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Modeling Poliovirus Transmission and Responses in New York State

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Abstract

Background.—In July 2022, New York State (NYS) reported a case of paralytic polio in an unvaccinated young adult, and subsequent wastewater surveillance confirmed sustained local transmission of type 2 vaccine-derived poliovirus (VDPV2) in NYS with genetic linkage to the paralyzed patient.

Methods.—We adapted an established poliovirus transmission and oral poliovirus vaccine evolution model to characterize dynamics of poliovirus transmission in NYS, including consideration of the immunization activities performed as part of the declared state of emergency.

Results.—Despite sustained transmission of imported VDPV2 in NYS involving potentially thousands of individuals (depending on seasonality, population structure, and mixing assumptions) in 2022, the expected number of additional paralytic cases in years 2023 and beyond is small (less than 0.5). However, continued transmission and/or reintroduction of poliovirus into NYS and

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Supplementary Data

Supplementary materials are available at *The Journal of Infectious Diseases* online. Consisting of data provided by the authors to benefit the reader, the posted materials are not copy-edited and are the sole responsibility of the authors, so questions or comments should be addressed to the corresponding author.

other populations remains a possible risk in communities that do not achieve and maintain high immunization coverage.

Conclusions.—In countries such as the United States that use only inactivated poliovirus vaccine, even with high average immunization coverage, imported polioviruses may circulate and pose a small but nonzero risk of causing paralysis in nonimmune individuals.

Keywords

New York; immunization; modeling; outbreak; polio

Global polio immunization and eradication efforts have substantially reduced poliomyelitis cases [1], although the polio eradication endgame faces substantial hurdles [2]. Continued poliovirus transmission and oral poliovirus vaccine (OPV) use pose risks of importation into polio-free countries, such as the United States, with the potential to restart transmission and cause paralytic polio in undervaccinated communities [3]. In 1997, the United States adopted a sequential schedule of inactivated poliovirus vaccine (IPV) followed by OPV (IPV/OPV), and in 2000 switched to an IPV-only schedule for all routine immunization (RI) [4]. This transition eliminated the very small, but nonzero incidence of vaccine-associated paralytic polio (VAPP), which had become the primary form of polio cases reported [4, 5].

After 2000, the United States rarely reported polio cases or evidence of transmission. In 2005, detection of nonparalytic vaccine-derived poliovirus infection in an immunodeficient child with no known exposure to live polioviruses provided evidence that polioviruses imported from other countries could lead to transmission in undervaccinated US communities [6]. In 2009, the United States reported VAPP in a 44-year-old woman with common variable immunodeficiency who likely became infected 12 years earlier when her child received OPV [7]. Before 2022, the last reported US polio case occurred in 2013 in an immigrant child with severe combined immunodeficiency who received OPV in India [8].

In July 2022, New York State (NYS) reported a case of paralytic polio in an unvaccinated adult from Rockland County, which has the third lowest pediatric IPV coverage in NYS [9, 10]. Subsequent wastewater testing showed sustained transmission of genetically linked circulating vaccine-derived poliovirus type 2 (cVDPV2) in Rockland and neighboring counties [9, 11]. Whole-genome sequencing analyses of wastewater samples by laboratories in the United States, United Kingdom, and Israel identified common genetic sequences that suggested linkages between the contemporaneously circulating viruses in all 3 countries [11–13]. Subsequently, Canada reported wastewater detection of related viruses [14], and Israel reported a paralytic case in February 2023 [15].

The 2022 reported NYS polio case and sustained detections of polioviruses in wastewater raised questions about the likelihood of continued transmission and additional cases. Prior US modeling studies anticipated the potential for transmission following importation of a live poliovirus [3, 5, 16–18]. These studies identified undervaccinated communities as at risk for paralytic cases despite high overall national vaccine coverage [3, 5, 16–18]. Here, we model the transmission of the poliovirus importation that occurred in NYS to explore the dynamics of the outbreak and highlight opportunities for better risk assessment,

management, and communication of this and potential future outbreaks in undervaccinated communities in IPV-only countries.

METHODS

We obtained information about the index patient, vaccination coverage, and wastewater sampling from relevant public health authorities (see Supplementary Material). We modeled transmission of the poliovirus imported into NYS in 2022 by identifying and characterizing the undervaccinated communities with the potential of sustaining local transmission. We divided the population between outbreak counties of Rockland, Orange, Sullivan, and Kings, which reported repeated detections of polioviruses in wastewater with genetic linkage to the index patient, and nonoutbreak counties in NYS (Figure 1). We subdivided these populations into general and undervaccinated subpopulations (ie, outbreak counties general [OG] and undervaccinated [OU]; nonoutbreak counties general [NG] and undervaccinated [NU]). The general subpopulations represent communities with vaccination coverage consistent with RI levels reported for the whole state, while the undervaccinated subpopulations represent communities with lower vaccination coverage [10, 19]. This structure provided a conceptual and functional representation of the NYS population that groups people by levels of vaccination and risk.

We applied a previously developed deterministic, differential equation-based poliovirus transmission and OPV evolution model [20, 21] with US-specific inputs [3, 5, 16] adapted to NYS. The model divides the population into 8 immunity states (fully susceptible, maternally immune, and 6 partially immune states resulting from different numbers of live poliovirus infections and/or effective IPV doses). Properly modeling poliovirus transmission requires consideration of all these immunity states because individuals with prior vaccine-induced or infection-induced immunological protection can become (re) infected and participate in transmission, although they do so without clinical detection. Only fully susceptible individuals (ie, those with no type-specific immunity) may become paralyzed when infected. Less than 1 case of paralysis occurs in 2000 infections (<0.05%) by type 2 wild poliovirus (WPV), with lower risk for OPV-related strains [20, 21]. Individuals with live poliovirus-induced immunity participate less in transmission than those with IPV-only immunity, making the birth cohorts since 2000 an important contributor to transmission [16]. We modeled infection as a multistage process that accounts for different poliovirus types, routes of transmission, waning, and evolution from fully attenuated Sabin OPV to fully reverted strains that behave like the homotypic WPV [20, 21] (Supplementary Table 1).

Given uncertainty about the extent of mixing between individuals from different subpopulations, we considered 5 mixing matrices including 2 bounding scenarios of complete isolation, in which no mixing between any subpopulations occurs and homogeneous mixing, in which each subpopulation receives contacts from all other subpopulations. To examine the effect of various mixing behaviors, we considered subpopulation isolation, in which the undervaccinated subpopulations (OU, NU) remain isolated from the general subpopulations (OG, NG), but mix between themselves; no isolation, in which 95% of contacts come from the 2 subpopulations of the same vaccination levels while the remaining 5% come from both of the other 2 subpopulations; and partial

isolation, in which 95% of contacts come from each undervaccinated subpopulation while the remaining 5% come only from the 2 general subpopulations (Supplementary Table 2).

We characterized historical NYS immunization (Supplementary Figure 1). We simulated the cVDPV2 introduction by assuming multiple contacts with individuals of all ages in the undervaccinated subpopulation of the outbreak counties at a high-spread–potential gathering (eg, a lifecycle celebration, reception, concert) [9] on 1 March 2022, with an individual excreting a type 2 poliovirus less attenuated than type 2 Sabin OPV using model evolution stage 10 [20, 22]. Consistent with the NYS emergency efforts (see Supplementary Material), we included IPV catch-up immunizations between 21 July 2022 and 8 January 2023 for individuals <20 years old in the undervaccinated subpopulations. NYS made IPV doses available to individuals in the outbreak counties and some nonoutbreak counties, but the actual numbers of doses delivered to unvaccinated individuals above those that would have remained unvaccinated is not known. We assumed the delivery of approximately 12 000 IPV doses due to the outbreak in the outbreak counties undervaccinated subpopulation (OU), and approximately 12 500 IPV doses in the nonoutbreak counties undervaccinated subpopulation (NU). As a sensitivity analysis, we explored the impact of not administering these additional IPV doses or administering them all to the general subpopulations (OG and NG).

We simulated population immunity using effective immune proportion (EIP) [3, 5, 16, 23]. EIP integrates over all immunity states for all individuals and measures the overall population immunity to polio. Poliovirus transmission can be sustained when EIP falls below its threshold (designated EIP*). With basic reproduction number (R_0) changing over time due to seasonality (and varying by serotype and setting), we also report the mixing-adjusted net reproduction number (R_n), which shows the average number of secondary infections generated by a single infectious individual considering the relative potential contribution to transmission of all individuals in the population as well as mixing between age groups and subpopulations [23]. For $R_n > 1$, each new infection generates at least 1 new infection and transmission of existing or imported poliovirus can continue. When $R_n < 1$ for a sufficiently long duration, then transmission will eventually die out. We performed all simulations using JAVA™ programming language in the integrated development environment Eclipse™, and used a model time horizon extending through 2026 [20, 21].

RESULTS

As the outbreak unfolded, public health authorities reported the timing and incidence of poliovirus detections in wastewater using various formats [9–11, 19]. We present the information through June 2023 in the form of county-level detection signals by the week of detection for counties that performed wastewater testing during any given week, which shows the basis for designating Rockland, Orange, Sullivan, and Kings counties as outbreak counties (Figure 1*A*). A positive signal represents a type 2 poliovirus detection with (n = 91) or without (n = 1) genetic linkage to the index patient, or a strain for which the genetic information is inadequate to establish linkage to the index patient (n = 5). Negative detections represent negative samples (n = 3748) or samples in which a poliovirus was not definitively found (n = 29). The index patient presented in June 2022 (week 25), which

occurs at the leading portion of the cluster of positive detections in the summer/fall of 2022. The reduced number of positive detections after October 2022 likely reflects the combination of seasonal variability, vaccination, and transmission die-out as the virus has spread through the undervaccinated population, resulting in increased population immunity.

Figure 1*B* shows the geographic extent of the outbreak and wastewater surveillance at the county level. The sampled sewer sheds vary in size and population covered, resulting in nonhomogenous wastewater detection sensitivities. To juxtapose the geography of the outbreak with risk, Figure 1*C* presents 2022 NYS immunization coverage indicators by county using different metrics available early in the outbreak [10, 19] (see Supplementary Material).

Table 1 shows the expected incidence of paralytic cases by subpopulation over time and under different population mixing assumptions. Under all mixing assumptions, the expected cases in 2023 drop below 0.2, even if the transmission does not stochastically die out. As anticipated, the highest likelihood of detecting a second case in 2023 occurs in the undervaccinated subpopulations of the outbreak counties.

Although the likelihood of detecting additional paralytic cases in NYS is small, sustained poliovirus transmission reflected the participation of thousands of individuals, primarily as asymptomatic, subclinical or nonparalytic poliovirus infections that do not meet the clinical criteria or count as polio cases. Figure 2 and Supplementary Figure 2 show the monthly incidence of new infections by immunity state under different mixing assumptions for the undervaccinated population of the outbreak counties (left panels) and the NYS totals (right panels). The results show most new infections occurred or would occur in individuals with prior immunity induced by a prior live poliovirus infection, including OPV immunization, or from IPV-only immunization (ie, those born since 2000). These results reflect the overall relatively high population immunity in NYS and demonstrate the extent of asymptomatic participation in transmission. The thousands of individuals likely infected in 2022 represents a large number of people in absolute numbers, but a small fraction of the total NYS population.

Assuming complete isolation of all subpopulations provides a theoretical lower bound of the possible extent of spread of poliovirus transmission in the subpopulations (Supplementary Figure 2*A*). Complete isolation leads to 0.05 expected cases in 2023, which we approximate as a 5% probability of having 1 or more paralytic cases in 2023 (Table 1). Alternatively, homogeneous mixing, which simulates the population of NYS as a single, well-mixed population, provides a theoretical upper bound of the possible spread of poliovirus transmission (Supplementary Figure 2*B*). However, given the assumed homogeneous large and well-mixed population with relatively high overall immunity (ie, no preferentially mixing undervaccinated groups), the model shows a very low chance that the introduced virus would spread sufficiently to get detected by surveillance (Table 1).

Assuming subpopulation isolation, in which mixing between the 2 undervaccinated subpopulations occurs freely, allows poliovirus to spread to the undervaccinated subpopulation of the nonoutbreak counties (Figure 2*A*). Given additional spread potential

into the other undervaccinated populations, the low level of poliovirus transmission continues until mid-2024. This scenario represents the highest burden of infections in undervaccinated subpopulation of the outbreak counties, with an estimated over 16 000 individuals participating in transmission during the 2022–2024 period (Figure 2*A*, left panel), and >14 000 of these in 2022.

The more realistic mixing assumptions of no isolation allow for some contacts of undervaccinated subpopulations with the individuals from general populations and vice versa (Figure 2*B*). Here, poliovirus transmission continues at a low level until February 2024, with 96% of new infections occurring in 2022. This scenario also represents the highest burden of total infections, with an estimated almost 30 000 individuals participating in transmission over the 2022–2024 period (Figure 2*B*, right panel), and approximately 28 000 of these in 2022.

Finally, for partial isolation of the undervaccinated subpopulations (Figure 2*C*) the majority of infections occur in 2022, more than 80% of which occur in the undervaccinated subpopulation of the outbreak counties (Figure 2*C*, left panel). Some residual infections in this deterministic model last through January 2024, but the probability of new paralytic cases in 2023 and beyond remains very small (Table 1).

Increasing the amplitude of the seasonality (Supplementary Figure 3) increases the transmission and the number of expected paralytic cases, but it also increases the chances of die out during the low season. For example, with seasonality of 0.35, die out occurs using the deterministic threshold in the model for all mixing assumptions, but die out does not occur for subpopulation isolation mixing for lower seasonality assumptions.

Additional IPV doses administered during the NYS emergency likely played a relatively small role with respect to slowing transmission and preventing cases in 2022. Longer term, these additional IPV doses will protect individuals who otherwise would have remained susceptible to becoming paralyzed if infected by a poliovirus, assuming their administration into the undervaccinated populations (Supplementary Figure 4). However, sensitivity analysis shows that not administering these additional IPV doses or administering them to the general populations would not have changed the dynamics of ongoing transmission and/or future outbreaks.

The EIP from 1990–2025 (Figure 3*A*) highlights the decline in population immunity following the 1997 shift to IPV/OPV sequential vaccination and 2000 shift to IPV-only, because unlike OPV, IPV does not spread secondarily beyond the individual recipient. The oscillation of the EIP* reflects seasonality, such that during some months, the threshold required to prevent transmission increases and narrows the gap to or falls below the EIP. The declining trend in EIP drops slightly more rapidly in 2020 due to disruptions in immunization coverage because of the coronavirus disease 2019 (COVID-19) pandemic. The increase in EIP in 2022 reflects the transmission of the outbreak virus, which induces immunity in infected individuals. Figure 3*A* shows the expected population immunity will continue to fall below EIP* (the level required to prevent sustained transmission) for some

parts of the year, which implies ongoing risk of similar outbreaks in NYS in the future. Figure 3*B* shows R_n with values >1 capable of supporting sustained transmission.

DISCUSSION

Despite sustained transmission of imported cVDPV2 in NYS in 2022–2023, the likelihood of identifying other polio cases from this outbreak poliovirus in 2023 and beyond appears small. However, these results should not minimize the potentially significant implications of circulating polioviruses in the United States and other IPV-only countries.

The report of paralytic poliomyelitis in NYS served as a potent reminder to polio-free countries that imported polioviruses remain a threat as long as polioviruses circulate anywhere in the world. In addition, poliovirus infections can result in prolonged or chronic infection in patients with primary immunodeficiencies, which in turn can become sources of virus reintroduction in the population, and can lead to the development of immunodeficiency-associated VAPP so long as the infection persists [24].

Polioviruses can cross geographic borders, putting undervaccinated individuals anywhere at risk. Genetic linkage between the cVDPV2s identified in wastewater in the United States, United Kingdom, Israel, and Canada provide a clear indication of this risk. Our findings demonstrate the possibility of low-level sustained transmission given current levels of population immunity in NYS and ongoing transmission of cVDPV2s globally. The modeling results and wastewater surveillance data tell a consistent story, with only 1 isolated positive environmental detection through June 2023. However, it will take some time with active surveillance and no additional positive detections to gain confidence that transmission has died out, as opposed to continuing at undetectable levels because of seasonality and locally diminished pool(s) of susceptible individuals. The possibility of continued transmission remains, with additional detections potentially increasing with seasonality in mid-2023.

Modeling US poliovirus transmission provides insights for countries that use only IPV in RI. A 2012 study of trends in US vulnerability to importations [16] characterized the expected decreases in population immunity to transmission [25] following the shift from OPV to IPV-only RI. Modeling identified the possibility of sustained transmission of imported polioviruses in undervaccinated communities with high IPV-only coverage before the epidemiological observation of this phenomenon in Israel [26]. Although Israel shifted to an IPV-only RI in 2004, after detecting type 1 WPV transmission in 2013, Israel used bivalent OPV (containing types 1 and 3) to respond after its interventions with IPV failed to stop transmission [27]. More recently, the use of IPV to stop transmission of cVDPV2 succeeded in China [28], but not in Tajikistan, which later used type 2 novel OPV to successfully stop transmission [29]. Time will tell whether the IPV used in the 2022 United States, United Kingdom, and Israel cVDPV2 outbreaks successfully stopped transmission.

Disruptions in RI during the COVID-19 pandemic may have reduced coverage and population immunity [30], and thus increased the risks of sustained transmission in United States and elsewhere. A recent health economic analysis provided estimates of the number of potential VAPP cases expected from giving different OPV formulations to all Americans

in 2020 [31]. Although responding to the NYS outbreak would not involve reintroducing OPV for all Americans, the analysis suggests that the risks and costs of using any OPV may outweigh its benefits for some outbreaks [31]. If poliovirus transmission continues in NYS, this may lead to discussion about using OPV to respond.

This modeling has limitations [20, 21] in addition to uncertainty about actual mixing dynamics and seasonality in NYS. We used a deterministic model such that the results represent the expected average behavior, which may differ from real-life given stochastic variability. Moreover, we used a simplified, deterministic approach to characterize poliovirus transmission die-out. In reality, poliovirus transmission can take off or die out by chance, which motivates further stochastic analyses, as well as an analysis of the quality of surveillance information. We also note limitations in the availability of information about the characteristics of various populations, including historical immunization data, size, and extent of various at-risk populations, seasonality, and information about mixing behavior among various social, ethnic, religious groups, and other specific subpopulations. Prior modeling and 1-way sensitivity analyses that we performed to explore the impacts of changing seasonality assumptions implied longer transmission with lower (or no) seasonality if the importation restarted transmission, or more intense transmission with higher seasonality. Despite these limitations, our results provide insights into the likely dynamics of poliovirus transmission in NYS, and may help to guide public health expectations, actions, and policy decisions.

Surveillance data continue to be of value in monitoring the outbreak status, but the surveillance data in NYS are limited by the complex nature of the sewage system in this densely populated region [11, 32]. Wastewater sampling pools over large populations in NYS and could miss signals from low level transmission events or low volume excretion from individuals with primary immunodeficiencies who may continue prolonged excretion while remaining in areas with limited surveillance. In addition, several communities of concern rely on local septic systems that are not captured in the public sewer systems that are the current source of wastewater for surveillance.

This model suggests poliovirus transmission will die out in NYS, if it did not already, but that wastewater sampling in the summer/fall of 2023 might show an uptick of detections. If transmission continues, or if another independent importation of this virus occurs in 2023, we do not anticipate a high probability of additional cases caused by cVDPV2 in NYS. This is true even though the outbreak virus only affected a small fraction of the NYS population and unimmunized individuals remain at risk. The transmission potential of the outbreak virus is unlikely to lead to substantial spread, like this importation, and even with transmission the probability of paralysis is low. However, the possibility of importation of a more transmissible and/or more virulent poliovirus (eg, a type 1 cVDPV or more virulent and transmissible cVDPV2) could lead to 1 or more additional cases.

The consequences of disruptions in RI during the COVID-19 pandemic increased global cVDPV2 risks and may have lowered the overall population immunity in NYS, which increased the size of the population at risk and the potential for sustained transmission. While the outbreak motivated some to seek IPV and NYS delivered thousands of doses

during the emergency, undervaccination remains an important issue. The risk of poliovirus circulation remains in undervaccinated communities in NYS and elsewhere as long as global circulation continues. Overall, this modeling of the 2022 NYS outbreak supports the notion that in countries that use only IPV for RI, imported polioviruses may not die out immediately even in the background of high immunization rates, and pose ongoing risks of paralysis in nonimmune individuals. Improvements in routine childhood immunization coverage are needed in undervaccinated close-knit communities, protecting the population from the deleterious health effects of vaccine-preventable illnesses, including paralysis due to polioviruses given ongoing risks of importation.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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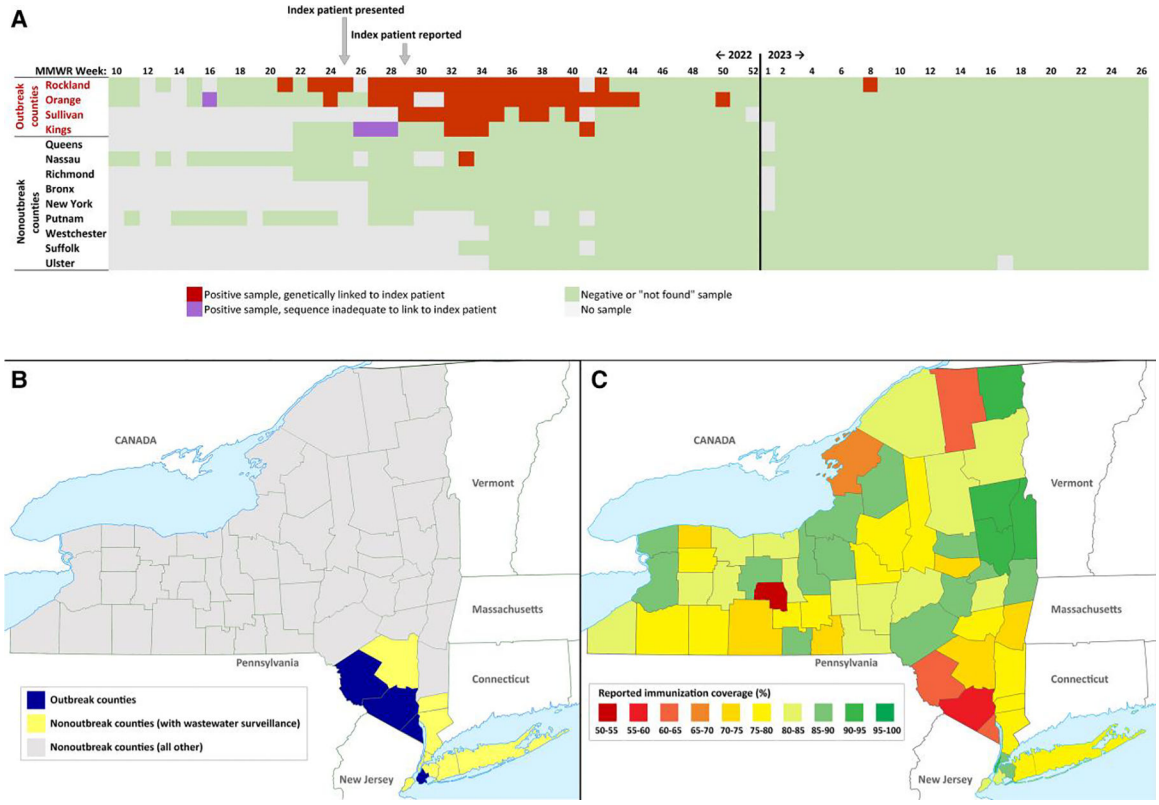

Figure 1.

A, New York State (NYS) wastewater surveillance results for outbreak counties, as well as the nonoutbreak counties that reported wastewater surveillance results. Each colored box shows the surveillance outcome for the corresponding NYS counties, indicating weeks with at least 1 positive sample result (red and purple boxes), only negative or indeterminate sample results (green boxes), or no wastewater surveillance results (light gray). The index patient presented with paralysis onset in June 2022 (week 25), and the case was reported in July 2022 (week 29), with designation of weeks of the year based on the convention used by the Morbidity and Mortality Weekly Report (MMWR) corresponding to a 52-week year. The vertical black line between weeks 52 and 1 represents 1 January 2023. Each county may include more than 1 sewer shed and multiple sampling sites, for which we aggregate at the county level. For Kings County, the 1 sewer shed that was repeatedly positive included a small portion of Queens, which we attributed to Kings County only. Not specifically shown are three 24-hour composite specimens and 14 large-volume specimens collected to increase sensitivity of wastewater surveillance in critical times and/or regions. Nonoutbreak counties that have not been subject to wastewater surveillance are not listed; see county map in (*B*). *B*, Map of outbreak and nonoutbreak counties with and without wastewater surveillance. *C*, Variability in reported polio immunization coverage by county based on the best available, different metrics reported by the New York City Department of Health and Mental Hygiene and the New York State Department of Health at the beginning of the outbreak [10, 19].

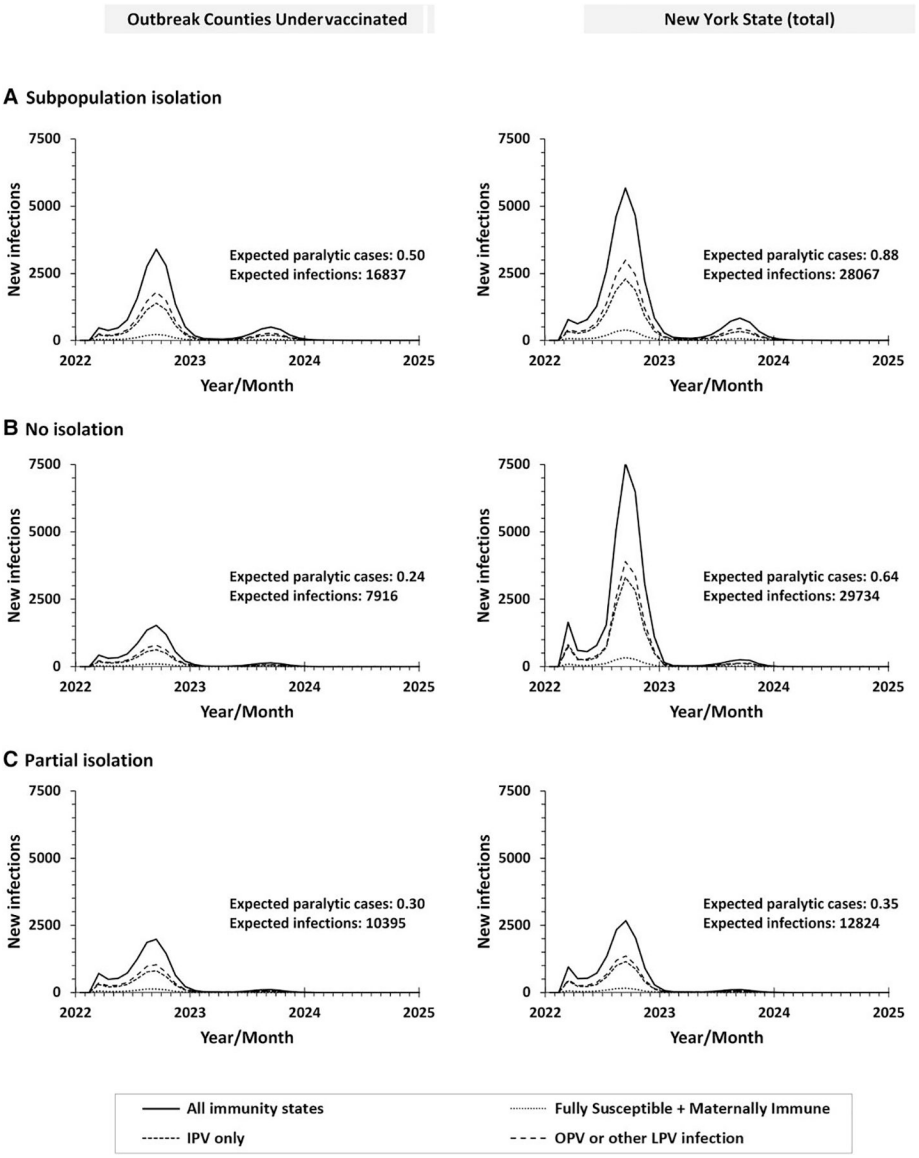

Figure 2.

Monthly new infections by prior immunity state under different mixing assumptions. *A–C*, For each mixing assumption, new infections in the undervaccinated population of the outbreak counties are shown on the left, and the total number of expected new infections for New York State on the right. Text insets in each panel show the corresponding expected paralytic cases (derived from Table 1) and the total expected infections (area under the solid curve). See Supplementary Figure 1 for the bounding scenarios of complete isolation and homogeneous mixing. Abbreviations: IPV, inactivated poliovirus vaccine; LPV, live poliovirus; OPV, oral poliovirus vaccine.

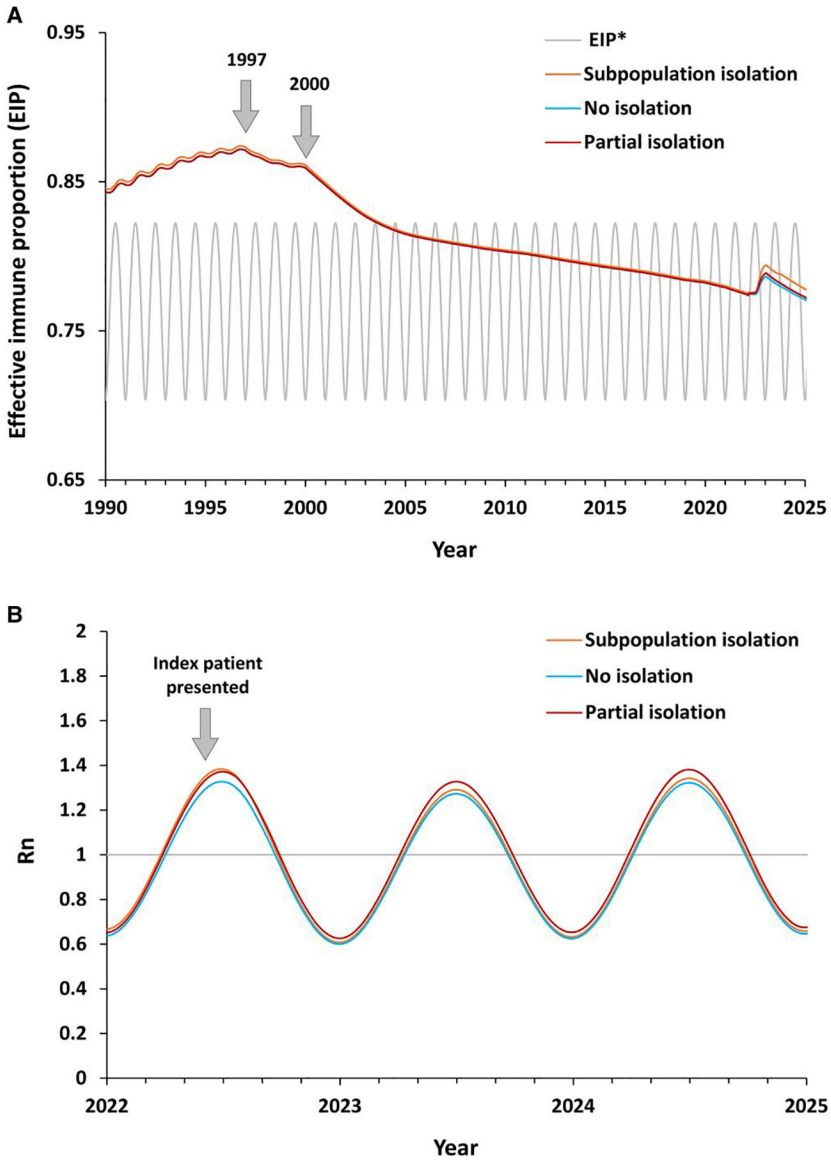

Figure 3.

A, Effective immune proportion (EIP) for the outbreak counties undervaccinated subpopulation for 3 mixing assumptions showing the decline in population immunity starting with the shift in routine immunizations to inactivated poliovirus vaccine/oral poliovirus vaccine (IPV/OPV) (1997) and then to IPV-only (2000). EIP* shows the threshold below which the population can sustain imported transmissions, with oscillation in the threshold for potential die out (EIP*) reflecting seasonality. The transient increase in EIP in 2022 reflects the population immunity gained by transmission of the outbreak virus in New York State (NYS). Population immunity will continue to fall in the future, implying ongoing seasonal risk of future outbreaks in NYS. *B*, Net reproduction number (R_n) for NYS for 3 mixing assumptions between 2022 and 2025 highlights the risk of sustained transmission of imported type 2 polioviruses when $R_n > 1$, as occurred with the index patient presenting in June of 2022.

Table 1.

Expected Paralytic Cases by Subpopulation Under Different Model Mixing Assumptions for the New York State Poliovirus Outbreak by Year for 2022–2024

	2022	2023	2024
Complete isolation	0.53 (0.41)	0.05 (0.05)	0
OU	0.53 (0.41)	0.05 (0.05)	0
OG	0	0	0
NU	0	0	0
NG	0	0	0
Homogeneous mixing	0	0	0
OU	0	0	0
OG	0	0	0
NU	0	0	0
NG	0	0	0
Subpopulation isolation	0.75 (0.53)	0.13 (0.12)	0
OU	0.43 (0.35)	0.07 (0.07)	0
OG	0	0	0
NU	0.33 (0.28)	0.05 (0.05)	0
NG	0	0	0
No isolation	0.59 (0.45)	0.04 (0.04)	0
OU	0.21 (0.19)	0.02 (0.02)	0
OG	0.05 (0.05)	0	0
NU	0.16 (0.15)	0.02 (0.02)	0
NG	0.17 (0.16)	0	0
Partial isolation	0.33 (0.28)	0.02 (0.02)	0
OU	0.29 (0.25)	0.02 (0.02)	0
OG	0.04 (0.04)	0	0
NU	0	0	0
NG	0	0	0

For each nonzero value, the number in parentheses represents the probability of detecting at least 1 paralytic case given the corresponding expected value in a Poisson distribution.

Abbreviations: NG, nonoutbreak counties general; NU, nonoutbreak counties undervaccinated; OG, outbreak counties general; OU, outbreak counties undervaccinated.