

MOLECULAR HIV SURVEILLANCE: A GLOBAL REVIEW OF HUMAN RIGHTS IMPLICATIONS



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CONTENTS

EXECUTIVE SUMMARY	4
GLOSSARY OF TERMS	5
WHAT IS THIS BRIEFING PAPER AND WHO IS IT FOR?	7
WHAT IS MOLECULAR HIV SURVEILLANCE? HOW AND WHY IS IT BEING USED?	8
Molecular HIV Surveillance for research	11
Molecular HIV Surveillance for public health intervention	12
Where is Molecular HIV Surveillance being used and who is being targeted?	14
Where does the data for Molecular HIV Surveillance come from?	15
What tools are used to undertake Molecular HIV Surveillance?	16
WHAT ARE THE CONCERNS WITH MOLECULAR HIV SURVEILLANCE?	19
Consent and autonomy violations	19
Lack of community consultation and engagement	21
Stigma on targeted communities	22
Privacy and data protections	23
Concerns about “proving” direct transmission	24
Concerns about HIV criminalisation	25
RECOMMENDATIONS	27
Recommendations for researchers and scientists	27
Recommendations for public health practitioners	28
Recommendations for legal system experts and actors	29
Recommendations for people living with HIV	29
METHODOLOGY	30
APPENDIX: LITERATURE REVIEWED	31
Peer-reviewed scientific literature	31
Community, research, and government grey literature	34

EXECUTIVE SUMMARY

Molecular HIV surveillance (MHS) is an umbrella term that describes a wide range of practices focused on the monitoring of HIV variants and the differences and similarities between them for scientific research, public health surveillance and intervention. This briefing paper was developed for people living with HIV, activists, legal experts, and human rights campaigners to understand the complexities and consequences of MHS – a growing research and public health surveillance practice that has concerning implications for human rights.

To conduct MHS, scientists rely on the results of HIV genetic sequencing tests taken from people living with HIV – these tests are often done to determine if the individual has a strain of HIV that is resistant to certain treatments. Interest in, and use of, MHS is increasing globally. In some places, MHS is being conducted in ways that puts the rights of people living with HIV in jeopardy. Depending on the circumstances, the reuse of genetic sequencing data is often done without the explicit consent of the individual or communities.

Researchers and public health practitioners are conducting MHS in countries which actively criminalise HIV non-disclosure, exposure and/or transmission. In addition, increased surveillance of people who use drugs, people who sell or buy sex, migrants, and gender and sexual minorities living with HIV, typically leads to greater precarity, stigma, discrimination, and criminalisation. HIV experts and advocates have raised human rights concerns about this technology, including: consent and autonomy; lack of community consultation; increased stigma on targeted communities; privacy and data protections; whether or not the technology can be used to “prove” direct transmission; and how MHS may intensify HIV criminalisation within communities who are already marginalised and oppressed.

To develop this briefing paper, a global scoping review of a literature on MHS was conducted – with 92 pieces of scientific, community, and expert literature from academic peer-reviewed journals, and grey literature from governments and community-based organisations examined overall. Throughout the review process, insight was sought from leading MHS advocates from around the world.

RECOMMENDATIONS

Based on our global scoping review of MHS research and intervention literature, we have produced a number of recommendations for a wide range of stakeholders which can be found at the end of the document. The most important of these are:

1. Take seriously and act upon community concerns about MHS.
2. Respect the bodily autonomy and integrity of people living with HIV in all our diversity.
3. MHS implementers must demonstrate a clear public health benefit that outweighs the potential harms of MHS, including by ensuring protections (i.e., data privacy, legal protections, social harms prevention, etc). These demonstrated benefits of MHS must measurably include people living with HIV.
4. Providers ordering HIV sequencing must inform people living with HIV about how their blood and data are being used for MHS purposes and be allowed to withdraw consent if they so wish, without fear of negative consequences to their HIV treatment and care.
5. Implementers of MHS should publicly advocate against punitive or coercive laws and policies aimed at people living with HIV and ensure that MHS is never used in criminal, civil, or immigration investigations or prosecutions.

GLOSSARY OF TERMS

MHS is highly technical, and practitioners use many complex scientific terms. To effectively respond to concerns of this growing practice, it is important that impacted individuals and communities understand some of the complex technicalities. Below is a starting list of a number of the key terms used in MHS research and practice.

Cluster	Cluster is an epidemiological term used to describe a group of health events – from infectious disease to cancer diagnoses – that are closely grouped—or “clustered”—in both time and geographic place. In MHS, a cluster is a specific and technical term used to define genetic relatedness between samples of HIV taken from different people. Researchers compare viral mutations from various sources to identify genetic similarities and differences where transmissions are happening at a rapid rate. Genetic similarities are determined by analysing how closely related RNA and DNA of the HIV are (human DNA is not analysed in this process). If scientists identify a group of similar viral mutations where HIV has been transmitted – <i>close to the same time, and in the same location</i> – this is known as a cluster. In some cases, clusters are also known as “transmission networks”, or “risk networks”. Being identified as part of a cluster does not mean that the people whose blood is being examined have ever come into contact with each other, it only means that there are genetic similarities between the samples of HIV taken from members of the cluster, as determined by the various tools used by researchers. People who are not living with HIV are also identified as belonging to specific clusters/transmission networks through a combination of molecular surveillance and contact tracing.
Cluster detection and response	Cluster detection and response (CDR) is the term used by the United States Centers for Disease Control and Prevention and public health departments across the United States to describe the actions taken once a cluster is identified. These actions may include efforts to link people to care and diagnostics and can also involve – in some instances – contacting police agencies.
Criminalisation	Criminalisation is the process by which certain social behaviours, activities, and individuals are socially classified into crime and criminals. When an issue is criminalised, it becomes understood as something that should be addressed via a criminal legal system and controlled with the threat of punishment, as opposed to being addressed in other ways. Criminalisation may relate broadly to many issues, including drugs, migration, sex work, poverty, and also HIV, where specific laws and policies are developed to regulate and control that issue through policing and the criminal legal system.
Directionality	A term used to describe time-bound relationships between HIV genetic sequences. Some tools used in molecular epidemiology can indicate whether viruses are related, and which strain or sample is “older” and “younger.” This is known as directionality, where relationships between strains of the virus are reconstructed in a time-bound, linear direction, like a family tree. Scientists are interested in understanding the directionality of HIV transmission so they can see how closely linked different people may be in a specific cluster and how the virus evolves over time.
Direct transmission	Information on directionality can be used to try and determine if one individual transmitted HIV to another individual, which is known as direct transmission. The scientific method to determine direct transmission is not currently 100% accurate, so inferring who transmitted to whom is only an informed guess. Some researchers are adamant that MHS cannot determine, for example, that Sample A is the source of HIV transmission resulting in Sample B, because the technology only shows <i>relatedness</i> between two samples and is not advanced enough at this time to determine direct transmission between only two people. However, researchers are working to advance the technology to be able to definitively determine direct transmission, although this is likely only possible in highly specialised research settings. However, HIV genetic information can be combined with other sources of information, such as medical records and contact tracing, to infer as to who transmitted HIV to whom.
Genetic sequence	The individual genetic RNA and DNA make-up of a single strain of HIV is commonly referred to as a genetic sequence. Each genetic sequence is taken from a blood sample and is then digitised into a unique code for MHS analysis. A genetic sequence can be used for individual patient care or can be used to identify relatedness to sequences from other people. Once a genetic sequence becomes code it can also be widely shared and stored in large databases for use by many researchers.

HIV criminalisation	HIV criminalisation is the unjust use of criminal and similar laws, policies and practices to police, regulate, control, and punish people living with HIV based on their HIV-positive status. Laws or policies differ around the world and can criminalise a range of activities including alleged HIV non-disclosure prior to sex, potential or perceived HIV exposure through many different means, or unintentional transmission of the virus.
Inference (infer)	Inference is a term used by scientists for the practice of trying to reach a conclusion based on observation, evidence, and reasoning. To infer a conclusion means it is a best guess, and not something that is conclusively proven. In MHS studies and in public health efforts, scientists and public health practitioners may try to infer direction or even direct transmission based on various sources of information.
Informed consent	Informed consent is a cornerstone of ethical scientific research and practice and means that individuals who participate in research should do so voluntarily, understanding the purpose, and its risks and potential benefits, as fully as possible. Where a person has the capacity to understand this information, and the ability to act on it voluntarily, the decision to participate is generally seen as an expression of having the autonomy to decide for oneself. Respect for autonomy is the guiding principle behind informed consent practices, to ensure violations and abuses in research and practice are mitigated.
Longitudinal cohort research study	A longitudinal study is a form of research study which follows participants – often from a specific cohort – over a prolonged period of time, often years and even decades. A cohort study is a particular form of longitudinal study that samples a specific cohort – which is a group of individuals that share a common characteristic, such as a positive HIV diagnosis.
Molecular HIV surveillance	Molecular surveillance for HIV, or MHS, is an umbrella term used to encompass a wide range of research and public health practices, and it can come by many different names, including, <i>HIV cluster detection and response</i> , <i>HIV genotype analysis</i> , <i>HIV genetic sequencing</i> , <i>HIV phylogenetic surveillance</i> , among others. Using a range of molecular genetic research techniques, scientists conduct molecular surveillance research to examine evolutionary relationships, similarities and differences between different viral strains of HIV. There are diverse aims of MHS, but generally, the research and public health goals are to understand viral transmission and drug resistance patterns, and to locate areas where new transmissions are happening rapidly so as to intervene and prevent new transmissions. The practice is often done without consent and has multiple privacy and human rights implications.
Phylogenetic analysis	Phylogenetic analysis compares the genetic sequences of organisms by estimating their evolutionary relationship to one another. In MHS, phylogenetic analysis is applied to the genetic sequences of HIV taken from people living with HIV. The viruses are compared using a phylogenetic tree, which is similar to a family tree – to show how close or far apart different sequences are. These phylogenetic trees are used to assist with inferring evolutionary relationships, and similarities and differences between individual HIV strains.
Public health surveillance	Public health is the name usually given to a government department or institution that responds to various health issues and should not be confused as a general term to describe the concept of community health and well-being. Public health departments systematically collect and analyse health-related data to plan, implement, and evaluate public health interventions. This system is understood as public health surveillance, and practitioners in these systems implement MHS in some countries.
Recency assay	A recency assay, also known as a RITA (Recent Infection Testing Algorithm) test, is a tool used by researchers which looks at the levels and proportions of certain antibodies in the blood of someone living with HIV, to estimate whether HIV acquisition was recent – within the previous 4 to 6 months – or if HIV has been present for longer. The tool can generally infer whether or not HIV has been recently acquired, but it is not 100% accurate due to individual variations in the timing of HIV-related antibody production. Used in combination with other MHS tools, recency assays have been able to assist in improving the accuracy of analyses to infer direct transmission.

WHAT IS THIS BRIEFING PAPER AND WHO IS IT FOR?

This paper is focused on the issue of molecular HIV surveillance (referred to throughout this briefing paper as MHS) to help support people living with HIV, activists, legal experts, and human rights campaigners to understand the complexities and consequences of MHS, which is a growing research and public health surveillance practice that has concerning implications for human rights.

Forms of HIV molecular genetic analysis for scientific research, and public health surveillance and intervention – are being implemented and scaled-up across the globe. As the practice has grown, so too have the concerns from communities of people living with HIV, ethicists, and human rights and civil liberties advocates. There have been widespread human rights concerns about the practice, notably around the technology's implications for consent and autonomy and the potential for intensified stigma and criminalisation resulting from the outcomes of MHS research and public health interventions.

To respond to this context, this briefing paper was developed from a detailed global scoping review of literature on MHS, with 93 pieces of scientific, community, and expert literature from academic peer-reviewed journals, and grey literature from governments and community-based organisations examined overall. Throughout the review process, insight was sought from leading MHS advocates from around the world.

The goal of this paper is to help increase the understanding of what MHS is and the implications of MHS for individuals and organisations working to advance the rights and well-being of people living with HIV. With increased knowledge on the practices of MHS, individuals and organisations can be better equipped to advocate for ending research and surveillance practices with a potential to harm the rights, autonomy, and well-being of people living with HIV.

This briefing paper begins with a detailed explanation of what MHS is and how it is used across the globe, including how the technology works, where it is being conducted, and by whom. The report then describes the growing human rights concerns relating to the use of this technology, specifically as they concern: consent and autonomy; lack of community consultation; increased stigma on targeted communities; privacy and data protections; the technology used to identify direct transmission; and intensified criminalisation. The paper then lists recommendations for the use of MHS which were gathered from the survey of international literature and from members of the Expert Advisory Group. The report concludes with a methodology section that describes how information for this briefing paper was gathered.

HIV JUSTICE WORLDWIDE

HIV JUSTICE WORLDWIDE is a growing, global movement to shape the discourse on HIV criminalisation as well as share information and resources, network, build capacity, mobilise advocacy, and cultivate a community of transparency and collaboration.

The mission of HIV JUSTICE WORLDWIDE is to seek to abolish criminal and similar laws, policies and practices that regulate, control, and punish people living with HIV based on their HIV-positive status.

We believe that this HIV criminalisation is discriminatory, a violation of human rights, undermines public health, and is detrimental to individual health and well-being.

To learn more, and to join the movement, please visit: www.hivjusticeworldwide.org

WHAT IS MOLECULAR HIV SURVEILLANCE? HOW AND WHY IS IT BEING USED?

Epidemiologists, public health practitioners, and infectious disease specialists increasingly use genetic analysis when seeking to understand, identify, manage, and control various disease outbreaks such as influenza, tuberculosis, food-borne disease, COVID-19, and HIV. Generally, such approaches can be called *molecular surveillance*. Molecular surveillance for HIV, or MHS, is an umbrella term used to encompass a wide range of research and public health practices, and it can come by many different names, including, *HIV cluster detection and response*, *HIV genotype analysis*, *HIV genetic sequencing*, *HIV phylogenetic surveillance*, among others.

To conduct MHS, scientists rely on the results of HIV genetic sequencing tests taken from individual people living with HIV during routine HIV care in order to test for antiretroviral (ARV) drug resistance, known as genotyping. Depending on the country, people living with HIV may undergo resistance testing when commencing or changing ARVs, or they may have only limited access, for example, through participation in a research study which has more advanced diagnostics than the local healthcare system.

When seeking healthcare, or participating in a research study, newly diagnosed people living with HIV receive a series of blood tests. Blood tests help to indicate the type of HIV someone has, and if any mutations make their version of the virus resistant to certain medications. There are multiple types of HIV, and the virus is constantly mutating and changing. These blood tests are used for individual resistance testing. The results reveal the unique genetic make-up of individual strains of HIV and are used to ensure healthcare professionals provide the correct care and choose the most effective treatment for the person living with HIV. These samples are stored in a database, sometimes linked with an individual's health records and other times anonymised. It is these samples that are used for MHS without specific consent or permission, which can then be re-used for phylogenetic analysis, where they are compared against a wide range of other samples from many people.¹

¹ Stanford Health Care. "HIV Drug Resistance Testing."

The results from these tests are then used for surveillance purposes and are the foundations on which MHS is conducted. Depending on the circumstances, the reuse of genetic sequencing data may be done with or without consent or knowledge of the people from whom the sequences are taken – and the broader communities of people living with HIV.

Along with the genetic sequences derived from resistance testing, multiple other sources of data and information can be collated for MHS analysis, such as demographic details covering age, sex, gender, sexuality, race, ethnicity, location, as well as information on behavioural and other socio-economic characteristics, such as whether the sample has been taken from someone who is known, or assumed, to be a sex worker, a migrant, or a person who use drugs.

This practice can be conducted by academic researchers, and state-run public health authorities, which is further outlined in the following sections.

One of the apparent justifications promoted for undertaking MHS is that it has been much cheaper to operationalise, as noted by one research team in Canada, "by making secondary use of routinely collected HIV genotypes, this approach is cost-effective, attains near real-time

monitoring of new cases, and can be implemented in all settings in which HIV genotyping is the standard of care.”² However, the costs of this practice, costs of follow-up public health interventions, and increased surveillance on the lives and human rights of people living with HIV are not accounted for when discussions of cost-effectiveness are heralded by practitioners of molecular HIV surveillance.

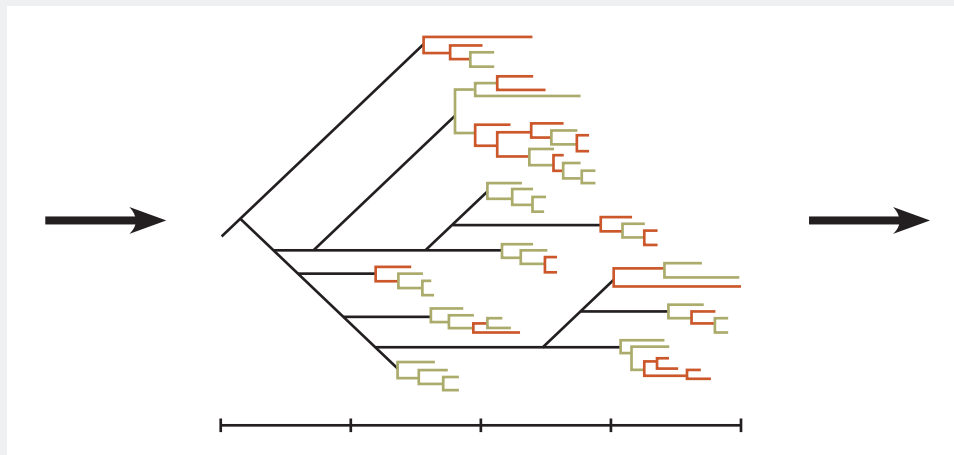
In the following sections, we look at the various uses of MHS, for research and public health intervention, as well as where MHS is being deployed, and what tools are used to conduct MHS research.

PHYLOGENETIC ANALYSIS

There is no standardised way to conduct MHS research, as techniques and technologies vary, but a key component of all MHS research and intervention is *phylogenetic analysis*. Phylogenetic analysis compares the genetic sequences of organisms and determines their relatedness and connectedness.

Phylogenetics is a well-established scientific discipline, but one that is commonly used to study viral dynamics within populations of organisms, rather than to suggest direct virological links between specific individuals.

In MHS, phylogenetic analysis is applied to genetic sequences of HIV taken from people living with HIV. The viruses are then compared using a phylogenetic tree, which is similar to a family tree – to show how close or far apart different sequences are. These phylogenetic ‘gene trees’ are used to assist with inferring evolutionary relationships, and similarities and differences between individual HIV strains. An evolutionary ‘gene tree’ is constructed based on a hypothesis about the relatedness of the samples via a common ancestor on the tree.³



Phylogenetics alone cannot conclusively infer direct relationships between two genetic sequences. Leading experts agree that phylogenetic analysis cannot, for example, tell if Sample A is the source of HIV transmission resulting in Sample B, because there could always be individual samples that were not collected between Sample A and B. In 2018, the Expert Consensus Statement on the Science of HIV in the Context of Criminal Law, issued and signed by international leaders in the biomedical fight against HIV, highlights that “phylogenetic analysis alone cannot prove beyond reasonable doubt that one person infected another.”⁴

While on its own the technology cannot prove direct transmission from one person to another, scientists are increasingly using phylogenetic analysis in concert with other MHS

² Poon, Art et al. “Near real-time monitoring of HIV transmission hotspots from routine HIV genotyping: an implementation case study.” *The Lancet HIV*. 2016.

“the costs of this practice, costs of follow-up public health interventions, and increased surveillance on the lives and human rights of people living with HIV are not accounted for when discussions of cost-effectiveness are heralded by practitioners of molecular HIV surveillance.”

³ Kidd, Paul. “Phylogenetic analysis as expert evidence in HIV transmission prosecutions.” *HIV Australia*. 2016.

⁴ Barré-Sinoussi, Françoise et al. “Expert consensus statement on the science of HIV in the context of criminal law.” *J Int AIDS Soc*. 2018.

tools, and in highly controlled research settings, with aims to increase the reliability of direct transmission inferences.^{5,6} As the technology has become more accessible, its role in HIV epidemiological MHS research and public health investigations and interventions has increased, resulting in greater concerns from human rights experts and other activists.

PHYLOGENETICS FOR FORENSICS

HIV-related phylogenetic analysis technology has been around since the early 1990s, and on its own, and not as part of MHS studies, phylogenetic analysis has been used as a forensic tool in HIV criminalisation cases in some parts of the world.⁷ The tool has been used during investigation and in court as evidence in attempts to prove, or to disprove, direct transmission in cases where one (or more) people allege that someone has unlawfully transmitted HIV to someone else. In many of these cases, phylogenetic analysis is only examining a very small number of individuals, which differs from MHS studies that often include hundreds and thousands of samples. In some cases, phylogenetic analysis has helped to exonerate individuals who had been investigated by authorities or criminally charged due to alleged HIV exposure or non-disclosure.^{8,9}

The Expert Consensus Statement on the Science of HIV in the Context of Criminal Law¹⁰ calls for a cautious use of phylogenetic analysis as a measure only used to discount possible offences. Guidance for prosecutors in HIV-related criminal cases in England and Wales clearly states that phylogenetic analysis must be used before a case comes to court, and if there are no genetic similarities, the case cannot proceed. However, relatively few countries' laws require that transmission be proved and very few countries have guidance for prosecutors on HIV-related criminal cases. The United Nations Development Programme (UNDP) released global guidance in June 2021 that included detailed suggestions on the correct use of phylogenetic analysis in criminal cases.¹¹ In Canada, provincial prosecutors used information from the open access Los Alamos genetic database as evidence, and while the judge noted the data could not prove infection, it was useful "circumstantial evidence"¹² that has been widely accepted in legal cases to identify relationships between genetic samples.

⁵ Taylor, Barbara and Hugo Sapién. "Determining the Direction of Human Immunodeficiency Virus Transmission: Benefits and Potential Harms of Taking Phylogenetic Analysis One Step Further." *Clinical Infectious Diseases*. 2020.

⁶ Zhang, Yinfeng et al. "Evaluation of Phylogenetic Methods for Inferring the Direction of Human Immunodeficiency Virus (HIV) Transmission: HIV Prevention Trials Network (HPTN) 052." *Clinical Infectious Diseases*. 2021.

⁷ Abecasis, Ana, Marta Pingarilho, and Anne-Mieke Vandamme. "Phylogenetic analysis as a forensic tool in HIV transmission investigations." *AIDS*. 2018.

⁸ Carter, Michael. "Prosecution for reckless HIV transmission in England ends with not guilty verdict." *Aidsmap*. 9 August 2006.

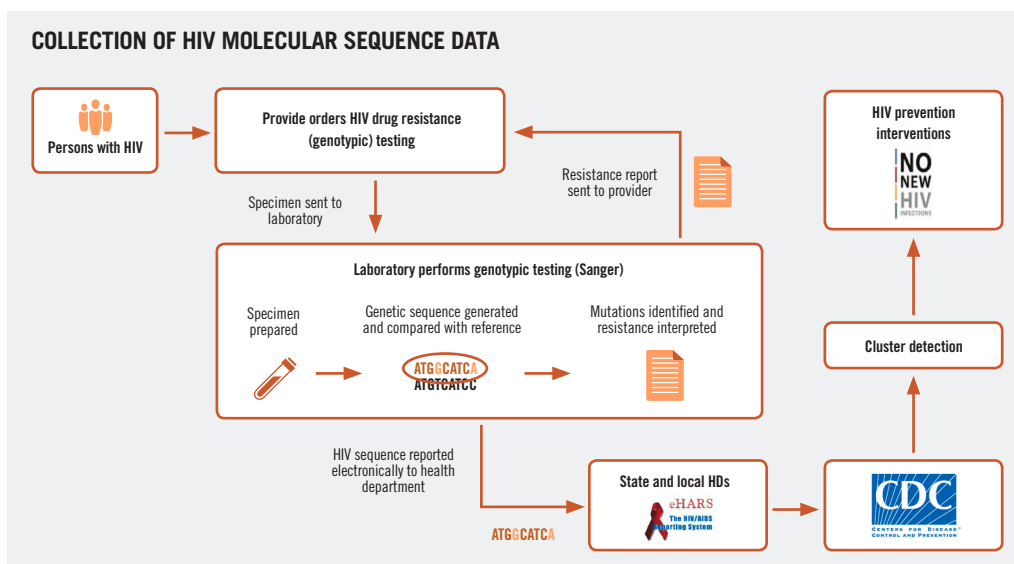
⁹ Bernard, Edwin J. "Reckless HIV transmission case dismissed due to insufficient evidence (amended)." *Aidsmap*. 11 February 2008.

¹⁰ Barré-Sinoussi, Françoise, et al. *Expert consensus statement on the science of HIV in the context of criminal law*. 2018.

¹¹ UNDP. "Guidance for prosecutors on HIV-related criminal cases." 2021.

¹² R. v. Aziga, 2008 (ON S.C.)

This illustration from the United States Centers for Disease Control and Prevention indicates the flow of data from people living with HIV to MHS research and intervention.



Source: CDC. "Detecting and Responding to HIV Transmission Clusters: A Guide for Health Departments DRAFT Version 2.0." June 2018.

MOLECULAR HIV SURVEILLANCE FOR RESEARCH

MHS is widely used around the world for epidemiological research to understand the prevalence of different viral subtypes in certain areas, patterns of drug resistance, and to identify areas where transmissions are happening at a rapid rate (often identified as *clusters*, *transmission networks*, or *risk networks*).

For research, MHS takes place in a number of general ways, either as one aspect of analysis for large-scale longitudinal cohort research studies, or other research projects, where participants are recruited in a research or clinical setting using standard study recruitment methods. In some cases, such research also aims to try to infer who transmitted HIV to whom.¹³

Participation in research studies requires initial patient consent, which is a cornerstone of ethical science. Each country has different consent standards, but it is against medical and scientific ethics to conduct research on people without their knowledge, or without informing them of the potential risks and benefits involved in the specific research. Informed consent is voluntary and means that people living with HIV will have a research project explained to them, and then asked if they consent to participate. They then have the choice to decide if they want to be involved in the research or not, or they could withdraw at a later date.

In some cases, the consent process may involve informing the person living with HIV that what they provide during the research study (e.g., blood tests) may be used in the other research for multiple future uses and different kinds of secondary analysis, including MHS. But the content and extent of the information provided during the consent processes varies and may be lacking. In some cases, with both large longitudinal cohort studies and other research studies, the anonymised genetic sequences of all participants in the study are available online indefinitely in databases for a wide range of future research projects. This means that a person living with HIV may have provided consent to participate in an initial research project but might not know that their unique genetic sequence is now available for other researchers to use and study.

¹³ Zhang, Yinfeng et al. "Evaluation of Phylogenetic Methods for Inferring the Direction of Human Immunodeficiency Virus (HIV) Transmission: HIV Prevention Trials Network (HPTN) Q52." *Clinical Infectious Diseases*. 2021.

"it is against medical and scientific ethics to conduct research on people without their knowledge, or without informing them of the potential risks and benefits involved in the specific research."

MOLECULAR HIV SURVEILLANCE FOR EPIDEMIOLOGICAL RESEARCH



COUNTRY EXAMPLE: UNDERSTANDING VIRAL SUBTYPES IN BANGKOK, THAILAND

Researchers in Thailand conducted genetic analysis on samples collected from a longitudinal study of gay men and other men who have sex with men in Thailand who were diagnosed with HIV from 2009 to 2015. The goal of the study was to support vaccine research and development by understanding the genetic diversity of the virus in Thailand and Asia at large. The researchers utilised data from the Los Alamos National Laboratory HIV Database to conduct transmission network analysis. The analysis suggests that one strain and subtype of HIV is prominent in Thailand, but there was a slight rise in certain strains which were traditionally located in concentrated epidemics among certain populations. As a result, the study recommends a wide range of prevention and treatment approaches because populations are becoming more connected.

The research was conducted with an informed consent process, but it is unclear if the researchers explained how people's blood samples would be used in an ongoing way for MHS. This means that people may have only consented to have a blood sample taken but may not have been provided with detailed information about what that blood sample would be used for in the future. Furthermore, it is unclear if the samples from the Los Alamos National Laboratory HIV Database were used with informed consent. Many

people living with HIV are unaware that their own genetic sequences are housed in the database, and that those samples can be widely used by researchers around the world.

Source: Bangkok, Thailand – Chang, David et al. “Molecular epidemiology of a primarily MSM acute HIV-1 cohort in Bangkok, Thailand and connections within networks of transmission in Asia.” *J Int AIDS Soc.* 2018.

MOLECULAR HIV SURVEILLANCE FOR PUBLIC HEALTH INTERVENTION

MHS is used in certain regions of the world – most notably in North America and certain European countries – by health departments. The aim is to rapidly and accurately identify similar strains of the virus that can be connected into what are known as *clusters*, that may not be captured by other routine public health investigations as close to “real time” as possible, where transmission clusters are taking place. Authorities then intervene with “enhanced public health” approaches to connect people to treatment and care or testing and diagnostics. When conducted by public health authorities, the practice can be called *Cluster Detection and Response*, as the surveillance information is not only studied, but also acted upon by public health practitioners as various forms of direct intervention in people’s lives.

According to MHS practitioners, public health responses designed to follow up on patterns identified through MHS purport to link people to care and diagnostics,^{14, 15} but there are concerns among activists and communities living with HIV that they may involve more coercive outcomes. US-based networks of people living with HIV have called for a suspension (moratorium) on MHS used for public health intervention in the country due to a range of ongoing concerns, including that public health workers may lack cultural competencies and may act in racist, homophobic, transphobic, and drug use stigmatising ways, exacerbate criminalisation, and could fuel ongoing issues of mistrust between public health authorities and people living with HIV.¹⁶

In some countries, the outcome of HIV-related public health investigations may lead to legally mandated treatment and counselling, or even intervention by law enforcement. In Canada, for example, legal public health orders, which can be the outcome of a public health investigation, can mandate people living with HIV to live under a curfew, attend regular counselling, use condoms and/or take antiretroviral medications, disclose their condition to all potential sex partners (regardless of whether or not they are virally suppressed and undetectable), along with other measures – including engaging law enforcement – if the person is deemed to be a public health risk by authorities.^{17, 18}

As pointed out by US networks of People Living with HIV in their call for an MHS moratorium, such coercive approaches by public health authorities may heighten stigma and could lead to criminalisation, deportation, or other negative outcomes.¹⁹

¹⁴ Sizemore, Lindsey et al. “Using an Established Outbreak Response Plan and Molecular Epidemiology Methods in an HIV Transmission Cluster Investigation, Tennessee, January-June 2017.” *Public Health Reports.* 2020.

¹⁵ Smith, Davey et al. “A Public Health Model for the Molecular Surveillance of HIV Transmission in San Diego, California.” *AIDS.* 2009.

¹⁶ US People Living with HIV Caucus (US PLHIV Caucus). “Open Letter to the CDC: Networks of People Living with HIV Demand a Moratorium on Molecular HIV Surveillance.” *ActionNetwork.* 2021.

¹⁷ Proctor, Jason. “Vancouver police search for subject of unprecedented HIV-medication order.” *CBC.* 6 June 2019.

¹⁸ McClelland, Alexander. “‘Lock This Whore Up’: Legal Violence and Flows of Information Precipitating Personal Violence against People Criminalised for HIV-Related Crimes in Canada.” *European Journal of Risk Regulation.* 2019.

¹⁹ US People Living with HIV Caucus (US PLHIV Caucus). “Open Letter to the CDC: Networks of People Living with HIV Demand a Moratorium on Molecular HIV Surveillance.” *ActionNetwork.* 2021.

INVESTIGATING CLUSTERS & PUBLIC HEALTH INTERVENTIONS



COUNTRY EXAMPLE: HOW CLUSTERS ARE INVESTIGATED IN THE UNITED STATES

MHS is used across the United States for public health interventions, as mandated by the US Centers for Disease Control and Prevention (CDC) – where the practice is more commonly known as *cluster detection and response*. Below are the steps that the CDC asks public health departments to take to investigate a cluster:

- Identify the underlying transmission cluster and risk network (e.g., undiagnosed cases, diagnosed cases without a sequence, persons at risk for HIV)
- Identify factors possibly associated with transmission
- Understand possible connections between cases in a cluster
- Assess potential risk for ongoing transmission
- Determine what potential interventions might be effective

Source: CDC. “Detecting, Investigating, and Responding to HIV Transmission Cluster.” 2018.



COUNTRY EXAMPLE: CLUSTER ANALYSIS OF MIGRANT TRANSGENDER SEX WORKERS IN MILAN, ITALY

Researchers in Italy conducted an MHS study examining clusters focused on 156 genetic sequences from transgender sex workers living with HIV, many of whom were also migrants. The samples were collected between 1999 and 2015 from a hospital in Milan. The study aimed to examine the country of origin of the HIV strains, as well as clusters – or the genetic relationships – between trans women and heterosexual men, and also gay men and other men who have sex with men. The primary location for HIV acquisition was identified as South America.

Source: Milan, Italy – Lai, Alessia et al. “Contribution of transgender sex workers to the complexity of the HIV-1 epidemic in the metropolitan area of Milan.” *Sexually Transmitted Infections*. 2020.

The advancement of MHS for public health intervention in the United States is being rolled out widely, where all people living with, and susceptible to, HIV are affected. The approach is being hailed by the United States CDC as “a critical step toward bringing the nation closer to the goal of no new infections”.²⁰ The CDC is promoting this approach as a way to collect information on everyone living with HIV, including communities who are not commonly connected to government health systems, such as people who use drugs, migrants, Black, Indigenous, and other people of colour, people who sell sex, gay men and other men who have sex with men, adolescents, people who live in poverty, and people in rural communities.

²⁰ CDC. “HIV Cluster and Outbreak Detection and Response.”

MHS FOR PUBLIC HEALTH INTERVENTION



COUNTRY EXAMPLE: INTERVENING IN AN OUTBREAK AMONG GAY MEN IN VANCOUVER, CANADA

In June 2014, the MHS monitoring system in British Columbia, Canada detected the expansion of a cluster by eleven new cases during three months, including eight cases with transmitted drug resistance. The cluster comprised young gay men and other men who have sex with men, who were contacted for “enhanced public health follow-up to ensure linkage to care and treatment initiation.” That involved public health authorities directly contacting the young men and encouraging them to seek care and testing. The additional benefit of MHS is questionable, however, because all of the nine cases associated with this follow-up had already been linked to care, and five cases had already started treatment.

Source: British Columbia, Canada – Poon, Art et al. “Near real-time monitoring of HIV transmission hotspots from routine HIV genotyping: an implementation case study.” *The Lancet HIV*. 2016.

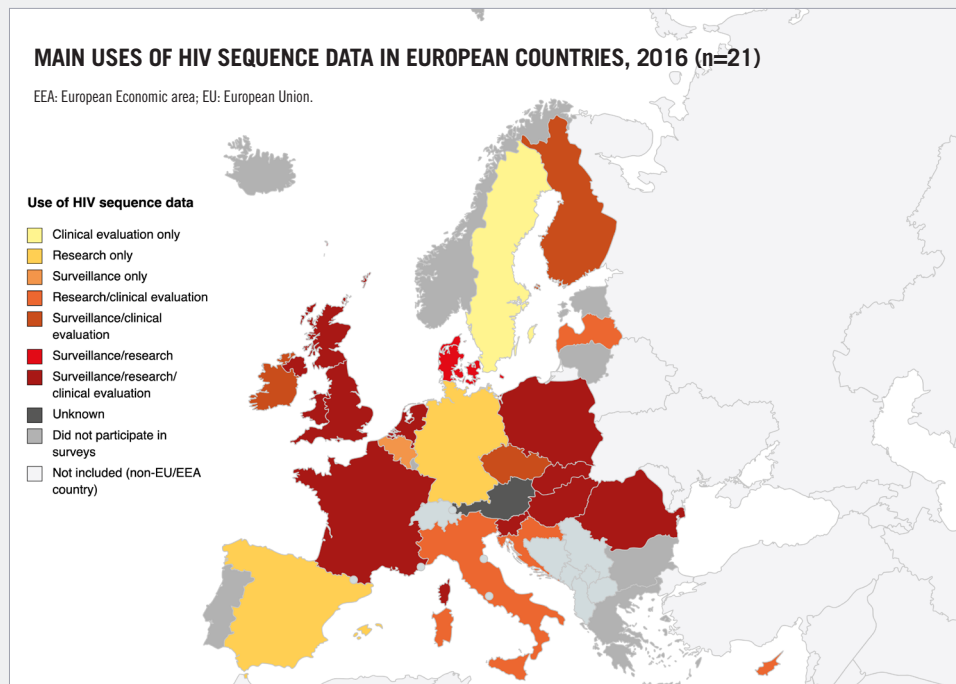
WHERE IS MOLECULAR HIV SURVEILLANCE BEING USED AND WHO IS BEING TARGETED?

MHS is being mobilised across all regions of the world in many countries for a wide range of varied purposes. In parts of North America and Europe, public health departments have mandated the use of MHS to inform ongoing surveillance and intervention, where rights to consent and privacy are suspended. In other regions, MHS is primarily utilised for epidemiological research to identify viral subtype and resistance patterns.

In countries around the world with active criminalisation regimes targeting populations most impacted by HIV, MHS studies have often focused on gay men and other men who have sex with men, trans women, people who sell sex and/or use drugs, and migrants. However, discussions about the impact of MHS research and intervention on criminalisation and human rights are often very limited in the literature. Due to the public availability of some MHS data sets, via genetic sequencing databases, researchers from around the world can freely study various regions and countries, based on what data is available and has been submitted to public databases.

MOLECULAR HIV SURVEILLANCE IMPLEMENTATION: EUROPEAN UNION

In 2017, researchers conducted a study to assess the MHS capacity of European Union countries and found that nineteen out of twenty-one countries reported using HIV sequence data at the national level for drug resistance testing and subtype testing. Fifteen of the countries also used phylogenetic analysis to examine transmission events, while thirteen countries used HIV sequence data for surveillance purposes at the national level. Of most concern is the fact that nine EU countries indicated that clinical, epidemiological, and sequence data were routinely linked for analysis.



Source: Keating, Patrick et al. "Assessment of HIV molecular surveillance capacity in the European Union." *Eurosurveillance*. 2017.

WHERE DOES THE DATA FOR MOLECULAR HIV SURVEILLANCE COME FROM?

While all of the data used for MHS studies originates from the blood of people living with HIV, once a genetic sequence is converted into digital code, it can be housed in multiple places, widely shared, and used for varied research purposes – often without the knowledge of people living with HIV from whom the data originated.

The primary sites where data originates for MHS analysis are: *databases of genetic sequences, public health surveillance systems, drug resistance surveillance programs, clinical settings, cohort research studies, and other research studies.* Genetic sequencing data moves between different sites in various ways. Data might originate in a clinical setting, and also be reported to a government public health authority, where it is then sent to a government-run public health surveillance system. That same data may then also be used for research (as clinical sites are also often research sites), and clinical researchers might also send all their data to a genetic sequencing database.

DATABASES OF HIV GENETIC SEQUENCES AND DRUG RESISTANCE SURVEILLANCE PROGRAMMES

To conduct MHS related research, epidemiologists can use publicly available data sets, via genetic sequencing and drug resistance databases, or also private databases owned by healthcare companies. For public databases, researchers around the world can freely study various regions and countries, based on what data is available and has been submitted to the databases.

UNITED KINGDOM DRUG RESISTANCE DATABASE (link: <http://www.hivrdb.org.uk/>)

This is a centralised database where all routine resistance tests are received annually from fifteen participating virology laboratories across the United Kingdom. On the database website it notes that: “where possible, tests are linked (using pseudo-anonymised patient identifiers) to clinical data, the UK Seroconverter Register, and to surveillance data at Public Health England.”

LOS ALAMOS NATIONAL LABORATORY HIV DATABASE (link: <https://www.hiv.lanl.gov/content/index>)

This is a leading genetic sequencing database, which includes a wide range of sequences from around the world. The database is open access, and according to the website “the number of sequences in the HIV database is still increasing. In total, at the end of 2017, there were 812,586 sequences in the HIV Sequence Database, an increase of 8.5% since the previous year.”

STANFORD UNIVERSITY HIV DRUG RESISTANCE DATABASE (link: <https://hivdb.stanford.edu/>)

This drug resistance database is housed at Stanford University and, as indicated by the website, is noted as being a: “curated public database, to represent, store and analyse HIV resistance data. It houses virus sequences from 213,273 persons and includes genotypes from 15 clinical trials.”

SPREAD PROGRAMME (STRATEGY TO CONTROL SPREAD OF HIV DRUG RESISTANCE)

(link: <https://www.esar-society.eu/spread-surveillance-program>)

SPREAD is a HIV-drug resistance surveillance program executed under the authority of the European Society for translational Antiviral Research. Within the SPREAD program clinicians, virologists, and epidemiologists from 28 European countries are actively involved in the surveillance of transmission of drug resistant HIV.

GLOBAL HIV DRUG RESISTANCE SURVEILLANCE NETWORK(link: <https://www.who.int/drugresistance/hivaids/network/en/>)

The Global HIV Drug Resistance Surveillance Network is being developed by WHO in collaboration with the International AIDS Society, which aims to provide information necessary to develop effective treatment strategies; to support and complement programmes aimed at increasing HIV therapy availability; and to assist in targeting and implementing strategies to prevent drug resistance.

MHS data is often combined with other available public health, clinical, and behavioural data. In many cases, to conduct MHS studies, genetic sequence data is combined with other sources of data, such as demographic data including age, sex, gender, sexuality, race, ethnicity, location, as well as information on behavioural and other socioeconomic characteristics, such as someone who is known, or assumed, to be a sex worker, migrant, or person who use drugs, all of which can come from a diverse range of sources.

DATA-SHARING FROM MULTIPLE SOURCES FOR MHS**COUNTRY EXAMPLES: CANADA AND RUSSIA**

One study conducted in Montreal, Canada, titled “Large cluster outbreaks sustain the HIV epidemic among gay men and other men who have sex with men in Quebec,” outlines how multiple data sources were used to conduct MHS, including sequencing data from government public health surveillance, along with clinical and behavioural data from a local research cohort study on rapid HIV testing, noting they combined: “phylogenetic analysis [...] genetic sequence datasets from the provincial genotyping programme with clinical and behavioural data from the Montreal [...] rapid testing site cohorts to assess underlying factors implicated in HIV transmission among MSM.” Similarly, another study in the Krasnoyarsk Region of Russia, noted that along with genetic sequence data, the study also got access to “demographic, clinical data and treatment information”, which were collected by physicians from the patients’ medical charts.

Sources: Bremmer, Bluma et al. “Large cluster outbreaks sustain the HIV epidemic among MSM in Quebec.” *AIDS*. 2017; and Neshumae, Dmitry. “Molecular Surveillance of HIV-1 Infection in Krasnoyarsk Region, Russia: Epidemiology, Phylodynamics, and Phylogeography.” *Current HIV Research*. 2019.

WHAT TOOLS ARE USED TO UNDERTAKE MOLECULAR HIV SURVEILLANCE?

A range of diverse computational and algorithmic tools are used to undertake MHS analysis. The tools are often open-access software packages, available online, which can be used for free by anyone with a powerful enough computer. Published peer-reviewed literature on MHS tools demonstrates their uses, promotes their success, and encourages their uptake. Epidemiologists, infectious disease specialists, and public health practitioners, use diverse and varied arrangements of MHS tools to undertake their analyses.

Tools designed to undertake MHS aim to estimate genetic relationships between HIV sequences. As technology develops, some of these tools are able to determine if the strains of

“The tools are often open-access software packages, available online, which can be used for free by anyone with a powerful enough computer.”

HIV are related, and this information can be used to estimate who transmitted HIV to who. One such tool is PHYLOSCANNER, the developers of which note:

“Great care must be taken to correctly interpret the ancestry of pathogens infecting individuals. Even if ancestry were established beyond any doubt, individual X’s pathogen being ancestral to individual Y’s pathogen does not imply that X infected Y: The pathogen could have passed through unsampled intermediate hosts.”

While there is a scientific consensus that it is impossible for phylogenetics alone to prove direct transmission, it remains to be seen when combined with other MHS tools, or conducted in controlled settings, if phylogenetic technologies will advance to the point where direct transmission can be determined conclusively. In a 2021 longitudinal cohort study, researchers state they were able to infer direct transmission with up to 93.3% accuracy. However, their research was conducted under highly controlled conditions, and they had detailed information on the sex partners of each participant in the study.²¹ The researchers note that outcomes of their study would not be reproducible in the real world, as all the unknowns and gaps in data make such analysis impossible.

However, the ability of some MHS practitioners of phylogenetics to continue to seek to infer direct transmission events alone poses great risks to people living with HIV – many of whom belong to populations already targeted or treated unfairly by criminal legal systems. The ongoing push to try and infer *who transmitted whom*, and the resulting research, could easily be misinterpreted or miscommunicated in the media, or taken up incorrectly by police, or in courts, and could increase stigma and further HIV criminalisation.

The ongoing drive to prove *who transmitted whom* through this technology comes from the same impetus that drives HIV criminalisation, which is rooted in an outdated stigmatising logic that there are certain individuals we must identify, blame, and detain in order to control communicable disease transmission. Such responses view HIV transmission as highly individualised, where certain people are labelled as vectors of transmission, and viewed as the only ones who hold responsibility for transmission. However, communicable diseases, such as HIV, are profoundly social, where we all hold accountability and responsibility, and to respond effectively requires large structural social changes to ensure all people are supported and have access to what they need to realise their health and wellbeing.

²¹ Zhang, Yinfeng et al. “Evaluation of Phylogenetic Methods for Inferring the Direction of Human Immunodeficiency Virus (HIV) Transmission: HIV Prevention Trials Network (HPTN) Q52.” *Clinical Infectious Diseases*. 2021.

“The ongoing push to try and infer who transmitted whom, and the resulting research, could easily be misinterpreted or miscommunicated in the media, or taken up incorrectly by police, or in courts, and could increase stigma and further HIV criminalisation.”

Name	What the tool does
HIV-TRANSMISSION Cluster Engine (HIV-TRACE)	This tool was created by researchers at the University of California, San Diego to generate network diagrams of clusters based on genetic data.
Secure HIV-TRACE	This is a version of HIV-TRACE that is mandated by the CDC to be used across the United States to conduct local analysis at public health departments.
PHYLOSCANNER	Developed by researchers at the University of Oxford and the Imperial College of London, this tool aims to allow for the inference of the direction of transmission from sequenced data. The developers note that there can be unsampled sequences, but that the tool can identify transmission chains.
Bayesian Evolutionary Analysis Sampling Trees (BEAST)	Software created by the University of Auckland to examine the temporal evolutionary rates and similarities between sequences. BEAST allows people to use a different approach – known as Bayesian – to doing phylogenetics and molecular epidemiology.

RITA (Recent Infection Testing Algorithm)

RITA is an algorithm that can assist with estimating whether infection is recent or not in people already diagnosed as HIV positive. RITA takes the result of a recency assay and combines it with other patient information to give an overall estimate of when an infection might have occurred. Like MHS, it is not accurate enough to determine timing of HIV acquisition definitively.²²

Cluster Picker

Developed by researchers at the University of Edinburgh, this tool identifies and analyses clusters of sequences. The tool, like all of the above ones, allows researchers to compare pathogen transmission dynamics between genetic sequences so as to define and construct clusters.

²² Bernard EJ et al. "Estimating the likelihood of recent HIV infection: Implications for criminal prosecution." National Aids Trust (NAT). 2011.

WHAT ARE THE CONCERNS WITH MOLECULAR HIV SURVEILLANCE?

This section summarises the main themes of the grey material we collected and the peer-reviewed papers that critique the use of MHS. There is a large and growing body of literature that explores the ethical concerns surrounding these tools. Experts and advocates have been involved in working groups and meetings with researchers, health departments, and agencies to discuss their apprehensions about MHS. Key human rights concerns with MHS include:

- Consent and autonomy,
- Lack of community consultation,
- Increased stigma on targeted communities,
- Privacy and data protections,
- Technology being used to “prove” direct transmission, and
- Intensified criminalisation.

There is an understanding that there needs to be a balance between the privacy of people living with HIV and any possible benefits to public health. In fact, several of the critiques against MHS often couch their recommendations in a manner that still allows for limited use of MHS. However, advocates argue that the unaddressed concerns can damage trust between people living with HIV and health departments and healthcare workers, potentially deterring people from seeking care. Furthermore, advocates claim that the information gained from MHS is redundant because the populations at risk have often been identified and connected to care and services using existing surveillance methods that do not have the same ethical concerns as MHS. Thus, advocates and people living with HIV have called on researchers and public health departments to provide stronger explanations on how the results of MHS can better serve the lives of people living with HIV, instead of just being a new advanced surveillance technology that tells us what we already know on the ground. However, in response to criticism, practitioners of MHS maintain that “the public good of HIV surveillance justifies this approach”²⁵ However, this argument misses that the suspension of rights and any resulting harms done to people living with HIV are still harms done to the public. People living with HIV are a part of the public and harms done to the human rights of communities of people living with HIV have wide-ranging impacts for all of society. If communities of people living with HIV are made more precarious, under increased surveillance, they will have less capacity and ability to flourish, contribute and participate to support themselves and each other.

“Furthermore, advocates claim that the information gained from MHS is redundant because the populations at risk have often been identified and connected to care and services using existing surveillance methods that do not have the same ethical concerns as MHS.”

²⁵ Wertheim, Joel et al. “Consent and criminalisation concerns over phylogenetic analysis of surveillance data – Author’s Reply.” *Lancet HIV*. 2019.

CONSENT AND AUTONOMY VIOLATIONS

At the heart of all of the concerns are consent and autonomy violations. As explained earlier, much of the MHS research uses gene sequences from samples that are obtained from HIV genetic sequence databases, public health department surveillance systems, and drug resistance surveillance programmes. People living with HIV give consent to their blood sample being sequenced to identify if they have a strain of HIV that is resistant to certain drug treatment. However, many people do not consent to having their data used in any other way outside of informing their doctor to receive better care. The patient has no idea their data is stored in databases and that anyone outside of their doctor would have access to it. Many public health departments and researchers around the globe argue that MHS is simply just another

piece of public health information and that they have a right to collect it to monitor infectious diseases and prevent further spread. This is a similar argument used for names-based HIV surveillance in the U.S. and across the world.²⁴ However, the four principles of medical ethics — autonomy, beneficence, non-maleficence, and justice²⁵ — strongly suggest that to respect the human rights of people living with HIV, we must respect their right to make informed decisions. Experts and advocates who raise concerns about consent and autonomy argue that without informed consent, health departments are undermining trust with people living with HIV and their advocates because MHS raises concerns about confidentiality.

²⁴ Lee et al. "Ethical Justification for Conducting Public Health Surveillance Without Patient Consent." 2012

²⁵ Beauchamp, Tom. and James Childress. *Principles of Biomedical Ethics*. Oxford University Press, 2019.

CONSENT AND AUTONOMY IN MOLECULAR HIV SURVEILLANCE RESEARCH



COUNTRY EXAMPLE: UNITED STATES STUDY ASKING PEOPLE LIVING WITH HIV IF THEY WOULD CONSENT TO PARTICIPATE IN PHYLOGENETIC RESEARCH

In one study in Boston, MA, U.S., researchers approached 90 patients to see if they would provide informed consent to phylogenetic research. Half of the patients approached did not consent to participate, mostly after reading the study materials and consent form. Reasons for not participating included unwillingness to discuss their HIV status, privacy and confidentiality concerns, disinterest, and lack of time. The researchers note that the high opt-out rates and concerns about discussing one's HIV status reflect to some extent the stigma surrounding HIV in Boston.

Source: Rudolph et al. "Informed Consent for HIV phylogenetic research: A case study of urban individuals living with HIV approached for enrollment in an HIV study." *EHQUIDAD*. 2020.



COUNTRY EXAMPLE: UNITED KINGDOM STUDY ASKING ABOUT THE ACCEPTABILITY OF USING PHYLOGENETIC DATA IN CLINICAL AND PUBLIC HEALTH PRACTICE

Researchers conducted focus groups and in-depth interviews with 40 individuals in Brighton and London, England. The participants were a mix of HIV-positive gay men and other men who have sex with men, HIV-positive Black African men and women, HIV-negative gay men and other men who have sex with men, and healthcare workers in the HIV field. The conclusion of the study was that acceptance of the use of phylogenetic data was dependent on the perceived risks and the public health benefits. Furthermore, if phylogenetic data was used without addressing certain concerns (mainly informed consent, data protections, and benefits to HIV-positive communities), there was a potential risk of individuals disengaging from testing or care.

Source: Mulka et al. "What is the acceptability of using phylogenetic data in clinical and public health practice?" *British HIV Association Conference*. 2019.



COUNTRY EXAMPLE: CHINESE STUDY WHERE CONSENT WAS PROVIDED, BUT THE CONTENT OF CONSENT WAS UNCLEAR

The Zhejiang Provincial Center of Disease Control and Prevention in China reviewed and approved an MHS study. The Institutional Ethics Committee approved the study because written informed consent was obtained by all 806 study participants. However, the authors of the study did not provide details on what information was communicated about genetic sequencing and ongoing future use of the data via the consent form and process. Unfortunately, this is the case with the overwhelming majority of studies across the globe.

Source: Fan et al. "Analysis of the Driving Factors of Active and Rapid Growth Clusters Among CRF07_BC-Infected Patients in a Developed Area in Eastern China." *Open Forum Infectious Diseases*. 2021.

"However, many people do not consent to having their data used in any other way outside of informing their doctor to receive better care. The patient has no idea their data is stored in databases and that anyone outside of their doctor would have access to it."



COUNTRY EXAMPLE: UNITED STATES STUDY WHERE INFORMED CONSENT FOR MHS AND FUTURE RESEARCH WAS PROVIDED

The UC San Diego Primary Infection Resource Consortium (PIRC) is the largest, most intensively studied, and well-characterised longitudinal cohort of acute and early HIV infected individuals in the U.S. In their consent form, they communicate to participants “Blood will be collected for storage for future HIV testing, other genetic testing, and other assays, as determined by the results of this and future studies.”

Source: UCSD Antiviral Research Center. “Consent to act as a research subject – AEHIV 042: Primary Infection Resource Consortium Network (PIRC-NET).” Protocol Version 1.2 [09JAN2020].

LACK OF COMMUNITY CONSULTATION AND ENGAGEMENT

Community engagement is a crucial and ethical component of research due to distrust of health research and medical care in historically marginalised communities. Virtually every piece of grey literature collected mentioned the importance of public health departments and researchers fostering a collaborative relationship with stakeholders in their local community. The general consensus is that most public health strategies, including identifying participants, providing targeted interventions, developing outbreak and communication plans, and protecting data, all involve working with community-based organisations. While some health departments have established contacts with affected communities, the degree of engagement varies. MHS research, public health surveillance, and public health intervention occurs without the explicit consent from people living with HIV, which increases the importance of community consultation and engagement to mitigate any potential social harm. Experts and advocates have not only called for more community engagement, but for MHS research to be helpful to communities living with HIV. Again, we recall the four principles of biomedical ethics, especially beneficence and non-maleficence. As others have argued, “Whenever we try to help others we inevitably risk harming them; health care workers, who are committed to helping others, must therefore consider the principles of beneficence and non-maleficence together and aim at producing net benefit over harm.”²⁶ HIV experts and advocates assert that community engagement should be centred throughout the research project and public health intervention to ensure that the research not only avoids harming people living with HIV but that it is ultimately beneficial for communities living with HIV.

“HIV experts and advocates assert that community engagement should be centred throughout the research project and public health intervention to ensure that the research not only avoids harming people living with HIV but that it is ultimately beneficial for communities living with HIV.”

²⁶ Gillon, Raanan. “Medical ethics: four principles plus attention to scope.” *Bmj*, p. 184. 1994.

COMMUNITY ENGAGEMENT



COUNTRY EXAMPLE: UNITED STATES CENTERS FOR DISEASE CONTROL AND PREVENTION COMMUNITY ENGAGEMENT EFFORTS

In 2019, the United States Centers for Disease Control and Prevention conducted three virtual meetings with “state and local health departments, representatives of community-based organisations including people with HIV, national organisations representing state and local health departments, academics, and experts in public health ethics and law” to discuss best practices in reducing harms and strengthening data protections. The number one theme of the discussions was the vital role of community engagement for any aspect of public health, especially MHS. “Many participants identified a need to go beyond HIV planning groups, and to make information and engagement accessible to broader communities. Public health agencies can work with communities and organisations to minimise distributive justice issues. Agencies can be aware that communities of color are at increased risk of HIV transmission, as well as often being targeted by policing and immigration enforcement, and consider these perspectives.”

Source: CDC. “Meeting summary: Responsible Use of HIV Cluster Data for Public Health Action: Amplifying Benefits, Minimising Harms.” <https://www.cdc.gov/hiv/programresources/guidance/cluster-outbreak/responsible-use.html>

STIGMA ON TARGETED COMMUNITIES

MHS is consistently applied to historically marginalised and criminalised communities. This includes gay men and other men who have sex with men, trans women, sex workers, people who use drugs (primarily those who inject drugs), migrants, and people experiencing homelessness. There is a risk that focusing on these identities can reinforce negative perceptions about these communities. This is especially true when public statements from researchers and public health departments use loaded language with negative connotations (see Greece example, below). Increased stigma of HIV and historically marginalised communities may exacerbate discrimination, which can occur in all aspects of society. HIV-related stigma and discrimination can deter individuals from HIV testing and learning their status, obtaining treatment, or staying in care.²⁷ If research focused less on individual identities and more on structural factors that increase the probability of acquiring HIV, such as laws and policies that create barriers to accessing prevention and treatment, then that research could decrease discrimination and conclude with a call for a reallocation of resources at a societal level that would reduce inequalities and decrease HIV transmission. Furthermore, much of the results of these MHS studies are already known to people living with HIV and experts working on the ground and could be obtained using existing disease investigation processes utilised by public health departments.

²⁷ Stockton, Melissa A., Kayla Ginger, and Laura Nyblade. “A scoping review of the role of HIV-related stigma and discrimination in noncommunicable disease care.” *PLoS ONE*, 2018.

MOLECULAR HIV SURVEILLANCE RESEARCH MAY NOT ADDRESS THE ROOT CAUSES OF HIV DISPARITIES



COUNTRY EXAMPLE: GREEK STUDY

As mentioned previously, much of the MHS research uses data from historically marginalised communities and can increase stigma and discrimination, rather than decreasing a “blaming” mentality or addressing societal factors of HIV transmission. One study in Athens, Greece used MHS to trace the most probable country of origin of HIV seroconversion of HIV-positive migrants who inject drugs. The goal of the study was to investigate if “transmissions occur more frequently among migrants than among Greek nationals.” The results of the study suggest that most migrants acquire HIV post-migration from other migrants and not from Greeks. However, this study does not reference any societal factors, such as criminalisation of irregular migration or drug use in Greece. Instead, the study focused on how “migrants engage in riskier behaviours with other migrants (at least from their own nationality) than with Greeks...[and] that migrants’ risk networks are primarily with other migrants.” This type of research risks being perceived as further stigmatising those it studies, as it does not seek out to address societal barriers against access to prevention and treatment of HIV, and instead focuses on the identities and behaviours of individuals or marginalised communities.

Source: Paraskevis et al. “Molecular Tracing of the Geographical Origin of Human Immunodeficiency Virus Type 1 Infection and Patterns of Epidemic Spread Among Migrants Who Inject Drugs in Athens.” 2017.

PRIVACY AND DATA PROTECTIONS

MHS tools raise the most concern when they combine multiple data streams from different sources on the individuals they are studying. At their most restrictive, MHS uses fully anonymised data that cannot be traced back to individuals or connected to multiple data streams. However, proponents of MHS have argued that for the most effective public health interventions, more data must be combined. This is alarming from a human rights perspective and is further complicated because public health agencies have historically shared their data with researchers, and funders of such research often require the resulting data to be made public. Experts and advocates have stressed that data should be ethically collected and protected. Some have called for a balance between anonymity and data protection with public health and scientific objectives, but that balance is easier said than done.

In 2011, the CDC published a report titled “Data Security and Confidentiality Guidelines for HIV, Viral Hepatitis, Sexually Transmitted Disease, and Tuberculosis Programs: Standards to Facilitate Sharing and Use of Surveillance Data for Public Health Action” to reach the goal of balancing privacy and data protections with the aims of public health and research. However, as technology continues to advance, true anonymisation becomes harder to obtain. Increases in computational power has made it easier for anonymised data to be re-identified, especially when combined with multiple data streams.²⁸ Thus, the 2011 guidelines are no longer at the forefront of ethics and privacy. Furthermore, as much of this data is collected and used without informed consent, additional ethical considerations should be in place.

“Experts and advocates have stressed that data should be ethically collected and protected. Some have called for a balance between anonymity and data protection with public health and scientific objectives, but that balance is easier said than done.”

²⁸ Rocher, Luc, Julien Hendrickx, and Yves-Alexandre de Montjoye. “Estimating the success of re-identification in incomplete datasets using generative models.” *Nature Communications*. 2019.

PRIVACY CONCERNS



COUNTRY EXAMPLE: IDENTIFYING AN OUTBREAK AMONG PEOPLE WHO USE DRUGS IN SEATTLE, UNITED STATES

MHS was used to confirm the relationship of an outbreak found through traditional contact tracing techniques in houseless individuals in northern Seattle who were identified as sex workers and/or injected drugs. The study was able to identify individuals who had not been included as part of the cluster through traditional contact tracing. Additionally, in media articles that resulted from the cluster detection and response initiatives, the exact street that individuals lived on was publicly published. This violation of privacy could have led to increased stigma, discrimination, and even violence. Broadcasting the address of where individuals lived could have increased policing, increased community surveillance and vigilantism, resulting in discrimination, and further stigmatisation of this already marginalised community.

Source: Golden, Matthew et al. "Outbreak of Human Immunodeficiency Virus Infection Among Heterosexual Persons Who Are Living Homeless and Inject Drugs — Seattle, Washington, 2018." *MMWR*. 2019.

As HIV is highly stigmatised and criminalised across the globe, people living with HIV and advocates fear that MHS data will intentionally or inadvertently identify people living with HIV and/or HIV transmission events. This data could harm countless individuals and groups of people, as marginalised and criminalised communities are often those studied. The largest risk is if the data is shared with law enforcement, the judicial system, and extra-judicial groups targeting people living with HIV. Any breach of confidentiality, inadequate anonymisation, or non-public health uses of this data can increase distrust with health systems and have ripple effects on the livelihood of people living with HIV. For example, the first criminal case in Scotland where an individual was prosecuted for transmitting HIV used forensic evidence that was obtained by a police warrant which forced researchers to re-identify MHS data originally obtained for a study on HIV in prison.²⁹ Situations like this can undermine health care goals because it can waiver people's beliefs that their healthcare data will only be used for their healthcare.

²⁹ Bird, Sheila M. and Andrew J. Leigh Brown. "Criminalisation of HIV transmission: implications for public health in Scotland." *BMJ*. 2001.

CONCERNS ABOUT "PROVING" DIRECT TRANSMISSION

The issue of trying to prove direct transmission is controversial and is addressed by many researchers, with widely varying views. In addition, many researchers are not clear in their definitions and conflate *directionality* with *direct transmission*, making it challenging for non-scientists to understand or engage in the debates. Directionality refers to analysing if one strain of HIV is related to another strain, and which strain is technically older. This analysis is widespread, and the science is consistent. Direct transmission, however, is a form of analysis seeking to understand if, for example, Sample A is the source of HIV transmission resulting in Sample B – in other words, that this person transmitted HIV to that person. The science behind direct transmission is still contested, and there is concern that such analysis is harmful if it is misused and misunderstood in criminalisation cases, or other instances, such as coercive treatment or immigration proceedings.

DETERMINING DIRECT TRANSMISSION

EXAMPLE: PHYLOSCANNER

In 2021, researchers used PHYLOSCANNER in a study examining genetic sequences from the HPTN 052 study, and according to their study, they were able to infer the direction of HIV transmission in 31 of the 32 couples examined (96.9%). There were no cases where the incorrect transmission direction (partner to index) was inferred. This is an example of correctly determining the ancestry between two samples of HIV *and not who transmitted HIV to whom*. It is critically important to mark the distinction between direction of transmission and direct transmission events. In the HPTN 052 example, what has been identified is direction of transmission (Person X's HIV is ancestral to Person Y's) and not direct transmission (Person X transmitted to Person Y).

Source: Zhang, Yinfeng et al. "Evaluation of Phylogenetic Methods for Inferring the Direction of Human Immunodeficiency Virus (HIV) Transmission: HIV Prevention Trials Network (HPTN) 052." *Clinical Infectious Diseases*. 2021.

"MHS and the attempt to prove direct transmission is dangerous when claims are believed or misinterpreted in the media and in the courts."

The leading experts agree that phylogenetic analysis cannot tell if Sample A is the source of HIV transmission resulting in Sample B because there can always be individual samples that were not collected between Sample A and B.³⁰ For example, one article stated, "although MHS can identify HIV transmission networks experiencing recent and rapid HIV transmission, [direct transmission] (who transmitted the virus to whom) cannot be determined using molecular data."³¹ However, other authors claim that as technology advances, it may be possible to eventually "prove" direct transmission. One paper stated, "phylogeny cannot determine the [direct path] of HIV transmission without extensive clonal sequencing of the virus populations."³² While the consensus on the current technology is clear, some researchers are still trying to "prove," in controlled settings, that direct transmission can be inferred or determined. For instance, in one study, the authors stated, direct transmission "was assessed through a stratified age and sex prevalence analysis based on the probability of one sampled individual transmitting to another within a cluster being a function of the sequencing coverage and the prevalence in the population."³³ However, even though direct transmission cannot currently be "proven," MHS and the attempt to prove direct transmission is dangerous when claims are believed or misinterpreted in the media and in the courts. The stigma, discrimination, and criminalisation of people living with HIV are reasons why "proving" direct transmission has been a key concern for people living with HIV and advocates for years.

³⁰ Barré-Sinoussi, Françoise et al. "Expert consensus statement on the science of HIV in the context of criminal law." *J Int AIDS Soc*. 2018.

³¹ Tookes, Hansel et al. "Rapid Identification and Investigation of an HIV Risk Network Among People Who Inject Drugs - Miami, FL, 2018." *AIDS Behavior*, 2020.

³² Poon et al. "Near real-time monitoring of HIV transmission hotspots from routine HIV genotyping: an implementation case study."

³³ De Oliveira et al. "Transmission networks and risk of HIV infection in KwaZulu-Natal, South Africa: a community-wide phylogenetic study."

CONCERNS ABOUT HIV CRIMINALISATION

There are more than 110 countries that assign criminal liability to people living with HIV who are accused of perceived or potential exposure and/or transmission of HIV. However, few countries have laws that need the prosecution to prove transmission; most prosecute allegations of non-disclosure, potential or perceived exposure and simply assume 'criminal' HIV transmission has taken place when the complainant(s) are also living with HIV. All of the previous concerns ultimately converge on how MHS can lead to further accusations that may result in criminal cases. In every jurisdiction in the world, even where health privacy laws exist, MHS data, along with other medical records, can always be subpoenaed by a court and be used as evidence in a criminal investigation or court case if police or prosecutors can persuade a judge to do so. If MHS evidence were included in an investigation or trial, and the results only inferred that the HIV strain of one person was "older" than the strain of another, but the limitations of this evidence were not clearly explained and understood, this could be enough for a conviction. When MHS is used in a country with active HIV criminalisation regimes, this "may lead to a reluctance to

test, failure to disclose contacts and/or refusal of resistance testing. There is evidence that these effects have already occurred. The likelihood of misuse and abuse of these data is high,” especially for historically marginalised and criminalised communities.³⁴ While MHS evidence could be used to prove that a defendant did *not* transmit HIV, access to such data for the defence is extremely limited. Moreover, science often fails to compete against bias in criminal legal systems, which still incarcerate people living with HIV for allegedly using their saliva as a “deadly weapon,” though salivary transmission of HIV is scientifically impossible.³⁵ In most contexts, it is much more likely that MHS would be used *against* overpoliced and over-incarcerated populations than it would be used successfully in their defence.

³⁴ Coltart et al. “Ethical Considerations in Global HIV Phylogenetic Research.”

³⁵ Satta, Mark. “Spitting at Science: The Unjustified Criminalisation of Spitting While HIV-Positive” in *Bill of Health*. Petrie-Flom Center at Harvard Law School. 25 February 2019.

While HIV criminalisation has been a topic that advocates and people living with HIV have been concerned about for decades, only seven of the peer reviewed MHS studies explicitly mentioned that HIV criminalisation was a topic that researchers should consider when undertaking MHS studies. The researchers in these seven studies stated that, at a minimum, jurisdictions should consider the ethical implications of selecting persons with specific, readily identifiable characteristics (race/ethnicity, sexual orientation, and transmission risk) for targeted interventions. However, some papers went further and explained in more detail how HIV criminalisation can negatively impact all aspects of public health goals and the practice of MHS itself.

RESEARCH STUDIES OUTLINES HIV CRIMINALISATION AS A BARRIER TO MOLECULAR HIV SURVEILLANCE



COUNTRY EXAMPLE: UNITED STATES STUDY ON MHS FOR PUBLIC HEALTH INTERVENTION PROPOSES THE DECRIMINALISATION OF HIV

The study researchers indicate: “To further the usefulness and safety of these methods, we also propose decriminalisation of unintended HIV transmission during consensual exposure [emphasis added] and legal recognition that *phylogenetic linkage using pol sequences does not prove beyond a reasonable doubt that transmission between partners occurred* [emphasis added].”

Source: Smith et al. “A Public Health Model for the Molecular Surveillance of HIV Transmission in San Diego, California.” *AIDS*. 2009.



COUNTRY EXAMPLE: CANADIAN MHS STUDY ON GAY MEN AND OTHER MEN WHO HAVE SEX WITH MEN IDENTIFIES CRIMINALISATION AS A BARRIER

The study researchers indicate: “Another challenge for the implementation of HIV phylogenetic monitoring is finding the balance between protecting an individual’s right to privacy and right to refuse medical care, and the public health responsibility to prevent the onward transmission of HIV. *This dilemma is exacerbated by the criminalisation of HIV exposure or transmission* [emphasis added], because the same phylogenetic methods used for characterising transmission hotspots have also been misused to prosecute individuals for the transmission of HIV. It is further compounded by the widespread use of the terms “transmission network” or “transmission cluster” to refer to genetically similar virus populations, which implicitly equates a phylogenetic relationship with a transmission event. On the contrary, a molecular phylogeny cannot establish whether the virus was transmitted directly from one individual to another because of the extensive diversity of HIV within hosts and the potential for transmissions through unknown third parties. Furthermore, a phylogeny cannot establish the directionality of HIV transmission without extensive clonal sequencing of the virus populations.”

Source: Poon, Art et al. “Near real-time monitoring of HIV transmission hotspots from routine HIV genotyping: an implementation case study.” *The Lancet HIV*. 2016.

RECOMMENDATIONS

The following recommendations were developed through the following ways: a) by synthesising existing recommendations we examined in our literature scoping review, to identify the most common themes that arose from scholars and activists concerns on MHS, and b) through ongoing consultation with members of our Expert Advisory Group. These recommendations are not exhaustive in scope, rather they are a base starting point from which to begin our collective work to address concerns on MHS.

The five overarching recommendations are:

- 1 Take seriously and act upon community concerns about MHS.**
- 2 Respect the bodily autonomy and integrity of people living with HIV in all our diversity.**
- 3 MHS implementers must demonstrate a clear public health benefit that outweighs the potential harms of MHS, including by ensuring protections (i.e. data privacy, legal protections, social harms prevention, etc). Demonstrated benefits of MHS must measurably include people living with HIV.**
- 4 Providers ordering HIV sequencing must inform people living with HIV about how their blood and data are being used for MHS purposes and be allowed to withdraw consent if they so wish, without fear of negative consequences to their HIV treatment and care.**
- 5 Implementers of MHS should publicly advocate against punitive or coercive laws and policies aimed at people living with HIV and ensure that MHS is never used in criminal, civil, or immigration investigations or prosecutions.**

For our more detailed recommendations, we have organised them for different stakeholders:

- HIV researchers and scientists,
- Public health practitioners,
- Legal system experts and actors, and
- People living with HIV and their advocates.

While we have placed these recommendations into individual stakeholder categories, many of these recommendations are valid for other areas and stakeholders.



RECOMMENDATIONS FOR RESEARCHERS AND SCIENTISTS

Researchers and scientists have a duty to conduct their work ethically and follow best practices throughout every step of their work, from study design to communicating the results to larger audiences. Therefore:

Studies should be designed to produce knowledge that is the most useful and does the least amount of harm to communities living with HIV.

Researchers should consult with stakeholders, especially people living with HIV, throughout the process to gain full engagement, ensure the balance between community benefit and potential harm, and lessen fears.

Researchers should consider the legal risks of phylogenetic studies by understanding HIV criminalisation laws in the jurisdiction of the study and where data are stored. Additionally, HIV researchers and scientists should be committed to dismantling HIV criminalisation laws.

Robust security measures should be taken with all data, including de-identification, refusing funding from organisations that require publicising data, and having an appropriate committee or board to review data sharing requests.

Informed consent is always required in clinical research, but research involving HIV sequencing must take the most comprehensive, dynamic, and ongoing approach to informed consent. This includes opt-in measures, explaining to participants prior to consent how their data could be used in future studies, and required comprehension assessments to ensure that participants fully understand the risks and benefits of their participation in the study.

Researchers should be prepared to pause, end their study, and not publish findings if any part of the process was not conducted ethically or if the results are potentially more harmful than helpful to communities of people living with HIV.



RECOMMENDATIONS FOR PUBLIC HEALTH PRACTITIONERS

Public health policymakers and practitioners have a duty to ensure that all responses to HIV are grounded in human rights. Therefore:

People in the public health field should monitor policies and practices for any potential discriminatory and stigmatising impact on communities of people living with HIV. If there is potential for harm, people in the public health field should advocate for reform.

Public health surveillance interventions should be people-centred, developed, and conducted using a cultural responsiveness framework. This includes de-linking interventions from law enforcement and not pursuing investigations that can harm people or make their home or workplace unstable.

Public health for people living with HIV should include more than just treatment. For example, if a cluster is identified amongst people who use drugs, multiple other supports and resources, along with HIV treatment, should be provided to people connected to the cluster.

To lessen the stigmatisation and criminalisation of people living with HIV, specific information that could be used to identify individuals in a cluster should not be shared with the media, the police, or the wider public. If findings must be shared, it is up to public health workers to ensure no misinformation is reported, that the story is not sensationalised, and that communities are not further stigmatised or criminalised. When misinformation is reported, public health authorities should publicly correct it.

The bodily autonomy of people living with HIV should be respected and advocated for. This includes informed consent and explaining to people living with HIV how their biometric data can be repurposed in the future for public health. Furthermore, if public health data can be accessed by other agencies (e.g. law enforcement, immigration enforcement, housing), people living with HIV have a right to know and the opportunity to opt out or protect their data.



RECOMMENDATIONS FOR LEGAL SYSTEM EXPERTS AND ACTORS

Public health laws, regulations, and policies have a profound effect on the health of communities and should be created using evidence-based approaches. Furthermore, laws, regulations, and policies that stigmatise, discriminate against, and/or criminalise communities undermine public health goals and diminish human rights. Therefore:

Countries that have them should repeal all HIV criminalisation laws and all countries should ensure non-discriminatory human rights and up-to-date science-based guidance exists for the criminal legal system that severely limits the overly broad use of the criminal law as it relates to allegations of HIV non-disclosure, potential or perceived exposure, and unintentional transmission.

Countries should increase investments in evidence-based programmes that are proven to reduce HIV transmission and acquisition, including community-led responses to criminalisation of people living with HIV, gender identity, sex work, and drug use.

Government funding to public health departments and researchers should be contingent on strong data protections and creating a positive human rights atmosphere for people living with HIV. This includes understanding the legal safeguards and required processes and protections for disclosing public health information to immigration, emergency services and law enforcement.

Phylogenetic analyses should only be used to exonerate individuals in cases related to HIV criminalisation.



RECOMMENDATIONS FOR PEOPLE LIVING WITH HIV

People living with HIV, whether as activists, experts, or ordinary people, can contribute towards addressing the potential harms of MHS. Therefore:

Learn about your local public health surveillance system to understand if MHS is being used in your community.

Advocate against the many intersectional ways that criminalisation and surveillance impact members of the HIV community, including people of trans experience, immigrants, gay and bisexual men, people of colour, people who use drugs, and sex workers.

Be aware of and consider how criminalisation and surveillance impacts members of the HIV community, including people of trans experience, immigrants, gay and bisexual men, people of colour, people who use drugs, and sex workers.

METHODOLOGY

This project utilised a scoping review methodology to understand the quality and scope of the literature on MHS. The goal was to understand where, how, by who, and in what ways MHS is being used globally. As outlined by Tricco, et al. (2018), scoping reviews are useful for answering broad questions, such as, “what is the nature of the evidence for this intervention” or “what is known about this concept?”³⁶ To collect the data for this project, we utilised the PubMed database and Google Scholar. When gathering our data, we sought to ensure: a global scope with a diversity of site countries, a diversity of uses of MHS (surveillance, public health intervention, etc.), a diversity of populations, the most recent articles, and the most cited articles. Our search included terms that address our criteria, terms that are related to MHS, and terms related to the geographical locations and populations. For example, some of the terms we used include phylogenetic, molecular, HIV, men who have sex with men, transgender, and geographical regions.

There were thousands of results for journal articles published between 2000 and 2021. To manage the large quantities of studies, our approach was not to summarise the entire body of MHS research, but rather to garner a representative sample of MHS studies that met our criteria. As a result, when we saw multiple studies in the same country, or looking at the same population, we limited our analyses, and excluded studies. Articles were manually screened, first by title, and then by abstract to assess relevance based on our eligibility criteria. We also focused on the most cited articles and the newest articles. To date, we have included and examined 72 articles. We have divided the articles into two areas for analysis: peer-reviewed MHS studies 50 and peer-reviewed articles on MHS studies 22.

In addition to the peer-reviewed articles, we also conducted a search for grey literature. Grey literature is any document that is produced by any level of government, academic, business, and industry. Examples of grey literature include presentations, reports, memos, white papers, policies and procedures. The grey literature was obtained by reaching out to various listservs and asking members to submit documents. We reached out to the SERO and HIV JUSTICE WORLDWIDE listservs for documents. To date, we have included and examined 20 pieces of grey literature. In total we have examined at least 92 pieces of literature on MHS.

³⁶ Andrea C. Tricco, Erin Lillie, Wasifa Zarin, et al. (2018). [PRISMA Extension for Scoping Reviews \(PRISMA-ScR\): Checklist and Explanation](#), *Annals of Internal Medicine*.169:467-473.

APPENDIX: LITERATURE REVIEWED

PEER REVIEWED LITERATURE

Title of Article	Year Published	Authors	Journal
Phylogenetic analysis as a forensic tool in HIV transmission investigations	2018	Abecasis, Ana, et al.	AIDS
Molecular surveillance of HIV-1 field strains in Nigeria in preparation for vaccine trials	2002	Agwale, S.M et al.	Vaccine
Analysis of HIV-1 pol sequences from Panama: Identification of phylogenetic clusters within subtype B and detection of antiretroviral drug resistance mutations	2009	Ahumada-Ruiz, Sara et al.	Infection, Genetics and Evolution
HIV genotypes and primary drug resistance among HIV seropositive blood donors in Brazil: role of infected blood donors as sentinel populations for molecular surveillance of HIV	2013	Alencar, CS et al.	J Acquir Immune Defic Syndr
Opioid Use Fueling HIV Transmission in an Urban Setting: An Outbreak of HIV Infection Among People Who Inject Drugs—Massachusetts, 2015–2018	2020	Alpren, Charles et al.	American Journal of Public Health
HIV-1 Diversity, Transmission Dynamics and Primary Drug Resistance in Angola	2014	Bártolo, Inês et al.	PLOS ONE
We Are People, Not Clusters!	2020	Bernard, Edwin J. et al.	American Journal of Bioethics
Large cluster outbreaks sustain the HIV epidemic among MSM in Quebec	2017	Brenner, Bluma G, et al.	AIDS
The Power and Pitfalls of HIV Phylogenetics in Public Health	2013	Brooks, James & Paul Sandstrom	Canadian Journal of Public Health
Detailed Transmission Network Analysis of a Large Opiate-Driven Outbreak of HIV Infection in the United States	2017	Campbell, Ellsworth et al.	The Journal of Infectious Diseases
Molecular epidemiology of a primarily MSM acute HIV-1 cohort in Bangkok, Thailand and connections within networks of transmission in Asia	2018	Chang, David et al.	Journal of the International AIDS Society
Molecular Epidemiology of HIV Type 1 Subtypes in Taiwan: Outbreak of HIV Type 1 CRF07-BC Infection in Intravenous Drug Users	2006	Chang, Sui-Yuan et al.	AIDS Research and Human Retroviruses
Molecular epidemiology identifies HIV transmission networks associated with younger age and heterosexual exposure among Korean individuals	2016	Chin, Bum Sik et al.	Journal of Medical Virology
Consent and criminalisation concerns over phylogenetic analysis of surveillance data	2019	Chung, Cecilia et al.	The Lancet HIV
Ethical Considerations in Global HIV Phylogenetic Research	2018	Coltart, C. E. et al.	The Lancet HIV
Molecular HIV Surveillance: Balancing Outbreak Detection and Control and the Rights of Persons Living With HIV	2020	Cranston, Kevin	American Journal of Public Health
Molecular HIV Surveillance: Balancing Outbreak Detection and Control and the Rights of Persons Living With HIV	2020	Cranston, Kevin	American Journal of Public Health
Conceptualizing a Bioethics of the Oppressed: Oppression, Structure, and Inclusion	2020	Croce, Yoann Della	The American Journal of Bioethics
HIV-1 Transmission Cluster With T215D Revertant Mutation Among Newly Diagnosed Patients From the Basque Country, Spain	2009	Cuevas, Maria Teresa et al.	J Acquir Immune Defic Syndr
Molecular HIV Surveillance and Public Health Ethics: Old Wine in New Bottle	2020	Dawson, Liza & Stephen Latham	The American Journal of Bioethics
Addressing Ethical Challenges in US-Based HIV Phylogenetic Research	2020	Dawson, Liza et al.	The Journal of Infectious Diseases
Transmission networks and risk of HIV infection in KwaZulu-Natal, South Africa: a community-wide phylogenetic study	2017	de Oliveria, Tulio et al	The Lancet HIV
HIV-1 Genetic and Contact Networks Among Men Who Have Sex With Men May Inform Public Health Efforts	2018	Dennis, Ann M.	American Journal of Public Health

Two Independent HIV Epidemics in Saint Petersburg, Russia Revealed by Molecular Epidemiology	2015	Dukhovlina, Elena et al.	AIDS Research and Human Retroviruses
First Molecular Surveillance Report of HIV Type 1 in Injecting Drug Users and Female Sex Workers along the U.S.–Mexico Border	2007	Eyzaguirre, L. et al.	AIDS Research and Human Retroviruses
Analysis of the Driving Factors of Active and Rapid Growth Clusters Among CRF07_BC-Infected Patients in a Developed Area in Eastern China	2021	Fan, Qin et al.	Open Forum Infectious Diseases
Patterns of Transmitted HIV Drug Resistance in Europe Vary by Risk Group	2014	Frentz, Dineke et al.	PLOS ONE
Methodological synthesis of Bayesian phylodynamics, HIV-TRACE, and GEE: HIV-1 transmission epidemiology in a racially/ethnically diverse Southern U.S. context	2021	Fujimoto, Kayo et al.	Nature
Considerations for Modernized Criminal HIV Laws and Assessment of Legal Protections Against Release of Identified HIV Surveillance Data for Law Enforcement	2019	Galletly, Carol et al.	American Journal of Public Health
Phylogenetic Surveillance of Viral Genetic Diversity and the Evolving Molecular Epidemiology of Human Immunodeficiency Virus Type 1	2007	Gifford, Robert et al.	Journal of Virology
Outbreak of Human Immunodeficiency Virus Infection Among Heterosexual Persons Who Are Living Homeless and Inject Drugs — Seattle, Washington, 2018	2019	Golden, Matthew R. et al.	MMWR Morbidity Mortality Weekly Report
Molecular Surveillance of HIV-1 in Madrid, Spain: a Phylogeographic Analysis	2011	Gonzalez-Alba, Jose et al.	Journal of Virology
Genetic clusters and transmission in transgender women	2019	Gräf, Tiago and Joshua T. Herbeck	The Lancet HIV
Can Directionality of HIV Transmission be Predicted by Next-Generation Sequencing Data?	2018	Günthard, Huldrych F. and Roger Kouyos	The Journal of Infectious Diseases
Ethical Convergence and Ethical Possibilities: The Implications of New Materialism for Understanding the Molecular Turn in HIV, the Response to COVID-19, and the Future of Bioethics	2020	Guta, Adrian, Marilou Gagnon, and Morgan Philbin	The American Journal of Bioethics
Benefit of HIV Molecular Surveillance is Unclear, but Risks to Prevention Norms Are Clear	2020	Haire, Bridget	The American Journal of Bioethics
Defining HIV-1 transmission clusters based on sequence data	2017	Hassan, Amin S. et al.	AIDS
Increasing proportions of HIV-1 non-B subtypes and of NNRTI resistance between 2013 and 2016 in Germany: Results from the national molecular surveillance of new HIV-diagnoses	2018	Hauser, Andrea et al.	PLOS ONE
A Geographic Hotspot and Emerging Transmission Cluster of the HIV-1 Epidemic Among Older Adults in a Rural Area of Eastern China	2020	Jiang, Jun et al.	AIDS Research and Human Retroviruses
Assessment of HIV molecular surveillance capacity in the European Union, 2016	2017	Keating, Patrick et al.	Eurosurveillance
Foreign Born Individuals with HIV in King County, WA: A Glimpse of the Future of HIV?	2017	Kerani, Roxanne et al.	AIDS and Behavior
Phylogenetic analysis as expert evidence in HIV transmission prosecutions	2016	Kidd, Paul	Australian Federation of AIDS Organisations (AFAO)
HIV-TRACE (TRANSMISSION CLUSTER ENGINE): a Tool for Large Scale Molecular Epidemiology of HIV-1 and Other Rapidly Evolving Pathogens	2018	Kosakovsky Pond, Sergei L. et al.	Molecular Biology and Evolution
Detailed Molecular Surveillance of the HIV-1 Outbreak Among People who Inject Drugs (PWID) in Athens During a Period of Four Years	2017	Kostaki, Evangelia et al.	Current HIV Research
Contribution of transgender sex workers to the complexity of the HIV-1 epidemic in the metropolitan area of Milan	2020	Lai, Alessia, et al.	Sexually Transmitted Infections
Ethical Justification for Conducting Public Health Surveillance Without Patient Consent	2012	Lee, Lisa et al.	Health Policy and Ethics
Assessing the HIV-1 epidemic in Brazilian drug users: a molecular epidemiology approach	2015	Lindenmeyer Guimarães, Monick et al.	PLOS ONE
The rise of molecular HIV surveillance: implications on consent and criminalization	2019	McClelland, Alexander et al.	Critical Public Health
How to build an HIV out of care watch list: Remaking HIV surveillance in the era of treatment as prevention	2020	Molldrem, Stephen	First Monday
Reassessing the Ethics of Molecular HIV Surveillance in the Era of Cluster Detection and Response: Toward HIV Data Justice	2020	Molldrem, Stephen et al.	American Journal of Bioethics
HIV-1 molecular epidemiology evidence and transmission patterns in the Middle East and North Africa	2011	Mumtaz, Ghina et al.	Sexually Transmitted Infections

Molecular Surveillance of HIV-1 Infection in Krasnoyarsk Region, Russia: Epidemiology, Phylodynamics and Phylogeography	2019	Neshumae, Dmitry et al.	Current HIV Research
Using Molecular HIV Surveillance Data to Understand Transmission between Subpopulations in the United States	2020	Oster, Alexandra et al.	Journal of Acquired Immune Deficiency Syndromes
Identifying clusters of recent and rapid HIV transmission through analysis of molecular surveillance data	2018	Oster, Alexandra et al.	Journal of Acquired Immune Deficiency Syndromes
Molecular Tracing of the Geographical Origin of Human Immunodeficiency Virus Type 1 Infection and Patterns of Epidemic Spread Among Migrants Who Inject Drugs in Athens	2017	Paraskevis, Dimitrios et al.	Current HIV Research
Near real-time monitoring of HIV transmission hotspots from routine HIV genotyping: an implementation case study	2016	Poon, A et al.	The Lancet HIV
Automated analysis of phylogenetic clusters	2013	Ragonnet-Cronin, Manon et al.	BMC Bioinformatics
HIV transmission networks among transgender women in Los Angeles County, CA, USA: a phylogenetic analysis of surveillance data	2019	Ragonnet-Cronin, Manon et al.	The Lancet HIV
Sources of HIV infection among men having sex with men and implications for prevention	2016	Ratmann, O. et al.	Science Translational Medicine
Geographic and Temporal Trends in the Molecular Epidemiology and Genetic Mechanisms of Transmitted HIV-1 Drug Resistance: An Individual-Patient- and Sequence-Level Meta-Analysis	2015	Rhee, Soo-Yon et al.	PLOS Medicine
Identifying Transmission Clusters with Cluster Picker and HIV-TRACE	2016	Rose, Rebecca et al.	AIDS Res Hum Retroviruses
Informed Consent for HIV phylogenetic research: A case study of urban individuals living with HIV approached for enrollment in an HIV study	2020	Rudolph, Abby E., Omar Martinez, Robin Davison, andChineye Brenda Amuchi	EHQUIDAD
HIV-1 Sub-Subtype A6: Settings for Normalised Identification and Molecular Epidemiology in the Southern Federal District, Russia	2020	Schlösser, Madita et al.	Viruses
Using an Established Outbreak Response Plan and Molecular Epidemiology Methods in an HIV Transmission Cluster Investigation, Tennessee, January - June 2017	2020	Sizemore, Lindsey et al.	Public Health Methodology
A Public Health Model for the Molecular Surveillance of HIV Transmission in San Diego, California	2009	Smith, Davey M., Susanne May, Samantha Tweeten, Lydia Drumright, et al.	AIDS
Determining the Direction of Human Immunodeficiency Virus Transmission: Benefits and Potential Harms of Taking Phylogenetic Analysis One Step Further.	2021	Taylor, Barbara S. and Hugo Sapien	Clinical Infectious Diseases
Rapid Identification and Investigation of an HIV Risk Network Among People Who Inject Drugs –Miami, FL, 2018	2019	Tookes, Hansel et al.	AIDS and Behaviour
PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity	2018	Wymant, Chris et al.	Molecular Biology and Evolution
Use of molecular HIV surveillance data and predictive modeling to prioritize persons for transmission-reduction interventions	2020	Xia, Qiang et al.	AIDS
Prevalence, Molecular Epidemiology and Drug Resistance Pattern of Human Immunodeficiency Virus Type 1 among Injecting Drug Users in Lahore, Pakistan	2021	Yaqub, Saima et al.	Pakistan J. Zool.
Transmission of HIV-1 drug resistance in Switzerland: a 10-year molecular epidemiology survey	2007	Yerly, Sabine et al.	AIDS
Evaluation of Phylogenetic Methods for Inferring the Direction of Human Immunodeficiency Virus (HIV) Transmission: HIV Prevention Trials Network (HPTN) 052	2021	Zhang, Yinfeng et al	Clinical Infectious Diseases

COMMUNITY, RESEARCH, AND GOVERNMENT GREY LITERATURE

Title of Document	Year Published	Authors	Organization
Best Laid Plans: Community concerns about HIV Molecular Testing	Unknown	Aaron Cogle	National Association of People with HIV Australia (NAPWAH)
NYC Strategy to Ending the HIV Epidemic	Unknown	Bisrat Abraham	NYC Department of Health
Meeting summary Responsible Use of HIV Cluster Data for Public Health Action: Amplifying Benefits, Minimizing Harms	2020	CDC	CDC
PowerPoint Presentation: HIV Data in Action	2018	CDC	CDC
Sample Press Release 1: PWID	2018	CDC	CDC
Sample Press Release 2: MSM	2018	CDC	CDC
Key Considerations for Engaging With News Media During a Cluster Response	2018	CDC	CDC
End the HIV Epidemic: An HIV Tracing Discussion, Part 2: How Molecular HIV Surveillance data are used in research - Seattle & King County's HIV Tracing Work	2021	Diana Tordoff	Seattle & King County Public Health
ECDC strategic framework for the integration of molecular and genomic typing into European surveillance and multi-country outbreak investigations	2019	European Centre for Disease Prevention and Control	European Centre for Disease Prevention and Control
Ethical considerations for a public health response using molecular HIV surveillance data	2017	Evans, D. et al.	Project Inform and Northwestern University
Learning about the Recent Infection Testing Algorithm (RITA)	2016	Health Service Executive	Health Service Executive
End the HIV Epidemic: An HIV Tracing Discussion, Part 1: Soliciting Community Feedback to Inform Public Health - Seattle & King County's HIV Tracing Work	2021	Jsani Henry & Roxanne Kerani	Seattle & King County Public Health
Using Molecular HIV Surveillance Data to Guide Public Health Practice in NYC	2017	Lucia Torian	NYC Department of Health
What is the acceptability of using phylogenetic data in clinical and public health practice?	2019	Mulka L, Pollard A, Vera JH, Leigh Brown A, Farsides B, Bernard E, Williams, M, Cassell J.	British HIV Association Conference
HIV Data Privacy and Confidentiality: Legal & Ethical Considerations for Health Department Data Sharing	2018	NASTAD	NASTAD (National Alliance of State and Territorial AIDS Directors)
Detecting and Responding to HIV Transmission Clusters: A Guide for Health Departments June 2018	2018	National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention	CDC
Big Ideas: Policy Action Can Increase Community Support for HIV Cluster Detection (Policy Brief)	2019	O'Neill Institute for National & Global Health Law	Georgetown Law
Quick Take: Using Cluster Detection to End the HIV Epidemic	2019	O'Neill Institute for National & Global Health Law	Georgetown Law
Consent form for Primary Infection Resource Consortium Network	2020	Primary Infection Resource Consortium Network	University of California
Molecular HIV Surveillance - Genotype Clusters Talking Points	2017	Texas Health and Human Services	Texas Health and Human Services
Molecular HIV Surveillance Cluster Response & Community Engagement	2017	The Bureau of HIV/STD and Viral Hepatitis Prevention	Houston Health Department