

Sustained detection of type 2 poliovirus in London sewage between February and July, 2022, by enhanced environmental surveillance



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Summary

Background The international spread of poliovirus exposes all countries to the risk of outbreaks and is designated a Public Health Emergency of International Concern by WHO. This risk can be exacerbated in countries using inactivated polio vaccine, which offers excellent protection against paralysis but is less effective than oral vaccine against poliovirus shedding, potentially allowing circulation without detection of paralytic cases for long periods of time. Our study investigated the molecular properties of type 2 poliovirus isolates found in sewage with an aim to detect virus transmission in the community.

Methods We performed environmental surveillance in London, UK, testing sewage samples using WHO recommended methods that include concentration, virus isolation in cell culture, and molecular characterisation. We additionally implemented direct molecular detection and determined whole-genome sequences of every isolate using novel nanopore protocols.

Findings 118 genetically linked poliovirus isolates related to the serotype 2 Sabin vaccine strain were detected in 21 of 52 sequential sewage samples collected in London between Feb 8 and July 4, 2022. Expansion of environmental surveillance sites in London helped localise transmission to several boroughs in north and east London. All isolates have lost two key attenuating mutations, are recombinants with a species C enterovirus, and an increasing proportion (20 of 118) meet the criterion for a vaccine-derived poliovirus, having six to ten nucleotide changes in the gene coding for VP1 capsid protein.

Interpretation Environmental surveillance allowed early detection of poliovirus importation and circulation in London, permitting a rapid public health response, including enhanced surveillance and an inactivated polio vaccine campaign among children aged 1–9 years. Whole-genome sequences generated through nanopore sequencing established linkage of isolates and confirmed transmission of a unique recombinant poliovirus lineage that has now been detected in Israel and the USA.

Funding Medicines and Healthcare products Regulatory Agency, UK Health Security Agency, Bill & Melinda Gates Foundation, and National Institute for Health Research Medical Research Council.

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Introduction

Poliovirus, the aetiological agent of paralytic poliomyelitis, is a member of the Enterovirus species C (family *Picornaviridae*, genus *Enterovirus*) and exists in three different serotypes, named poliovirus type 1, 2, and 3, respectively. The poliovirus genome consists of a single RNA positive strand molecule approximately 7400 nucleotides in length that contains a region coding for structural and non-structural proteins flanked by 5' and 3' short non-coding regions (appendix pp 3–4).

Before vaccination against polio was introduced in the UK in the 1950s, there were epidemics resulting in as many as 8000 cases of paralytic poliomyelitis each year and up to 750 deaths. The last outbreak of polio in the UK was in the late 1970s, and the last case of naturally

occurring polio in the UK was in 1984.¹ The WHO European region has been certified as polio-free since 2002.² However, despite the substantial reduction in the number of polio cases worldwide since the launch of the Global Polio Eradication Initiative in 1988, important challenges remain in 2022.³ There remain some areas in Afghanistan and Pakistan where wild poliovirus type 1 transmission has never been eliminated. In addition, there has been substantial transnational emergence and spread of circulating vaccine-derived polioviruses in recent years causing outbreaks across multiple countries worldwide and posing a major challenge to the polio eradication end game.⁴ Consequently, the risk of international spread of poliovirus is designated a Public Health Emergency of International Concern by WHO.⁵

Lancet 2022; 400: 1531–38

Published Online

October 12, 2022
[https://doi.org/10.1016/S0140-6736\(22\)01804-9](https://doi.org/10.1016/S0140-6736(22)01804-9)

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See Online for appendix

Research in context

Evidence before this study

The Global Polio Eradication Initiative identifies delayed detection of poliovirus transmission as one of the greatest risks to the programme. Since 2016, the initiative has invested heavily in environmental surveillance in low-income and middle-income countries as a supplement to surveillance for cases of acute flaccid paralysis. In high-income countries that rely solely on inactivated poliovirus vaccine for protection, implementation of poliovirus environmental surveillance is highly variable. We searched for articles reporting poliovirus environmental surveillance in inactivated poliovirus vaccine-using countries using the search term “polio*” and (“environmental surveillance” or sewage or wastewater or environment) and (“inactivated poliovirus vaccine” or IPV) in any field, in the Web of Science core collection covering 1970 to the search date (Sept 8, 2022), with no language restrictions. After screening 115 articles, we found 11 reporting environmental surveillance detection of poliovirus in seven inactivated poliovirus vaccine-only countries, or provinces, (Italy, the Netherlands, Israel, Argentina [Cordoba province], Japan, Indonesia [Yogyakarta province], and Switzerland). Most of these detections were Sabin-like viruses without evidence of circulation. Only in Israel was there evidence of poliovirus circulation: an imported wild-type poliovirus, which led to the reintroduction of oral poliovirus vaccine.

In all cases, poliovirus was detected by cell culture followed by molecular typing and sequencing, which is labour-intensive and time-consuming. In one case (Israel), direct molecular detection based on quantitative PCR was also used to allow quantification of virus copy numbers.

Added value of this study

We have implemented poliovirus environmental surveillance in the UK since 2014, following WHO recommended methods based on cell culture. Between Feb 8 and July 4, 2022, we isolated 118 genetically linked polioviruses derived from the serotype 2 Sabin vaccine strain in multiple sites in the sewage network serving north and east London. Whole-genome sequencing shows that these viruses share a unique recombination event in the non-structural region and have lost the key attenuating mutations affecting neurovirulence. Their prevalence, distribution, and continued evolution indicate local transmission, with some isolates from May, 2022 onwards being classified as vaccine-derived poliovirus, showing six to ten nucleotide changes in the VP1 region. We additionally found that nested PCR amplification and nanopore sequencing of poliovirus direct from sewage concentrates can provide a rapid method for detection and characterisation of these viruses.

Implications of all the available evidence

Polio environmental surveillance in London allowed early detection of vaccine-derived poliovirus transmission and a rapid public health response, including enhanced surveillance and a vaccination campaign with inactivated poliovirus vaccine. Whole-genome sequencing and direct detection by nanopore sequencing gave rapid sequence information that has helped track the spread and evolution of the virus. These methods could facilitate more widespread adoption of poliovirus environmental surveillance in Europe and worldwide.

More than 90% of all vaccine-derived outbreaks are from the Sabin 2 strain and have occurred in areas with persistently low immunisation coverage. It is therefore important to maintain sensitive surveillance for poliovirus globally following WHO recommendations.^{6,7}

Environmental surveillance by testing wastewater samples has been a valuable tool for tracking the distribution of viruses such as polio and non-polio enteroviruses and notably, in recent years, for monitoring the prevalence of different SARS-CoV-2 variants during the COVID-19 pandemic.⁸ In particular, a key advantage of this method is low sampling bias, as it captures all people in the catchment area and not only those that show symptoms and seek medical help. Environmental surveillance plays an important supplemental role to clinical surveillance for the detection of poliovirus and has helped to trace the elimination of wild poliovirus in some areas^{9–12} and to monitor the disappearance of vaccine virus after vaccination campaigns in countries such as Cuba, New Zealand and Japan.^{13–15} Environmental surveillance is particularly relevant in countries using only inactivated polio vaccine as it is understood that

although inactivated virus is highly effective against paralytic polio, it is less effective at inducing intestinal immunity and interrupting poliovirus transmission as compared with live-attenuated oral polio vaccine or natural infection.^{16,17} This is the reason why poliovirus can circulate undetected for long periods of time in countries using inactivated polio vaccine, even in those with high vaccination coverage such as Israel, where widespread circulation of wild type 1 virus imported from Pakistan, in the absence of reported paralytic cases, was identified through environmental surveillance in 2013.¹⁸

Sequence characterisation of poliovirus isolates from surveillance activities is crucial to confirm detection, distinguish vaccine-related from wild-type polioviruses, and identify genetic linkages between isolates to identify patterns of circulation. Nucleotide substitutions accumulate with time in the poliovirus genome according to a molecular clock that can be used to estimate how long a vaccine-related virus strain has been replicating since vaccine administration.¹⁹ The gene coding for capsid VP1 protein is commonly used for this analysis, but in some cases whole-genome analysis is necessary to confirm genetic linkage between different poliovirus isolates.

Sporadic detection of vaccine-like viruses containing a few mutations from the Sabin vaccine strains is expected following vaccination campaigns. However, finding related viruses with multiple mutations, separated in time and geographical space, is indicative of possible virus transmission in the community. The UK Health Security Agency (UKHSA) has developed detailed national guidelines for polio surveillance, investigation, and management that rely on the number, frequency of isolation, and sequence properties of poliovirus isolates identified through clinical and environmental surveillance.²⁰

We have been conducting routine environmental surveillance for poliovirus in two different cities in the UK, Glasgow and London, since 2014.²¹ As we have previously reported in the UK and as has been seen in other inactivated polio vaccine-using countries, vaccine-like poliovirus isolates can be sporadically detected in wastewater samples, most likely imported from countries still using oral polio vaccine for routine immunisation and outbreak response.^{21,22} We identified two type 1, two type 2, and eight type 3 vaccine-like poliovirus isolates between 2017 and 2021; all were genetically unrelated, contained few mutations compared with oral polio vaccine, and represented independent events with no related viruses identified in subsequent samples, hence providing no evidence for local poliovirus transmission.

Here, we use conventional cell culture methods for the identification of poliovirus in sewage samples, direct detection by nanopore sequencing (DDNS), and a novel nanopore protocol to quickly generate whole-genome sequences of multiple type 2 poliovirus isolates identified in sequential sewage samples from London between Feb 8 and July 4, 2022, to better understand their natural history and geographical spread, with an aim to guide public health interventions to protect children from developing paralytic polio and to stop virus transmission.

Methods

Sewage sample collection and processing

This study covers the analysis of sewage samples collected between Jan 11 and July 4, 2022. Sampling sites are shown

in maps in figure 1 and are listed in the appendix (pp 4–5). Samples are analysed in the WHO Global Specialised Laboratory for Polio at the National Institute for Biological Standards and Control (Potters Bar, UK) following the WHO recommended stepwise process that includes concentration, virus isolation in cell culture, and molecular characterisation.^{21,23–26} Methods for sample

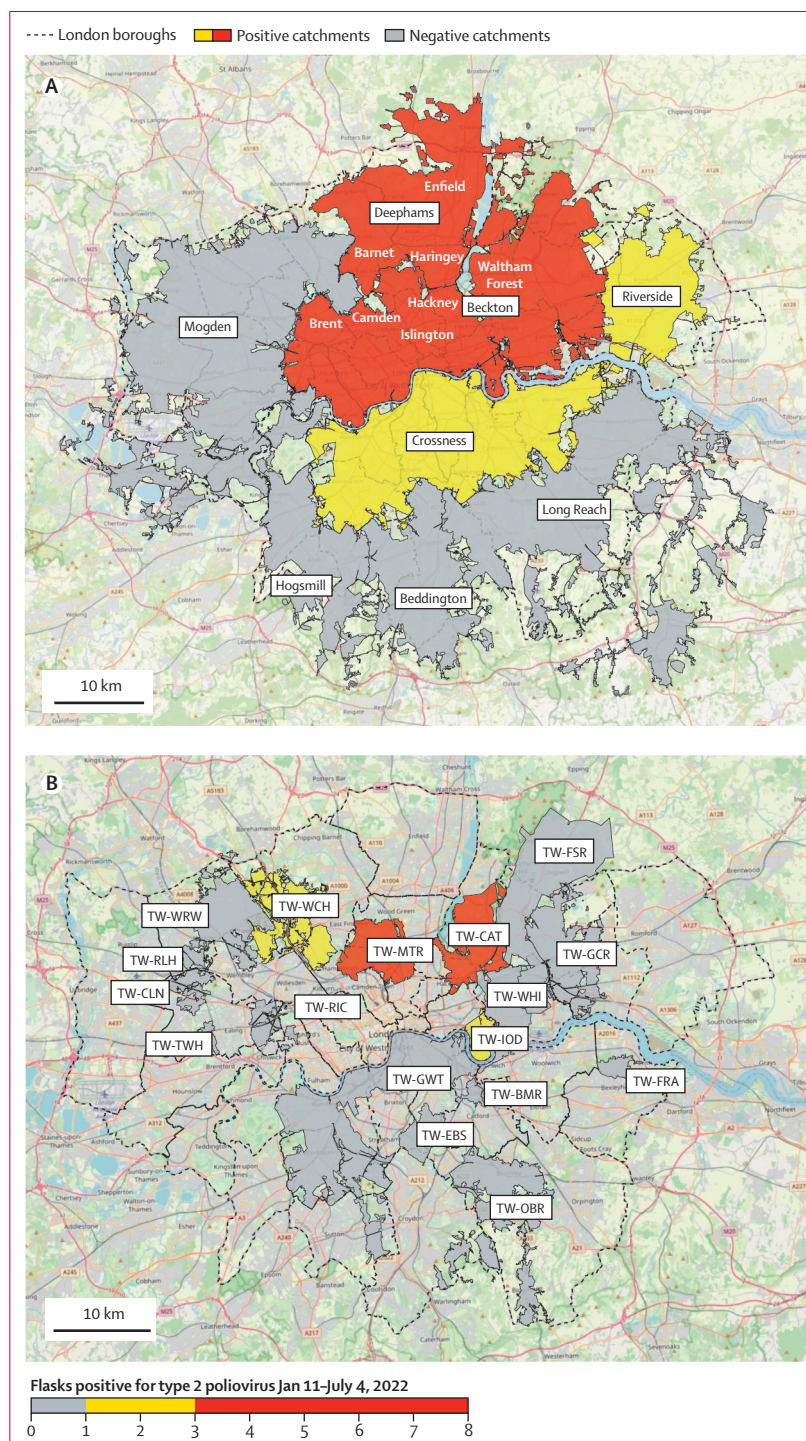


Figure 1: Location of London sewage sites sampled for poliovirus detection

The location of type 2 poliovirus isolations in London sewage is shown in maps displaying main sewage treatment works (A) or network treatment works sites (B). Catchment areas were coloured by poliovirus prevalence; areas with sustained type 2 poliovirus detection or high virus concentration if only one sample was tested (samples producing $\geq 50\%$ of type 2-positive cell flasks) in red; areas with only occasional detection or low virus concentration in yellow (samples producing $< 50\%$ of type 2-positive cell flasks); and sampling sites with negative results in grey. A sample from TW-10D site collected on June 20, 2022, produced four type 2-positive cell flasks, but samples collected on June 13 and July 4, 2022, from the same site were negative, so it was coloured in yellow.

TW=treatment works. BMR=Brookmill Road. CAT=Cadogan Terrace. CLN=Costons Lane Northolt Lane. EBS=Effra Branch Sewer. FRA=Fraser Road. FSR=Folkstone Road. GCR=Gaoisgoine Road. GWT=Greenwich Terminal. 10D=Isle of Dogs. MTR=Martaban Road. OBR=Old Bromley Road. RIC=Richford Street. RLH=Rayners Lane Harrow. TWH=Trummers Way Hanwell. WCH=Watserdale Close Hendon. WHI=West Ham Inlet. WRW=Watkin Road Wembley.

collection and processing of raw sewage are described in the appendix (pp 1–3).

Identification, sequencing, phylogenetic analysis, and direct detection of the isolates

Sewage concentrates were analysed for the presence of poliovirus by virus isolation in rhabdomyosarcoma and mouse L20B cells followed by whole-genome RT-PCR amplification using widely established protocols (appendix p 2).

Whole-genome RT-PCR products were sequenced using Oxford Nanopore Technologies and Illumina protocols (appendix pp 2–3). For convenience and quick results, all poliovirus whole-genome PCR products were sequenced using nanopore following similar methods to those we have previously described.²⁴ A large number of poliovirus whole-genome PCR products were also sequenced by Illumina technology (n=73) using methods described before^{21,23,24} and producing nearly identical sequences to those from nanopore but helping resolve a few ambiguities.

Poliovirus type 2 sequences obtained in this study were aligned to the serotype 2 Sabin vaccine strain reference genome sequence (AY184220) using the program ClustalW (within Geneious). Bootstrapped maximum likelihood neighbour-joining trees were constructed using Nextstrain software. Phylogenetic trees were plotted in the R statistical programming language using ggtree.

A protocol based on the DDNS method²⁴ that we and others have recently developed for the direct detection of poliovirus from stool samples was also used. We modified the protocol to use type 2 poliovirus-specific primers to

improve the sensitivity for type 2 poliovirus detection by reducing the background of VP1 sequences from co-circulating species C enteroviruses obtained with the original protocol. Briefly, 0.4–1.2 mL of sewage concentrate was used to extract RNA using the MagMAX Viral RNA Isolation Kit. Extracted RNA was used in nested PCR amplification reactions using poliovirus–enterovirus primers and PCR products were sequenced by nanopore as described above.

Statistical analysis

Statistical analysis and molecular clock-based inference of the date of oral polio vaccine administration leading to the vaccine-derived poliovirus were done using GraphPad Prism (version 9) software. Poliovirus sequencing data were processed and analysed using Geneious (version 10.2.3), MEGA X, and Nextstrain software as described here.

Role of the funding source

The funders of the study had no role in study design, data collection, data analysis, data interpretation, or writing of the report.

Results

Two poliovirus type 2 vaccine-like isolates were detected in a sample collected on Feb 8, 2022 from London Beckton sewage treatment works, with a catchment area of approximately 3 million people and covering areas north of the River Thames in London. Following three subsequent negative samples, genetically related type 2 poliovirus isolates have been identified in increasing concentration, meaning that an increasing proportion of cell culture flasks with a positive type 2 poliovirus isolation among the eight flasks inoculated with each sewage concentrate were observed in samples collected from the London Beckton area since April 12, 2022 (figure 2, appendix pp 4–5).

Extensive sampling efforts were conducted to localise the area in which virus transmission could be occurring and to guide vaccination responses. Beckton sewage treatment works was subdivided into smaller sub-catchment areas and sampling was also expanded to other large London sewage treatment works plants outside Beckton to investigate whether type 2 poliovirus was present in a wider area. As shown in figures 1 and 2, the location of positive sampling sites indicates that the virus is mainly present in some areas within Beckton and bordering areas to the north and west covering several north London boroughs. Sampling has also detected virus in lower concentration and frequency in areas adjacent to the Beckton catchment area to the south and to the east (figures 1, 2; appendix pp 4–5). However, as only sporadic type 2 poliovirus isolations have occurred from these areas, it is not clear whether the virus has established sustained transmission there or if the detections are due to travel from the affected areas. All negative sewage

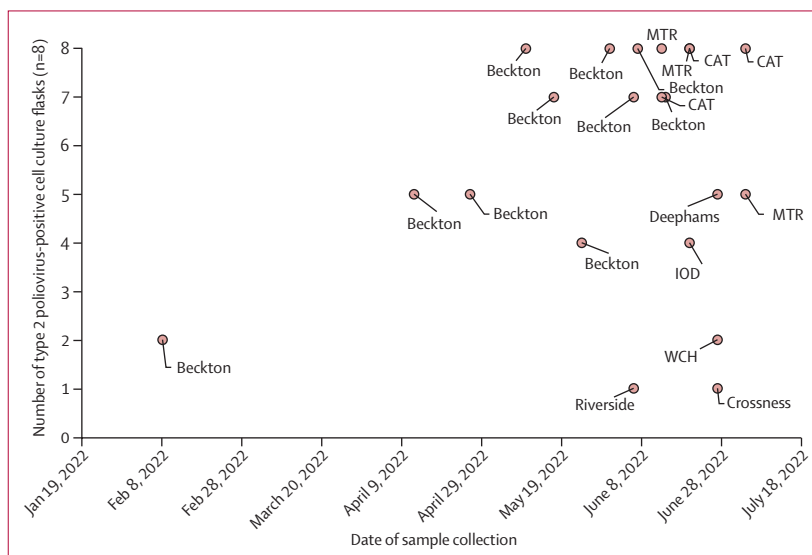


Figure 2: Type 2 poliovirus isolations from London sewage samples

The number of cell flasks with a positive type 2 isolation result per sample is shown. Date and location of sample collection are indicated in the figure. Eight cell flasks (five with rhabdomyosarcoma plus three with L20B) were infected with each sewage concentrate. Samples with a negative isolation result are not represented but are listed in the appendix (pp 4–5). CAT=Cadogan Terrace. IOD=Isle of Dogs. MTR=Martaban Road. WCH=Waterside Close Hendon.

concentrates produced full cytopathic effect in rhabdomyosarcoma cells within 4–5 days of inoculation as expected from the high prevalence of human enteroviruses in sewage and confirming the adequacy of the sample.

A total of 118 type 2 poliovirus isolates have been identified in 21 of 52 sewage samples collected in London between Feb 8 and July 4, 2022. Each isolate represents a single positive cell culture. In addition to type 2 poliovirus isolates, we identified three type 1 and six type 3 poliovirus vaccine-like isolates in the 52 sewage samples tested from London between Jan 11 and July 4, 2022 (appendix pp 4–5), all containing few mutations from oral polio vaccine strains without any indication of genetic linkage except via the Sabin parent strain. During this period, we have continued testing monthly samples from Glasgow. None of the samples contained type 2 poliovirus isolates and only one sample, collected on March 30, 2022, was found to contain a type 3 poliovirus vaccine-like isolate unrelated to any of the London type 3 poliovirus isolates.

Whole-genome sequencing revealed that all type 2 poliovirus isolates are related to the Sabin 2 vaccine strain and show the same recombinant genetic structure between type 2 poliovirus and an unidentified species C enterovirus strain with crossover point at nucleotide 5139 (appendix pp 3–4). Phylogenetic analysis based on whole-genome sequence comparisons indicates high sequence diversity between the type 2 London sewage isolates, even among isolates within the same sample, with viruses diversifying into multiple lineages over time, consistent with circulation in the population (figure 3). Only two sewage samples (ENV-22-027 and ENV-22-117) contained two isolates with identical sequences among the seven and five isolates found in those samples, respectively. Most type 2 poliovirus isolates (n=98) are defined as vaccine-like poliovirus (fewer than six nucleotide changes in VP1 region), but some (n=20) are classified as vaccine-derived type 2 poliovirus containing between six and ten nucleotide changes in the VP1 region from the Sabin 2 vaccine strain. The vaccine-derived sequences appear to group in at least three distinct genetic sub-clusters that include type 2 poliovirus isolates from different sampling sites (figure 3). The first vaccine-derived poliovirus isolate was identified in a sewage sample collected from London Beckton main site on May 24, 2022. As shown in figure 4, a linear regression analysis based on the number of capsid nucleotide sequence differences from the Sabin 2 vaccine strain (mean values for each sample if multiple flasks were positive) versus date of sample collection, estimated the date of administration of the dose of oral polio vaccine leading to this type 2 poliovirus transmission event to be Dec 23, 2021 (95% CI Oct 28, 2021, to Jan 26, 2022).

All 118 type 2 poliovirus isolates share six mutations from the Sabin 2 vaccine strain. These include reversions at the two main Sabin 2 attenuating sites: A481G in the 5' non-coding region (5' NCR) and VP1-I143V in the

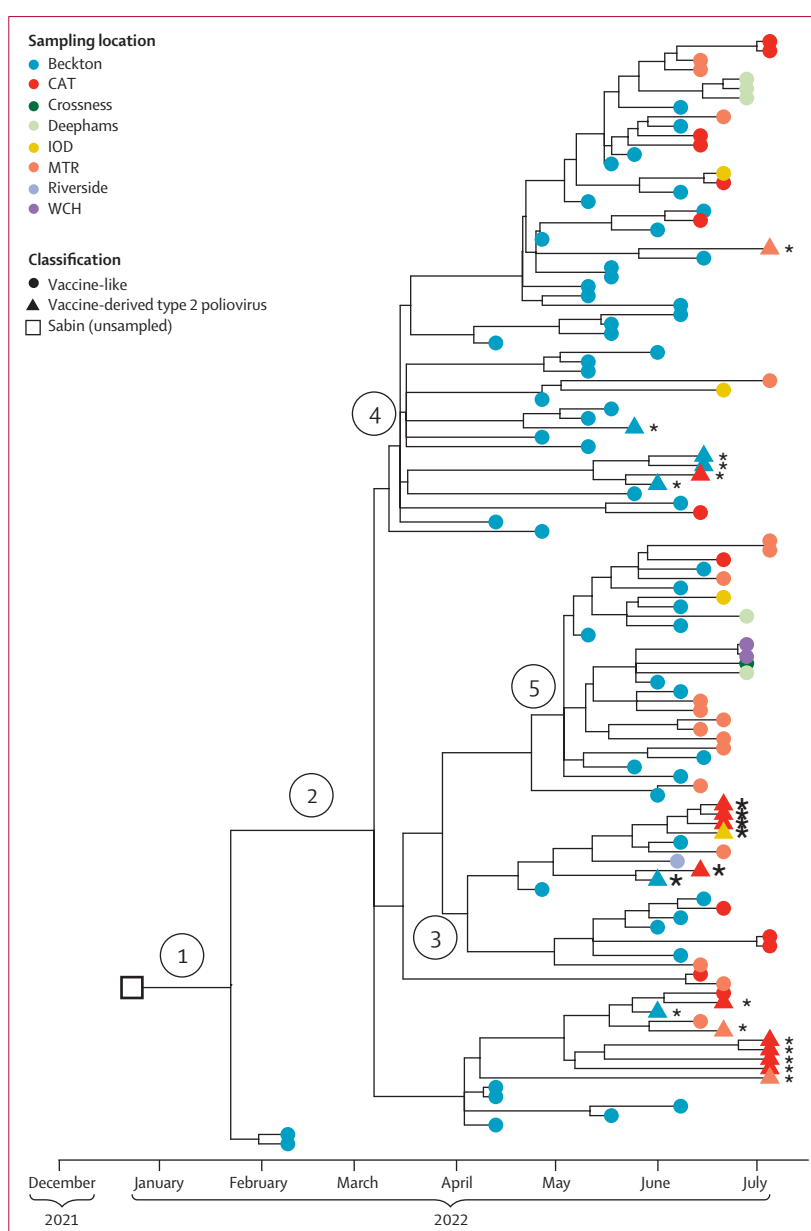


Figure 3: Tree showing phylogenetic relationship between all 118 type 2 poliovirus isolates by the analysis of whole-genome nucleotide sequences using the maximum likelihood method and Tamura-Nei model
The inferred Sabin origin date is shown at the root of the tree. Symbols are coloured by sampling site. Vaccine-derived and Sabin-like viruses are shown as different shapes with vaccine-derived type 2 poliovirus highlighted by an asterisk. Numbers 1–5 in open circles indicate groups of mutations acquired at each stage of virus evolution that are shared by viruses derived from that branch and are described in the appendix (pp 5–6). CAT=Cadogan Terrace. IOD=Isle of Dogs. MTR=Martaban Road. WCH=Waterside Close Hendon.

VP1 capsid protein. This pattern implies reversion to neurovirulent virus. 11 additional mutations were acquired between Feb 8 and April 12, 2022, and were carried forward and viruses further mutated at different nucleotide positions diversifying in different genetic sub-lineages (figure 3; appendix pp 5–6).

Although all results in this paper are based on the gold standard method for poliovirus detection in sewage

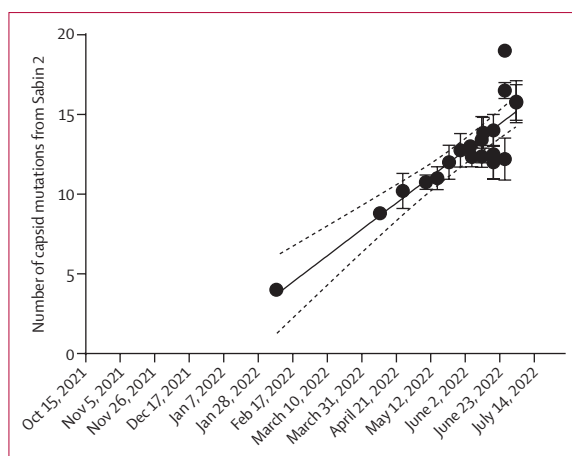


Figure 4: Estimation of the date of initial vaccination with Sabin 2

The figure represents mean values of the number of capsid mutations from Sabin 2 vaccine strain (GenBank ID AY184220) for each of the 21 type 2-positive samples (with bars indicating standard error of the mean plotted) plotted by date of sample collection. Dashed lines show 95% CI bands of the best-fit line. The data were adjusted to a linear function for the accumulation of nucleotide substitutions ($y=0.07871 \times x - 3507$; $r^2=0.79$). The date of initial Sabin 2 infection that led to the type 2 isolates identified in the London sewage was estimated by simple linear regression extrapolating the line for the evolution rate of nucleotide substitutions backwards to 0 capsid substitutions.

recommended by WHO and based on virus isolation in cell cultures, we also used the DDNS method²⁴ for the direct detection of type 2 poliovirus from a selected number of sewage samples that had been shown to contain a wide range of poliovirus concentration. As shown in the appendix (p 7), type 2 poliovirus detection using Y7/Q8 primers for the second nested PCR reaction as in the original protocol, had reduced sensitivity for type 2 poliovirus detection as compared with virus isolation. Type 2 poliovirus was missed from one of the samples that had been shown to be positive by virus isolation. This reduced sensitivity was due to RNA from a coxsackievirus A20 strain cocirculating with type 2 poliovirus in the same area being amplified with the Y7/Q8 primers. A coxsackievirus A15 strain was also detected in a sample negative for type 2 poliovirus (appendix p 7). When using type 2-specific primers in the second nested PCR reaction, sensitivity was increased and we were able to detect type 2 poliovirus in a sample that had been negative by virus isolation (appendix p 7).

Discussion

The geographical spread, frequency, and concentration of type 2 poliovirus isolates from London sewage samples and their high genetic diversity indicate virus transmission in areas of north and east London that might extend to adjacent neighbourhoods. In addition, the loss of the two main Sabin 2 attenuation mutations in all type 2 London sewage poliovirus isolates implies their probable reversion to a neurovirulent phenotype increasing the risk of type 2 poliovirus infections causing paralytic poliomyelitis. These findings have warranted an

urgent public health response including enhanced surveillance and a vaccination campaign with inactivated polio vaccine among children 1–9 years old in London.

Extensive whole-genome characterisation of all 118 type 2 poliovirus isolates identified unique genetic features such as a recombinant structure between the type 2 poliovirus and an unidentified enterovirus C strain and several unique mutations acquired during virus evolution. These unique genetic signatures show an unequivocal genetic link between all 118 type 2 poliovirus isolates, which share a common single origin, and can be used to easily identify genetically related viruses from elsewhere. 20 vaccine-derived isolates were identified among the 118 type 2 poliovirus isolates, including vaccine-derived type 2 poliovirus from sewage sites with adjacent but non-overlapping catchment populations, indicating local circulation. The level of detail on the early evolution of type 2 vaccine poliovirus generated in this study is unprecedented and highlights the value of whole-genome sequencing, which allowed the early detection of poliovirus transmission in London by establishing high-resolution linking between vaccine-like and vaccine-derived poliovirus isolates. In our example, viruses appear to have evolved in multiple directions from a single origin, with many London sewage type 2 poliovirus isolates only sharing one or two common VP1 nucleotide changes from the Sabin 2 vaccine strain, which means that genetic linkage between them is not apparent from just the VP1 sequences. In light of these results, it might be necessary to refine the definition of circulating vaccine-derived virus, currently based on VP1 sequence comparisons, to ensure the early and rapid detection of poliovirus transmission events such as the one ongoing in the UK. This might be currently more relevant in countries that have been polio-free for many years but can be expanded globally when we get closer to the poliovirus eradication endgame.

The use of next-generation sequencing, which is increasingly accessible and affordable, will help expand sequencing capacity to polio laboratories worldwide. Nanopore sequencing provides great portability and control over time to results, allowing us to get whole-genome sequences within 24 h of viruses being collected from cell cultures, with the additional advantage of producing long reads covering the entire poliovirus genome that confirmed the type 2 poliovirus recombinant structure. Nanopore whole-genome sequencing complements the recently described DDNS method that allows the direct detection of poliovirus from stool samples,²⁴ substantially reducing the time between samples arriving in the laboratory and availability of VP1 sequences, which is crucial in areas of active poliovirus transmission. We are actively working on trying to adapt the DDNS method for the direct detection of poliovirus from sewage samples and early results with samples reported here suggest this will be possible with some modifications of the original protocol. We will need to extend this validation to the detection of all three poliovirus types. This will allow a

faster testing of greater number of sewage samples and the selection of those positive for virus isolation and further testing.

Poliovirus transmission in London reminds us that no country is safe from polio until eradication is achieved globally. Similar events in 2022 in Israel²⁷ and the USA,^{28,29} where the first paralytic polio cases since 1989 and 2013 respectively have been reported, act as further reminders and have generated broad public interest. Early evidence indicates that the vaccine-derived poliovirus type 2 strain associated with the polio case in the USA and related type 2 poliovirus isolates found in the New York sewage are genetically linked with the London sewage isolates described here and with type 2 poliovirus isolates recently found in sewage samples from Israel.^{28,29} Full investigation is currently ongoing to confirm and better understand the link between the isolates from the three countries as new type 2 poliovirus sequences continue to emerge.

Our detection of poliovirus through environmental surveillance has several limitations. First, although upstream sampling can help localise transmission, stool surveys among healthy individuals or poliomyelitis case reports are required to conclusively identify infected individuals and communities participating in transmission.³⁰ Children in some communities in north London are under-vaccinated and could be the focus of the current outbreak, which might explain the detection of genetically linked viruses in Israel and New York, but this is not confirmed. Second, we relied on two different sampling methods based on a grab or composite sample. The composite sample method is preferred and is likely to be more sensitive, but it is not possible at all sampling points. Finally, we only used direct molecular detection methods with a subset of samples. Further testing with the DDNS method will help generate more data on the performance of this method and its potential to accelerate poliovirus detection.

The results shown here represent the first evidence of poliovirus transmission in the UK since 1984.¹ It is crucial that public health measures are adopted and guided by our environmental surveillance findings following the national polio guidelines set up by UKHSA. No cases of polio have been clinically identified during this period and the risk to the wider population is still assessed as low. However, the Joint Committee on Vaccination and Immunisation noted that coverage for the 3-dose primary schedule in 1-year-olds in London is well below the average achieved for the UK and uptake of the pre-school booster in 5-year-olds is even lower.³¹ The high-density populations in the areas affected and the number of individuals under-vaccinated in those boroughs suggests that there is significant potential for the vaccine-derived type 2 poliovirus to continue to spread. There is significant overlap between the local authorities with the lowest vaccine coverage and where vaccine-derived virus has been detected.³² In order to prevent cases of paralysis occurring and attempt to interrupt transmission, the Joint

Committee on Vaccination and Immunisation advised that an inactivated polio vaccine booster vaccination campaign targeting children aged 1 to 9 years in London should be rolled out urgently, starting in the London boroughs where vaccine-derived type 2 poliovirus has been detected and then expanding to all London boroughs.³¹ In addition to the expansion of environmental surveillance, health authorities have implemented enhanced clinical and laboratory surveillance. The UK National Health Service is also strengthening ongoing work to improve uptake nationally in the routine childhood programme. In London, active call–recall of unvaccinated and partially vaccinated children under the age of 5 years is already underway through primary care, with a planned phased extension up to 18 years of age.³³

Further interventions will continue to be guided by findings from environmental surveillance, which provides a sensitive and flexible tool to detect circulating or imported polioviruses. This includes enhanced sampling and addition of new sites targeting smaller communities following any positive detection to help localise transmission. The value of environmental surveillance in the detection and public health response to infectious disease threats is becoming increasingly apparent based on our experience with poliovirus, and that with SARS-CoV-2 and other pathogens.

Contributors

JM conceptualised the study and wrote the original draft. JM, AZea, VS, and MR designed and supervised the study. JM, EB, DK, TW, MM, and AT curated the data. JM, DK, and NCG did the formal analysis. DK, TW, EB, AT, MM, RM, CT, AGS, and JOA investigated the samples. JM, NCG, DK, TW, EB, AT, MM, RM, CT, AGS, JOA, AZea, AZeb, and MJW wrote the methodology. VS and MR were involved in project administration. JM, NG, MJW, VS, and MR were in charge of resources. All authors reviewed and edited the manuscript. All authors had full access to all the data in the study and had final responsibility for the decision to submit for publication.

Declaration of interests

We declare no competing interests.

Data sharing

Nucleotide sequences determined in this study are available from the NCBI sequence database with GenBank numbers OP410363–OP410480.

Acknowledgments

We thank Mihaela Cirdei and Julian Hand from the UK Health Security Agency (UKHSA) for arranging collection and transport of raw sewage samples. We thank members of the UKHSA NICC72 IMT–Vaccine Derived Polio Virus 2 for helpful discussions and feedback. Sewage analysis is based on independent research commissioned and funded by the National Institute for Health Research (NIHR) Policy Research Programme (National Institute for Biological Standards and Control Regulatory Science Research Unit) and Medicines and Healthcare products Regulatory Agency. This work was also supported by grants from the Bill & Melinda Gates Foundation (OPP1207299, INV-024477). NCG acknowledges funding from the UK Medical Research Council (MRC) Centre for Global Infectious Disease Analysis (reference MR/R015600/1), jointly funded by the MRC and the UK Foreign, Commonwealth, and Development Office (FCDO), under the MRC/FCDO Concordat agreement and is also part of the EDCTP2 programme supported by the EU. The views expressed in this publication are those of the authors and not necessarily those of the funders, the National Health Service, the NIHR, the Department of Health, arm's length bodies, or other government departments.

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