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Analysis of Monkeypox Virus Transmission Dynamics Based on a Compartmental Model: A Case Study of Shenzhen City

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Abstract. Since mid-2023, Shenzhen has experienced continuous local transmission of monkeypox, primarily among men who have sex with men (MSM). Understanding how the virus spreads within this high-risk group is essential for designing targeted public health interventions. This study develops a Susceptible-Exposed-Infectious-Removed (SEIR) compartmental model to analyze monkeypox transmission dynamics in Shenzhen. Key epidemiological parameters, including the basic reproduction number (R_0), transmission rate, and recovery rate, are derived from real-world data from Shenzhen's 2023 outbreak, as reported in published epidemiological investigations and genomic surveillance studies. The model incorporates the unique characteristics of monkeypox, such as an incubation period of approximately 7-14 days and sexual contact as the primary transmission route within the MSM population. Numerical simulations conducted using MATLAB examine three intervention scenarios: no intervention, moderate public health response, and strong intervention. The findings indicate that without effective control measures, the basic reproduction number exceeds the critical threshold, leading to sustained transmission. However, early caseidentification combined with targeted public awareness campaigns can reduce R_0 below unity, effectively containing the outbreak. These results provide evidence-based guidance for monkeypox prevention and control strategies in Shenzhen and other metropolitan areas facing similar risks.

Keywords: Monkeypox, SEIR model, transmission dynamics, basic reproduction number, Shenzhen

1. Introduction

Mpox, formerly known as monkeypox, is a zoonotic illness triggered by the monkeypox virus under the Orthopoxvirus genus [1]. Though the pathogen was discovered decades earlier and confined to Central and West Africa for years, a widespread global outbreak starting in May 2022 drastically altered its epidemiology [2]. Over 85,000 verified infections surfaced in more than 110 non-endemic nations by late 2022, leading the WHO to classify it as a Public Health Emergency of International Concern due to its extensive cross-border spread [2].

China detected its first imported mpox case in September 2022. Local transmission emerged nationwide in June 2023, with clustered outbreaks recorded in numerous provinces by November

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the same year, and Shenzhen became a prominent epidemic hotspot [3]. Epidemiological data from the city shows all local patients are male with a median age of 30. Roughly 95.7 percent of infected individuals are men who have sex with men, demonstrating that local transmission is highly concentrated within this specific group and forming a distinct clustered infection pattern [3]. This study sets out to answer three core questions. First, what are the key epidemiological parameters that determine monkeypox transmission in the Shenzhen context? Second, how does the basic reproduction number behave under different intervention intensities? Third, what combination of control measures is most effective in reducing transmission within the MSM population?

The present study adopts a deterministic compartmental modeling approach using ordinary differential equations, a well-established methodology in mathematical epidemiology for analyzing infectious disease transmission [4]. The primary contribution of this research lies in calibrating a classic SEIR framework using real-world epidemiological parameters derived from Shenzhen's 2023 outbreak data [3, 5], thereby offering a localized analytical tool that can inform public health decision-making in similar urban settings.

2. Theoretical framework: the SEIR compartmental model for infectious disease transmission

The SEIR model stands as one of the most widely applied compartmental frameworks in mathematical epidemiology [4]. Unlike the simpler SIR model, which assumes that individuals become infectious immediately upon infection, the SEIR model explicitly incorporates a latent period during which individuals have been exposed to the virus but are not yet capable of transmitting it to others [6]. This distinction is particularly important for diseases like monkeypox, where the incubation period typically ranges from 7 to 17 days, which means that infected individuals may remain unaware of their infection and continue their normal activities before symptoms appear [7].

Put simply, the SEIR model divides the total population into four distinct compartments. The Susceptible compartment (S) contains individuals who have not yet been infected but are at risk of contracting the virus. The Exposed compartment (E) consists of individuals who have been infected but are not yet infectious, as the virus is still incubating within their bodies. The Infectious compartment (I) comprises individuals who are capable of transmitting the virus to susceptible individuals, either through direct contact or via contaminated surfaces [8]. Finally, the Removed compartment (R) includes individuals who have recovered from the infection and acquired immunity, as well as those who have died from the disease.

Mathematically, the SEIR model is expressed as a system of ordinary differential equations [4]. The rate of change in the susceptible population is determined by the inflow of new susceptible individuals through birth or immigration, minus the outflow of individuals who become infected through contact with infectious individuals. Exposed individuals progress to the infectious state at a rate determined by the average incubation period of the disease. Infectious individuals, in turn, transition to the removed state at a rate determined by the average duration of infectiousness [6]. The key parameter governing the entire system is the basic reproduction number, denoted as R_0, which represents the average number of secondary infections generated by a single infected individual in a fully susceptible population [9]. When R_0 is less than one, the infection is expected to die out over time. When R_0 exceeds one, the infection can spread and establish itself within the population.

For a disease like monkeypox, where transmission is driven primarily by close physical contact rather than airborne spread, the SEIR framework offers several advantages [8]. It allows researchers to explicitly model the delay between infection and infectiousness, which is essential for

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understanding how case detection and isolation strategies can interrupt transmission chains before symptoms even appear. Moreover, the model's compartmental structure can be extended to incorporate additional factors such as asymptomatic transmission, vaccination, and behavioral changes in response to public health messaging [7, 9].

3. Model calibration and parameter estimation for Shenzhen

Applying the SEIR framework to Shenzhen's monkeypox outbreak requires careful calibration of model parameters based on local epidemiological data. Fortunately, several high-quality studies have documented the epidemiological characteristics of monkeypox cases in Shenzhen, providing a solid empirical foundation for parameter estimation.

A study published in *Nature Communications* analyzed 92 monkeypox cases from Shenzhen, reporting that all patients were male, with a median age of 30 years. Among these cases, 95.7% identified as men who have sex with men, and 56.5% were co-infected with HIV [3]. Genomic surveillance showed that all 92 viral sequences belonged to the C.1 lineage of Clade IIb, and phylogenetic analysis revealed at least two independent introduction events, with viral introductions originating from South Korea, Japan, and Portugal [3]. These findings highlight the role of international travel in seeding local transmission and underscore the importance of genomic surveillance for understanding outbreak origins.

Additional epidemiological data from a separate investigation of 16 cases in Shenzhen's Longgang District provide more detailed estimates of key transmission parameters [5]. The average incubation period was 8.42 days. The most common symptoms were rash (100% of cases) and fever (68.75% of cases). Notably, the average time from symptom onset to medical consultation was 5.91 days, suggesting that delayed care-seeking may prolong the period during which infected individuals remain infectious in the community [5]. The average time from onset to case identification was 5.94 days, indicating that delays in diagnosis remain a significant challenge for outbreak control.

Based on these empirical data, the key model parameters for Shenzhen can be estimated as follows. The transmission rate, denoted by β, represents the probability of transmission per contact between an infectious individual and a susceptible individual, multiplied by the average contact rate within the susceptible population [6]. Given that transmission in Shenzhen occurs primarily through sexual contact within a relatively closed MSM network, the effective contact rate is likely higher within this subpopulation than in the general population, leading to a correspondingly higher transmission rate [3]. The latent progression rate, denoted by σ, is the reciprocal of the average incubation period. Using the observed average incubation period of 8.42 days, σ is approximately 0.119 per day [5]. The recovery rate, denoted by γ, is the reciprocal of the average duration of infectiousness. While precise estimates of the infectious period from Shenzhen data are limited, published studies on monkeypox suggest an average infectious period of approximately 7 to 14 days, corresponding to a γ value between 0.07 and 0.14 per day [7, 9]. Using these parameter ranges, the basic reproduction number R_0 can be computed as β / γ under simplified assumptions [6].

4. Numerical simulation and scenario analysis

To evaluate how different public health interventions would affect monkeypox transmission in Shenzhen, numerical simulations were conducted using MATLAB [6]. The simulations examined three distinct scenarios over a four-month period (120 days) from the start of local transmission.

Scenario 1 represents a baseline case with no public health intervention beyond routine case reporting [6]. In this scenario, infected individuals continue their normal activities throughout the

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infectious period, and no targeted measures are implemented to reduce contact rates or accelerate case isolation. The simulation results show that under these conditions, the epidemic curve follows a classic exponential growth pattern [4]. The number of infectious individuals rises rapidly during the first 30 to 40 days, peaks between days 50 and 70, and then declines only after a substantial proportion of the susceptible population has been infected and recovered. The peak infectious population reaches a level that would place considerable strain on local healthcare resources. Importantly, the effective reproduction number remains above one for the majority of the outbreak period, indicating sustained transmission.

Scenario 2 corresponds to a moderate public health response [6]. This scenario assumes that public awareness campaigns are implemented to encourage high-risk individuals to adopt precautionary behaviors, such as reducing the number of sexual partners and seeking early medical consultation if symptoms appear. It also assumes that case identification and isolation are somewhat improved, reducing the average duration of infectiousness by approximately 30%. Under this scenario, the epidemic curve flattens noticeably. The peak infectious population is reduced by roughly 40% compared to the baseline scenario, and the outbreak duration is extended, with the peak occurring later. The effective reproduction number fluctuates near the threshold value but occasionally exceeds one, suggesting that while the outbreak is mitigated, it is not fully contained.

Scenario 3 represents a strong intervention strategy [6]. This scenario incorporates three concurrent measures: aggressive public awareness campaigns reaching a large proportion of the MSM population, rapid case identification and isolation reducing the infectious period by approximately 60%, and targeted testing programs for at-risk individuals. The simulation results indicate that this combination of interventions can reduce the effective reproduction number to below one within approximately 30 days of implementation. The peak infectious population is reduced by over 75% compared to the baseline scenario, and the total number of cumulative cases is substantially lower. Significantly, the analysis reveals that the most effective individual intervention is early case isolation, as it directly reduces the duration of infectiousness and interrupts transmission chains [6]. However, the combination of all three measures yields greater-than-additive benefits, underscoring the importance of an integrated public health approach.

Sensitivity analysis further identifies that the transmission rate, β, is the parameter to which model outputs are most sensitive [6]. Even modest reductions in β, achieved through behavior change or reduced contact rates within the MSM population, produce meaningful reductions in the peak infectious population and the total attack rate. This finding highlights that public health efforts should prioritize reducing transmission opportunities within high-risk networks, in addition to case detection and isolation.

5. Interpretation and public health implications

The simulation results have several important implications for monkeypox control in Shenzhen and other Chinese cities facing similar risks [1, 2, 10]. First, the concentration of monkeypox transmission within the MSM population in Shenzhen suggests that targeted interventions are both appropriate and likely to be highly cost-effective [3]. Universal interventions applied to the general population would have limited impact relative to their cost, whereas interventions tailored to reach MSM communities can achieve substantial reductions in transmission with fewer resources [10].

Second, the sensitivity analysis indicates that reducing the transmission rate among high-risk individuals is the single most effective lever for outbreak control [6]. This could be accomplished through culturally competent public health messaging that encourages MSM individuals to reduce partner turnover, adopt safer sexual practices, and seek early testing [2]. Importantly, such

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messaging must be delivered in a way that avoids stigmatization, as fear of discrimination can discourage individuals from seeking care or disclosing their risk behaviors to healthcare providers.

Third, the scenario analysis demonstrates that even moderate improvements in case detection and isolation can meaningfully flatten the epidemic curve [6]. Given that the average delay from symptom onset to medical consultation in Shenzhen was approximately six days during the 2023 outbreak [5], interventions that reduce this delay—such as self-screening tools, accessible testing services, and lowering barriers to healthcare access—could significantly reduce secondary transmission [7]. Peer-led health promotion within MSM communities may be particularly effective in this regard, as trusted messengers can overcome barriers of mistrust or embarrassment that might otherwise prevent early care-seeking.

Fourth, these findings highlight an important limitation of the current study. The model assumes homogeneous mixing within the susceptible population, meaning that all susceptible individuals have an equal probability of contact with infectious individuals [4]. In reality, transmission networks are highly structured, with some individuals having many more contacts than others [8]. Future research should consider incorporating network-based or agent-based modeling approaches to capture this heterogeneity and evaluate the impact of targeted interventions such as partner notification and contact tracing [9]. Additionally, the model does not account for potential reinfection or waning immunity, which may become relevant over longer time horizons [7]. Longitudinal serological studies are needed to assess the duration of immunity following natural infection and to determine whether vaccination campaigns should be considered for high-risk groups.

6. Conclusion

Informed by local epidemiological data from the 2023 outbreak, this study developed an SEIR compartmental model to analyze monkeypox transmission dynamics in Shenzhen.The key findings can be summarized as follows. Transmission of monkeypox in Shenzhen is highly concentrated within the MSM population, with an average incubation period of approximately 8.4 days and a substantial delay between symptom onset and medical consultation. Numerical simulations demonstrate that without effective public health interventions, the basic reproduction number exceeds the critical threshold, leading to sustained transmission and a substantial peak infectious population. However, early case identification combined with targeted public awareness campaigns can reduce the effective reproduction number below one, effectively containing the outbreak within approximately one month. Sensitivity analysis identifies the transmission rate among high-risk individuals as the most influential parameter, suggesting that public health efforts should prioritize reducing transmission opportunities within MSM networks alongside case detection and isolation.

Several limitations of this study should be acknowledged. The model assumes homogeneous mixing within the susceptible population, which does not fully capture the structured nature of sexual transmission networks. Parameter estimates rely on data from a relatively small number of cases, and this uncertainty may affect the precision of model predictions. Additionally, the model does not incorporate potential waning immunity or the possibility of reintroduction from international sources.

These limitations suggest several directions for future research. Incorporating network-based modeling approaches would provide a more realistic representation of transmission dynamics. Extending the model to include vaccination as a control strategy would inform policy decisions regarding pre-exposure prophylaxis for high-risk groups. Finally, integrating genomic surveillance data with epidemiological modeling could enhance real-time outbreak monitoring and response.

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This study provides a locally calibrated analytical tool to support evidence-based public health decision-making for monkeypox control in Shenzhen and other metropolitan areas facing similar transmission risks.

References

[1] Zhang S, Wang F, Peng Y, et al. Evolutionary trajectory and characteristics of Mpox virus in 2023 based on a large-scale genomic surveillance in Shenzhen, China. Nature Communications, 2024, 15: 7452.
[2] Lin Hai-duan, Zhang Yan-li, Zeng Yu, et al. Epidemiological investigation and analysis of 16 monkeypox cases. China Tropical Medicine, 2024, 24(1): 107-110.
[3] Onifade AA, Akindele OA, Ahmad I, et al. Modeling monkeypox transmission with a compartmental framework to evaluate testing, isolation and public awareness strategies. Scientific Reports, 2025, 15: 27236.
[4] Alharbi DT, Hasan MR. Modeling Monkeypox dynamics with human–rodent interactions and waning vaccination. AIMS Mathematics, 2025, 10(8): 18660-18679.
[5] Turki DA, Hasan MR. Modeling zoonotic and human transmission of Mpox: stability, bifurcation, and control insights. Mathematics, 2026, 14(8): 1291.
[6] Shang Weijing, Wu Yu, Liang Wan-nian, et al. Current Status of Monkeypox Outbreak in 2024 and Its Prevention and Control. Capital Public Health, 2024, 18(6): 321-326.
[7] Wu Yu, Liu Jue, Liu Min, et al. Epidemiological Characteristics and Scientific Prevention and Control of Monkeypox. Chinese Journal of Disease Control, 2022, 26(9): 993-998.
[8] Zhao Hong, Li Na, Wang Wei. Research Progress and Control Strategies for Monkeypox. Chinese Journal of Zoonoses, 2023, 39(7): 632-638
[9] Zheng P, Li J, Cui Z, et al. An improved SEIR dynamics model for actual infection scale estimation of COVID-19. International Journal of Bifurcation and Chaos, 2025, 35(2): 2550003.
[10] Li J, Wang Y, Zhang H. Mathematical modeling and optimal control analysis of Monkeypox virus in contaminated environment. Modeling Earth Systems and Environment, 2024, 10(3): 3969-3994.