

Role of behaviour change in controlling the 2022 Paris mpox outbreak

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The 2022 mpox outbreak led to a rapid case surge among men who have sex with men (MSM) in previously unaffected regions, followed by a sudden decline, whose drivers remain unclear. We developed a network model of mpox transmission among MSM based on sexual behaviour data, focusing on the Paris region epidemic. Our analysis tested three drivers for the decline: postexposure prophylaxis vaccination, immunity among highly active MSM and behavioural adaptations, either uniform in the population or based on individual risk factors. Behavioural changes adopted by 49% (95% confidence interval 47–51%) of MSM, regardless of risk factors, best explained the decline, preventing an estimated 68% (15–99%) of potential cases in summer 2022. To validate model predictions, we analysed data from the 2023 ERAS survey and found that 46% (45–48%) of MSM in the region reported reducing their number of sexual partners during that period—closely matching model estimates. In contrast, postexposure prophylaxis vaccination and immunity among highly active MSM were insufficient to halt the outbreak. Both model predictions and survey results underscore the role of widespread, spontaneous behavioural adaptations, regardless of risk profile, in driving the epidemic downturn. These findings highlight the importance of effective risk communication and community engagement in outbreak management.

The 2022 global outbreak of mpox marked an international public health crisis¹. Endemic in Western Africa, monkeypox virus clade II rapidly spread to Western Europe, then through Central and Southern Europe, to North America, Latin America and the rest of the world, driven largely by international travel and extensive underdetected dissemination². By 23 July 2022, with more than 23,000 cases reported in 94 countries, the World Health Organization (WHO) declared mpox a Public Health Emergency of International Concern. As cases surged worldwide, a major concern was the mode of transmission.

The spread of mpox in 2022 was indeed remarkably different from previous outbreaks. Unlike previous mpox outbreaks that remained

geographically limited to known endemic areas, the global outbreak predominantly affected men who have sex with men (MSM)³ and was largely associated with sexual transmission¹. A key factor driving the rapid dissemination was the heterogeneity of sexual networks in the MSM community. A small number of individuals with an exceptionally high number of sexual partners largely amplified the disease spread, creating conditions for sustained human-to-human transmission that led to explosive case growth^{2,4}.

However, the explosive rise was soon followed by a sudden decline in viral circulation. This occurred as countries were struggling to implement control efforts through vaccination and risk communication. It

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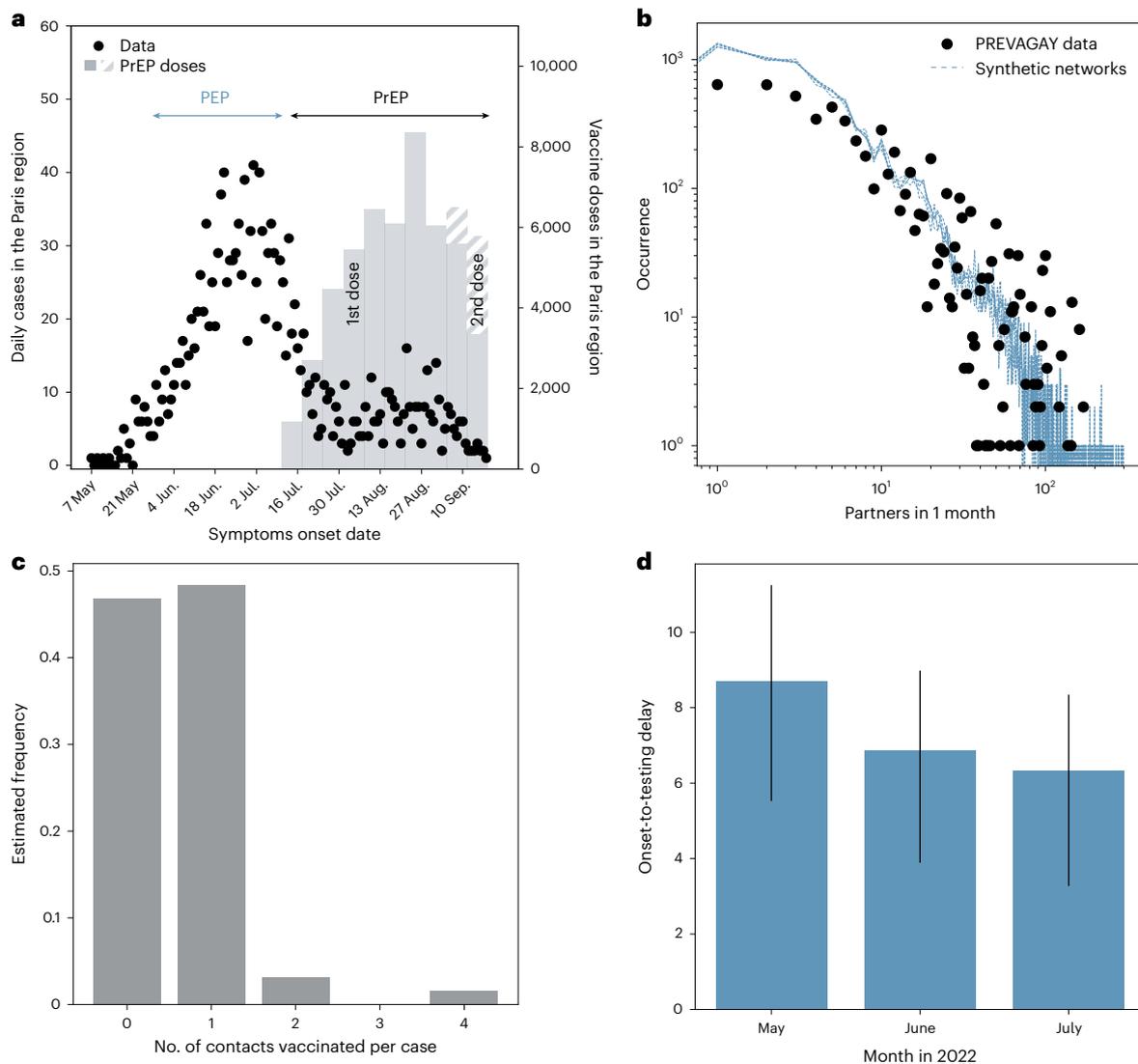


Fig. 1 | Surveillance, behavioural and vaccination data. **a**, Mpx cases in the Paris region from 7 May to 18 September 2022 (points, left y axis), together with 1st (solid bars) and 2nd (dashed bars) doses of PrEP vaccines in the Paris region (right y axis). **b**, Occurrence of the monthly number of sexual partners in the PREVAGAY survey and in five synthetic networks, in log–log scale. **c**, Frequency of

vaccinated contacts per mpx case estimated from contact tracing data. **d**, Onset-to-testing delay estimates by month. Fitted values and interquartile ranges of Gamma distributions estimated from onset-to-testing delays data ($n = 78$ for May, $n = 506$ for June, $n = 276$ for July).

remains uncertain whether these measures contributed to slow down the epidemic. Indeed, the rapid infection of highly active MSM could have already led to infection-induced immunity at the population level^{5,6} or individuals may have spontaneously avoided risk in response to public health messaging^{7,8}. The interplay between these factors is complex and context specific, with timing and impact varying across countries^{6,9–15}, depending on factors such as the time of first importations², vaccination campaign onset and resource availability. In France, vaccine postexposure prophylaxis (PEP) of contacts of confirmed cases began on 27 May, shortly after the first confirmed case on 19 May, but was initially limited to 802 doses over 45 days. Mass pre-exposure mpx vaccination (mpox PrEP, hereafter referred to as PrEP) only began after the epidemic had peaked, both nationally and in the Paris region (Île-de-France), where the peak occurred in late June (week 26, 27 June to 3 July). Public health communication campaigns targeting MSM intensified over this period¹⁶. Clarifying the roles of both public health efforts and individual actions is critical for developing more effective strategies for future outbreaks.

We developed a data-driven network model of mpx transmission to identify the drivers behind the observed decline in mpx cases among MSM during summer 2022. The study focused on the Paris region, which

reported the majority of cases in France (63% at the time of the peak) and has the largest MSM community in the country¹⁷. Our analysis tested three main drivers: PEP vaccination, infection-induced immunity and behavioural changes driven by different factors. Results were then validated with surveillance data and postoutbreak behavioural survey responses.

Results

To investigate the causes of the sharp decline in mpx cases among MSM in the Paris region during summer 2022, we developed a stochastic, data-driven network model of sexual transmission that integrated behavioural survey data, case surveillance and vaccination timelines. The model simulated mpx spread on dynamic networks constructed from sexual behaviour data and considered varying assumptions about transmission dynamics and sexual network topology, including degree assortativity and venue-based correlations. We tested three hypotheses to explain the observed epidemic decline. First, that PEP vaccination contributed to the downturn, which we evaluated by comparing epidemic trajectories with and without vaccination, based on real-world rollout data. Second, that the decline was consistent with infection-induced immunity as the sole driver, which we assessed by treating the

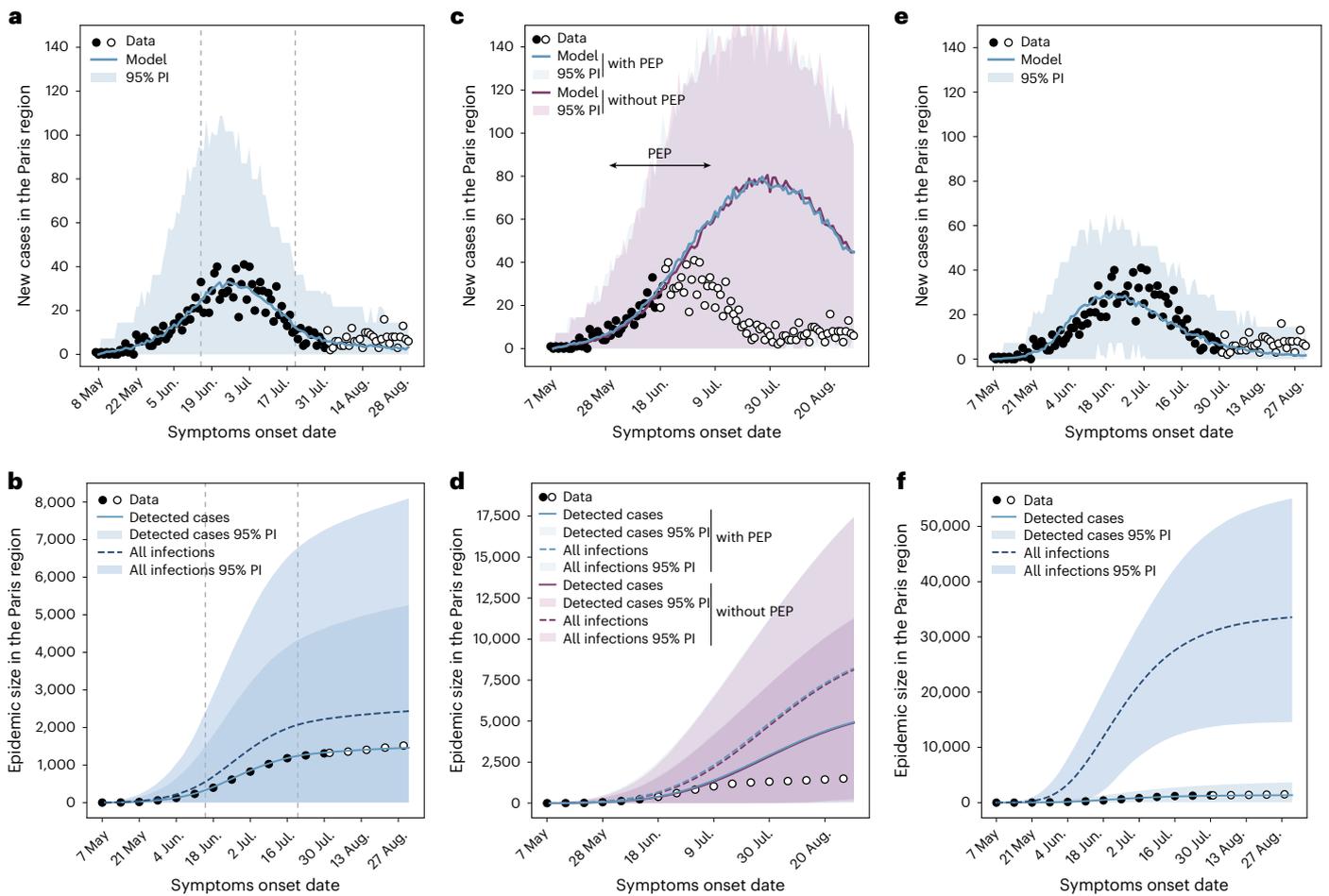


Fig. 2 | Model predictions for the three hypotheses. a, b, Mpx cases in the Paris region (filled points refer to the data used for inference) and model predictions under the behavioural change hypothesis, assuming homogeneous change of behaviour across MSM (best-fit model) showing reported new cases (a) and epidemic size (b). **c, d**, Data versus model predictions under the PEP vaccination

hypothesis, scenarios with and without PEP vaccination, new cases (c) and epidemic size (d). **e, f**, Data versus model predictions under the infection-induced immunity hypothesis, new cases (e) and epidemic size (f). All model predictions are presented as means with 95% PI (shaded areas) obtained from $n = 250$ stochastic runs.

level of case underdetection as a free parameter to explore the plausibility of extensive unobserved transmission. Third, that spontaneous behavioural adaptations were responsible, which we examined through three alternative mechanisms: a uniform reduction in sexual activity across the MSM population, reductions preferentially among the most sexually active or changes triggered by recent exposure to diagnosed cases. For each scenario, we fitted model outputs to surveillance data and used model selection criteria to determine the best explanation. Finally, we validated model predictions using independent behavioural data from the 2023 ERAS survey, which documented self-reported reductions in sexual activity during the outbreak.

Model and data

To simulate mpx transmission dynamics, we first constructed synthetic sexual contact networks reflecting the structure and heterogeneity of MSM partnerships in the Paris region. These time-varying networks were parameterized using behavioural survey data on age, number of sexual partners (Fig. 1b) and attendance at different types of commercial venues^{18,19}. By design, the networks incorporate venue-based correlations, as connections between individuals were only possible if they reported attending the same type of venue. This structure, directly derived from the data, reflects the increased likelihood of contact among individuals sharing the same sexual and social contexts. Mpx transmission on sexual contacts was modelled with a stochastic susceptible-exposed-infected-isolated-recovered scheme adapted to include case detection

(Supplementary Fig. 1). We considered the effect of smallpox vaccination, of the PEP vaccination given to contacts of cases from 27 May to 10 July (Fig. 1c) and of the PrEP vaccination starting on 11 July, according to data on vaccine doses administered and the vaccination guidelines defined by the Haute Autorité de Santé and Santé publique France^{20–22} (Supplementary Table 1). We used data on mpx cases obtained from Santé publique France (Fig. 1a), reporting on age, area of residence, dates of symptoms onset and testing, smallpox vaccination status and self-identification as a MSM (91% of answering cases). Based on a total of 996 mpx cases with complete data for the period of May to August 2022, we estimated a reduction of the mean onset-to-testing delay from 8.7 (interquartile range 5.5–11.2) days in May to 6.9 (3.9–9.0) days in June, and 6.3 (3.3–8.3) days in July (Fig. 1d). The decreasing trend was confirmed through an analysis of variance test ($P < 10^{-6}$).

Drivers of the outbreak decline

To understand which factors contributed to the observed decline in mpx cases, we simulated the epidemic under three distinct hypotheses, each grounded in a different potential mechanism of epidemic control. For each hypothesis, we defined a specific modelling and fitting strategy aligned with the nature of the assumed driver—vaccination, immunity buildup or behavioural adaptation. We then compared simulated outcomes to observed case data and assessed model performance using information criteria to determine which scenario best reproduced the epidemic trajectory.

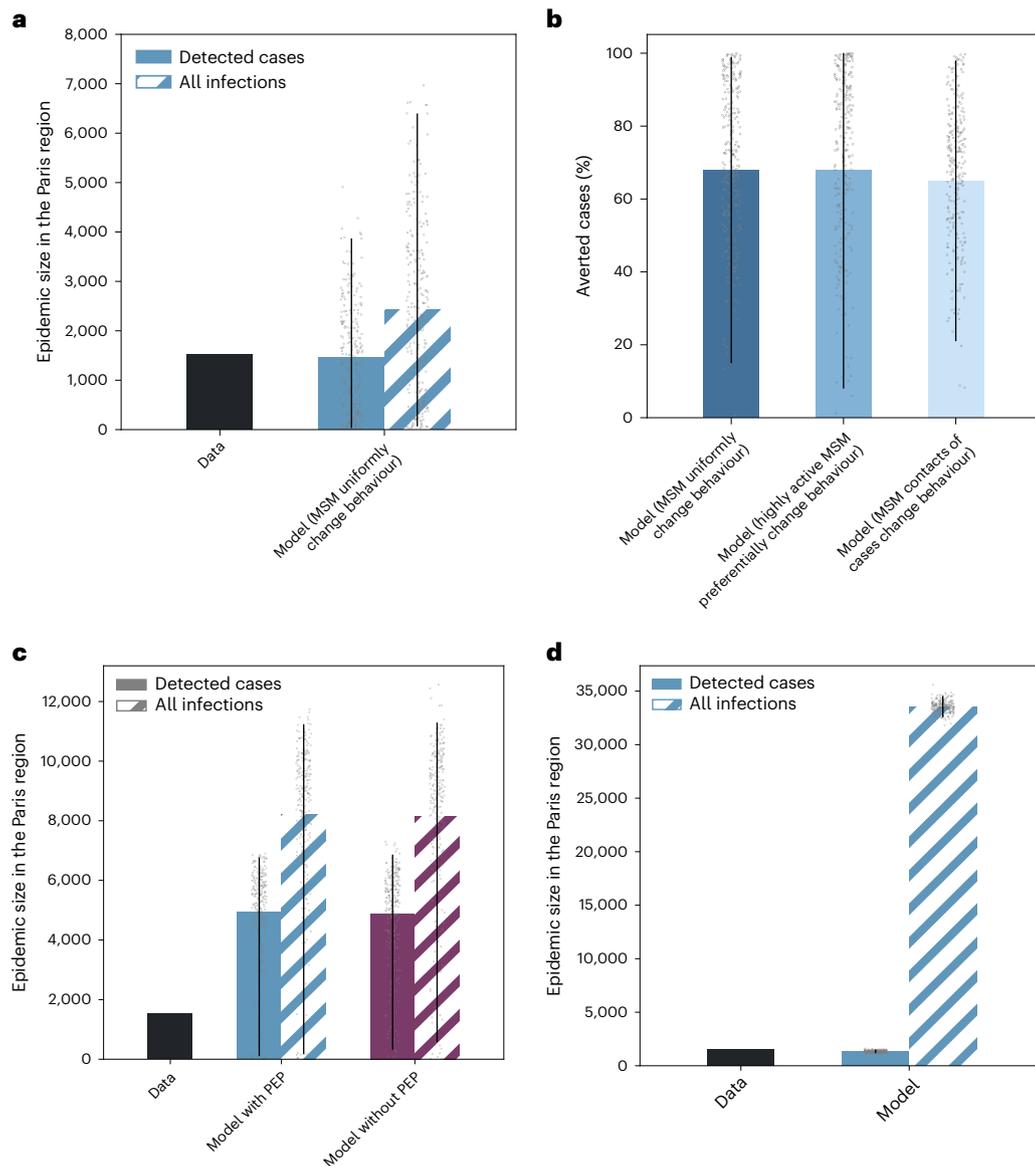


Fig. 3 | Epidemic size and averted cases. **a**, Epidemic size in the Paris region on 31 August 2022, data versus model predictions in the behavioural change hypothesis, assuming homogeneous change of behaviour across MSM (best-fit model). **b**, Predicted percentage with 95% PI of averted mpox cases in the Paris region from 7 May to 31 August 2022 for the three assumptions considered under the behavioural change hypothesis. Predicted percentages were computed

averaging over $n = 250$ stochastic simulations (grey points). **c**, As in **a**, data versus model predictions with 95% PI under the PEP vaccination hypothesis, showing the two cases with and without PEP vaccination. **d**, As in **a**, data versus model predictions under the infection-induced immunity hypothesis. Model predictions are presented as means with 95% PI obtained from $n = 250$ stochastic runs (grey points).

For the PEP vaccination hypothesis, we fitted only the early rise of cases and then compared simulations with and without vaccination to assess its impact. For the infection-induced immunity hypothesis, we fitted the full epidemic curve—including the vaccination phase—by treating the detection probability as a free parameter to capture the potential contribution of undetected infections to population-level immunity. For the behavioural change hypothesis, we considered three patterns of behavioural adaptations among uninfected and unvaccinated MSM: uniform reductions in sexual activity across the population, reductions concentrated among the most sexually active or reductions triggered by recent exposure to diagnosed cases. In this case, model fitting was conducted in two steps: we first estimated baseline transmission by fitting the early rise of the epidemic, and then second calibrated the extent and coverage of behavioural change using the observed decline. Behavioural changes were assumed to occur from mid-June to mid-July, with specific dates selected through the Akaike Information Criterion (AIC).

Among all drivers, the model that best explained the observed epidemic decline considered a uniform reduction in risk across the MSM population. It closely matched the observed epidemic curve (Figs. 2a,b and 3a), reproducing peak time, magnitude and epidemic size. It estimated that 49% (95% confidence interval (CI) 47–51%) of MSM reduced their sexual contacts by 93% (95% CI 86–98%). This adaptation, occurring gradually between 15 June and 20 July (Table 1), led to a 39% (95% prediction interval (PI) 35–41%) reduction in sexual contacts, ultimately driving the epidemic decline. By comparing the best-fit model simulations to those without behavioural changes, we found that risk reduction prevented 68% (95% PI 15–99%) of mpox cases during the study period (Fig. 3b). The infection dynamics from the best-fit model showed rapid progression, particularly among highly active MSM early in the epidemic. Despite representing only 0.4% of the MSM population, individuals with over 100 sexual contacts per month accounted for 6% (95% PI 0–13%) of early cases, declining to 4% (95% PI 0–13.5%) in the later phase (Extended Data Fig. 1a). We found

Table 1 | Fit results of behavioural change models

Model	MSM changing behaviour (% of the MSM population)	Reduction in sexual activity	Avoided sexual contacts	Averted cases	Period of behavioural changes	AIC
MSM uniformly changing behaviour	49% (47–51%)	93% (86–98%)	39% (35–41%)	68% (15–99%)	15 June–20 July	413.25
Highly active MSM preferentially changing behaviour	19% (17–25%)	96% (82–100%)	41% (35–44%)	68% (8–100%)	21 June–26 July	430.62
MSM contacts of cases change behaviour	8% (0.4–13%) ^a	100% (95–100%)	28% (2–42%)	65% (21–98%)	21 June–2 August	452.34

^aFor this model, we fitted the percentage c of the contacts of mpox cases and obtained $c=100%$ (95–100%), resulting in the percentage of the MSM population reported. Models are ranked by increasing AIC. Data in the columns of ‘MSM changing behaviour’ and ‘Reduction in sexual activity’ are fit estimates with 95% CI; data in the columns ‘Avoided sexual contacts’ and ‘Averted cases’ are means with 95% PI obtained from $n=250$ independent stochastic runs.

that 17% (95% PI 0–72%) of these highly active individuals were infected at peak time. The predicted mean age of mpox cases increased from 33 years (95% PI 20–57) in May to 38 years (95% PI 20–63) in July (t -test $P < 10^{-6}$), aligning with surveillance data (Extended Data Fig. 1b). Simulations estimated that 25% (95% PI 5–53%) of mpox cases occurred in individuals vaccinated against smallpox, consistent with surveillance data (Extended Data Fig. 1c).

To validate our model selection, we analysed responses from the 2023 ERAS survey²³, a behavioural survey that collected self-reported data on sexual activity, health and mpox-related behaviours among MSM in France (Methods). The analysis showed that 46% (95% CI 45–48%) of MSM in the Paris region reported reducing their sexual partners during summer 2022, aligning closely with our model prediction (Fig. 4a). Importantly, in the survey response data we found no significant correlation between sexual activity levels and individual risk-reduction behaviours ($P = 0.3$), further supporting our model ability to capture behavioural changes across different activity levels (Fig. 4b). In contrast, the two rejected behavioural models did not align with observed behavioural patterns. The first model, which assumed that highly active MSM were the primary drivers of behavioural change, required only 19% (95% CI 17–25%) of MSM to reduce sexual contacts to achieve epidemic control (Table 1 and Extended Data Fig. 2). However, this underestimated the community-wide behavioural change indicated by survey data (Fig. 4a). The second model, which attributed behavioural changes to recent contacts of detected cases, predicted an even more modest adaptation (8%, 95% PI 0.4–13%, Table 1 and Extended Data Fig. 3). Both models failed to reproduce the change of behaviour reported by survey respondents with fewer than 50 partners per month (Fig. 4c,d).

Next, we examined the role of PEP vaccination, testing whether it alone could explain the epidemic decline. Simulations with and without PEP vaccination yielded identical epidemic trajectories (Fig. 2c), confirmed by a chi-square test ($P = 1.0$). This suggested that PEP vaccination had no significant impact on the epidemic trajectory. Most importantly, the model failed to replicate the observed incidence of cases, predicting a delayed peak by 29 days (95% PI 1–57) and a 3.5-fold higher incidence (95% PI 0.3–5.6). By 31 August, the model predicted 4,939 (95% PI 104–6,773) detected mpox cases, corresponding to 8% (95% PI 0.2–10%) of the MSM population—3.2 times higher than observed (Figs. 2d and 3c). Even a lower detection probability ($P_d = 20%$)—which would imply more undetected infections and higher natural immunity—could not replicate the peak timing and magnitude, leading to a longer-lasting and higher epidemic wave (Extended Data Fig. 4). We also tested whether infection-induced immunity might have curbed the epidemic, assuming broader viral circulation than what was observed. This scenario allowed the model to estimate the proportion of undetected infections. While it provided a good fit to the epidemic curve (Fig. 2e), it required an implausibly low case detection rate of only $P_d = 4%$ (95% CI 4–5%) of the cases be reported. Under this scenario, 52% (95% PI 50–53%) of the MSM population in the Paris region—amounting to 33,561 individuals (95% CI 32,432–34,661)—would have had to contract mpox by the end of August (Figs. 2f and 3d).

Fitted values, estimated behavioural adaptations and AIC values are reported for each model in Supplementary Table 5.

Sensitivity analyses

We refitted the model with uniform behavioural changes among MSM to assess the impact of different assumptions explored in the sensitivity tests (Supplementary Table 6). We compared the results using the AIC (Supplementary Table 7). When considering a detection probability of $P_d = 80%$, the model produced similar performance and outputs (Extended Data Fig. 5c,d). In contrast, assuming $P_d = 20%$ or that the vaccine protected against both infection and transmission resulted in considerably worse fits (Extended Data Fig. 5a,b). If unrecognized mpox infections transmitted less than detected cases, a slightly smaller reduction in risk behaviour (84%, 95% PI 77–92%) was needed to explain the epidemic decline compared to the best-fit model (Extended Data Fig. 6). In addition, allowing smallpox-vaccinated MSM to also change their behaviour required a higher percentage of sexual contacts (52%, 95% PI 49–54%) to be avoided to reproduce the downturn, since some of these contacts were at lower risk of infection due to prior vaccination (Extended Data Fig. 7). Overall, the other sensitivity tests, including considering networks with a higher degree assortativity, showed no substantial changes in results and none improved the fit compared to the best-fit model (Supplementary Figs. 6–8).

Discussion

According to our analysis, a substantial change in behaviour in almost half the MSM in the Paris region was the key factor in curbing the 2022 mpox epidemic and triggering its decline. These findings agree with postoutbreak behavioural survey data. In contrast, our model indicated that implemented PEP vaccination or infection-induced immunity were insufficient to explain the early downturn of the outbreak.

The reduction in risk behaviour was likely due to heightened community awareness about mpox, as indicated by the shorter onset-to-testing period over time pointing to better disease recognition and treatment seeking. Our model identified 15 June 2022 as the onset for the progressive reduction in sexual contacts, in line with a wide-reaching communication campaign by authorities targeting the MSM community¹⁶. Without risk reduction, our analysis showed that the epidemic would have lasted longer and reached a substantially larger scale, peaking in late July with three times as many cases. About half the MSM were predicted to have reduced their sexual contacts in response to the outbreak—consistent with behavioural changes reported in 46% of MSM in the Paris region and 50% of MSM in Western Europe⁸. The model suggested a 90% reduction in sexual contacts by MSM, which may have resulted from several sources: a reduction in the number of partnerships⁸; the adoption of safer sex practices reducing transmission risk per contact—the WHO survey reported that 54% of respondents avoided drug use in sexual settings⁸, and modelling results estimated a 61–87% drop in sexual transmission in Italy¹⁵; or even being away from the region—21% of French mpox cases having travelled abroad in June or July 2022, for example²⁴. We found no evidence that change in behaviour

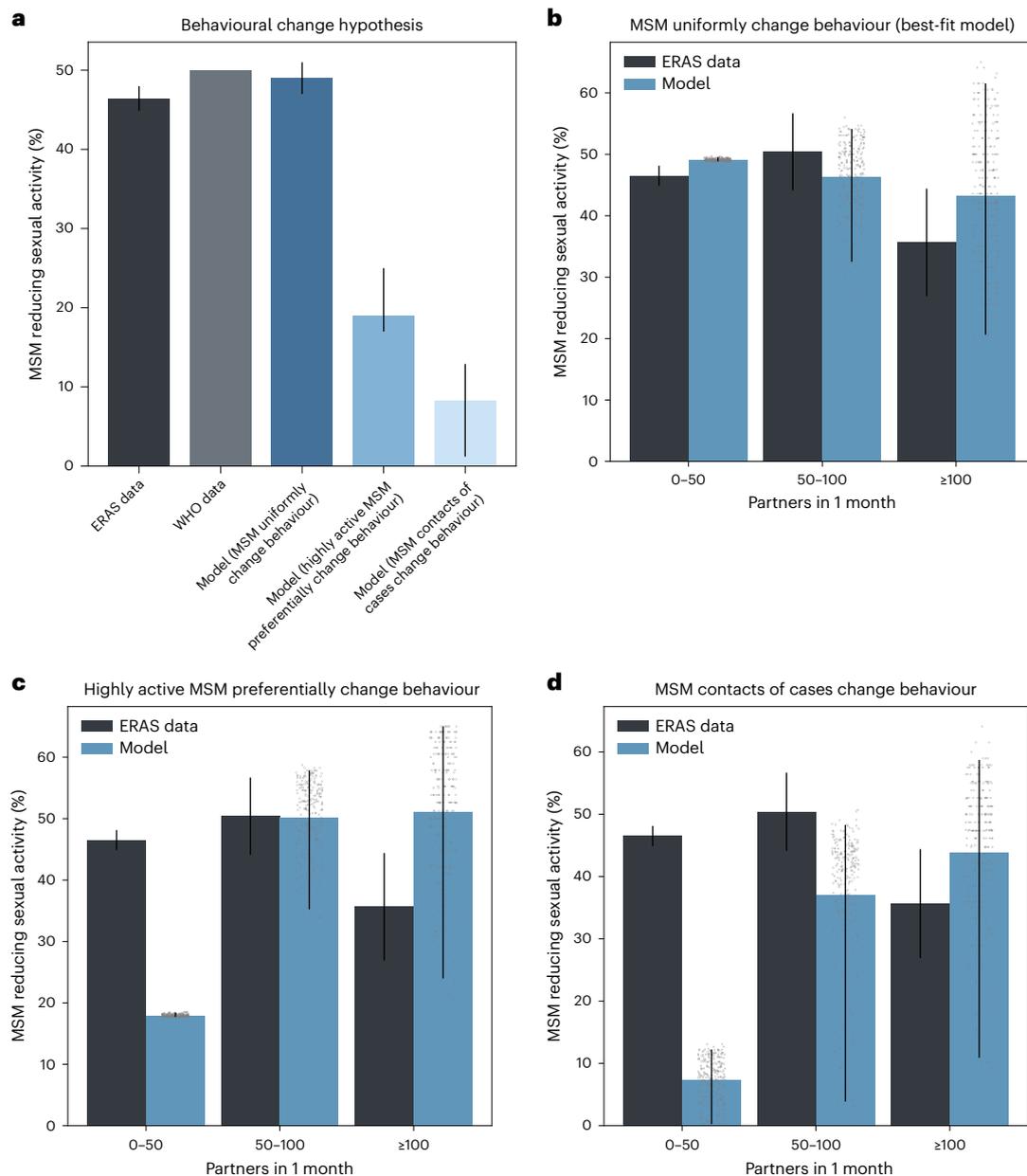


Fig. 4 | Change of behaviour. **a**, Percentage of MSM reducing sexual activity: survey data versus maximum-likelihood model estimates with 95% CI. CI in the data were computed as binomial proportion CI ($n = 3,965$ data points). **b**, Percentage of MSM reducing sexual activity stratified by the monthly number of partners: survey data versus model predictions in the assumption of uniform change of behaviour across MSM (best-fit model). Model predictions are

presented as means with 95% PI obtained from $n = 250$ stochastic runs (grey points). CI in the data were computed as binomial proportion CI ($n = 3,606$ for 0–50 monthly partners, $n = 244$ for 50–100 monthly partners, $n = 115$ for 100+ monthly partners). **c**, As in **b** in the assumption of a change of behaviour based on sexual activity. **d**, As in **b** in the assumption of a change of behaviour based on recent exposure to a diagnosed case.

was linked to high sexual activity or recent exposure to diagnosed mpox cases. Indeed, the observed proportion of MSM required to change behaviour under these hypotheses did not match that reported in the ERAS survey, especially among lower-risk individuals. ERAS data also showed no significant correlation between respondents' levels of sexual activity and their reduction in sexual partnerships during the 2022 mpox outbreak, further confirming that the adoption of risk-reducing behaviours was widespread throughout the community.

Surveillance data from France and other affected countries showed a rapid, explosive surge in cases early in the outbreak². This has been reported to be driven by the heavy-tailed distribution of sexual partnerships among MSM, where a small number of individuals have disproportionately many partners, and fuel the outbreak fast acceleration^{2,4,25}. Networks built from sexual behavioural survey data

reproduced the hierarchical spread of the outbreak²⁶, with highly active MSM accounting for a larger proportion of cases during the growth phase than in the decline (6% versus 4%), mirroring observed trends²⁴. While our analysis showed that about half of MSM reduced sexual contacts, we also found that reducing contacts in the most sexually active would have required only 19% of MSM reducing risk behaviour to yield the same impact on the outbreak. This suggests that prioritizing high-risk groups should be favoured, especially when vaccine supplies are limited. The large spontaneous change in behaviour may not be sustainable in the long term, beyond our study period, and individuals who initially altered their behaviour may eventually return to their previous activity levels. However, WHO data shows that 23% of MSM in Western Europe were still reducing their sexual activity 1 year later⁸, suggesting a lasting impact from the 2022 epidemic wave.

We found no measurable population-level impact from PEP vaccination. This likely stems from both the limited availability of doses early in the outbreak and the substantial operational challenges in implementing the strategy. Contacts could not be documented systematically for all cases: by 7 July 2022, contact tracing had been reported for only 145 of 656 diagnosed cases, and for nearly half of cases with available data, no contacts were ultimately vaccinated. Even when contacts were identified, 83% of vaccinated individuals received the dose beyond the recommended 4-day postexposure window²⁷, limiting its effectiveness. These findings suggest that access to diagnosis, low levels of declared contacts and delays in reaching vaccination centres hindered the impact of the PEP strategy. In contrast, once the epidemic declined, PrEP vaccination contributed to long-term control^{6,9,13,28} by protecting individuals before exposure and overcoming many of the logistical challenges seen with PEP implementation.

International reports on the mechanisms responsible for the 2022 mpox epidemic decline showed different results. Our findings differ markedly from previous work suggesting that the accumulation of immunity among highly active MSM drove the observed epidemic fadeout globally⁵. Here we found that only 17% of highly active MSM were predicted to be infected before the epidemic peak, although they contributed a disproportionate share to infected cases (6% of cases despite representing only 0.4% of the population). For saturation to explain the course of the epidemic, our model required that approximately half of the entire MSM community would have been infected by summer 2022, corresponding to only 4% of cases being detected. While detection probabilities during the 2022 mpox outbreak remain undetermined in France, estimates from similar countries^{15,29,30} range between 60% and 80%. We used a 60% detection probability³⁰ as a reference value and found that increasing it to 80% produced similar results and model fit. Lowering the detection probability to 20% in our model led to a considerably worse fit of the observed wave. Taken together, these results indicate that behavioural adaptation primarily drove the epidemic decline, with only secondary contribution of infection-induced immunity.

Substantial behavioural adaptations are consistent with results from two modelling studies on the UK outbreak^{9,13}. They estimated that the epidemic decline resulted from 45% reduction in the sexual partner rate in one model¹³, and from a 40% decrease in the transmission rate in another⁹. These estimates are close to the 39% reduction in sexual contacts resulting from our best fit, although the second study also acknowledges an important role of infection-induced immunity. In the Netherlands, even if the epidemiological situation (1,000 cases by 8 August³¹) was similar to that in the Paris region (1,357 cases by the same date), behavioural changes were not as instrumental to the reduction in cases, given that a reduction by 15–20% was sufficient to account for the decline⁶. Two studies in the USA found that PrEP vaccination and behavioural changes together prevented between 64% and 84% of cases^{12,14}. However, the mpox outbreak started later in the USA and peaked in mid-August², whereas the PrEP vaccination campaign had begun on 26 June. This gave the USA ample time for postvaccine collective immunity to considerably protect the population and contribute to the epidemic decline. Although both studies recognize the role of behavioural adaptations, it was less important than in the French context where PrEP started well after the decline.

This study presents some limitations. First, we did not model presymptomatic transmission³², similarly to other modelling studies^{9,13,14}. Asymptomatic transmission was addressed by including undetected milder cases and testing lower transmissibility in our sensitivity analyses, without altering our main findings. Second, we assumed a constant detection probability over time. As a result, part of the estimated behavioural change could be due to an increased detection rate over time. However, our findings on behavioural change are supported by postoutbreak survey data and hold in the range 60% to 80% for case detection, estimated for other countries^{11,30}. Third, ERAS is based on a

convenience-based sample recruited online and through social media, as is often the case for surveys related to MSM³³. The findings from this survey may not fully represent the experiences of everyone in the community. Fourth, our networks constructed from sexual behavioural survey data are not degree assortative. However, sensitivity analyses increasing degree assortativity levels showed no impact on the results. By contrast, venue-based correlation is intrinsic to the network construction—derived from co-attendance to specific venue types—and reflects the increased likelihood of connection among individuals sharing the same sexual and social contexts. Finally, our three scenarios for sexual contact reduction did not cover all possible nuances. Better documenting these aspects could be the objective of future surveys.

Our findings highlight the critical role of adaptive community behaviour in successfully controlling outbreaks like mpox. This is especially relevant during periods when vaccination coverage is still increasing³⁴. It underscores the power of effective risk communication as a cornerstone of outbreak management, particularly when targeting highly-vulnerable communities. In the ongoing mpox crisis^{1,34,35}, as new waves of infection caused by clade I, vaccine distribution challenges and transmission across various settings persist, these insights are yet more vital. Empowering communities with timely, clear and accessible information can drive substantial behavioural changes that, when combined with vaccination efforts, can substantially reduce transmission. Future public health strategies for emerging pathogens must prioritize a dual approach: fostering behavioural adaptations while accelerating and expanding vaccine access to ensure both short-term mitigation and long-term epidemic control.

Methods

MSM definition

MSM refers to all men who engage in sexual relations with other men. The words ‘men’ and ‘sex’ are interpreted differently in diverse cultures and societies and by the individuals involved. Therefore, the term encompasses the large variety of settings and contexts in which male-to-male sex takes place, regardless of multiple motivations for engaging in sex, self-determined sexual and gender identities, and various identifications with any particular community or social group³.

Mpox surveillance data

Data on the mpox outbreak were reported to Santé Publique France³⁶ (French Public Health Agency), including age, area of residence, dates of symptoms onset and testing, smallpox vaccination status and self-identification as a MSM (91% of answering cases). We accessed surveillance data for the Paris region, which included 1,616 mpox cases with symptoms onset or testing dates between 7 May and 22 September 2022 (Fig. 1a). Among these, 33 cases had missing or misreported symptoms onset dates, but valid testing dates. For these, we imputed symptoms onset dates from the onset-to-testing delay obtained from cases with complete data (Supplementary Table 2 and Supplementary Fig. 2). During the study period from 7 May to 31 August, 1,530 cases were included in the analysis, 30 with imputed onset dates.

Vaccination data

Smallpox vaccination in France was mandatory until 1979. Therefore, all MSM in the synthetic network born up to 1979 (47% of the population) were considered vaccinated against smallpox. The efficacy of first-generation vaccines against developing mpox was originally estimated as 85% (ref. 37). Part of the protection, however, may have been lost throughout the years. In this work, we considered a vaccine effectiveness of 71%, recently estimated for France³⁸, and the case of a vaccine effectiveness of 85% was tested for sensitivity.

During the 2022 outbreak, the third-generation Modified Vaccinia Ankara smallpox vaccine Imvanex (called Jynneos in the USA) was used against mpox in France²⁰. Data on third-generation vaccine doses administered in the Paris region in the study period included PEP doses

for at-risk contacts from 27 May to 10 July, and PrEP doses starting on the 11 July (Fig. 1a). There were two phases of the vaccination campaign, as reported in Supplementary Table 1. In the first phase starting on 27 May 2022²⁰, vaccines were offered to at-risk contacts of detected cases as PEP due to limited resources. The Haute Autorité de Santé indicated to administer the vaccine in the first 4 days following the at-risk contact and no later than 14 days^{21,22}. A total of 468 PEP vaccine doses were administered in the Paris region between 27 May and 10 July. We modelled the PEP vaccination process by randomly selecting and vaccinating a number n of contacts established by mpox cases within the preceding 14 days. The value of n was sampled from the distribution of vaccinated at-risk contacts per detected case, estimated from available contact tracing data (Fig. 1c). During the initial PEP phase, contact tracing coverage was limited and the vaccination campaign had programmatic difficulties. Contacts were reported for only 145 of 656 diagnosed cases by early July, and among 64 cases with available vaccination data, 47% had no contacts vaccinated. The median number of reported at-risk contacts was two per case (Supplementary Fig. 3), likely an underestimate. To account for these limitations, we ensured that all PEP doses distributed in the Paris region during this phase were administered to case contacts in the simulation.

Owing to the limited dose availability in the PEP phase, we considered that only MSM not vaccinated against smallpox could receive the PEP vaccination. We considered 89% vaccine effectiveness 14 days after administration, derived from studies conducted in Spain^{39,40} and the USA⁴¹. A recent meta-review largely reduced the estimate of the effectiveness of PEP vaccination to 20% (ref. 42). This does not impact our conclusions, since in our results we did not find a measurable population-level impact of the PEP vaccination even with the higher estimate used in our study.

In the second phase starting on 11 July²¹, vaccines became available on a voluntary basis as PrEP. The Haute Autorité de Santé recommended the vaccination of individuals at risk, prioritizing multipartner MSM, transgender individuals and sex workers. In our simulations, we administered the vaccines according to the data on the distributed number of doses per week. Vaccine effectiveness 14 days after administration was set to 78% according to available estimates^{40,43}.

PREVAGAY survey, time-varying sexual contact network construction and MSM population estimate

We used data from the 2015 PREVAGAY survey of sexual behaviour and HIV serostatus conducted among MSM in France^{18,19}. The survey was designed to include MSM only, where MSM were self-declared. MSM were eligible if they were at least 18 years old, had sex with men in the previous 12 months, and could read and speak French. A total of 2,646 MSM reported sociodemographic data, such as age and place of residence, and sexual habits, in terms of number of sexual partners and attendance at MSM commercial venues. We used data from the 1,089 MSM living in Paris. Of these respondents, 44% declared having more than 10 sexual partners in the previous month, and 8% declared more than 50 partners. Survey participants were asked to indicate if they attended gay venues in the past 12 months, including bars and clubs without sex, saunas with sex, backrooms or darkrooms, clubs or sex clubs and if they used internet dating sites or geolocalized gay dating apps.

From PREVAGAY data, we built stochastic time-varying networks of sexual contacts among MSM in the Paris region¹⁸. In this approach, MSM are represented by nodes in the network and time-varying sexual partnerships are represented by edges connecting two MSM and changing every day. Data allowed the reporting of sexual contacts occurring in specific venue types (for example, saunas, backrooms, clubs and online dating) that we combined in a single network. We simulated partnerships in a synthetic population of 10,000 MSM, assigning to each MSM the following features taken from the PREVAGAY data according to sampling weights: age, monthly number of

sexual partners and information on his attendance or not at each venue type. We interpreted sexual contacts reported in the survey as single-day partnerships in our daily sexual contact networks. For each venue type, network realizations were generated by sampling from power-law distributions fitted to the venue-specific reported number of monthly sexual partners. Power-law distributions provided a better fit than Weibull alternatives (Supplementary Table 3). The distribution of the monthly number of sexual contacts of the generated networks is shown in Fig. 1b and in Supplementary Fig. 4 for the venue-specific plots. The fit is poorer when stratifying per venue, and this is likely to be influenced by rounding in self-reported partner numbers. Specifically, the network was constructed by assigning a number of monthly partners to each MSM for each venue type by sampling the corresponding fitted power-law distribution 6 times, representing 6 months. To preserve the individual sexual behaviour over time, the sampled numbers were sorted and assigned to individuals in the same order each month. We distributed the partners over time according to a multinomial distribution over the days of each month. We then generated the time-varying network corresponding to the sequence of 180 daily occurring partnerships in the MSM population using the configuration model⁴⁴, pairing MSMs according to date and place of encounter^{18,45}. The networks incorporated venue-based correlation, as individuals could only be connected if they reported attending the same type of venue. However, they were not degree assortative, therefore we also tested alternative versions of the sexual networks imposing a certain level of degree assortativity. To take into account variability in the network building, we considered 5 stochastic realizations of the sexual network, and we confirmed the robustness of results to specific realizations of the network by considering 50 network configurations (Supplementary Fig. 9).

The synthetic population of 10,000 MSM is a scaled representation of the estimated 65,000 MSM in the Paris region (26% of the estimated 250,000 multipartner MSM in France^{21,46}). To compare simulation outputs to observed data—such as reported case counts or vaccine doses administered—we rescaled model outputs by a factor of 6.5 to align with the total target population size.

Degree-assortative sexual contact networks

The sexual contact networks generated from PREVAGAY survey data are not degree assortative—that is, nodes do not preferentially connect with others of similar degree. To explore the potential impact of assortative mixing, we applied a rewiring algorithm to increase degree assortativity while preserving the daily degree distribution (Supplementary Fig. 5). The algorithm was applied independently to each day of the temporal networks, ignoring venue information. The steps of the algorithm can be summarized as follows. For each pair of connected nodes A and B, we define a distance $d(A, B) = |k_A - k_B|$ where k_A and k_B are the degrees of node A and node B, respectively. All connected pairs are sorted by decreasing distance. Starting from the top of the list (pair (A, B)), the algorithm searches for another connected pair (C, D) satisfying the following conditions:

- A, B, C and D are all distinct nodes
- Links (A, D) and (B, C) do not already exist
- Rewiring reduces the degree distance:
 $d(A, B) + d(C, D) > d(A, D) + d(C, B)$

When a pair is found, links (A, B) and (C, D) are replaced by (A, D) and (C, B). This process is repeated iteratively. The algorithm stops when the variance in the last 10 assortativity values falls below 10^{-20} , indicating convergence.

ERAS 2023 survey

Since 2017, Santé publique France has conducted a web-based Enquête rapport au sexe [relation to sex] survey called ERAS once every 2 years to monitor the use of different means of HIV prevention among MSM in

France²³. The 2023 edition was conducted from 24 February to 6 April 2023. Participants were recruited via a variety of digital media. Banners were posted directly on geolocated gay dating applications and gay affinity information sites. They were also posted on social networks, targeting profiles similar to those of visitors to the Sexosafe prevention website²³. The inclusion criteria for participation were being male and 18 years of age or older. The survey included questions about registered sex at birth, gender, sexual orientation definition and number of sexual partners in the past 6 months (male, female and transgender male or transgender female). The survey had 23,502 respondents, 3,965 (16.9%) of whom were multipartner MSM living in the Paris region. We restricted our analysis to this subset. The survey was divided into four main sections: sociodemographic characteristics, lifestyle and socialization data, health data, and sexual and preventive behaviour over the last 6 months and during the last sexual encounter. In addition, the survey asked respondents whether they reduced their sexual activity in the summer of 2022 during the mpox epidemic. Participants were also asked whether they were diagnosed with mpox.

Ethics statement

All surveillance data were anonymized before use. Surveillance was considered as noninterventional research only requiring the nonopposition of the patient (article L1211 of the French public health code).

The PREVAGAY study was authorized by the Comité de protection des personnes Île-de-France IX (no. 2014-A01605-42). The ERAS study was approved by Inserm’s Ethics Evaluation Committee (IRB00003888 avis no. 23-989). Participants in both studies gave their informed consent.

Mpox transmission model

We described mpox transmission on the network of sexual contacts among MSM using a stochastic susceptible-exposed-infected-isolated-recovered agent-based model, adapted to include case detection. A susceptible individual (S) establishing a sexual contact with an infectious individual can contract the infection with a given probability (transmissibility β) per sexual contact. Following infection, the individual becomes exposed (E) but cannot yet transmit. After the latency period, he becomes infectious entering one of the two following infectious compartments: I_d if detected with detection probability P_d , or I (undetected) otherwise. The detection probability P_d was fixed to 60% (ref. 30) and varied for sensitivity ($P_d = 20\%, 80\%$), except when testing the infection-induced immunity hypothesis where P_d was fitted. After the onset-to-testing period, I_d enters isolation (Q) where we assumed he abstains from any sexual contact, therefore preventing further transmission. After the infectious period or the isolation phase, the individual enters the recovery state (R, R_d), becoming fully immune to the disease. The model was stratified to account for smallpox vaccination status at the start of the simulations, rolling vaccination over time in the study period for both vaccine PEP and PrEP. The model is illustrated in Supplementary Fig. 1 and was informed with the parameter values reported in Supplementary Table 4.

Adaptive behaviour models

We explored three models of behavioural changes in uninfected and unvaccinated MSM: uniform changes across the population, changes based on sexual activity or triggered by recent exposure to diagnosed cases. Adaptive changes were modelled from mid-June to mid-July 2022, with the reduction lasting through the study period. We tested 9 periods starting on 15 June, 18 June or 21 June 21, lasting 4 to 6 weeks. The reduction level r and the percentage c of MSM reducing contacts were estimated by fitting each model to the epidemic decline. The models differed in how MSM were selected and in the definition of the percentage c . In the first two models we considered that a daily percentage of MSM adapted their behaviour, resulting in a gradual change in the population reducing their risk, amounting to an overall

percentage c of MSM. MSM were chosen with a uniform probability in the population in the first model, and with a probability proportional to their sexual activity in the second model. The third model instead was based on exposure to detected cases. We assumed that a percentage c of MSM who had a sexual interaction with a case in the 14 days prior to the case detection reduced their sexual activity. MSM were chosen uniformly among case contacts.

Inference framework

We simulated a population of 10,000 MSM and rescaled it to match the Paris region population of 65,000. We averaged over 250 stochastic simulations to compute the expected epidemic curve and fitted the model to observed case counts through a (pseudo-) likelihood approach⁴⁷, described here.

Y_t was used for the observed daily incidence of mpox cases that we consider as the observed data, X_t for the variables describing the status of the population over time (t) and θ for the parameters to be estimated. In our model, the distribution of Y_t is specified by $P(Y_t | X_t)$; it is a compound binomial, as new cases arise as a proportion of all infected or susceptible pairs that are linked in the contact network at a given time. We approximated this binomial distribution by a Poisson distribution, which is appropriate since incidence remains small with respect to the size of the simulated population:

$$P_\theta(Y_t | X_t) \sim \text{Poisson}(Y_t | H(X_t, \theta))$$

where $H(X_t | \theta)$ is the expected incidence computed in the model. Likewise, given that the epidemic process is Markovian in discrete time, $P_\theta(X_t)$ is specified by the initial state $P_\theta(X_0)$ and the conditional probabilities $P_\theta(Y_j | X_{j-1})$, $1 \leq j \leq t$.

The log likelihood of the observed incidence up to time T can be computed as follows:

$$\begin{aligned} \log P_\theta(Y_1, \dots, Y_T) &= \int_{X_0, \dots, X_T} \log P_\theta(Y_1, \dots, Y_T | X_1, \dots, X_T) \\ &\prod_{1 \leq t \leq T} P_\theta(X_t | X_{t-1}) P(X_0) dX_0 \dots dX_T = \int_{X_0, \dots, X_T} \sum_{1 \leq t \leq T} \log \text{Poisson} \\ &(Y_t | H(X_t, \theta)) \prod_{1 \leq t \leq T} P_\theta(X_t | X_{t-1}) P(X_0) dX_0 \dots dX_T \end{aligned}$$

that is, averaging over all trajectories compatible with observed incidence. The integral can be approximated by the Monte Carlo method as:

$$\frac{1}{k} \sum_{1 \leq k \leq K, 1 \leq t \leq T} \log \text{Poisson}(Y_t | H(X_t^k, \theta))$$

where X_t^k are a set of K trajectories obtained by simulation under $P_\theta(X_t)$.

Last, we approximate this quantity to the first order as

$$\sum_t \log \text{Poisson}(Y_t | H^*(X_t | \theta))$$

where

$$H^*(X_t) = \frac{1}{K} \sum_{1 \leq k \leq K} H(X_t^k, \theta)$$

that is, we replace the average probability over individual trajectories by the probability of the mean trajectory.

Therefore, the algorithm for the likelihood estimation works as follows: (1) first obtain the mean incidence over time by averaging 250 trajectories simulated with the model; then (2) use Poisson distribution to compute the likelihood. As we had at maximum two free parameters, we performed a grid search to find the maximum likelihood, using a quadratic approximation to smooth the response surface and locate the maximum.

The number of fitted parameters depended on the hypothesis considered. In all cases, we fitted the rate of transmission per sexual contact (β) and the date of introduction of 10 seeds (t_0), explored between 6 May and 20 May. For the PEP vaccination hypothesis, the fit was performed on the early case rise up to 18 June, for simulations with and without vaccination. We associated likelihood ratio 95% CI to the estimate of β . For the infection-acquired immunity hypothesis, we fitted the model to the full epidemic curve and estimated P_d as well, associating 95% bootstrap CI to their estimates. For behavioural changes, we first fitted β and t_0 on the early rise (with likelihood ratio 95% CI), then estimated c and r (as described earlier) on the remaining trajectory—maintaining β and t_0 fixed. When the parameter set corresponding to the maximum likelihood was on the border of the domain we took it as the maximum likelihood estimate (MLE). In this case, we computed the likelihood ratio 95% CI rounded to the closest points of the explored grid. Otherwise, we associated to the estimates of c and r a 95% bootstrap CI.

The best-fit model was determined using AIC. Simulations without change in behaviour served as a counterfactual.

Sensitivity analysis

We conducted a total of seven sensitivity analyses. They were performed on the hypothesis and assumption of the best-fit model, that is under the behavioural change hypothesis assuming a homogeneous change of behaviour, to assess how these aspects impact the results of the best-fit model.

- (1) Detection probability. The model was parameterized with a detection probability $P_d = 60\%$ estimated for Portugal³⁰ (except when evaluating the infection-acquired immunity hypothesis where P_d was fitted). In absence of an estimate specific for France, we repeated our analyses with a lower ($P_d = 20\%$) and a higher ($P_d = 80\%$) probability of detection.
- (2) Asymptomatic infections. Our model does not formally distinguish between asymptomatic and symptomatic infections, but instead differentiates between undetected and detected cases. However, undetected mpox infections are typically those showing milder or no symptoms. In this perspective, and following prior assumptions on presymptomatic transmissibility⁹, we repeated our analysis assuming that undetected cases (I stage) would have a 20% lower transmissibility than detected cases (I_d stage).
- (3) Vaccination. Owing to the uncertainty about the type of protection vaccines provide, we tested the case of vaccine effectiveness against both infection and transmission. We assumed the same effectiveness, similar to previous modelling work⁶. In another test, we repeated our analysis parameterizing the model with the first available estimate of the effectiveness of the first-generation vaccine ($VE_{inf,1st} = 85\%$)³⁷.
- (4) Behavioural change. In our main analysis, we assumed that only nonvaccinated MSM would change behaviour. We carried out a sensitivity test lifting this assumption and also taking into account vaccinated MSM changing behaviour.
- (5) Degree assortativity. We increased the level of degree assortativity of the networks and assessed the robustness of behavioural change results to this network aspect.

Statistical analyses and validation

Monthly changes in onset-to-testing delays were tested by analysis of variance. We compared mpox incidence with and without vaccination using a chi-square test. We compared the mean ages of infected cases over successive months (t -tests).

Uncertainty on model estimates were provided by the 95% PI.

Model selection was validated against ERAS and WHO⁸ survey data, analysing behavioural change responses across MSM populations in the Paris region and reported estimates for Western Europe, respectively.

We analysed the responses from the ERAS 2023 survey, considering MSM respondents residing in the Paris region who had at least two male sexual partners in the previous six months. We computed the percentage of respondents who declared having reduced the number of sexual partners in summer 2022. The associated error was estimated by computing a binomial proportion confidence interval using a normal approximation. The reduction in the number of sexual partners was also analysed stratified by sexual activity. We performed a logistic regression to examine the correlation between the number of sexual partners and having changed behaviour or otherwise during summer 2022.

We also compared the predicted proportion of MSM changing behaviour with published estimates from a cross-sectional electronic survey conducted by WHO between 19 May and 31 May 2023 to explore the experiences of gay, bisexual and other MSM during the first year of the mpox outbreak⁸. The survey was undertaken in 23 affected countries in Europe and the Americas, including France. WHO advertised the survey using in-app direct messages and/or pop-ups through four geospatial dating applications. Inclusion criteria for participation were being 18 years old or older, and identifying as a gay or bisexual man, an MSM, or as a trans- or gender-diverse person, and agreeing to participate in the survey. The survey had 16,875 eligible respondents, 8,151 (48.3%) from Western Europe.

Simulations were developed and executed in C++ (version 14.2.0). Data processing and analyses were carried out in Python (version 3.8.10). Network construction and the quadratic approximation of the fitting procedure were carried out using R (version 4.2.3).

Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

Data availability

All data used to parameterize the model, run the simulations and generate the findings—including age-informed sexual contact networks, parameter values and vaccination data—are publicly available together with the model code in the GitHub repository associated with this study (<https://github.com/EPICx-lab/mpox-behavioral>). Access to individual-level data from the PREVAGAY and ERAS surveys, which contains sensitive information on sexual behaviour and health, is restricted. These data can be made available to researchers upon request to Annie Velter, subject to approval of the proposed analyses and agreement to adhere to security, confidentiality and collaborative conditions. Source data are provided with this paper.

Code availability

Our code, usable to reproduce all our experiments, is publicly available at the GitHub repository (<https://github.com/EPICx-lab/mpox-behavioral>).

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Author contributions

V.C. conceived and designed the study. D.M., O.R., P.-Y.B. and M.M. contributed to the methodology. D.M. and M.M. analysed the surveillance data. O.R. and P.-Y.B. developed the code for the generation of the MSM sexual network. D.M. developed the code for the inference and the modelling of the transmission dynamics, ran the simulations and analysed the data. A.V. coordinated the ERAS survey, contributing to its design, online publishing and data management. A.V. and D.M. analysed the ERAS survey data. All authors interpreted the results. D.M. and V.C. wrote the initial manuscript draft. All authors edited and approved the final version of the article.

Competing interests

The authors declare no competing interests.

Additional information

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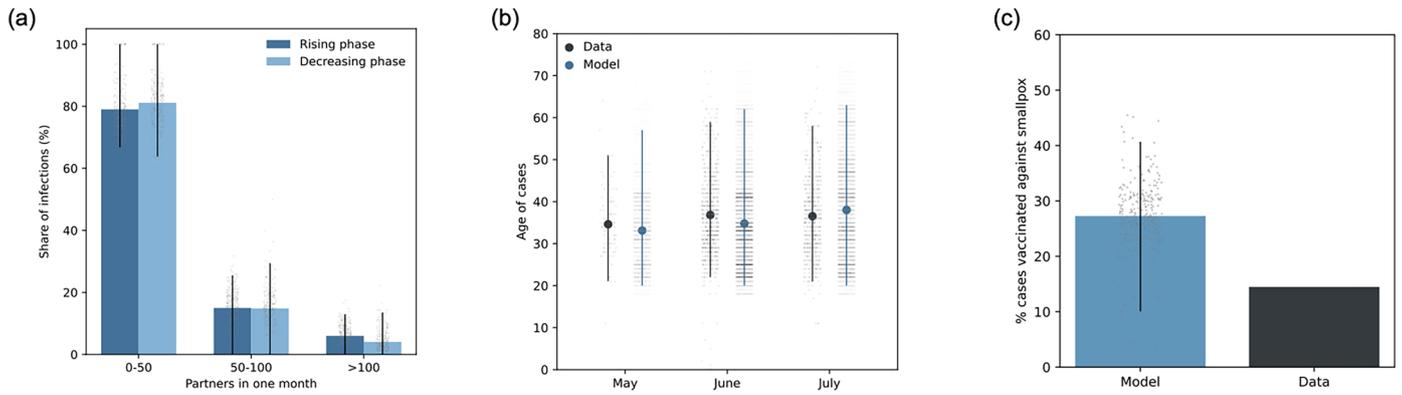
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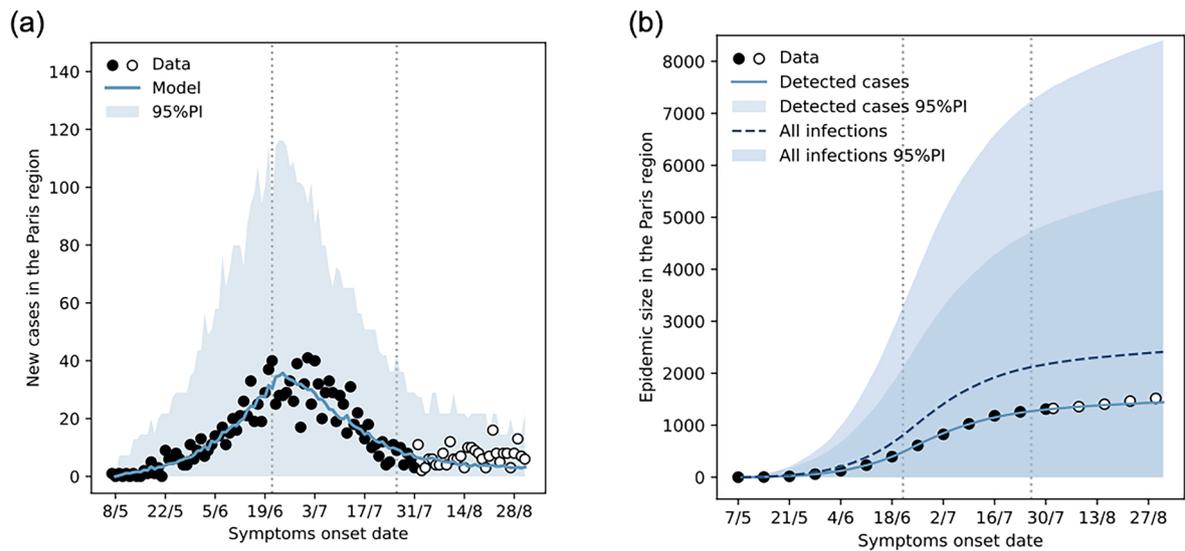
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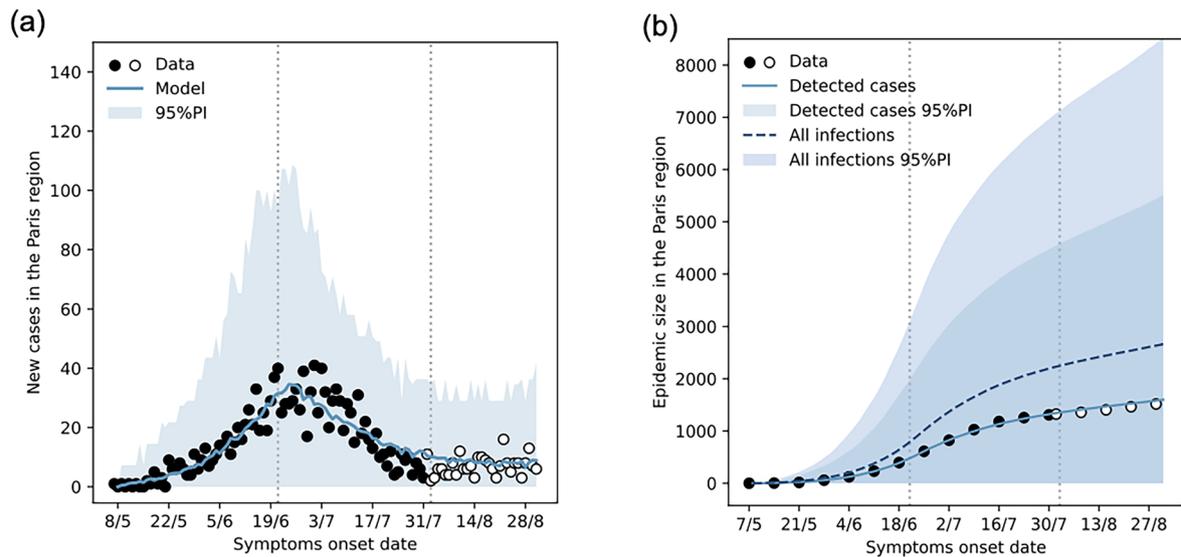
Extended Data Fig. 1 | Best-fit model results. a: Share of infection in the rising and the decreasing phases of the outbreak stratified by the monthly number of sexual partners. Model predictions are presented as means with 95% prediction intervals obtained from $n = 250$ stochastic runs (grey points). **b:** Age of mpox cases stratified by month from May to July 2022, data vs. model predictions

presented as means with 95% prediction intervals obtained from $n = 250$ stochastic runs (grey points). **c:** Percentage of mpox cases vaccinated against smallpox, data vs. model predictions presented as means with 95% prediction intervals obtained from $n = 250$ stochastic runs (grey points).



Extended Data Fig. 2 | Highly active MSM preferentially changing behavior. a, b: Behavioral change hypothesis, assuming highly active MSM preferentially change behavior, mpxv cases in the Paris region (filled points refer to the data used for

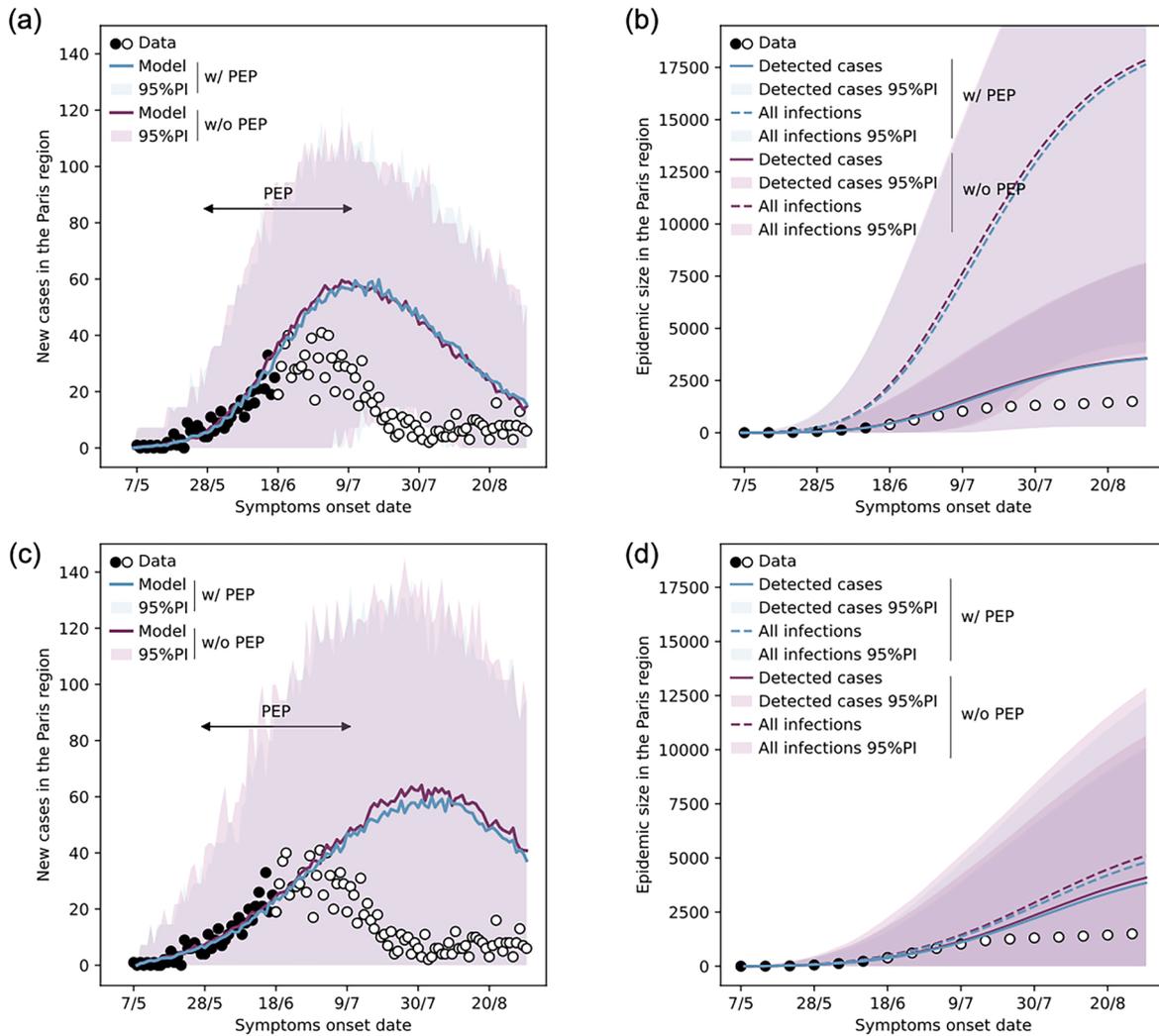
inference) and model predictions. Model predictions are presented as means with 95% prediction intervals (shaded areas) obtained from $n = 250$ stochastic runs. The left panel (a) reports incident cases, and the right panel (b) the epidemic size.



Extended Data Fig. 3 | MSM contacts of cases changing behavior.

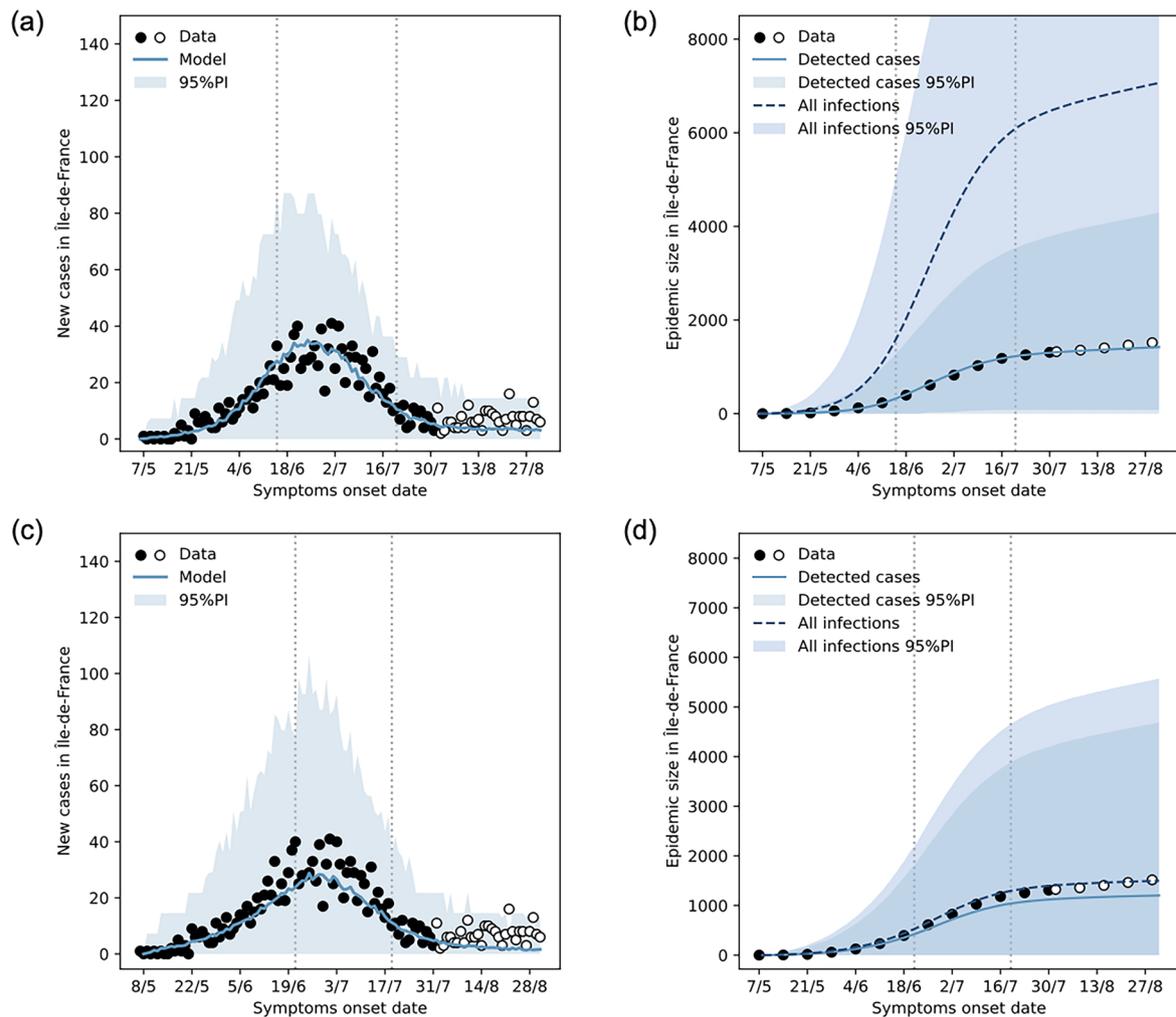
a,b: Behavioral change hypothesis, assuming MSM contacts of cases changing behavior, mpox cases in the Paris region (filled points refer to the data used for

inference) and model predictions. Model predictions are presented as means with 95% prediction intervals (shaded areas) obtained from $n = 250$ stochastic runs. The left panel (a) reports incident cases, and the right panel (b) the epidemic size.



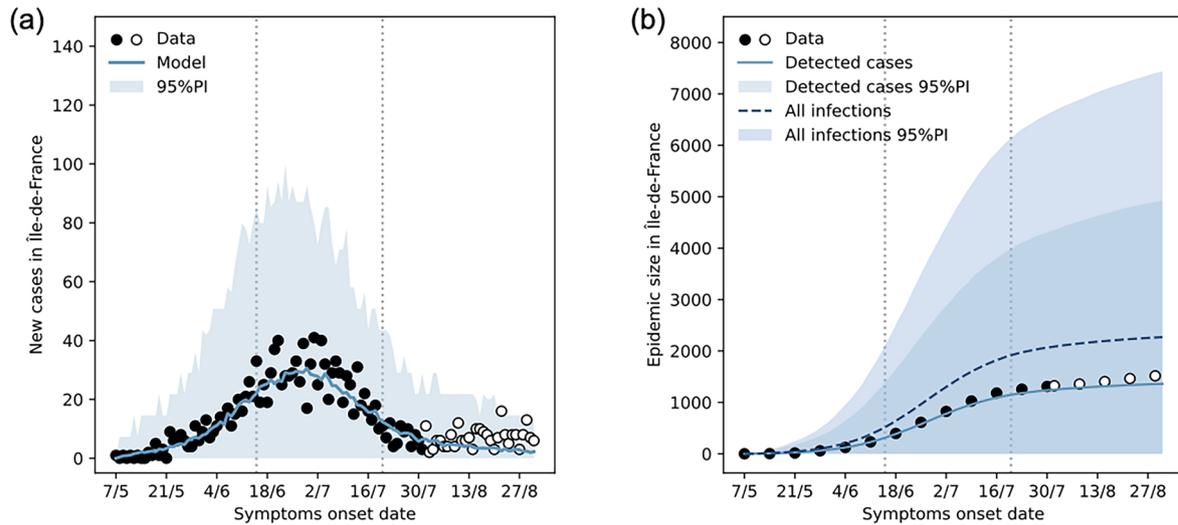
Extended Data Fig. 4 | PEP vaccination hypothesis with $p_d = 20\%$ and $p_d = 80\%$. **a,b:** Mpox cases in the Paris region (filled points refer to the data used for inference) and model predictions in the scenarios with and without PEP vaccination assuming a detection probability $p_d = 20\%$. Model predictions are presented as means with 95% prediction intervals (shaded areas) obtained from $n = 250$ stochastic runs. The left panel (a) reports incident cases, and the right panel (b) the epidemic size. The model predicted a delayed peak by 13 days (95%PI -9-43) and a 2.6-fold higher incidence (95%PI 1.4-4.0). By August 31, the

model predicted 3,534 (95%PI 2,556-4,031) detected mpox cases, corresponding to 5% (95%PI 4-6%) of the MSM population—2.3 times higher than observed. **c,d:** As in (a,b) assuming a detection probability $p_d = 80\%$. Model predictions are presented as means with 95% prediction intervals (shaded areas) obtained from $n = 250$ stochastic runs. The model predicted a delayed peak by 31 days (95%PI -24-58) and a 2.8-fold higher incidence (95%PI 0-4.9). By August 31, the model predicted 3,844 (95%PI 54-6,442) detected mpox cases, corresponding to 6% (95%PI 0.1-10%) of the MSM population—2.5 times higher than observed.



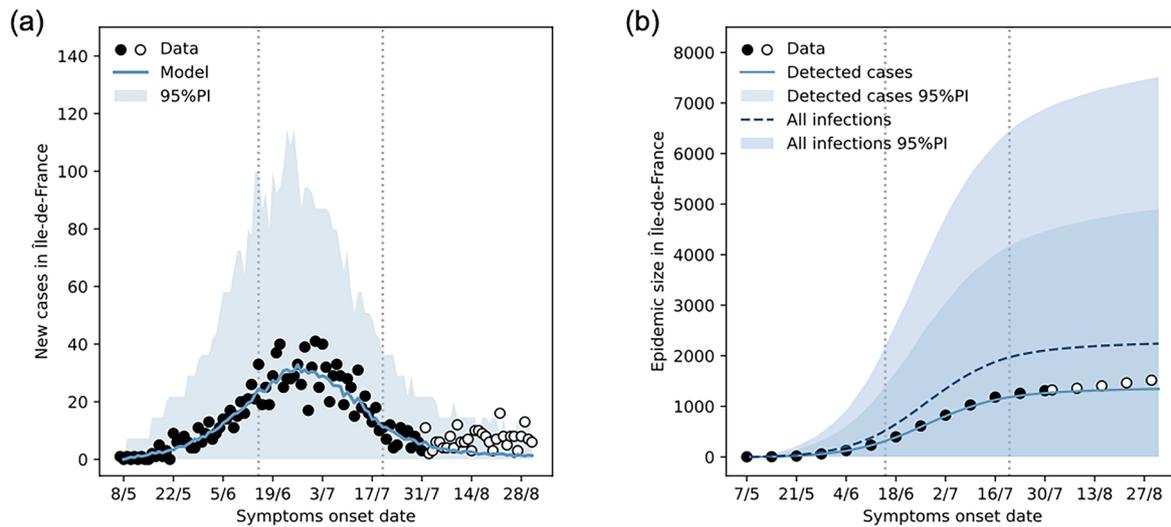
Extended Data Fig. 5 | Impact of lower ($p_d = 20\%$) and of higher ($p_d = 80\%$) detection probability. Results refer to the model with uniform behavioral changes among MSM. **a,b:** Mpx cases in the Paris region (filled points refer to the data used for inference) and model predictions, assuming $p_d = 20\%$. Model predictions are presented as means with 95% prediction intervals (shaded areas) obtained from $n = 250$ stochastic runs. The left panel (**a**) reports incident cases, and the right panel (**b**) the epidemic size. The model resulted in a considerably worse fit than the best-fit model (Supplementary Table 7) and estimated that 53% (95% CI 50-53%) of the MSM reduced their sexual contacts by

100% (95% CI 95-100%). This adaptation, occurring gradually between June 15 and July 20, was predicted to lead to a 44% (95%PI 41-46%) reduction in sexual contacts and 59% (95%PI 24-99%) averted mpx cases during the study period. **c,d:** As in (**a,b**) assuming $p_d = 80\%$. The model produced a similar performance and output to the best-fit model (Supplementary Table 7) and estimated that 53% (95% CI 50-53%) of the MSM reduced their sexual contacts by 85% (95% CI 85-100%). This adaptation, occurring gradually between June 21 and July 19, led to a 38% (95%PI 34-41%) reduction in sexual contacts and 71% (95%PI 18-99%) averted mpx cases during the study period.



Extended Data Fig. 6 | Impact of lower transmissibility of asymptomatic cases. Results refer to the model with uniform behavioral changes among MSM. **a,b:** Mpox cases in the Paris region (filled points refer to the data used for inference) and model predictions. Model predictions are presented as means with 95% prediction intervals (shaded areas) obtained from $n = 250$ stochastic runs. The left panel (a) reports incident cases, and the right panel (b) the epidemic size. Under this hypothesis, the model fitted worse than best-fit model

(Supplementary Table 7). It estimated that 51% (95% CI 46-56%) of the MSM in the population reduced their sexual contacts by (84% (95% CI 77-92%)), i.e. a slightly smaller reduction compared to the best-fit model. This adaptation, occurring gradually between June 21 and July 20, was expected to lead to a 37% (95% PI 33-39%) reduction in sexual contacts and 71% (95% PI 26-99%) averted mpox cases during the study period.



Extended Data Fig. 7 | Impact of allowing also vaccinated MSM to change behavior. Results refer to the model with uniform behavioral changes among MSM. **a,b:** Mpx cases in the Paris region (filled points refer to the data used for inference) and model predictions. Model predictions are presented as means with 95% prediction intervals (shaded areas) obtained from $n = 250$ stochastic runs. The left panel (a) reports incident cases, and the right panel (b) the

epidemic size. The model fitted worse than the best-fit model (Supplementary Table 7) and estimated that 89% (95% CI 80-98%) of the MSM in the population reduced their sexual partnerships by 75% (95% CI 68-83%). This spontaneous adaptation, occurring gradually between June 15 and July 20, was estimated to lead to a 52% (95%PI 49-54%) reduction in sexual contacts and 71% (95%PI 27-100%) averted mpx cases during the study period.

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All data used to parameterize the model, run the simulations, and generate the findings—including age-informed sexual contact networks, parameter values, and vaccination data—are publicly available together with the model code in the GitHub repository associated with this study (<https://github.com/EPIcx-lab/mpox->

behavioral). Access to individual-level data from the PREVAGAY and ERAS surveys, which contain sensitive information on sexual behavior and health, is restricted. These data can be made available to researchers upon request to Annie Velter, subject to approval of the proposed analyses and agreement to adhere to security, confidentiality, and collaborative conditions. Source Data files for all data presented in graphs within the Figures and Extended Data are published alongside the paper.

Research involving human participants, their data, or biological material

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Reporting on sex and gender	Surveillance data contained self-identification as MSM (yes/no). 2015 PREVAGAY survey was proposed to MSM only. MSM were self-declared. 2023 ERAS survey contained self identification about the gender ("male", "female", "non-binary", "other: "), and about the sex at birth.
Reporting on race, ethnicity, or other socially relevant groupings	Survey and surveillance data were not specifically sampled based on race or ethnicity. Surveillance and ERAS data were restricted to the Paris region (Île-de-France); PREVAGAY data to Paris. ERAS data were filtered to consider MSM respondents only (98% of Île-de-France's respondents).
Population characteristics	The characteristic of the sample of the various data sources are described in the Methods (sections: ERAS 2023 survey, PREVAGAY survey, time-varying sexual contact network construction, and MSM population estimate, Mpox surveillance data). Both PREVAGAY and ERAS surveys contained socio-demographic, health-related and sexual-related information; ERAS contained also mpox-related questions. We used information on the number of sexual partners in the past month, age, attended sex-related venues of the PREVAGAY survey. We used information on the number of sexual partners in the past 6 months and mpox-related behavioral changes in 2022 in the ERAS survey. Both survey were addressed to MSM.
Recruitment	Data on the mpox cases were reported, anonymized, to Santé Publique France (French Public health Agency). Participants to the 2015 PREVAGAY surveys were recruited in commercial gay venues in five French cities (Paris, Lyon, Lille, Montpellier/Nîmes/Béziers, Nice). Such commercial gay venues could be sex-related (Sauna, Backroom, sex-club) or non sex-related (Bar, Club without backroom). The survey was specifically proposed to individuals self-defined as MSM. Participants to the 2023 ERAS survey were recruited via a variety of digital media. Banners were posted directly on geolocated gay dating applications and gay affinity information sites. They were also posted on social networks, targeting profiles similar to those of visitors to the Sexosafe prevention website visitors.
Ethics oversight	All surveillance data were anonymized before use. Surveillance was considered as non-interventional research only requiring the non-opposition of the patient (article L1211 of the French public health code). The PREVAGAY study was authorized by the Comité de protection des personnes Île-de-France IX (n°2014-A01605-42). The ERAS study was approved by Inserm's Ethics Evaluation Committee (IRB00003888 avis n°23-989). Participants in both studies gave their informed consent.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

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Sample size	In the fitting procedure, at each iteration, we averaged 250 stochastic simulations (50 for each of the 5 networks we generated) obtained from the same parameter sets to compute the average expected value for the likelihood. We chose simulations number to ensure a relative precision at least 10% on the variance estimates (based on the normal assumption - $SD(s^2)/s^2 = 2/n$, which gives $n > 200$ for at least 10% relative precision). We conducted a sensitivity analysis for the number of networks. Sample sizes of surveillance data, PREVAGAY data, and ERAS data are provided in the main manuscript.
Data exclusions	Our study focused on the Paris region (Île-de-France). All other data are excluded.
Replication	The study contains several stochastic models: the generation of the networks, the epidemic model, the imputation of missing dates of symptom onset. Each network generation and each model replication were independently executed. We tested the reproducibility of our findings by varying the number of networks from 5 to 50 and the number of from stochastic runs from 250 to 2500.
Randomization	Our study is observational and population-based in nature, and involves no intervention. Randomization of subjects is therefore not applicable.
Blinding	Our study is observational and population-based in nature, and involves no intervention. Blinding techniques are therefore not applicable.

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