 high-quality datasets from Mpox cases and 3 from sewage samples, each with at least 80% genome coverage at 10× sequencing depth, for mutation profile analysis.

Phylogenetic Analysis

The quality and lineage of the assembled genome were evaluated using NextClade with the pre-built clade IIb dataset (18). Genome sequences from representative clades (or lineages) were downloaded from the GISAID database and subjected to multiple alignments with the reference genome (GenBank: NC_063383.1) using NextClade. The meta-information on the sequences used is provided in Supplementary Tables S1 and S2. To avoid including false-positive mutations introduced by sequencing errors, only the region from 1,500 to 190,000 bp was retained for further analysis, as previously described (7,11). A phylogenetic tree was constructed using IQtree2 (v2.3.6) with the GTR+F+I+G4 model, and the bootstrap value was set to 1,000 (19). Time calibration of the phylogenetic tree (i.e., tMRCA estimation) and population size inference were conducted using TreeTime (v0.11.4) (parameters: -reroot oldest -covariation -coalescent skyline) (20). Briefly, TreeTime estimates the mutation rate through linear regression of root-to-tip genetic distances against sampling time. Sequences with abnormally high mutation counts (classified as outliers) were excluded. A time-calibrated phylogenetic tree was generated using the branch2time function, while a skyline plot (reflecting effective population size changes) was constructed based on the coalescent theory. A haplotype network of the complete MPXV genome was generated using fastHaN with the modified_tcs algorithm (21).

RESULTS

Genome Sequencing of MPXV from Clinical Samples and Sewage Samples in Sichuan

Between June and October 2023, Sichuan Province reported 129 confirmed Mpox cases, including 120 in Chengdu, 6 in Leshan, and 1 each in Yibin, Neijiang, and Mianyang, none of whom had a recent travel history. Demographic data revealed that 99.2% of the patients were male (128/129), with ages ranging from

15 to 52 years (median=31.5), consistent with national trends (10). Clinical samples from 96 confirmed cases (94 in Chengdu, 1 each in Yibin and Mianyang) were collected, and most cases were identified between July and August (Supplementary Table S1 and Figure 1A). The ninth wastewater treatment plant in Chengdu, serving an urban area of 200 km², provided 26 influent samples that were collected twice a week from July to September 2023. All clinical and PCR-positive sewage samples (*n*=67) were subjected to amplicon sequencing, with 59 originating from mpox cases and 8 from sewage samples. Five MPOX case datasets and five sewage sample datasets with low coverage ratios (<80%) of the viral genome were filtered.

Genomic Characteristics and Phylogenetic Analysis of MPXV from Sichuan

The MPXV genome from mpox cases includes 46 high-quality sequences (defined by Nextclade as “good” or “mediocre” via the qc.overallStatus metric) and 9 low-quality ones. Three genome sequences were recovered from the sewage samples, with two having high-quality scores and one having low-quality scores. All newly sequenced genomes were assigned to the C.1 lineage (also known as B.1.3.1) and its sub-lineage, C.1.1, which belongs to the West African clade (Clade IIb). These newly assembled sequences were deposited in GenBank under the accession numbers C_AA103396.1 to C_AA103462.1 (Supplementary Table S1). Among the 58 sequences, 55 were classified as the C.1.1 lineage, which exhibited a distinct mutation (C149963T; OPG176:S52L). Integration of the newly sequenced genomes with published genomes revealed that the MPXV genomes in Sichuan clustered into multiple distinct groups (Figure 1B). Most sequences were grouped according to their respective lineages, except for one of the poor-quality sequences, which was possibly caused by sequencing errors. Furthermore, intercountry transmission events have been identified in China, Japan, the Republic of Korea, Portugal, the United States, and other countries.

Haplotype network diagrams offer an intuitive method for visualizing transmission relationships during both coronavirus disease 2019 (COVID-19) (22) and Mpox (9). To investigate potential MPXV import and local transmission in Sichuan, this study constructed a haplotype network using newly sequenced high-quality genomes and 351 evolutionarily closely related genomes downloaded

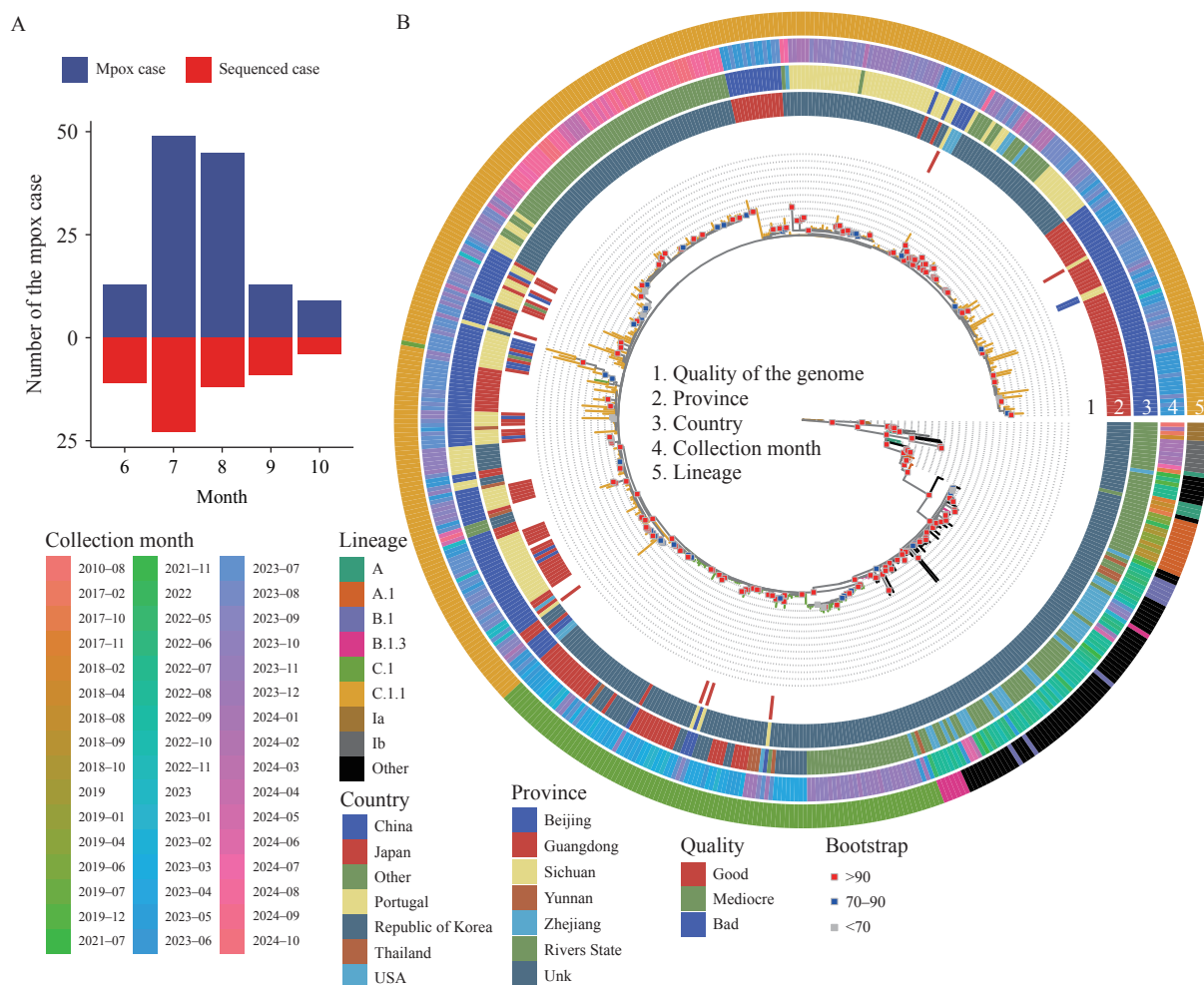


FIGURE 1. Genomic characteristics of MPXV from Mpox in Sichuan. (A) Number of confirmed Mpox cases and sequenced MPXV genomes; (B) Phylogenetic tree of the sequenced MPXV genomes and randomly selected published ones.

Note: Tips are color-coded according to their respective lineages. For clarity, bootstrap support values for branches are categorized into three confidence intervals (<70, 70–90, and >90), represented by gray, blue, and red rectangular shapes, respectively. Five concentric rings, numbered 1 to 5 from the innermost to outermost, indicate: 1) quality of newly sequenced viral genomes from Mpox cases; 2) geographic origins of sequences; 3) country-level origins; 4) collection dates; and 5) lineages. Rivers State is part of Nigeria; genomic sequences lacking province- or state-level administrative division information are labeled as "Unk" (Unknown). To enhance the clarity, we simplified the lineage categories by highlighting only the Ia/Ib/A/A.1/B.1/B.1.3/C.* lineages, while the remaining ones were categorized as "Other".

Abbreviation: MPXV=Monkeypox virus; Mpox=monkeypox.

from public databases. The newly sequenced genomes clustered into at least six groups within the network (Figure 2), suggesting multiple importation events and simultaneous local co-circulation in Sichuan. The largest cluster comprised 31 sequences and was closely related to the genomes reported in Beijing, Guangdong, and Yunnan PLADs in China and Portugal. The three smallest groups consisted of only a single Sichuan case, indicating the occasional importation of MPXV. Due to effective public health advocacy and monitoring measures, these clusters did not expand further.

Mpox Outbreaks in Sichuan Province Resulted from Multiple Importation Events

To investigate the evolutionary dynamics of MPXVs in Sichuan, this study temporally calibrated a phylogenetic tree using sample collection dates. Most clusters exhibited time to the most recent common ancestor (tMRCA) estimates between March and July 2023. Notably, a distinct cluster of cases ($n=25$) emerged exclusively in Sichuan from July to October 2023 (Figure 3A), demonstrating rapid localized

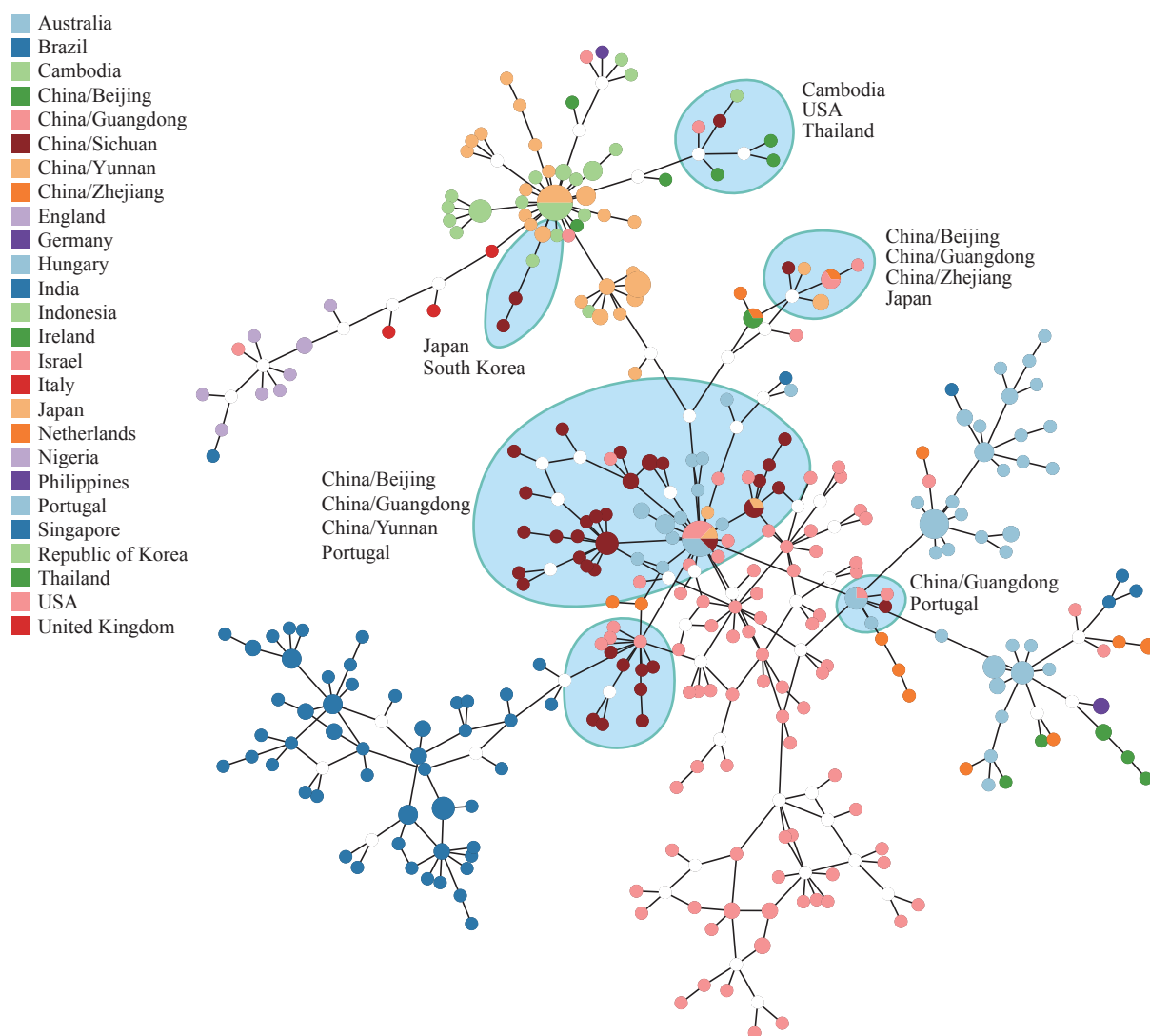


FIGURE 2. Haplotype network of the MPXV from Mpox in Sichuan.

Note: Haplotype network illustrates newly sequenced MPXV genomes from confirmed mpox cases in the Sichuan Province and representative genomes from other lineages. Six major transmission hubs (identified and highlighted in light blue) demonstrated clustering patterns. Node sizes were normalized according to the number of sequences. The sources of the closely related sequences within each hub are listed as references.

Abbreviation: MPXV=Monkeypox virus.

transmission. This study estimated the MPXV evolutionary rate by analyzing the temporal relationship between accumulated mutations and sampling dates, yielding a mutation rate of $5.23 \pm 0.5 \times 10^{-5}$ substitutions/site/year (Figure 3B), consistent with previous findings (11). The effective population size of MPXV showed a marked expansion beginning in early 2023, peaking in June 2023, followed by a sharp decline, consistent with the reported case numbers (Figure 3C). These findings underscore the efficacy of the recent mpox containment measures.

Sewage Samples Reflected the Mutational Spectrum of the MPXV Carried by Mpox Cases

Direct clinical sample collection faces ethical and logistic challenges, including patient privacy concerns. The utility of sewage sample-based surveillance systems for recovering viral genome fragments has been demonstrated in prior pathogen monitoring efforts, such as norovirus and SARS-CoV-2 tracking, which facilitate the detection of emerging mutations. A recent study reported successful retrieval of the full-length

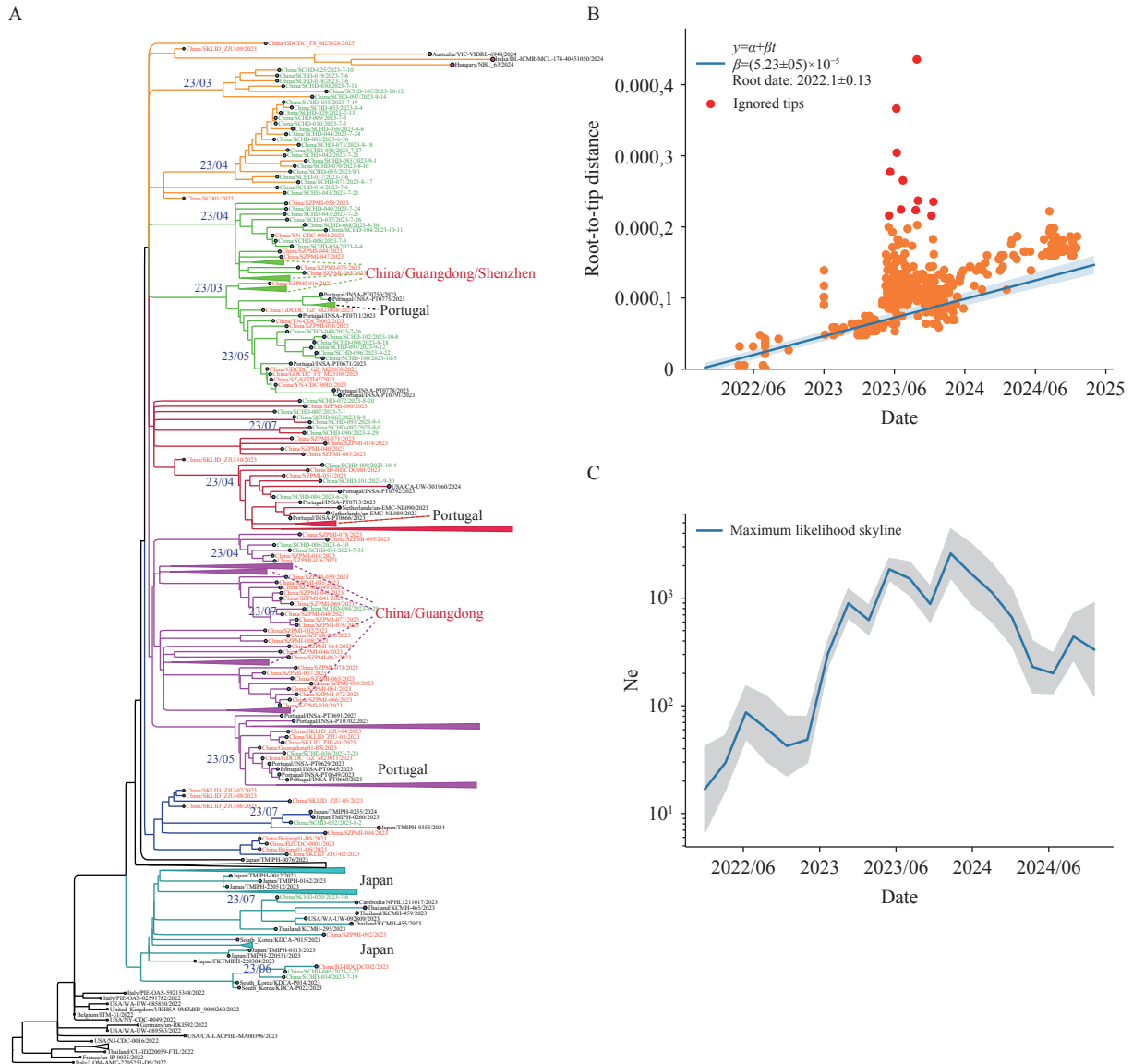


FIGURE 3. Phylodynamics of the 2023 Mpox Outbreak in Sichuan. (A) Time-calibrated phylogenetic tree of newly sequenced MPXV genomes; (B) Linear regression of root-to-tip divergence against sampling dates; (C) Temporal fluctuations in the effective population size (N_e) of MPXV.

Note: In panel A, MPXV genome sequences from Sichuan and those from other provinces/regions in China are labeled in green and red, respectively. A subset of sequences from Portugal, Japan, and other regions was collapsed. The time to the most recent common ancestor (tMRCA) of the newly sequenced MPXV and their closest relatives is annotated on the corresponding branch. In panel B, sequences with ambiguous quality or uncertain collection dates are color-coded in red. Abbreviation: MPXV=Monkeypox virus; Mpox=monkeypox.

MPXV genome from sewage samples (23). In this study, 26 sewage samples were collected, 8 of which tested positive for MPXV. Following viral particle enrichment and genome amplification, sequencing achieved a high coverage of the MPXV genome in the three samples. All sewage-derived viral genomes belonged to MPXV C.1.1 lineage, which matched the viral strains identified in locally transmitted cases. Comparative analysis of high-frequency mutations

between sewage-derived and clinical samples revealed that sewage detection encompassed all mutation sites observed in local infections, supporting the utility of sewage monitoring for tracking the evolution of MPXV (Figure 4A). However, distinct mutations were uniquely identified in both clinical cases and sewage samples (Figure 4B–C), underscoring the need for an integrated surveillance approach that combines clinical and environmental data to comprehensively assess the

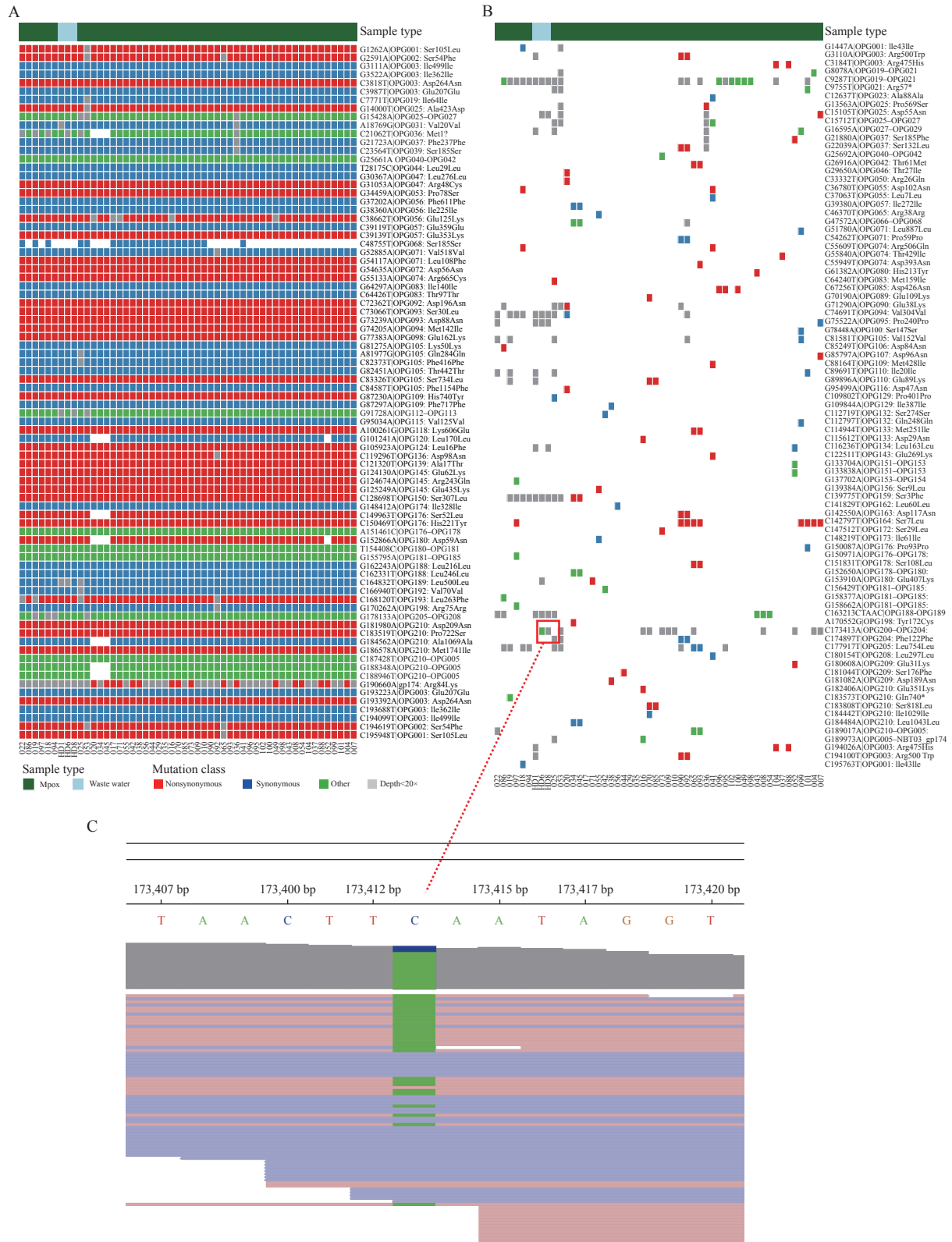


FIGURE 4. Mutation profiles of MPXV from Mpxv cases and sewage samples. (A) Profiles of high and low-frequency; (B) Mutation in the collected samples; (C) Distinct mutations identified in sewage sample HD01.

Note: Detailed information on the Mpxv and sewage samples is provided in [Supplementary Table S1](#).

Abbreviation: MPXV=Monkeypox virus.

genetic diversity of MPXV.

DISCUSSION

This study collected clinical and sewage samples from Sichuan Province, China in 2023, and conducted whole-genome sequencing of MPXV. Based on the phylogenetic analysis, the transmission characteristics and mutation trends of MPXV in this region were studied. Genomic analysis of MPXV samples from various regions in China, notably Sichuan, indicated that the strains responsible for local infections belonged to either subtype C.1 or C.1.1, consistent with previous reports (9,24). The newly sequenced genome did not reveal any notable high-frequency amino acid mutations in genes targeting drugs or vaccines, indicating the likelihood of effective control. Concerning the *F3L* gene, a key target for Mpox detection in China, no significant mutations were detected in the newly sequenced sequences, confirming the efficacy of existing detection primers in identifying the present cases of Mpox infection in China. In Sichuan, there is a dual-level interaction involving Mpox cases at both the national and provincial levels, underscoring the intricate nature of transmission and infection within the local population. Significant variations existed in the number of Mpox cases among the six clusters categorized by the haplotype network. Further analysis of the characteristics of each transmission cluster, based on on-site epidemiological investigation results will aid in the formulation of scientifically effective prevention and control strategies. Notably, most patients did not provide information regarding their activity trajectories or close contacts due to privacy protection concerns. Consequently, the transmission relationships inferred from the viral genome sequencing analysis could not be cross-validated against the actual infection processes in these cases. Phylogenetic tree and haplotype network analyses revealed that the genomic sequences of the Sichuan cases showed high similarity with sequences uploaded from countries/regions including Japan, Portugal, the United States, the Republic of Korea, the Netherlands, and Thailand. This suggests the potential import of Mpox cases from these regions into Sichuan. Notably, viral sequences from other Chinese provinces also clustered within the same 5/6 viral clades (Figure 2), indicating possible domestic transmission origins for the Sichuan cases. Owing to the challenges in conducting field epidemiological investigations, the precise origins of these viral clusters cannot be

definitively determined based solely on available genomic sequencing data.

Molecular evolutionary trend analysis showed that the evolutionary rate of MPXV in the West African evolutionary branch was significantly higher than that of the known double-stranded DNA viruses (25). Mutations that accumulate in the monkeypox virus after spreading across the population are largely attributable to host APOBEC3 editing (3). Wu et al. found that genetic mutations in early local cases of monkeypox virus infection in China followed this trend (9). This study examined variations in the effective population size of the MPXV C.1 and its sublineages from June 2022 to the present. The results show a significant shift in the expansion and contraction of the effective population. The transition occurred mainly in the first half of 2024, which is consistent with the trends in the number of Mpox cases in China and other countries or regions during the same period. The decline in MPXV population size was primarily attributable to effective prevention and control measures. These include vaccination campaigns, antiviral treatments, expedited diagnosis, and reduced direct contact with infected individuals through isolation protocols and social distancing policies. Nevertheless, the present count of confirmed monkeypox cases exceeds the pre-2022 levels, and the recent interspecies transmission of Clade I MPXV in Africa underscores the ongoing critical need for monkeypox prevention and control measures (26). The high-frequency mutations ($n=82$) consisted of 37 non-synonymous, 34 synonymous, and 11 intergenic events. A start codon loss mutation (C21062T) was observed in the *OPG036* gene in all C.1.1 genomes. However, whether this mutation disrupts the translation of OPG036 remains unclear. The observed ratio of *N* to *S* substitutions was significantly lower than the expected ratio (37/34 *vs.* 126,244/39,292; $P=9.11 \times 10^{-6}$; Fisher's Exact Test), indicating that the MPXV genome experiences purifying selection, consistent with findings from our recent study (7).

Due to the particularity of the transmission route of Mpox, there is a low proportion of proactive patients seeking medical treatment. Hence, conventional monitoring methods may not entirely depict the comprehensive scenario of an Mpox epidemic. An environmental monitoring system that specifically targets domestic sewage has been implemented globally to offer epidemiological insights into different pathogens at the population level, thus serving as a valuable supplement to individual case monitoring

(23,26–27). The WHO released interim guidelines in 2024, indicating that sewage and environmental monitoring can provide more information for the prevention and control of Mpox (28). The Mpox cases in Sichuan Province primarily originated from Chengdu. Sewage samples were collected for testing from the inflow of a major municipal water reclamation plant located in the central area of Chengdu City. These findings revealed a high level of consistency between the MPXV mutations identified in sewage samples and those found in the Mpox case samples. However, distinct mutations were also observed, suggesting a potential silent spread of the virus among individuals who did not seek medical attention. These results underscore the importance of sewage monitoring for enhancing infectious disease surveillance.

This study attempted to comprehensively incorporate publicly available sequencing data on indigenous Mpox in China. However, the included sequences covered only parts of the provinces and cities, which may have affected the results of the fine-scale molecular tracing analysis. Due to limitations, such as sampling strategies and difficulties in obtaining epidemiological information, this study did not sample close contacts of patients and the environment. Therefore, it is not possible to validate the transmission relationships between various transmission clusters divided by genomic sequencing based on epidemiological investigation results. Additionally, there is a limited understanding of the variations in immune status, clinical manifestations, and disease outcomes among patients from different transmission clusters, as well as their potential association with viral genomic mutations. Further research is needed to investigate whether MPXV can be transmitted to other animals through humans, because monkeypox has a wide range of natural hosts.

This study analyzed viral genome sequencing data from indigenous Mpox cases in Sichuan Province. These results indicate that these cases stem primarily from multiple distinct introductory events. The haplotype network and phylogenetic tree revealed at least six distinct local transmission clusters. Furthermore, three full-length MPXV genomes were successfully isolated from sewage samples collected from local communities. These sewage-derived MPXV genomes belong to the C.1.1 lineage, share all predominant mutations with viral strains detected in clinical cases, and exhibit a limited number of unique mutations. This finding suggests that sewage-based

MPXV surveillance may serve as a valuable complementary approach to the existing monitoring strategies. In summary, this study investigated the local transmission dynamics of Mpox in Sichuan Province. By integrating sequencing data from other provinces, this study provides a comprehensive overview of the epidemiology, transmission dynamics, and genomic variation trends of the endemic monkeypox virus in China, offering critical insights into evidence-based control strategies.

Conflicts of interest: No conflicts of interests

Ethical statement: Approved by the Sichuan CDC (approval no. SCCDCIRB 2024-014). All the patients were informed in advance and authorized to use their clinical samples for this study.

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SUPPLEMENTARY MATERIAL

SUPPLEMENTARY TABLE S1. The meta information of Mpox cases and wastewater samples.

Sequence ID	Sex/Sample type	Age	Collection_date	Region	Genotype	qc.overallStatus	Coverage (%)	Genebase accession number	Quality
SCHD-001	Male	38	2023/6/29	Chengdu, China	undetermined	/	/	/	
SCHD-004	Male	25	2023/6/30	Chengdu, China	C.1.1	good	99.78	C_AA103404.1	high
SCHD-005	Male	40	2023/6/30	Chengdu, China	C.1.1	bad	87.43	C_AA103405.1	low
SCHD-006	Male	52	2023/6/30	Chengdu, China	/	bad	30.37	C_AA103406.1	
SCHD-007	Male	34	2023/7/1	Chengdu, China	C.1.1	good	99.37	C_AA103407.1	high
SCHD-008	Male	34	2023/7/3	Chengdu, China	C.1.1	good	99.78	C_AA103408.1	high
SCHD-009	Male	38	2023/7/3	Chengdu, China	C.1.1	good	99.61	C_AA103409.1	high
SCHD-010	Male	30	2023/7/3	Chengdu, China	C.1.1	good	99.48	C_AA103410.1	high
SCHD-015	Male	31	2023/7/5	Chengdu, China	undetermined	/	/	/	
SCHD-016	Male	27	2023/7/6	Chengdu, China	C.1.1	good	98.78	C_AA103411.1	high
SCHD-017	Male	25	2023/7/6	Chengdu, China	C.1.1	good	99.02	C_AA103412.1	high
SCHD-018	Male	31	2023/7/6	Chengdu, China	C.1.1	good	96.93	C_AA103413.1	high
SCHD-019	Male	25	2023/7/6	Chengdu, China	C.1.1	mediocre	94.70	C_AA103414.1	high
SCHD-020	Male	29	2023/7/6	Chengdu, China	C.1	good	98.94	C_AA103415.1	high
SCHD-021	Male	27	2023/7/7	Chengdu, China	C.1.1	bad	82.42	C_AA103416.1	low
SCHD-022	Male	31	2023/7/8	Chengdu, China	C.1.1	bad	95.43	C_AA103417.1	low
SCHD-025	Male	32	2023/7/10	Chengdu, China	C.1.1	bad	90.43	C_AA103418.1	low
SCHD-026	Male	19	2023/7/11	Chengdu, China	undetermined	/	/	/	
SCHD-027	Male	30	2023/7/12	Chengdu, China	undetermined	/	/	/	
SCHD-028	Male	32	2023/7/13	Chengdu, China	undetermined	/	/	/	
SCHD-029	Male	32	2023/7/13	Chengdu, China	C.1.1	good	99.80	C_AA103419.1	high
SCHD-030	Male	39	2023/7/18	Chengdu, China	/	bad	23.20	C_AA103420.1	
SCHD-031	Male	38	2023/7/12	Chengdu, China	undetermined	/	/	/	
SCHD-032	Male	39	2023/7/18	Chengdu, China	undetermined	/	/	/	
SCHD-033	Male	39	2023/7/18	Chengdu, China	undetermined	/	/	/	
SCHD-034	Male	36	2023/7/19	Chengdu, China	C.1	good	99.70	C_AA103421.1	high
SCHD-035	Male	29	2023/7/19	Chengdu, China	C.1.1	good	99.83	C_AA103422.1	high
SCHD-036	Male	32	2023/7/20	Chengdu, China	C.1.1	good	95.06	C_AA103423.1	high
SCHD-037	Male	35	2023/7/26	Chengdu, China	C.1.1	good	99.89	C_AA103424.1	high
SCHD-038	Male	21	2023/7/27	Chengdu, China	C.1.1	good	99.95	C_AA103425.1	high
SCHD-039	Male	36	2023/7/27	Chengdu, China	undetermined	/	/	/	
SCHD-040	Male	25	2023/7/24	Chengdu, China	C.1.1	bad	83.14	C_AA103426.1	low
SCHD-041	Male	23	2023/7/21	Chengdu, China	C.1.1	good	99.78	C_AA103427.1	high
SCHD-042	Male	32	2023/7/21	Chengdu, China	C.1.1	good	99.94	C_AA103428.1	high
SCHD-043	Male	36	2023/7/21	Chengdu, China	C.1.1	good	99.72	C_AA103429.1	high
SCHD-044	Male	30	2023/7/24	Chengdu, China	C.1.1	good	99.91	C_AA103430.1	high
SCHD-045	Male	42	2023/7/22	Chengdu, China	C.1	good	99.94	C_AA103431.1	high
SCHD-046	Male	24	2023/7/22	Chengdu, China	undetermined	/	/	/	
SCHD-047	Male	35	2023/7/22	Chengdu, China	undetermined	/	/	/	

Continued

Sequence ID	Sex/Sample type	Age	Collection_date	Region	Genotype	qc.overallStatus	Coverage (%)	Genebase accession number	Quality
SCHD-048	Male	34	2023/7/29	Chengdu, China	undetermined	/	/	/	
SCHD-049	Male	30	2023/7/26	Chengdu, China	C.1.1	good	98.96	C_AA103432.1	high
SCHD-050	Male	27	2023/7/30	Chengdu, China	undetermined	/	/	/	
SCHD-051	Male	45	2023/7/31	Yibin, China	C.1.1	bad	70.11	C_AA103433.1	low
SCHD-052	Male	36	2023/8/2	Chengdu, China	C.1.1	good	99.77	C_AA103434.1	high
SCHD-053	Male	33	2023/8/4	Mianyang, China	C.1.1	bad	86.27	C_AA103435.1	low
SCHD-054	Male	51	2023/8/4	Chengdu, China	C.1.1	good	99.96	C_AA103436.1	high
SCHD-055	Male			Chengdu, China	C.1.1	good	99.91	C_AA103437.1	high
SCHD-056	Male	28	2023/8/6	Chengdu, China	C.1.1	good	99.90	C_AA103438.1	high
SCHD-057	Male	28	2023/8/6	Chengdu, China	undetermined	/	/	/	
SCHD-058	Male	29	2023/8/5	Chengdu, China	undetermined	/	/	/	
SCHD-059	Male	34	2023/8/1	Chengdu, China	undetermined	/	/	/	
SCHD-060	Male	35	2023/8/1	Chengdu, China	undetermined	/	/	/	
SCHD-061	Male	27	2023/7/31	Chengdu, China	undetermined	/	/	/	
SCHD-062	Male	32	2023/7/31	Chengdu, China	undetermined	/	/	/	
SCHD-063	Male	23	2023/8/4	Chengdu, China	undetermined	/	/	/	
SCHD-064	Male	39	2023/8/4	Chengdu, China	undetermined	/	/	/	
SCHD-065	Male	46	2023/8/9	Chengdu, China	C.1.1	good	97.79	C_AA103439.1	high
SCHD-066	Male	28	2023/8/3	Chengdu, China	undetermined	/	/	/	
SCHD-067	Male	31	2023/8/4	Chengdu, China	undetermined	/	/	/	
SCHD-068	Male	25	2023/8/4	Chengdu, China	undetermined	/	/	/	
SCHD-069	Male	29	2023/8/8	Chengdu, China	undetermined	/	/	/	
SCHD-070	Male	20	2023/8/10	Chengdu, China	C.1.1	good	99.80	C_AA103440.1	high
SCHD-071	Male	42	2023/8/17	Chengdu, China	C.1.1	good	99.27	C_AA103441.1	high
SCHD-072	Male	29	2023/8/20	Chengdu, China	C.1.1	bad	74.63	C_AA103442.1	low
SCHD-073	Male	28	2023/8/18	Chengdu, China	C.1.1	good	99.80	C_AA103443.1	high
SCHD-074	Male	37	2023/8/27	Chengdu, China	undetermined	/	/	/	
SCHD-075	Male	34	2023/8/25	Chengdu, China	undetermined	/	/	/	
SCHD-076	Male	24	2023/8/22	Chengdu, China	undetermined	/	/	/	
SCHD-077	Male	38	2023/8/22	Chengdu, China	undetermined	/	/	/	
SCHD-078	Male	47	2023/8/22	Chengdu, China	undetermined	/	/	/	
SCHD-079	Male	16	2023/8/23	Chengdu, China	undetermined	/	/	/	
SCHD-080	Male	42	2023/8/19	Chengdu, China	undetermined	/	/	/	
SCHD-081	Male	34	2023/8/19	Chengdu, China	undetermined	/	/	/	
SCHD-082	Male	39	2023/8/20	Chengdu, China	undetermined	/	/	/	
SCHD-084	Male	30	2023/8/25	Chengdu, China	undetermined	/	/	/	
SCHD-085	Male	23	2023/8/31	Chengdu, China	C.1.1	good	99.82	C_AA103444.1	high
SCHD-086	Male	37	2023/9/1	Chengdu, China	C.1.1	good	98.17	C_AA103445.1	high
SCHD-087	Male	37	2023/8/31	Chengdu, China	undetermined	/	/	/	
SCHD-088	Male	29	2023/8/30	Chengdu, China	C.1.1	good	99.85	C_AA103446.1	high
SCHD-089	Male	34	2023/8/29	Chengdu, China	C.1.1	bad	64.14	C_AA103447.1	low

Continued

Sequence ID	Sex/Sample type	Age	Collection_date	Region	Genotype	qc.overallStatus	Coverage (%)	Genebase accession number	Quality
SCHD-090	Male	31	2023/8/29	Chengdu, China	C.1.1	good	99.28	C_AA103448.1	high
SCHD-091	Male	38	2023/8/28	Chengdu, China	undetermined	/	/	/	
SCHD-092	Male	24	2023/9/9	Chengdu, China	C.1.1	mediocre	93.74	C_AA103449.1	high
SCHD-093	Male	36	2023/9/9	Chengdu, China	C.1.1	good	99.65	C_AA103450.1	high
SCHD-094	Male	18	2023/8/29	Chengdu, China	C.1.1	good	98.04	C_AA103451.1	high
SCHD-095	Male	29	2023/9/12	Chengdu, China	C.1.1	good	99.06	C_AA103452.1	high
SCHD-096	Male	32	2023/9/22	Chengdu, China	C.1.1	good	99.65	C_AA103453.1	high
SCHD-097	Male	29	2023/9/14	Chengdu, China	C.1.1	good	99.16	C_AA103454.1	high
SCHD-098	Male	37	2023/9/18	Chengdu, China	C.1.1	good	99.77	C_AA103455.1	high
SCHD-099	Male	29	2023/10/4	Chengdu, China	C.1.1	good	99.75	C_AA103456.1	high
SCHD-100	Male	29	2023/10/5	Chengdu, China	C.1.1	good	99.78	C_AA103457.1	high
SCHD-101	Male	31	2023/9/30	Chengdu, China	C.1.1	good	99.46	C_AA103458.1	high
SCHD-102	Male	28	2023/10/8	Chengdu, China	C.1.1	good	99.37	C_AA103459.1	high
SCHD-103	Male	34	2023/10/11	Chengdu, China	/	bad	55.78	C_AA103460.1	
SCHD-104	Male	35	2023/10/11	Chengdu, China	C.1.1	good	99.71	C_AA103461.1	high
SCHD-105	Male	31	2023/10/12	Chengdu, China	/	bad	52.46	C_AA103462.1	
HD1	Sewage	/	2023/7/24	Chengdu, China	C.1.1	mediocre	92.92	C_AA103396.1	high
HD2	Sewage	/	2023/7/31	Chengdu, China	/	bad	2.61	C_AA103397.1	
HD3	Sewage	/	2023/8/7	Chengdu, China	/	bad	4.40	C_AA103398.1	
HD4	Sewage	/	2023/8/10	Chengdu, China	/	bad	28.98	C_AA103399.1	
HD5	Sewage	/	2023/8/17	Chengdu, China	/	bad	5.90	C_AA103400.1	
HD6	Sewage	/	2023/8/24	Chengdu, China	C.1.1	good	94.72	C_AA103401.1	high
HD7	Sewage	/	2023/9/4	Chengdu, China	/	bad	43.52	C_AA103402.1	
HD8	Sewage	/	2023/9/14	Chengdu, China	C.1.1	good	95.37	C_AA103403.1	high

Abbreviation: Mpox=monkeypox.

SUPPLEMENTARY TABLE S2. The meta information of the sequences included in constructing the haplotype network

Name	Country	Province	Collection date	Sources	Revised collection date for treetime	Revised month
hMPXV/China/SCHD-004/2023-6-29	China	Sichuan	2023/6/29	This_study	2023-06-29	2023-06
hMPXV/China/SCHD-007/2023-7-1	China	Sichuan	2023/7/1	This_study	2023-07-01	2023-07
hMPXV/China/SCHD-009/2023-7-3	China	Sichuan	2023/7/3	This_study	2023-07-03	2023-07
hMPXV/China/SCHD-017/2023-7-6	China	Sichuan	2023/7/6	This_study	2023-07-06	2023-07
hMPXV/China/SCHD-008/2023-7-3	China	Sichuan	2023/7/3	This_study	2023-07-03	2023-07
hMPXV/China/SCHD-020/2023-7-6	China	Sichuan	2023/7/6	This_study	2023-07-06	2023-07
hMPXV/China/SCHD-010/2023-7-3	China	Sichuan	2023/7/3	This_study	2023-07-03	2023-07
hMPXV/China/SCHD-016/2023-7-6	China	Sichuan	2023/7/6	This_study	2023-07-06	2023-07
hMPXV/China/SCHD-038/2023-7-27	China	Sichuan	2023/7/27	This_study	2023-07-27	2023-07
hMPXV/China/SCHD-018/2023-7-6	China	Sichuan	2023/7/6	This_study	2023-07-06	2023-07
hMPXV/China/SCHD-041/2023-7-21	China	Sichuan	2023/7/21	This_study	2023-07-21	2023-07
hMPXV/China/SCHD-037/2023-7-26	China	Sichuan	2023/7/26	This_study	2023-07-26	2023-07
hMPXV/China/SCHD-034/2023-7-19	China	Sichuan	2023/7/19	This_study	2023-07-19	2023-07

Continued

Name	Country	Province	Collection date	Sources	Revised collection date for treetime	Revised month
hMPXV/China/SCHD-035/2023-7-19	China	Sichuan	2023/7/19	This_study	2023-07-19	2023-07
hMPXV/China/SCHD-029/2023-7-13	China	Sichuan	2023/7/13	This_study	2023-07-13	2023-07
hMPXV/China/SCHD-044/2023-7-24	China	Sichuan	2023/7/24	This_study	2023-07-24	2023-07
hMPXV/China/SCHD-036/2023-7-20	China	Sichuan	2023/7/20	This_study	2023-07-20	2023-07
hMPXV/China/SCHD-042/2023-7-21	China	Sichuan	2023/7/21	This_study	2023-07-21	2023-07
hMPXV/China/SCHD-045/2023-7-22	China	Sichuan	2023/7/22	This_study	2023-07-22	2023-07
hMPXV/China/SCHD-049/2023-7-26	China	Sichuan	2023/7/26	This_study	2023-07-26	2023-07
hMPXV/China/SCHD-043/2023-7-21	China	Sichuan	2023/7/21	This_study	2023-07-21	2023-07
hMPXV/China/SCHD-088/2023-8-30	China	Sichuan	2023/8/30	This_study	2023-08-30	2023-08
hMPXV/China/SCHD-054/2023-8-4	China	Sichuan	2023/8/4	This_study	2023-08-04	2023-08
hMPXV/China/SCHD-056/2023-8-6	China	Sichuan	2023/8/6	This_study	2023-08-06	2023-08
hMPXV/China/SCHD-100/2023-10-5	China	Sichuan	2023/10/5	This_study	2023-10-05	2023-10
hMPXV/China/SCHD-055/2023/8/1	China	Sichuan	2023/8/1	This_study	2023-08-01	2023-08
hMPXV/China/SCHD-065/2023-8-9	China	Sichuan	2023/8/9	This_study	2023-08-09	2023-08
hMPXV/China/SCHD-086/2023-9-1	China	Sichuan	2023/9/1	This_study	2023-09-01	2023-09
hMPXV/China/SCHD-070/2023-8-10	China	Sichuan	2023/8/10	This_study	2023-08-10	2023-08
hMPXV/China/SCHD-104/2023-10-11	China	Sichuan	2023/10/11	This_study	2023-10-11	2023-10
hMPXV/China/SCHD-095/2023-9-12	China	Sichuan	2023/9/12	This_study	2023-09-12	2023-09
hMPXV/China/SCHD-096/2023-9-22	China	Sichuan	2023/9/22	This_study	2023-09-22	2023-09
hMPXV/China/SCHD-052/2023-8-2	China	Sichuan	2023/8/2	This_study	2023-08-02	2023-08
hMPXV/China/SCHD-085/2023-9-1	China	Sichuan	2023/9/1	This_study	2023-09-01	2023-09
hMPXV/China/SCHD-097/2023-9-14	China	Sichuan	2023/9/14	This_study	2023-09-14	2023-09
hMPXV/China/SCHD-073/2023-8-18	China	Sichuan	2023/8/18	This_study	2023-08-18	2023-08
hMPXV/China/SCHD-071/2023-8-17	China	Sichuan	2023/8/17	This_study	2023-08-17	2023-08
hMPXV/Portugal/INSA-PT0649/2023	Portugal		2023-07-10	GISAID	2023-07-10	2023-07
hMPXV/China/SCHD-099/2023-10-4	China	Sichuan	2023/10/4	This_study	2023-10-04	2023-10
hMPXV/China/SCHD-102/2023-10-8	China	Sichuan	2023/10/8	This_study	2023-10-08	2023-10
hMPXV/China/SCHD-094/2023-8-29	China	Sichuan	2023/8/29	This_study	2023-08-29	2023-08
hMPXV/China/SZ-SZTH42/2023	China	Guangdong	2023-06-24	GISAID	2023-06-24	2023-06
hMPXV/China/SCHD-101/2023-9-30	China	Sichuan	2023/9/30	This_study	2023-09-30	2023-09
hMPXV/China/SCHD-098/2023-9-18	China	Sichuan	2023/9/18	This_study	2023-09-18	2023-09
hMPXV/Portugal/INSA-PT0671/2023	Portugal		2023-08-02	GISAID	2023-08-02	2023-08
hMPXV/China/YN-CDC-0002/2023	China	Yunnan	2023-06-28	GISAID	2023-06-28	2023-06
hMPXV/China/SCHD-093/2023-9-9	China	Sichuan	2023/9/9	This_study	2023-09-09	2023-09
hMPXV/China/SCHD-090/2023-8-29	China	Sichuan	2023/8/29	This_study	2023-08-29	2023-08
hMPXV/China/YN-CDC-0001/2023	China	Yunnan	2023-06-27	GISAID	2023-06-27	2023-06
hMPXV/Portugal/INSA-PT0645/2023	Portugal		2023-07-07	GISAID	2023-07-07	2023-07
hMPXV/Portugal/INSA-PT0791/2023	Portugal		2023-11-08	GISAID	2023-11-08	2023-11
hMPXV/China/YN-CDC-0003/2023	China	Yunnan	2023-07-03	GISAID	2023-07-03	2023-07
hMPXV/Portugal/INSA-PT0660/2023	Portugal		2023-07-26	GISAID	2023-07-26	2023-07
hMPXV/China/SZ-SZTH45/2023	China	Guangdong	2023-6-16	GISAID	2023-06-16	2023-06
hMPXV/Portugal/INSA-PT0656/2023	Portugal		2023-07-21	GISAID	2023-07-21	2023-07

Continued

Name	Country	Province	Collection date	Sources	Revised collection date for treetime	Revised month
hMPXV/Portugal/INSA-PT0733/2023	Portugal		2023-09-19	GISAID	2023-09-19	2023-09
hMPXV/Portugal/INSA-PT0629/2023	Portugal		2023-06-20	GISAID	2023-06-20	2023-06
hMPXV/Portugal/INSA-PT0713/2023	Portugal		2023-08-21	GISAID	2023-08-21	2023-08
hMPXV/Netherlands/un-EMC-NL089/2023	Netherlands		2023-10-15	GISAID	2023-10-15	2023-10
hMPXV/Portugal/INSA-PT0748/2023	Portugal		2023-09-29	GISAID	2023-09-29	2023-09
hMPXV/Portugal/INSA-PT0666/2023	Portugal		2023-08-01	GISAID	2023-08-01	2023-08
hMPXV/Portugal/INSA-PT0727/2023	Portugal		2023-09-12	GISAID	2023-09-12	2023-09
hMPXV/Brazil/RJ-FIOCRUZ-10491/2024	Brazil		2024-04-18	GISAID	2024-04-18	2024-04
hMPXV/Portugal/INSA-PT0775/2023	Portugal		2023-10-19	GISAID	2023-10-19	2023-10
hMPXV/Portugal/INSA-PT0711/2023	Portugal		2023-08-21	GISAID	2023-08-21	2023-08
hMPXV/Germany/BY-IMB-2541/2023	Germany		2023-11-22	GISAID	2023-11-22	2023-11
hMPXV/Portugal/INSA-PT0694/2023	Portugal		2023-07-18	GISAID	2023-07-18	2023-07
hMPXV/Portugal/INSA-PT0736/2023	Portugal		2023-09-19	GISAID	2023-09-19	2023-09
hMPXV/Portugal/INSA-PT0778/2023	Portugal		2023-10-27	GISAID	2023-10-27	2023-10
hMPXV/Portugal/INSA-PT0661/2023	Portugal		2023-07-26	GISAID	2023-07-26	2023-07
hMPXV/China/SZ-SZTH41/2023	China	Guangdong	2023-06-19	GISAID	2023-06-19	2023-06
hMPXV/USA/CA-UW-301960/2024	USA		2024-02-14	GISAID	2024-02-14	2024-02
hMPXV/Portugal/INSA-PT0744/2023	Portugal		2023-09-26	GISAID	2023-09-26	2023-09
hMPXV/USA/CA-CDPH-1M1000432/2023	USA		2023-10-14	GISAID	2023-10-14	2023-10
hMPXV/Portugal/INSA-PT0739/2023	Portugal		2023-09-24	GISAID	2023-09-24	2023-09
hMPXV/Portugal/INSA-PT0724/2023	Portugal		2023-09-08	GISAID	2023-09-08	2023-09
hMPXV/Ireland/un-NVRL-Z22IRL00908/2023	Ireland		2023-08-18	GISAID	2023-08-18	2023-08
hMPXV/Portugal/INSA-PT0799/2023	Portugal		2023-11-20	GISAID	2023-11-20	2023-11
hMPXV/Portugal/INSA-PT0750/2023	Portugal		2023-10-02	GISAID	2023-10-02	2023-10
hMPXV/Ireland/un-NVRL-Z22IRL00909/2023	Ireland		2023-08-31	GISAID	2023-08-31	2023-08
hMPXV/Portugal/INSA-PT0756/2023	Portugal		2023-10-06	GISAID	2023-10-06	2023-10
hMPXV/Portugal/INSA-PT0740/2023	Portugal		2023-09-22	GISAID	2023-09-22	2023-09
hMPXV/Portugal/INSA-PT0738/2023	Portugal		2023-09-22	GISAID	2023-09-22	2023-09
hMPXV/Portugal/INSA-PT0783/2023	Portugal		2023-10-29	GISAID	2023-10-29	2023-10
hMPXV/Portugal/INSA-PT0780/2023	Portugal		2023-10-29	GISAID	2023-10-29	2023-10
hMPXV/Portugal/INSA-PT0771/2023	Portugal		2023-10-12	GISAID	2023-10-12	2023-10
hMPXV/Portugal/INSA-PT0701/2023	Portugal		2023-08-07	GISAID	2023-08-07	2023-08
hMPXV/Portugal/INSA-PT0708/2023	Portugal		2023-08-10	GISAID	2023-08-10	2023-08
hMPXV/Portugal/INSA-PT0784/2023	Portugal		2023-11-01	GISAID	2023-11-01	2023-11
hMPXV/Portugal/INSA-PT0793/2023	Portugal		2023-11-07	GISAID	2023-11-07	2023-11
hMPXV/Portugal/INSA-PT0800/2023	Portugal		2023-11-18	GISAID	2023-11-18	2023-11
hMPXV/Netherlands/un-EMC-NL090/2023	Netherlands		2023-11-07	GISAID	2023-11-07	2023-11
hMPXV/Portugal/INSA-PT0741/2023	Portugal		2023-09-25	GISAID	2023-09-25	2023-09
hMPXV/Ireland/un-NVRL-G23IRL50393/2023	Ireland		2023-08-16	GISAID	2023-08-16	2023-08
hMPXV/Germany/un-IMB-2541/2023	Germany		2023-11-22	GISAID	2023-11-22	2023-11
hMPXV/Ireland/un-NVRL-Z22IRL00910/2023	Ireland		2023-08-28	GISAID	2023-08-28	2023-08
hMPXV/Portugal/INSA-PT0772/2023	Portugal		2023-10-12	GISAID	2023-10-12	2023-10

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Name	Country	Province	Collection date	Sources	Revised collection date for treetime	Revised month
hMPXV/Portugal/INSA-PT0787/2023	Portugal		2023-11-02	GISAID	2023-11-02	2023-11
hMPXV/Portugal/INSA-PT0768/2023	Portugal		2023-10-12	GISAID	2023-10-12	2023-10
hMPXV/Portugal/INSA-PT0767/2023	Portugal		2023-10-13	GISAID	2023-10-13	2023-10
hMPXV/Portugal/INSA-PT0757/2023	Portugal		2023-10-04	GISAID	2023-10-04	2023-10
hMPXV/Portugal/INSA-PT0734/2023	Portugal		2023-09-19	GISAID	2023-09-19	2023-09
hMPXV/Portugal/INSA-PT0806/2023	Portugal		2023-11-30	GISAID	2023-11-30	2023-11
hMPXV/Portugal/INSA-PT0759/2023	Portugal		2023-10-10	GISAID	2023-10-10	2023-10
hMPXV/Netherlands/un-EMC-NL092/2023	Netherlands		2023-12-18	GISAID	2023-12-18	2023-12
hMPXV/Portugal/INSA-PT0785/2023	Portugal		2023-10-31	GISAID	2023-10-31	2023-10
hMPXV/Portugal/INSA-PT0652/2023	Portugal		2023-07-19	GISAID	2023-07-19	2023-07
hMPXV/Netherlands/un-EMC-NL088/2023	Netherlands		2023-08-29	GISAID	2023-08-29	2023-08
hMPXV/Italy/PIE-OAS-59215348/2022	Italy		2022-09-05	GISAID	2022-09-05	2022-09
hMPXV/Netherlands/un-EMC-NL093/2023	Netherlands		2023-12-19	GISAID	2023-12-19	2023-12
hMPXV/Portugal/INSA-PT0794/2023	Portugal		2023-11-09	GISAID	2023-11-09	2023-11
hMPXV/Portugal/INSA-PT0809/2023	Portugal		2023-12-21	GISAID	2023-12-21	2023-12
hMPXV/Netherlands/un-EMC-NL098/2023	Netherlands		2023-12-19	GISAID	2023-12-19	2023-12
hMPXV/Italy/PIE-OAS-02591782/2022	Italy		2022-07-19	GISAID	2022-07-19	2022-07
hMPXV/Brazil/RS-CEVS-378/2023	Brazil		2023-11-08	GISAID	2023-11-08	2023-11
hMPXV/Brazil/SP-IAL-357531658/2024	Brazil		2024-02-28	GISAID	2024-02-28	2024-02
hMPXV/England/CDC_P3/2018	England		2018-09	GISAID	2018-09	2018-09
hMPXV/England/CDC_P2/2018	England		2018-09	GISAID	2018-09	2018-09
hMPXV/England/CDC_P1/2018	England		2018-09	GISAID	2018-09	2018-09
hMPXV/Nigeria/CBR-003/2019	Nigeria		2019-01-16	GISAID	2019-01-16	2019-01
hMPXV/Nigeria/CBR-053/2019	Nigeria		2019-07-01	GISAID	2019-07-01	2019-07
hMPXV/Singapore/CDC-01/2019	Singapore		2019	GISAID	2019	2019
hMPXV/Nigeria/CBR-052/2019	Nigeria		2019-06-08	GISAID	2019-06-08	2019-06
hMPXV/Israel/IIBR-01/2018	Israel		2018-10-04	GISAID	2018-10-04	2018-10
hMPXV/Brazil/SP-IAL-357514864/2024	Brazil		2024-02-22	GISAID	2024-02-22	2024-02
hMPXV/Nigeria/CBR-042/2019	Nigeria		2019-04-29	GISAID	2019-04-29	2019-04
hMPXV/Brazil/RJ-FIOCRUZ-10501/2024	Brazil		2024-05-14	GISAID	2024-05-14	2024-05
hMPXV/Hungary/NBL_63/2024	Hungary		2024-06-20	GISAID	2024-06-20	2024-06
hMPXV/Nigeria/CBR-040/2019	Nigeria		2019-04-29	GISAID	2019-04-29	2019-04
hMPXV/Brazil/PR-FIOCRUZ-10548/2024	Brazil		2024-07-19	GISAID	2024-07-19	2024-07
hMPXV/Brazil/RJ-FIOCRUZ-09217/2024	Brazil		2024-03-29	GISAID	2024-03-29	2024-03
hMPXV/United_Kingdom/UKHSA-0MZd8B_9000260/2022	United_Kingdom		2022-08	GISAID	2022-08	2022-08
hMPXV/Brazil/RJ-FIOCRUZ-10527/2024	Brazil		2024-08-16	GISAID	2024-08-16	2024-08
hMPXV/Brazil/RJ-FIOCRUZ-09216/2024	Brazil		2024-03-31	GISAID	2024-03-31	2024-03
hMPXV/Brazil/RJ-FIOCRUZ-09219/2024	Brazil		2024-04-08	GISAID	2024-04-08	2024-04
hMPXV/USA/IL-RIPHL-004-0142/2024	USA		2024-02-07	GISAID	2024-02-07	2024-02
hMPXV/Portugal/INSA-PT0815/2024	Portugal		2024-01-13	GISAID	2024-01-13	2024-01
hMPXV/Brazil/SP-IAL-357496487/2024	Brazil		2024-02-16	GISAID	2024-02-16	2024-02
hMPXV/Nigeria/CBR-039/2019	Nigeria		2019-04-29	GISAID	2019-04-29	2019-04

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Name	Country	Province	Collection date	Sources	Revised collection date for treetime	Revised month
hMPXV/China/HZCDC-0001/2023	China	Zhejiang	2023-06-15	GISAID	2023-06-15	2023-06
hMPXV/Portugal/INSA-PT0814/2024	Portugal		2024-01-15	GISAID	2024-01-15	2024-01
hMPXV/Brazil/RJ-FIOCRUZ-09215/2024	Brazil		2024-03-29	GISAID	2024-03-29	2024-03
hMPXV/Japan/TMIPH-0260/2023	Japan		2023-09-16	GISAID	2023-09-16	2023-09
hMPXV/Portugal/INSA-PT0752/2023	Portugal		2023-10-03	GISAID	2023-10-03	2023-10
hMPXV/Brazil/SP-IAL-357531200/2024	Brazil		2024-02-27	GISAID	2024-02-27	2024-02
hMPXV/Portugal/INSA-PT0807/2023	Portugal		2023-12-27	GISAID	2023-12-27	2023-12
hMPXV/Portugal/INSA-PT0776/2023	Portugal		2023-10-20	GISAID	2023-10-20	2023-10
hMPXV/Portugal/INSA-PT0781/2023	Portugal		2023-10-26	GISAID	2023-10-26	2023-10
hMPXV/Brazil/SP-IAL-357983351/2024	Brazil		2024-10-08	GISAID	2024-10-08	2024-10
hMPXV/Brazil/SP-IAL-357911339/2024	Brazil		2024-08-23	GISAID	2024-08-23	2024-08
hMPXV/Portugal/INSA-PT0774/2023	Portugal		2023-10-18	GISAID	2023-10-18	2023-10
hMPXV/Brazil/BA-LACEN-293860175/2024	Brazil		2024-08-07	GISAID	2024-08-07	2024-08
hMPXV/Portugal/INSA-PT0691/2023	Portugal		2023-07-15	GISAID	2023-07-15	2023-07
hMPXV/Ireland/D-NVRL-Z22IRL00925/2023	Ireland		2023-10	GISAID	2023-10	2023-10
hMPXV/Ireland/D-NVRL-Z22IRL00922/2023	Ireland		2023-10	GISAID	2023-10	2023-10
hMPXV/Brazil/SP-IAL-357975925/2024	Brazil		2024-10-02	GISAID	2024-10-02	2024-10
hMPXV/Portugal/INSA-PT0773/2023	Portugal		2023-10-17	GISAID	2023-10-17	2023-10
hMPXV/Japan/TMIPH-0353/2024	Japan		2024-01-25	GISAID	2024-01-25	2024-01
hMPXV/Portugal/INSA-PT0747/2023	Portugal		2023-09-26	GISAID	2023-09-26	2023-09
hMPXV/Brazil/SP-IAL-357897692/2024	Brazil		2024-08-14	GISAID	2024-08-14	2024-08
hMPXV/Portugal/INSA-PT0655/2023	Portugal		2023-07-21	GISAID	2023-07-21	2023-07
hMPXV/Brazil/SP-IAL-357640019/2024	Brazil		2024-04-03	GISAID	2024-04-03	2024-04
hMPXV/Brazil/SP-IAL-357886830/2024	Brazil		2024-08-06	GISAID	2024-08-06	2024-08
hMPXV/Portugal/INSA-PT0702/2023	Portugal		2023-08-08	GISAID	2023-08-08	2023-08
hMPXV/Portugal/INSA-PT0703/2023	Portugal		2023-08-10	GISAID	2023-08-10	2023-08
hMPXV/Brazil/RJ-UG_UFRJ_0572/2024	Brazil		2024-08-27	GISAID	2024-08-27	2024-08
hMPXV/Brazil/SP-IAL-357821026/2024	Brazil		2024-06-18	GISAID	2024-06-18	2024-06
hMPXV/Portugal/INSA-PT0685/2023	Portugal		2023-07-13	GISAID	2023-07-13	2023-07
hMPXV/Brazil/RJ-FIOCRUZ-10490/2024	Brazil		2024-04-10	GISAID	2024-04-10	2024-04
hMPXV/Brazil/SP-IAL-357899878/2024	Brazil		2024-08-15	GISAID	2024-08-15	2024-08
hMPXV/Brazil/SP-IAL-357979688/2024	Brazil		2024-10-06	GISAID	2024-10-06	2024-10
hMPXV/Brazil/SP-IAL-357904928/2024	Brazil		2024-08-19	GISAID	2024-08-19	2024-08
hMPXV/Brazil/SP-IAL-357941922/2024	Brazil		2024-09-11	GISAID	2024-09-11	2024-09
hMPXV/Brazil/SP-IAL-357921858/2024	Brazil		2024-09-01	GISAID	2024-09-01	2024-09
hMPXV/Thailand/KCMH-459/2023	Thailand		2023-12-12	GISAID	2023-12-12	2023-12
hMPXV/Brazil/SP-IAL-357882670/2024	Brazil		2024-08-02	GISAID	2024-08-02	2024-08
hMPXV/Brazil/SP-IAL-357981172/2024	Brazil		2024-10-04	GISAID	2024-10-04	2024-10
hMPXV/Brazil/SP-IAL-357903818/2024	Brazil		2024-08-19	GISAID	2024-08-19	2024-08
hMPXV/Brazil/RJ-UG_UFRJ_0568/2024	Brazil		2024-08-15	GISAID	2024-08-15	2024-08
hMPXV/Australia/VIC-VIDRL-6948/2024	Australia		2024-05-06	GISAID	2024-05-06	2024-05
hMPXV/Brazil/PR-FIOCRUZ-10549/2024	Brazil		2024-07-20	GISAID	2024-07-20	2024-07

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Name	Country	Province	Collection date	Sources	Revised collection date for treetime	Revised month
hMPXV/Thailand/KCMH-455/2023	Thailand		2023-12-01	GISAID	2023-12-01	2023-12
hMPXV/Brazil/SP-IAL-357802143/2024	Brazil		2024-06-06	GISAID	2024-06-06	2024-06
hMPXV/Brazil/SP-IAL-357792329/2024	Brazil		2024-06-02	GISAID	2024-06-02	2024-06
hMPXV/Cambodia/NPHL1211017/2023	Cambodia		2023-12-11	GISAID	2023-12-11	2023-12
hMPXV/USA/WA-UW-092809/2023	USA		2023-09	GISAID	2023-09	2023-09
hMPXV/South_Korea/KDCA-P019/2023	South_Korea		2023-04-19	GISAID	2023-04-19	2023-04
hMPXV/Brazil/SP-IAL-357798278/2024	Brazil		2024-06-04	GISAID	2024-06-04	2024-06
hMPXV/Brazil/SP-IAL-357899716/2024	Brazil		2024-08-15	GISAID	2024-08-15	2024-08
hMPXV/Portugal/INSA-PT0754/2023	Portugal		2023-10-04	GISAID	2023-10-04	2023-10
hMPXV/Brazil/RJ-UG_UFRJ_0554/2024	Brazil		2024-08-21	GISAID	2024-08-21	2024-08
hMPXV/Japan/TMIPH-0255/2024	Japan		2023-09-11	GISAID	2023-09-11	2023-09
hMPXV/Portugal/INSA-PT0751/2023	Portugal		2023-10-03	GISAID	2023-10-03	2023-10
hMPXV/USA/CA-LACPHL-MA00658/2024	USA		2024-07-24	GISAID	2024-07-24	2024-07
hMPXV/Brazil/SP-IAL-357944650/2024	Brazil		2024-09-15	GISAID	2024-09-15	2024-09
hMPXV/Brazil/SP-IAL-357933783/2024	Brazil		2024-09-08	GISAID	2024-09-08	2024-09
hMPXV/Brazil/SP-IAL-357914556/2024	Brazil		2024-08-26	GISAID	2024-08-26	2024-08
hMPXV/Brazil/SP-IAL-357994370/2024	Brazil		2024-10-16	GISAID	2024-10-16	2024-10
hMPXV/Portugal/INSA-PT0653/2023	Portugal		2023-07-21	GISAID	2023-07-21	2023-07
hMPXV/Brazil/SP-IAL-357949045/2024	Brazil		2024-09-17	GISAID	2024-09-17	2024-09
hMPXV/Brazil/SP-IAL-357929674/2024	Brazil		2024-09-04	GISAID	2024-09-04	2024-09
hMPXV/Brazil/RJ-FIOCRUZ-10502/2024	Brazil		2024-05-15	GISAID	2024-05-15	2024-05
hMPXV/Netherlands/un-EMC-NL110/2024	Netherlands		2024-08-07	GISAID	2024-08-07	2024-08
hMPXV/Brazil/SP-IAL-357928627/2024	Brazil		2024-09-04	GISAID	2024-09-04	2024-09
hMPXV/South_Korea/KDCA-P022/2023	South_Korea		2023-04-21	GISAID	2023-04-21	2023-04
hMPXV/Brazil/SP-IAL-357897410/2024	Brazil		2024-08-13	GISAID	2024-08-13	2024-08
hMPXV/Brazil/SP-IAL-357899889/2024	Brazil		2024-08-15	GISAID	2024-08-15	2024-08
hMPXV/Portugal/INSA-PT0716/2023	Portugal		2023-08-31	GISAID	2023-08-31	2023-08
hMPXV/Brazil/RJ-FIOCRUZ-10495/2024	Brazil		2024-05-02	GISAID	2024-05-02	2024-05
hMPXV/Brazil/SP-IAL-357909240/2024	Brazil		2024-08-21	GISAID	2024-08-21	2024-08
hMPXV/Brazil/RJ-UG_UFRJ_0553/2024	Brazil		2024-08-19	GISAID	2024-08-19	2024-08
hMPXV/Brazil/SP-IAL-357985080/2024	Brazil		2024-10-09	GISAID	2024-10-09	2024-10
hMPXV/Brazil/SP-IAL-357903632/2024	Brazil		2024-08-19	GISAID	2024-08-19	2024-08
hMPXV/Japan/TMIPH-220516/2023	Japan		2023-03-29	GISAID	2023-03-29	2023-03
hMPXV/Brazil/SP-IAL-357901450/2024	Brazil		2024-08-18	GISAID	2024-08-18	2024-08
hMPXV/Brazil/SP-IAL-357896065/2024	Brazil		2024-08-13	GISAID	2024-08-13	2024-08
hMPXV/South_Korea/KDCA-P006/2023	South_Korea		2023-04-06	GISAID	2023-04-06	2023-04
hMPXV/Japan/TMIPH-0318/2022	Japan		2023-01-25	GISAID	2023-01-25	2023-01
hMPXV/South_Korea/KDCA-P020/2023	South_Korea		2023-04-19	GISAID	2023-04-19	2023-04
hMPXV/Japan/TMIPH-220524/2023	Japan		2023-03-30	GISAID	2023-03-30	2023-03
hMPXV/South_Korea/KDCA-P010/2023	South_Korea		2023-04-13	GISAID	2023-04-13	2023-04
hMPXV/Brazil/SP-IAL-357903502/2024	Brazil		2024-08-19	GISAID	2024-08-19	2024-08
hMPXV/South_Korea/KDCA-P008/2023	South_Korea		2023-04-11	GISAID	2023-04-11	2023-04

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Name	Country	Province	Collection date	Sources	Revised collection date for treetime	Revised month
hMPXV/South_Korea/KDCA-P032/2023	South_Korea		2023-04-25	GISAID	2023-04-25	2023-04
hMPXV/Japan/TMIPH-0019/2023	Japan		2023-04-11	GISAID	2023-04-11	2023-04
hMPXV/Japan/TMIPH-0047/2023	Japan		2023-04-19	GISAID	2023-04-19	2023-04
hMPXV/Japan/TMIPH-0076/2023	Japan		2023-04-28	GISAID	2023-04-28	2023-04
hMPXV/South_Korea/KDCA-P013/2023	South_Korea		2023-04-15	GISAID	2023-04-15	2023-04
hMPXV/Japan/TMIPH-0310/2022	Japan		2023-01-25	GISAID	2023-01-25	2023-01
hMPXV/Brazil/SP-IAL-357718239/2024	Brazil		2024-04-30	GISAID	2024-04-30	2024-04
hMPXV/South_Korea/KDCA-P029/2023	South_Korea		2023-04-23	GISAID	2023-04-23	2023-04
hMPXV/Japan/TMIPH-0342/2022	Japan		2023-02-09	GISAID	2023-02-09	2023-02
hMPXV/Japan/FKTMIPH-220343/2023	Japan		2023-02-13	GISAID	2023-02-13	2023-02
hMPXV/South_Korea/KDCA-P012/2023	South_Korea		2023-04-15	GISAID	2023-04-15	2023-04
hMPXV/Japan/TMIPH-230002/2023	Japan		2023-03-31	GISAID	2023-03-31	2023-03
hMPXV/Portugal/INSA-PT0633/2023	Portugal		2023-06-25	GISAID	2023-06-25	2023-06
hMPXV/Japan/TMIPH-0126/2023	Japan		2023-05-15	GISAID	2023-05-15	2023-05
hMPXV/Thailand/KCMH-465/2023	Thailand		2023-12-28	GISAID	2023-12-28	2023-12
hMPXV/South_Korea/KDCA-P030/2023	South_Korea		2023-04-23	GISAID	2023-04-23	2023-04
hMPXV/Japan/TMIPH-0325/2022	Japan		2023-01-30	GISAID	2023-01-30	2023-01
hMPXV/South_Korea/KDCA-P007/2023	South_Korea		2023-04-10	GISAID	2023-04-10	2023-04
hMPXV/South_Korea/KDCA-P034/2023	South_Korea		2023-04-25	GISAID	2023-04-25	2023-04
hMPXV/South_Korea/KDCA-P016/2023	South_Korea		2023-04-18	GISAID	2023-04-18	2023-04
hMPXV/South_Korea/NMC-P003/2023	South_Korea		2023-05-03	GISAID	2023-05-03	2023-05
hMPXV/Thailand/KCMH-296/2023	Thailand		2023-07-03	GISAID	2023-07-03	2023-07
hMPXV/South_Korea/KDCA-P027/2023	South_Korea		2023-04-22	GISAID	2023-04-22	2023-04
hMPXV/South_Korea/KDCA-P028/2023	South_Korea		2023-04-22	GISAID	2023-04-22	2023-04
hMPXV/South_Korea/KDCA-P021/2023	South_Korea		2023-04-21	GISAID	2023-04-21	2023-04
hMPXV/Indonesia/JK-NIHRD-MP044/2023	Indonesia		2023-10-25	GISAID	2023-10-25	2023-10
hMPXV/Japan/FKTMIPH-220304/2023	Japan		2023-01-23	GISAID	2023-01-23	2023-01
hMPXV/South_Korea/KDCA-P009/2023	South_Korea		2023-04-12	GISAID	2023-04-12	2023-04
hMPXV/Japan/TMIPH-0162/2023	Japan		2023-06-02	GISAID	2023-06-02	2023-06
hMPXV/Japan/TMIPH-220512/2023	Japan		2023-03-28	GISAID	2023-03-28	2023-03
hMPXV/Japan/TMIPH-220323/2023	Japan		2023-01-30	GISAID	2023-01-30	2023-01
hMPXV/South_Korea/KDCA-P011/2023	South_Korea		2023-04-14	GISAID	2023-04-14	2023-04
hMPXV/Japan/TMIPH-220357/2023	Japan		2023-02-20	GISAID	2023-02-20	2023-02
hMPXV/South_Korea/KDCA-P024/2023	South_Korea		2023-04-21	GISAID	2023-04-21	2023-04
hMPXV/Japan/TMIPH-0129/2023	Japan		2023-05-17	GISAID	2023-05-17	2023-05
hMPXV/South_Korea/KDCA-P018/2023	South_Korea		2023-04-18	GISAID	2023-04-18	2023-04
hMPXV/South_Korea/KDCA-P005/2023	South_Korea		2023-03-13	GISAID	2023-03-13	2023-03
hMPXV/USA/WA-UW-066957/2023	USA		2023-06	GISAID	2023-06	2023-06
hMPXV/Japan/TMIPH-0072/2023	Japan		2023-04-28	GISAID	2023-04-28	2023-04
hMPXV/Japan/TMIPH-0085/2023	Japan		2023-05-01	GISAID	2023-05-01	2023-05
hMPXV/Japan/TMIPH-220510/2023	Japan		2023-03-28	GISAID	2023-03-28	2023-03
hMPXV/Indonesia/JK-NIHRD-MP010/2023	Indonesia		2023-10-20	GISAID	2023-10-20	2023-10

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hMPXV/Japan/TMIPH-0288/2023	Japan		2023-10-11	GISAID	2023-10-11	2023-10
hMPXV/Japan/TMIPH-0171/2023	Japan		2023-06-06	GISAID	2023-06-06	2023-06
hMPXV/South_Korea/KDCA-P015/2023	South_Korea		2023-04-18	GISAID	2023-04-18	2023-04
hMPXV/Japan/TMIPH-0082/2023	Japan		2023-05-01	GISAID	2023-05-01	2023-05
hMPXV/Japan/TMIPH-220531/2023	Japan		2023-03-31	GISAID	2023-03-31	2023-03
hMPXV/Thailand/KCMH-295/2023	Thailand		2023-07-03	GISAID	2023-07-03	2023-07
hMPXV/Japan/TMIPH-0112/2023	Japan		2023-05-11	GISAID	2023-05-11	2023-05
hMPXV/Japan/TMIPH-0144/2023	Japan		2023-05-20	GISAID	2023-05-20	2023-05
hMPXV/Japan/TMIPH-0017/2023	Japan		2023-04-06	GISAID	2023-04-06	2023-04
hMPXV/Brazil/SP-IAL-357981364/2024	Brazil		2024-10-07	GISAID	2024-10-07	2024-10
hMPXV/Japan/TMIPH-0267/2023	Japan		2023-09-22	GISAID	2023-09-22	2023-09
hMPXV/Thailand/KCMH-026/2023	Thailand		2023-05-12	GISAID	2023-05-12	2023-05
hMPXV/Brazil/SP-IAL-357934564/2024	Brazil		2024-09-09	GISAID	2024-09-09	2024-09
hMPXV/Philippines/RITM-007/2023	Philippines		2023-12-05	GISAID	2023-12-05	2023-12
hMPXV/Japan/TMIPH-0223/2023	Japan		2023-07-07	GISAID	2023-07-07	2023-07
hMPXV/India/DL-ICMR-MCL-174-40451050/2024	India		2024-09-09	GISAID	2024-09-09	2024-09
hMPXV/Brazil/RJ-UG_UFRJ_0552/2024	Brazil		2024-08-15	GISAID	2024-08-15	2024-08
hMPXV/South_Korea/KDCA-P017/2023	South_Korea		2023-04-18	GISAID	2023-04-18	2023-04
hMPXV/Japan/TMIPH-0100/2023	Japan		2023-05-06	GISAID	2023-05-06	2023-05
hMPXV/Brazil/SP-IAL-357909129/2024	Brazil		2024-08-19	GISAID	2024-08-19	2024-08
hMPXV/Netherlands/un-EMC-NL106/2024	Netherlands		2024-08-13	GISAID	2024-08-13	2024-08
hMPXV/Japan/TMIPH-0012/2023	Japan		2023-04-04	GISAID	2023-04-04	2023-04
hMPXV/Japan/TMIPH-0029/2023	Japan		2023-04-17	GISAID	2023-04-17	2023-04
hMPXV/Brazil/SP-IAL-357980969/2024	Brazil		2024-09-30	GISAID	2024-09-30	2024-09
hMPXV/Japan/TMIPH-0204/2023	Japan		2023-06-26	GISAID	2023-06-26	2023-06
hMPXV/Japan/TMIPH-0113/2023	Japan		2023-05-12	GISAID	2023-05-12	2023-05
hMPXV/Japan/TMIPH-0109/2023	Japan		2023-05-11	GISAID	2023-05-11	2023-05
hMPXV/Brazil/SP-IAL-357981061/2024	Brazil		2024-10-06	GISAID	2024-10-06	2024-10
hMPXV/China/GDCDC_GZ_M23050/2023	China	Guangdong	2023/6/16	GenBase	2023-06-16	2023-06
hMPXV/China/GDCDC_GZ_M23011/2023	China	Guangdong	2023/6/7	GenBase	2023-06-07	2023-06
hMPXV/China/SKLID_ZJU-10/2023	China	Guangdong	2023	GenBase	2023	2023
hMPXV/Brazil/SP-IAL-357938508/2024	Brazil		2024-09-10	GISAID	2024-09-10	2024-09
hMPXV/Brazil/SP-IAL-357890330/2024	Brazil		2024-08-07	GISAID	2024-08-07	2024-08
hMPXV/Brazil/RJ-FIOCRUZ-10505/2024	Brazil		2024-05-16	GISAID	2024-05-16	2024-05
hMPXV/Portugal/INSA-PT0803/2023	Portugal		2023-11-28	GISAID	2023-11-28	2023-11
hMPXV/Brazil/RJ-UG_UFRJ_0551/2024	Brazil		2024-08-09	GISAID	2024-08-09	2024-08
hMPXV/China/GDCDC_FS_M23108/2023	China	Guangdong	2023/6/22	GenBase	2023-06-22	2023-06
hMPXV/China/SZPMI-041/2023	China	Guangdong	2023/7/13	GenBase	2023-07-13	2023-07
hMPXV/Brazil/SP-IAL-357911479/2024	Brazil		2024-08-24	GISAID	2024-08-24	2024-08
hMPXV/Brazil/SP-IAL-357996884/2024	Brazil		2024-10-18	GISAID	2024-10-18	2024-10
hMPXV/China/SZPMI-038/2023	China	Guangdong	2023/7/7	GenBase	2023-07-07	2023-07
hMPXV/China/SZPMI-016/2023	China	Guangdong	2023/6/21	GenBase	2023-06-21	2023-06

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hMPXV/Portugal/INSA-PT0764/2023	Portugal		2023-10-13	GISAID	2023-10-13	2023-10
hMPXV/China/SZPMI-048/2023	China	Guangdong	2023/7/16	GenBase	2023-07-16	2023-07
hMPXV/China/Guangdong01-BS/2023	China	Guangdong	2023/6/1	GenBase	2023-06-01	2023-06
hMPXV/Portugal/INSA-PT0770/2023	Portugal		2023-10-12	GISAID	2023-10-12	2023-10
hMPXV/China/SZPMI-056/2023	China	Guangdong	2023/7/25	GenBase	2023-07-25	2023-07
hMPXV/China/SZPMI-076/2023	China	Guangdong	2023/8/14	GenBase	2023-08-14	2023-08
hMPXV/China/SZPMI-049/2023	China	Guangdong	2023/7/12	GenBase	2023-07-12	2023-07
hMPXV/China/SZPMI-043/2023	China	Guangdong	2023/7/14	GenBase	2023-07-14	2023-07
hMPXV/China/GDCDC_GZ_M23008/2023	China	Guangdong	2023/6/8	GenBase	2023-06-08	2023-06
hMPXV/China/SZPMI-024/2023	China	Guangdong	2023/7/2	GenBase	2023-07-02	2023-07
hMPXV/China/SZPMI-069/2023	China	Guangdong	2023/8/4	GenBase	2023-08-04	2023-08
hMPXV/China/SZPMI-032/2023	China	Guangdong	2023/7/2	GenBase	2023-07-02	2023-07
hMPXV/China/SKLID_ZJU-04/2023	China	Zhejiang	2023/7/28	GenBase	2023-07-28	2023-07
hMPXV/China/SZPMI-021/2023	China	Guangdong	2023/7/2	GenBase	2023-07-02	2023-07
hMPXV/China/SZPMI-004/2023	China	Guangdong	2023/6/16	GenBase	2023-06-16	2023-06
hMPXV/China/SKLID_ZJU-01/2023	China	Zhejiang	2023/7/17	GenBase	2023-07-17	2023-07
hMPXV/China/SZPMI-051/2023	China	Guangdong	2023/7/19	GenBase	2023-07-19	2023-07
hMPXV/China/SKLID_ZJU-09/2023	China	Guangdong	2023	GenBase	2023	2023
hMPXV/China/SZPMI-026/2023	China	Guangdong	2023/7/1	GenBase	2023-07-01	2023-07
hMPXV/China/SZPMI-035/2023	China	Guangdong	2023/7/5	GenBase	2023-07-05	2023-07
hMPXV/China/SZPMI-085/2023	China	Guangdong	2023/8/29	GenBase	2023-08-29	2023-08
hMPXV/China/SZPMI-008/2023	China	Guangdong	2023/6/13	GenBase	2023-06-13	2023-06
hMPXV/China/SZPMI-023/2023	China	Guangdong	2023/7/10	GenBase	2023-07-10	2023-07
hMPXV/China/SZPMI-005/2023	China	Guangdong	2023/6/16	GenBase	2023-06-16	2023-06
hMPXV/China/SZPMI-045/2023	China	Guangdong	2023/7/15	GenBase	2023-07-15	2023-07
hMPXV/China/SKLID_ZJU-03/2023	China	Zhejiang	2023/7/25	GenBase	2023-07-25	2023-07
hMPXV/China/SZPMI-028/2023	China	Guangdong	2023/6/29	GenBase	2023-06-29	2023-06
hMPXV/China/SZPMI-018/2023	China	Guangdong	2023/6/27	GenBase	2023-06-27	2023-06
hMPXV/China/SZPMI-039/2023	China	Guangdong	2023/7/11	GenBase	2023-07-11	2023-07
hMPXV/China/SZPMI-017/2023	China	Guangdong	2023/6/26	GenBase	2023-06-26	2023-06
hMPXV/China/SZPMI-066/2023	China	Guangdong	2023/7/31	GenBase	2023-07-31	2023-07
hMPXV/China/SZPMI-059/2023	China	Guangdong	2023/7/24	GenBase	2023-07-24	2023-07
hMPXV/China/SZPMI-033/2023	China	Guangdong	2023/6/30	GenBase	2023-06-30	2023-06
hMPXV/China/SZPMI-025/2023	China	Guangdong	2023/6/29	GenBase	2023-06-29	2023-06
hMPXV/China/SZPMI-029/2023	China	Guangdong	2023/6/30	GenBase	2023-06-30	2023-06
hMPXV/China/SZPMI-036/2023	China	Guangdong	2023/6/30	GenBase	2023-06-30	2023-06
hMPXV/China/SZPMI-015/2023	China	Guangdong	2023/6/21	GenBase	2023-06-21	2023-06
hMPXV/China/SZPMI-060/2023	China	Guangdong	2023/7/28	GenBase	2023-07-28	2023-07
hMPXV/China/SZPMI-040/2023	China	Guangdong	2023/7/16	GenBase	2023-07-16	2023-07
hMPXV/China/SZPMI-078/2023	China	Guangdong	2023/8/20	GenBase	2023-08-20	2023-08
hMPXV/China/SZPMI-072/2023	China	Guangdong	2023/8/14	GenBase	2023-08-14	2023-08
hMPXV/China/SZPMI-057/2023	China	Guangdong	2023/7/31	GenBase	2023-07-31	2023-07

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Name	Country	Province	Collection date	Sources	Revised collection date for treetime	Revised month
hMPXV/China/SZPML-013/2023	China	Guangdong	2023/6/19	GenBase	2023-06-19	2023-06
hMPXV/China/SZPML-065/2023	China	Guangdong	2023/8/5	GenBase	2023-08-05	2023-08
hMPXV/China/SZPML-031/2023	China	Guangdong	2023/6/30	GenBase	2023-06-30	2023-06
hMPXV/China/SZPML-022/2023	China	Guangdong	2023/7/2	GenBase	2023-07-02	2023-07
hMPXV/China/SZPML-006/2023	China	Guangdong	2023/6/14	GenBase	2023-06-14	2023-06
hMPXV/China/SZPML-037/2023	China	Guangdong	2023/7/1	GenBase	2023-07-01	2023-07
hMPXV/China/SZPML-073/2023	China	Guangdong	2023/8/12	GenBase	2023-08-12	2023-08
hMPXV/China/SZPML-030/2023	China	Guangdong	2023/6/30	GenBase	2023-06-30	2023-06
hMPXV/China/SZPML-058/2023	China	Guangdong	2023/7/24	GenBase	2023-07-24	2023-07
hMPXV/China/SZPML-077/2023	China	Guangdong	2023/8/14	GenBase	2023-08-14	2023-08
hMPXV/China/SZPML-095/2023	China	Guangdong	2023/10/14	GenBase	2023-10-14	2023-10
hMPXV/China/SZPML-061/2023	China	Guangdong	2023/7/29	GenBase	2023-07-29	2023-07
hMPXV/China/SZPML-009/2023	China	Guangdong	2023/6/21	GenBase	2023-06-21	2023-06
hMPXV/China/SZPML-050/2023	China	Guangdong	2023/7/13	GenBase	2023-07-13	2023-07
hMPXV/China/SZPML-074/2023	China	Guangdong	2023/10/10	GenBase	2023-10-10	2023-10
hMPXV/China/SZPML-027/2023	China	Guangdong	2023/6/30	GenBase	2023-06-30	2023-06
hMPXV/China/SZPML-088/2023	China	Guangdong	2023/9/12	GenBase	2023-09-12	2023-09
hMPXV/China/SZPML-054/2023	China	Guangdong	2023/7/24	GenBase	2023-07-24	2023-07
hMPXV/China/SKLID_ZJU-05/2023	China	Zhejiang	2023/7/31	GenBase	2023-07-31	2023-07
hMPXV/China/SZPML-071/2023	China	Guangdong	2023/8/4	GenBase	2023-08-04	2023-08
hMPXV/China/SZPML-007/2023	China	Guangdong	2023/6/10	GenBase	2023-06-10	2023-06
hMPXV/China/SZPML-083/2023	China	Guangdong	2023/8/27	GenBase	2023-08-27	2023-08
hMPXV/China/SKLID_ZJU-07/2023	China	Guangdong	2023	GenBase	2023	2023
hMPXV/China/SZPML-020/2023	China	Guangdong	2023/6/27	GenBase	2023-06-27	2023-06
hMPXV/China/Beijing01-OS/2023	China	Beijing	2023/6/1	GenBase	2023-06-01	2023-06
hMPXV/China/SKLID_ZJU-08/2023	China	Guangdong	2023	GenBase	2023	2023
hMPXV/China/SZPML-063/2023	China	Guangdong	2023/8/1	GenBase	2023-08-01	2023-08
hMPXV/China/Beijing01-BS/2023	China	Beijing	2023/6/1	GenBase	2023-06-01	2023-06
hMPXV/China/SZPML-067/2023	China	Guangdong	2023/7/29	GenBase	2023-07-29	2023-07
hMPXV/China/SZPML-019/2023	China	Guangdong	2023/6/27	GenBase	2023-06-27	2023-06
hMPXV/China/SZPML-034/2023	China	Guangdong	2023/7/2	GenBase	2023-07-02	2023-07
hMPXV/China/SZPML-092/2023	China	Guangdong	2023/10/7	GenBase	2023-10-07	2023-10
hMPXV/China/SZPML-047/2023	China	Guangdong	2023/7/14	GenBase	2023-07-14	2023-07
hMPXV/China/SKLID_ZJU-06/2023	China	Guangdong	2023	GenBase	2023	2023
hMPXV/China/SKLID_ZJU-02/2023	China	Zhejiang	2023/7/25	GenBase	2023-07-25	2023-07
hMPXV/China/SZPML-046/2023	China	Guangdong	2023/7/12	GenBase	2023-07-12	2023-07
hMPXV/China/SZPML-052/2023	China	Guangdong	2023/7/19	GenBase	2023-07-19	2023-07
hMPXV/China/SZPML-094/2023	China	Guangdong	2023/10/10	GenBase	2023-10-10	2023-10
hMPXV/China/SZPML-062/2023	China	Guangdong	2023/7/29	GenBase	2023-07-29	2023-07
hMPXV/China/SZPML-080/2023	China	Guangdong	2023/8/30	GenBase	2023-08-30	2023-08
hMPXV/China/SZPML-053/2023	China	Guangdong	2023/7/19	GenBase	2023-07-19	2023-07
hMPXV/China/SZPML-002/2023	China	Guangdong	2023/6/12	GenBase	2023-06-12	2023-06

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Name	Country	Province	Collection date	Sources	Revised collection date for treetime	Revised month
hMPXV/China/SZPMI-011/2023	China	Guangdong	2023/6/17	GenBase	2023-06-17	2023-06
hMPXV/China/GDCDC_FS_M23028/2023	China	Guangdong	2023/6/13	GenBase	2023-06-13	2023-06
hMPXV/China/SZPMI-075/2023	China	Guangdong	2023/8/17	GenBase	2023-08-17	2023-08
hMPXV/China/SZPMI-012/2023	China	Guangdong	2023/6/18	GenBase	2023-06-18	2023-06