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Estimated Testing, Tracing, and Vaccination Targets for Containment of the US Mpox Outbreak

Melanie H. Chitwood, MS; Jiye Kwon, MPH; Alexandra Savinkina, MSPH; Jo Walker, MPH; Alyssa Bilinski, MS, PhD; Gregg Gonsalves, PhD

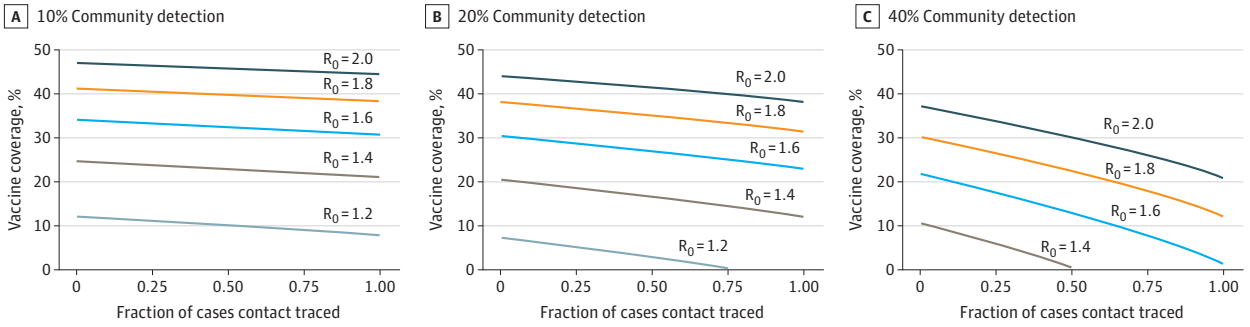
Introduction

As of November 2022, there have been more than 28 000 confirmed US mpox cases, predominantly among men who have sex with men (MSM).[1] Reducing transmission of mpox virus (hMPXV) is crucial to protect the health of MSM and reduce the risk of transmission in the general population. While testing, contact tracing, and vaccination can slow the spread of hMPXV, target levels of these measures have not been established. We aimed to estimate the levels of community testing, contact tracing, and vaccination required to reduce the effective reproduction number (R_t) of hMPXV to less than 1 for high-risk MSM (HR-MSM).

+ Supplemental content

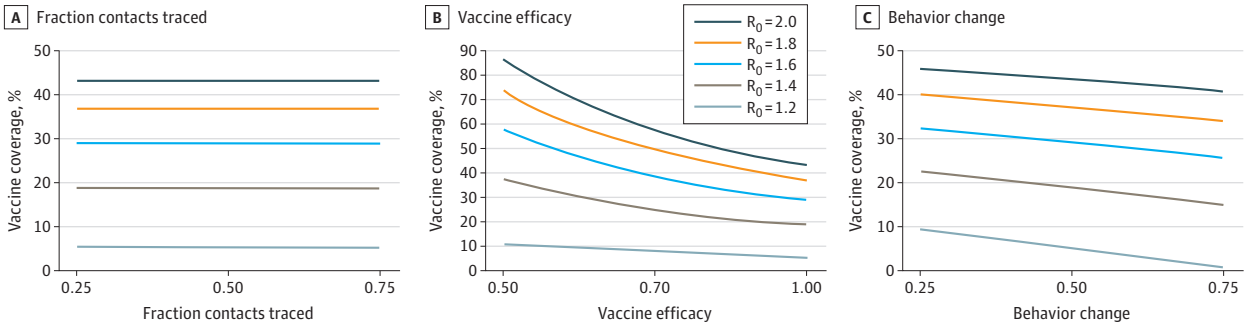
Author affiliations and article information are listed at the end of this article.

Figure 1. Frontier of Contact Tracing, Testing, and Vaccination Coverage to Reduce the Effective Reproduction Number to Less Than 1



The community detection rate varied across panels. Each line shows the efficient frontier for a given value of the basic reproduction number (R_O). Each point on the line can be interpreted as the minimum vaccination coverage at which the effective reproduction number remains less than 1 for a given value of R_O and contacts traced.

Figure 2. Association of Key Model Parameters With the Critical Threshold to Vaccinate



All panels assume a community detection rate of 20% and 25% of cases are contact traced. Each line shows the efficient frontier, describing the minimum vaccination coverage at which the effective reproduction number remains less than 1 for a given value of the basic reproduction number (R_O).

Methods

In this decision analytic model, we adapted a deterministic branching model to describe the transmission of hMPXV among HR-MSM[2] (eMethods and eFigure in Supplement 1). Infectious individuals are detected depending on the community detection rate and whether their source case underwent contact tracing (eFigure in Supplement 1). We assumed that community detection of a case reduced secondary infections by 50%, identifying a case early through contact tracing reduced secondary infections by 90%, and all detected cases have the same probability of being contact traced (eTables 1 and 2 in Supplement 1). We found the minimum level of vaccine coverage that would reduce R_t to less than 1, accounting for contact tracing and community detection. To reflect uncertainty in the basic reproduction number (R_0) in the HR-MSM population, we varied R_0 from 1.2 to 2.0.[3]

Analyses were conducted using R version 4.2.1 (R Project for Statistical Computing). This study does not qualify as human participant research; no institutional review board approval was sought, and informed consent was not required. The analysis follows relevant Consolidated Health Economic Evaluation Reporting Standards (CHEERS) reporting guidelines.

Results

We found that testing and contact tracing without vaccination can reduce R_t to less than 1 among HR-MSM if the R_0 is less than 1.4, at least 40% of cases are detected through community testing, and at least 50% of contacts are traced. With a moderate response (ie, ≥20% community detection; ≥25% of cases contact traced) the critical threshold to vaccinate ranges from 5% (R_0 = 1.2) to 43% (R_0 = 2.0) (**Figure 1**). In this scenario, 170 000 to 1.4 million full doses of the Modified Vaccinia Ankara-Bavarian Nordic vaccine (Bavarian Nordic) would need to be administered to 85 000 to 731 000 of the 1.7 million MSM who are eligible for preexposure prophylaxis (a proxy for HR-MSM) in the United States.[4,5]

The critical threshold to vaccinate was not sensitive to assumptions about the fraction of secondary cases detected through contact tracing (**Figure 2**A), but it was sensitive to assumptions about vaccine efficacy and the association of self-isolation with secondary infections. For example, if vaccine efficacy were 85%,[6] the critical threshold to vaccinate ranged from 6% (R_0 = 1.2) to 51% (R_0 = 2.0) in the moderate response scenario (Figure 2B). Similarly, as the association between self-isolation and secondary infections decreased, the critical threshold to vaccinate increased (Figure 2C).

Discussion

In this study, we simulated public health measures to reduce the spread of hMPXV in the United States. We found that the critical threshold to vaccinate depends on the R_0 of hMPXV and on public health measures. Rapid distribution of vaccinations to at least one-third of the HR-MSM population (at least 1.1 million doses), with increased testing and contact tracing, can support containment efforts in most modeled scenarios. Short-term behavioral changes, such as limiting intimate physical contacts, will support containment efforts but do not obviate the need for vaccination for long-term containment.

This analysis has several limitations. We estimated vaccine requirements assuming that sustained spread outside the HR-MSM population is negligible and vaccines are efficiently targeted to HR-MSM. Consequently, our estimates may represent a lower bound of doses needed. Furthermore, although we illustrated sensitivity of our results to variations in vaccine efficacy and reductions in secondary infections due to behavioral changes, these parameters remain uncertain. Overall, we believe this analysis provides a useful framework for quantitative targets toward hMPXV containment.

ARTICLE INFORMATION

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Corresponding Author: Melanie H. Chitwood, MS, Department of Epidemiology of Microbial Diseases, Yale School of Public Health, 60 College St, New Haven CT 06510 (melanie.chitwood@yale.edu).

Author Affiliations: Department of Epidemiology of Microbial Diseases, Yale School of Public Health, New Haven, Connecticut (Chitwood, Kwon, Savinkina, Walker, Gonsalves); Public Health Modeling Unit, Yale School of Public Health, New Haven, Connecticut (Chitwood, Kwon, Savinkina, Walker, Gonsalves); Department of Health Services, Policy, and Practice, Brown School of Public Health, Providence, Rhode Island (Bilinski); Department of Biostatistics, Brown School of Public Health, Providence, Rhode Island (Bilinski).

Author Contributions: Ms Chitwood had full access to all of the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis.

Concept and design: Kwon, Savinkina, Walker, Bilinski, Gonsalves.

Acquisition, analysis, or interpretation of data: Chitwood, Kwon, Savinkina, Walker, Gonsalves.

Drafting of the manuscript: Chitwood, Kwon, Savinkina, Gonsalves.

Critical revision of the manuscript for important intellectual content: All authors.

Statistical analysis: Chitwood, Kwon, Savinkina, Walker, Bilinski.

Supervision: Gonsalves.

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Data Sharing Statement: See Supplement 2.

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SUPPLEMENT 1.

eMethods.
eTable 1. Model Parameter Values
eTable 2. Estimation of Secondary Infections
eReferences.
eFigure. Model Schematic

SUPPLEMENT 2.

Data Sharing Statement

Supplemental Online Content

Chitwood MH, Kwon J, Savinkina A, Walker J, Bilinski A, Gonsalves G. Estimated testing, tracing, and vaccination targets for containment of the US mpox outbreak. *JAMA Netw Open.* 2023;6(1):e2250984. doi:10.1001/jamanetworkopen.2022.50984

This supplemental material has been provided by the authors to give readers additional information about their work.

Supplement

Methods

To describe the transmission of monkeypox virus (hMPXV) in a population of high risk men who have sex with men (HR-MSM), we adapted a deterministic branching model first developed for SARS-CoV-2[2]. The model by Bilinski et al. has compartments to account for detection at the asymptomatic, presymptomatic, or symptomatic stage. As transmission of hMPXV is presumed to only occur among symptomatic individuals[7], we removed the asymptomatic and presymptomatic states and transitions (Figure S1). We made additional changes to parameter values to account for the epidemiological differences between the two viruses (Table S1).

We use the model to assess three tools to reduce transmission of hMPXV: community detection, contact tracing, and vaccination. The model estimates the number of secondary infections arising from cases (Table S2). Cases can be detected either through community testing programs or as a result of contact tracing. Community testing identifies individuals once they are infectious; these individuals take measures to reduce their contacts by 50% over the infectious period. Contact tracing identifies individuals prior to the onset of infectiousness; these individuals enter quarantine and reduce their contacts by 90% over the infectious period. Undetected cases do not reduce their contacts and do not undergo contact tracing; the secondary infections arising from undetected cases can be detected through community testing only. All detected cases have the same probability of having their contacts traced. We estimated the rate of vaccination and contact tracing needed to lower R_t below 1, assuming community detection rates of 10%, 20%, and 40%.

Finally, we estimate the number of vaccine doses needed to support containment. Because the Jynneos vaccine requires two doses given at least four weeks apart[8], the number of doses needed is twice the number of individuals that need to be vaccinated. We make the simplifying assumptions that the Jynneos vaccine is 100% efficacious against infection, that protection is conferred immediately following the first dose, that no doses are wasted, and that doses are only given to HR-MSM. As a result, our estimates represent a lower bound on the number of doses needed in each scenario.

eTable 1 . Model Parameter Values

Parameter	**Value(s)**	**Source**
Probability of community case detection (k_c)	10%, 20%, 40%	Assumed
Probability of contact tracing case detection (k_t)	50%	Assumed
R0	1.2, 1.4, 1.6, 1.8, 2.0	(4)
Fraction of cases that are contact traced (p)	varies	Assumed
Duration of infectiousness (d)	21 days	(9)
Relative number of secondary infections from detected infections compared to undetected infections (q) ● note: this applies to cases that aren't contact traced but are detected through testing, as well as cases that are contact traced (all of which we assume are detected, see above). As a result, the overall transmissibility ratio $\frac{R_{contact\ traced}}{R_{not\ traced\ or\ otherwise\ detected}}$ is computed as the product of this parameter and $(1-\epsilon)$, see below	0.5	Assumed
Average daily rate of transmission for symptomatic cases not traced (b)	calibrated	
Additional reduction in secondary infections due to quarantine (ϵ, only applicable to cases that are contact traced)	80%	Assumed
Vaccination % (v)	Varies	

eTable 2. Estimation of Secondary Infections

Category	Formula
Not contact traced, detected	$r_{ND} = (1-v)bdq$
Not contact traced, undetected	$r_{NU} = (1-v)bd$
Contact traced, detected	$r_{TD} = (1-e)(1-v)bdq$
Contract traced, undetected	$r_{TU} = (1-e)(1-v)bd$

Where:

b= Average daily rate of transmission for cases not traced

d=duration of infectiousness

q=Relative number of secondary infections from detected infections compared to undetected infections

e=Isolation and quarantine efficacy

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eFigure. Model Schematic