Sarcouncil Journal of Internal Medicine and Public Health

ISSN(Online): 2945-3674

Volume- 05| Issue- 01| 2026

Research Article **Received:** 20-12-2025| **Accepted:** 15-01-2026 | **Published:** 31-01-2026

Enhancing Rapid Response to HIV Outbreaks: Lessons from U.S. Cluster Detection and Contact-Tracing Models

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Abstract: **Background:** The United States is required to control the epidemic of HIV by rapidly detecting and responding to clusters of its transmission. Starting to be used recently, the development of molecular surveillance, digital contact tracing, and data integration has changed the definition of outbreak intelligence, allowing rapid transmission networks to be identified nearly in real time. **Objective:** This narrative review sums up the evidence published in the past two years on the shift in U.S. cluster detection and response models, which focus on technological, operational, and ethical aspects of the matter that affect preparedness to outbreaks and precision prevention. **Approach:** The critical analysis of peer-reviewed articles and population health assessments (2020-2025) was conducted to reveal the emergent trends, gaps in knowledge, and issues in implementation. Instead of systematically listing cases, the review focuses on interpretive synthesis of molecular epidemiology, network-based contact tracing, and community engagement frameworks. **Findings:** Recent national implementation of the use of molecular cluster identification by the CDC and local jurisdictions has reduced response times and improved cross-sector coordination. Nonetheless, the differences in the capacity of the workforce, interoperability of data, and ethical governance are still significant obstacles. Some of these innovations, like AI-assisted outbreak forecasting and community-engaged surveillance models, have potential and need to be empirically validated and deployed equally. **Conclusion:** To improve the response to HIV outbreaks in a short time frame, the coordination of their data, sound ethical control, and permanent cooperation with the community are required. The experience of the U.S. molecular and contact-tracing models suggests that technological accuracy and social trust have to be balanced to provide sustained control of the epidemic.

Keywords: HIV cluster detection; molecular surveillance; digital contact tracing; outbreak response; precision public health.

INTRODUCTION

The speedy detection and reaction to concentrations of HIV spread continue to play a critical role in preventing new infections in the United States. Although there are significant progresses in biomedicine, including pre-exposure prophylaxis (PrEP) and antiretroviral treatment (ART), the transmission is not evenly spread, especially in marginalized groups. In turn, population health measures have shifted to precision prevention and have incorporated molecular epidemiology, contact tracing, and social network analysis to quickly identify and cut transmission clusters. The strategies are the foundation of the Ending the HIV Epidemic (EHE) program launched by the U.S. Centers for Disease Control and Prevention that will decrease the new infections by 90 percent by 2030 (Garcia *et al*., 2023). Molecular cluster detection, which is the identification of genetically linked HIV cases, signals that high-speed local transmission has emerged as a revolution in responding to outbreaks. Molecular techniques can be used to detect outbreaks almost in real-time by using viral sequence data collected as a normal part of routine surveillance, allowing specific interventions before these incidents can be transmitted extensively (France *et al*., 2025). Such a combination of genomic surveillance and traditional contact tracing is indicative of a paradigm shift in terms of future prediction of outbreaks as opposed to the retrospective identification of cases.

Cluster detection has a higher significance to the health of the people than its technical ingenuity. It revisits the conceptualization of epidemiologists in terms of transmission networks, which emphasizes the presence of interaction between biological determinants, behavioural determinants, and social determinants. It is empirically proven that timely and coordinated interventions prevent hundreds of secondary infections in the case of localized responses to clusters of HIV (Oster *et al*., 2022). On the other hand, the examples of delay in cluster identification, such as the one observed during the 2014-2015 epidemic in Scott County, Indiana, revealed the severe weak points in surveillance (Gonsalves and Crawford, 2018). These case studies emphasize the twofold need of timeliness and trust: effective data-sharing architectures should be accompanied by ethical measures to ensure societal trust. In addition, the COVID-19 pandemic has revived research on the topic of outbreak analytics and has made comparisons between HIV cluster surveillance and pathogen genomic tracing of respiratory viruses. The real-time cluster mapping and adaptive response algorithms in HIV surveillance systems are now

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DOI- https://doi.org/10.5281/zenodo.18444659

informed by cross-disciplinary innovations of these adjacent fields (Quilter *et al*., 2021).

Although the models of rapid reaction to outbreaks have made major progress in terms of detecting outbreaks, a few systemic and ethical issues are still hindering their complete usage. The number of data integration and interoperability challenges is also a significant challenge because local and federal systems do not work together effectively in the exchange of data due to their fragmentation. CDC has standardized protocols to detect molecular clusters, but because there is variability in electronic reporting at the state level, the protocols are not scalable (France *et al*., 2025). Additional issues that complicate the application of molecular surveillance include privacy and stigmatization; concerns of consent and data use, as well as the security of key populations, may undermine community involvement and trust (Oster *et al*., 2021). Inequality in how operations are carried out also remains, and in many cases, rural and under-resourced regions do not have the technical infrastructure or human capital needed to perform complex cluster analysis, which feeds inequity in responding to outbreaks (Philpott *et al*., 2022). Moreover, digital and molecular tools enhance the speed of detection, but the barrier to application of these findings in timely field interventions is presented by legal, logistical, and cultural barriers, which slow down contact tracing and containment efforts (Sizemore *et al*., 2020). It is against this backdrop that there is an urgent requirement to bridge these gaps by coming up with models that not only enhance technical detection but also lead to effective cooperation among agencies, disciplines, and communities.

The current CDC efforts focus on standardization and capacity development using the HIV Outbreak Coordination Unit (OCU) to simplify federal assistance in cluster investigations (Oster *et al*., 2022). The protocols of the OCU combine epidemiological intelligence with the genomic data, which provides multi-level coordination of the federal, state, and local partners. This is indicative of an increased appreciation that outbreak response is a governance issue, no less problematic than a scientific one. On the technological edge, predictive modeling of the transmission dynamics is now possible due to the development of machine learning and network analytics. Initial trials of applying these tools to the work of the public health departments have proven the better prioritization of partner services and prevention outreach (Garcia *et al*., 2023). At the same time, the local responses to outbreaks, including the West Virginia surge investigation, have honed the framework of the best practice of interagency coordination and use of data to make decisions (Quilter *et al*., 2021). The following evolutionary step in cluster detection systems is the synthesis of molecular, behavioral, and social data. Genomic-linked contact-tracing results and demographic risk profiles in the form of integrative dashboards are already widely implemented to provide near real-time surveillance and response planning. These platforms are the basis of the shift towards anticipatory rather than reactive public health intelligence.

Even though tools and systems of cluster detection and contact tracing exist, the effectiveness of these tools is empirically evaluated only sparingly. Little research has been conducted on systematically studying the effect of the combination of these approaches on outbreak containment in different jurisdictions in the United States. The majority of the existing analysis is mostly descriptive and not integrated into wider theories or predictive utility. This raises serious concerns about the urgent need for an interpretive synthesis to map the conceptual advancement, identify the gap in the research, and inform the creation of future generations of surveillance models. The most important open questions are how to increase the interoperability of data in disconnected public health systems, which ethical principles can reconcile the efficacy of molecular surveillance with personal privacy and community sovereignty, and what factors, including early detection triggers, immediate mobilization of the workforce, and standard data practices, are most readily replicable in different environments. These issues should be addressed in order to transform the current broken, reactive reactions into integrated epidemic intelligence systems.

The objective of this review is to synthesize the evidence that has been published since 2020 on the topic of HIV cluster detection and contact-tracing models in the U.S., specifically focusing on how molecular epidemiology, data systems, and rapid-response frameworks are integrated. Through the discussion of the trends in policy, technology, and ethics, it aims to illuminate the broad advances that have led to the current state of outbreak management, determine the current problems and research limitations of modern implementation, and suggest an imaginary roadmap of how future integration of real-time analytics, fair data control, and community-based strategies can occur. This paper approaches rapid response as a dynamic ecosystem, rather than a technical process, integrating scientific rigor, social fairness, and coordinated system-level response in accelerating national responses in ending the HIV epidemic.

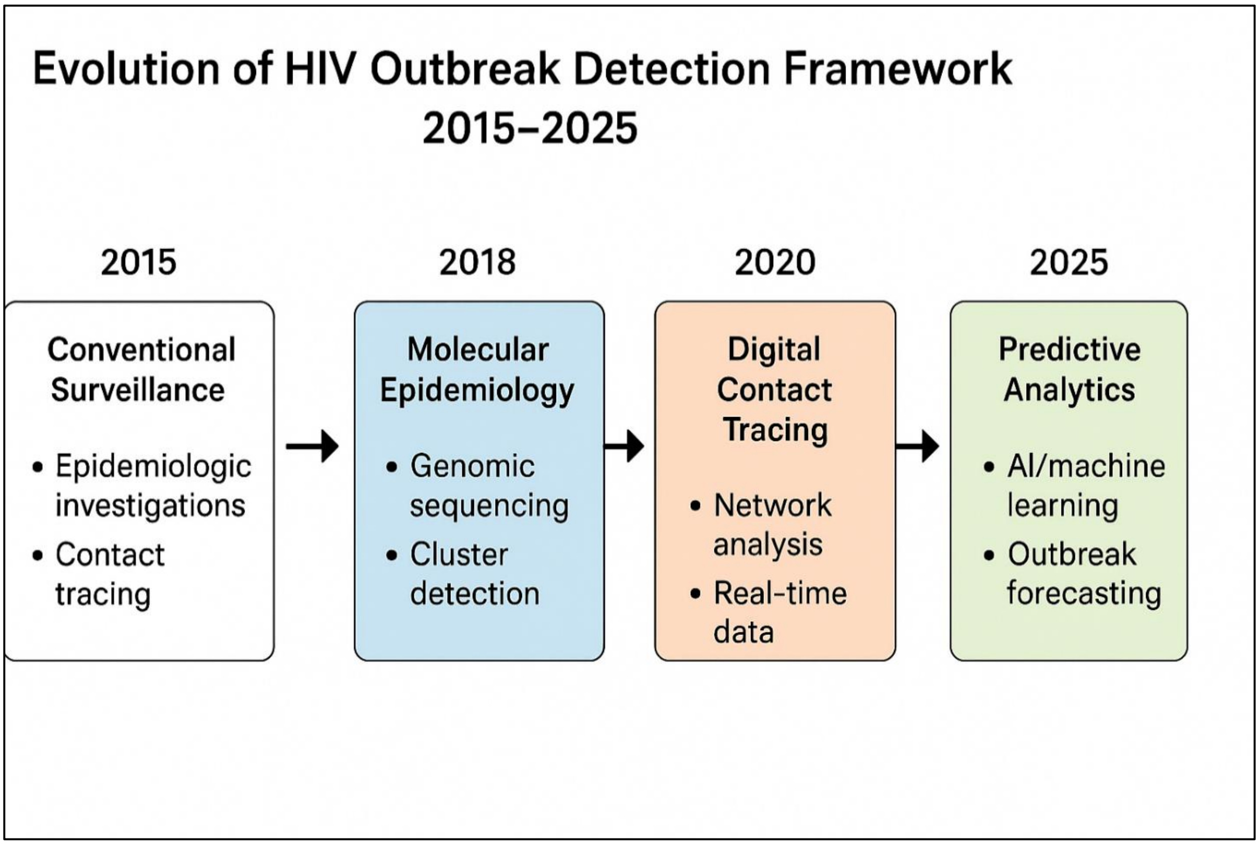

Figure 1: Evolution of HIV Outbreak Detection Framework, 2015-2025
Source: Author's construct, 2025

Emerging Trends and Thematic Analysis

The section is a synthesis of recent post-2020 developments in the United States in regards to the advancement of HIV cluster detection and contact-tracing systems. Thematic analysis shows that there are four dominant trends that influence this area: (1) Molecular surveillance and analytics innovations, (2) Digital and network-based contact tracing, (3) Ethical, social, and data justice, and (4) Future uses toward predictive and equitable response to epidemics. All the themes emphasize the interaction between technological innovation, community health operations, and ethical governance of outbreak control.

Molecular Surveillance and Real-Time Analytics: Evolution

The shift of HIV surveillance from passive case reporting to dynamic, molecular-driven intelligence is one of the most important achievements in the sphere of public health in the past decade. The Molecular HIV Surveillance (MHS) framework by the U.S. CDC has been implemented in almost every state and local health department since 2020, which allows the near-real-time detection of genetically related infections (France *et al*., 2025). These systems study sequences of HIV-1 pol genes received at diagnostic labs, where clusters are created according to genetic distance levels, which reveal the likelihood of rapid transmission.

The recent assessments have reflected significant growth in the time of response to outbreaks and coverage areas. with the use of the HIV-TRACE (Transmission Cluster Engine), automated detection pipelines have been implemented, which connect epidemiologic and molecular streams of data (Mehta *et al*., 2025). Detection latency is reduced more than 40 times compared to the systems used during the 2020s, which have made it possible to deploy contact-tracing teams and prevention services earlier.

Nonetheless, a high level of heterogeneity between jurisdictions remains. Other states with well-established data infrastructure, including New York and California, have built integrated dashboards that integrate MHS data with the field investigation metrics, whereas others are supported by manual cluster review committees (Garcia *et al*, 2023). This disproportionate application creates persistent inequities in capacity, training, and funding.

More importantly, it is now possible to predict the growth pathways of clusters with the convergence of machine learning and molecular data. In urban areas, pilot projects have shown that algorithmic models can preempt high-risk network expansions up to half a year early, which may be used to preempt intervention (Schuster *et al*., 2024). The models include the social network metrics, the viral diversity, and the rate of testing to estimate the velocity of transmission, which is where the new paradigm of anticipatory epidemiology is produced.

The shift towards predictive modeling as opposed to retrospective analysis represents a paradigm shift in the definition of outbreak intelligence. The MHS systems are now bio-surveillance systems, which have the capacity to connect genomics, behavior, and demography into cohesive analytic systems. However, the more refined the models of analysis, the more the need to have stringent ethical controls and open systems of governance.

National Digital and Network-Based Contact Tracing

In line with molecular innovations, contact-tracing systems have been digitally transformed. The core principles of traditional partner services involve the use of interviews and manual record searches to find and inform the contacts; however, recently, the network analytics and digital communication tools have become prominent to facilitate the process effectively.

The current CDC guidelines indicate the need to integrate molecular and social network data in a single dashboard to facilitate real-time partner notification and connection to care after 2020 (France *et al*., 2025). The digital tablet-equipped field teams are now able to visualize cluster networks, locate bridging nodes, and rank contacts according to proximity and transmission probability.

The West Virginia outbreak response in 2021 showed the strength of such an integrated model: the investigators could map a rapidly expanding range of injection-related HIV spread and implement harm-reduction services within days using a combination of genomic and contact data (Quilter *et al*., 2025). The same hybrid efforts are under trial in Atlanta and Chicago, where epidemiologists are working side by side with data scientists to bring the visualization of network development to a real-time view.

The Outbreak Coordination Unit (OCU), which was created by the CDC in 2020, is the hub of standardization of these processes. Its cross-jurisdictional procedures guarantee uniform definitions and data-sharing contracts and triage thresholds to act (Oster *et al*., 2022). With this coordination, responding to outbreaks has become more responsive, and the traditional boundaries between epidemiology, data science, and operations in the field are becoming less distinct.

Contact tracing has become a dynamic systems science through the integration of digital tracing and molecular analytics and is no longer a static, retrospective process. Nonetheless, there is still a lack of operational gaps in data interoperability and cross-platform integration. According to experts, until informatics pipelines are standardized and access to digital tools is equal, the situation in which some areas are more susceptible to outbreaks and slower in response will be maintained, and rural and underfunded areas will be overrepresented.

Ethical, Social, and Data Justice Considerations

Although molecular and digital advances hold potential to make advances in precision unmatched, they have also served as a kind of resurgence of ethical debates on privacy, consent, and surveillance justice. The higher the data granularity, the higher the possibility of being abused or stigmatized unwillingly, especially when considering the communities that are affected by HIV at a disproportionate rate.

Bioethicists have also expressed serious doubts regarding the absence of informed consent in the molecular cluster detection, with the majority of people whose viral sequences are analyzed not realizing that the information can be employed to conduct the public health linkage analysis (Molldrem & Smith, 2020). As a result, some have called for an HIV data justice framework that focuses on community autonomy, transparency, and participative governance on data use.

A succession of qualitative research indicates that mistrust and criminalization anxieties of the community may obstruct involvement in cluster studies (Watson 2023). Marginalized groups, in particular, Black, Latino, and LGBTQ+, report apprehensions about the use of molecular data in courts or as a means of strengthening stigmatization. Such apprehensions are amplified by the convergence of the two fields in the form of molecular surveillance with statistics on criminalization of HIV in certain states (Garcia *et al.*, 2023).

Moreover, the authors like Schuster *et al.* (2024) underline that the user experience is one of the key aspects of the ethical implementation, not only among the staff of medical institutions but also among those who have suffered. The survey conducted across the country helps highlight the importance of culturally competent communication and standardized training of health departments to communicate with their communities in a transparent way (Schuster *et al.*, 2024).

The most debatable issue is the need to consider the interests of the whole population and the rights of a person. HIV data ethical governance should transcend the compliance-based privacy models to participatory ethics, in which the affected communities actively co-design the surveillance models. Without a trustworthy, transparent, and mutually agreed-upon decision-making process, effective surveillance cannot be ethically viable (Molldrem and Smith, 2020).

One of the most promising conceptual frameworks which have arisen as a result of this discussion is the Community-Engaged Surveillance Framework (CESF), which focuses on the two-way communication, fair consent paradigm, and community-based interpretation of data. Epidemiologic accuracy could be preserved by future incorporation of CESF principles into CDC protocols to alleviate the issue of data justice.

New Future Applications and Systemic Integration

In the future, the U.S. system of response to HIV outbreaks is expected to grow its focus beyond cluster intelligence to predictive, adaptive, and equity-related public health intelligence. The integration of genomic, behavioral, and environmental data streams, also known as next-generation surveillance, is changing the epidemiologic environment.

The next-generation research suggests applying AI-based outbreak prediction, which would use both structured (sequence, case counts) and unstructured (social media, mobility patterns) data to anticipate locations of the outbreak acceleration (Mehta *et al.*, 2025). Initial experiments in pilot programs of CDC have been encouraging, as models can detect possible outbreak seed groups before the explosion grows exponentially.

At the same time, the rise of cloud-based surveillance systems can be used to ease any real-time cooperation between health departments, promote prompt triage and analytics (France *et al.*, 2025). This decentralization of analytic capacity democratizes response during outbreaks, whereby the local jurisdictions are given the powers to respond independently, and coordination among the federal government.

On the conceptual level, researchers such as Watson *et al.* (2022) recommend the use of narrative ethics approaches that place surveillance data in a wider context of lived experiences. According to them, the inclusion of community narratives in surveillance analytics is not just humanizing the response to public health but also enhances interpretive accuracy by placing data on a socio-cultural reality.

The future direction of HIV cluster detection will probably lead to systems integration and moral reflexivity. The principles of justice, equity, and local empowerment cannot be guaranteed through technological innovation alone to control the epidemic. Next-generation response systems should, therefore, act as learning ecosystems in that they should constantly evolve according to the community response, data performance, and ethical reflection.

FUTURE DIRECTIONS AND RESEARCH GAPS

Persistent Gaps in Molecular HIV Surveillance Capacity

Although molecular HIV surveillance (MHS) has revolutionized the way outbreaks are responded to, the coverage and practice of MHS is uneven across jurisdictions in the U.S. By 2025, approximately 70 percent of the HIV-reporting regions are wholly integrated with the MHS with local health departments, which creates surveillance blind spots in resource-restricted and rural areas (France *et al.*, 2025). Such differences are usually motivated by differences in skills in the workforce, bioinformatics ability, and availability of data system interoperability.

The next step of research should be directed at a scalable architecture that will allow sharing of real-time molecular data between the laboratories, local agencies, and, CDC. Cloud-based and privacy-protected repository development and standardized data pipelines would minimize latency and enable federated analyses across jurisdictions. Public-health payback would be better understood through comparative studies that measure the results in states that have and do not have integrated systems.

Integration and Interoperability of Data

The presence of technological fragmentation remains a barrier to the smooth flow of data between the molecular and behavioral surveillance systems and the clinical surveillance system. Garcia *et al*. (2023) found that the implementation of laboratory information systems to match public-health informatics systems produced significant obstacles in the delivery of information, and delays in confirming clusters and duplication of case records.

New machine-learning capabilities that can align heterogeneous data sets can eliminate these inefficiencies, but not many have undergone testing on a working scale. Automated linkage algorithms require rigorous pilot trials to test bias and provide equitable performance by subgroups of the population. HL7 FHIR extensions of genomic surveillance should also be included in the list of priorities for research to promote a nationwide harmonization.

Legal and Ethical Complexities of Using Surveillance Data

The issue of ethics has been one of the most serious and controversial, unsolved questions. Researchers stress that MHS tends to be functioning without a clear personal consent, which brings up the problem of autonomy and data justice (Molldrem and Smith, 2020). Respondents in the community are worried about the fact that genetic connections might accidentally expose some sexual or drug use network, and the participants would be stigmatized or criminalized (Shook *et al*., 2025).

More recent qualitative studies have started defining health-policy counterpublics as grass-roots movements in opposition to the expansion of federal surveillance and the promotion of participatory governance (Molldrem & Smith, 2024). Introducing these views into the formal policymaking would redefine the ethical supervision format from top-down compliance to co-production.

The next research question to address is the frameworks, like Community-Engaged Surveillance Models, by determining the impact of a shared decision-making framework, opt-in consent pilots, and data-stewardship boards on community trust and responsiveness. The current evidence gap on the balancing of epidemiologic utility and rights protection would be filled with an empirical assessment of these mechanisms.

Implementation Science and Needs in Workforce Development

In cluster detection and contact tracing, limited trained personnel are always determined as a bottleneck by operational research. According to Schuster *et al*. (2024), field epidemiologists are frequently bioinformatics illiterate in terms of sequence information interpretation, and data scientists are not necessarily knowledgeable in the context of health.

This gap could be bridged by a national competency framework in the practice of molecular epidemiology. There is an urgent need to have training programs that would incorporate genomic analysis, ethical reasoning, and outbreak communication skills. Through future research, blended learning models, mentorship pipelines, and regional centers of excellence that develop cross-disciplinary expertise ought to be assessed.

Factors that affect the successful adoption of the program could also be explained using implementation-science approaches. Gore *et al*. (2022) have discovered that social-network analysis with cluster detection was better at response targeting but necessitates long-term technical support and stakeholder buy-in to translate research innovations into the standard of public-health practice.

Technological Horizons: to Predictive and Point-of-Care Surveillance

The future platform is predictive analytics and decentralized diagnostics. According to Mehta *et al*. (2025), AI-based predictive models based on viral genetics, partner-services data, and social-determinant indicators may be used to predict cluster growth prior to a case surge. To incorporate these models into public-health dashboards, it will be necessary to have well-developed validation with actual outbreak trajectories.

At the same time, fast molecular point-of-care (POC) technologies are also becoming available and will have the potential to produce sequence data at the community level (Gavina *et al*., 2023). The introduction of portable sequencing platforms in high-incidence areas would reduce the working-weeks-time to hours to detect; however, technical and logistical challenges like cold-chain management, reagent costs, and secure data upload are significant research factors.

Translational and Equity Considerations

One of the lasting problems is the ability to ensure that surveillance innovations are translated fairly in relation to various communities. Historical marginalization leads to community mistrust, which reduces participation in testing and tracing programs. Shook *et al*. (2022) show that co-created messages with the addition of local advocates can make a huge difference in how acceptable molecular surveillance can be.

Translational studies in the future should assess models of community-based implementation of surveillance and compare the results of surveillance through local health workers and the central government. In addition, research ought to evaluate the interaction of social-determinant indicators of housing insecurity, patterns of substance use, and access to healthcare and cluster processes to inform targeted intervention.

Policy and Conceptual Research Priorities

Besides technical interventions, there is an increasing demand to re-theorize the response to outbreaks by using systems thinking. Molldrem and Smith (2020) state that the paramount issue is not the accuracy of data but the political ecology of surveillance, how data governance, resource flows, and community agency co-produce the results of epidemic control (Molldrem and Smith, 2020).

The structural dimensions should be interrogated by future research based on interdisciplinary interaction between bioethics, data science, and political sociology. Policy analysis must examine the impact of the federal funding mechanisms, legal environments, and cross-sector partnerships on responsiveness and trust. A more formal assessment system that incorporates quantitative performance measures (e.g., detection lag time) and qualitative social-impact measures would offer the comprehensive evidence base required to design policy in the next generation.

CONCLUSION

The last six months have been a period of change in the way HIV outbreaks are detected and responded to in the United States, with the incorporation of molecular surveillance, digital contact tracing, and data-driven analytics that have redirected the work of the U.S. in the area toward not reacting to cases but responding with intelligence on outbreaks. This narrative review is of the essence in light of the fact that, despite major technological and operational advancements, there are still structural, ethical, and equity-related issues that have to be resolved to enable a complete exploitation of these innovations.

Molecular cluster detection conducted nationwide by CDC and state partners has substantially enhanced the capacity to detect the transmission networks within almost real-time. Between 2020 and 2023, there were 298 molecular clusters reported to the CDC, of which 249 were initially identified at the state or local level, highlighting the sophistication of precise public health and rapid outbreak control. This combination of social network information and molecular data is a significant methodological innovation, which can be used to provide specific and resource-efficient interventions, but the uneven infrastructure and capacity of workforces limit scalability.

Ethical and social legitimacy issues, such as data privacy, informed consent, and community mistrust, particularly those involving genetic linkage information, are also difficult barriers that must be addressed through transparent and participatory forms of governance systems incorporated at every phase of the molecular surveillance programs. At the community level, ethical governance is an effective approach to sustainable implementation because fears of stigmatization are a barrier to engagement.

The new trends indicate the tendency towards predictive, equity-based, and community-incorporated outbreak response models. New technologies in the field of artificial intelligence make it possible to predict the growth of the cluster, and the portable sequencing technology will help to enhance the surveillance process in rural and resource-restricted regions. Nevertheless, the agility of the policy and the flexibility of funding systems are needed to be in step with the technological evolution and to protect civil liberties.

Suggestions on how this field can be developed further are institutionalization of interoperability standards to allow data exchange to be secure and real-time, investing in ethical infrastructure such as community advisory boards, improving workforce competency via integrated training, focusing on research to validate predictive models with ethical AI governance, and making equity a key performance indicator. These initiatives will help turn molecular surveillance into a proactive health equity framework to address the needs of marginalized populations instead of marginalizing them, enabling it to reduce the impact of molecular surveillance as a reactive tool to a crisis.

REFERENCES

1. France, A. M., Hallmark, C. J., Panneer, N., Billock, R., Russell, O. O., Plaster, M., & Oster, A. M. "Nationwide Implementation of HIV Molecular Cluster Detection by Centers for Disease Control and Prevention and State and Local Health Departments, United States." *Emerging Infectious Diseases* 31.Suppl 1 (2025): S80.
2. Garcia, M., Devlin, S., Kerman, J., Fujimoto, K., Hirschhorn, L. R., Phillips II, G., & McNulty, M. C. "Ending the HIV epidemic: Identifying barriers and facilitators to implement molecular HIV surveillance to develop real-time cluster detection and response interventions for local communities." *International journal of environmental research and public health* 20.4 (2023): 3269.
3. Gavina, K., Franco, L. C., Khan, H., Lavik, J. P., & Relich, R. F. "Molecular point-of-care devices for the diagnosis of infectious diseases in resource-limited settings–A review of the current landscape, technical challenges, and clinical impact." *Journal of Clinical Virology* 169 (2023): 105613.
4. Gonsalves, G. S., & Crawford, F. W. "Dynamics of the HIV outbreak and response in Scott County, IN, USA, 2011–15: a modelling study." *The lancet HIV* 5.10 (2018): e569-e577.
5. Gore, D. J., Schueler, K., Ramani, S., Uvin, A., Phillips, G., McNulty, M., & Schneider, J. "HIV response interventions that integrate HIV molecular cluster and social network analysis: A systematic review." *AIDS and Behavior* 26.6 (2022): 1750-1792.
6. Mehta, S. R., Chaillon, A., Wells, A. B., & Little, S. J. "Molecular HIV Surveillance: Beyond Cluster Detection and Response." *AIDS Research and Human Retroviruses* 41.4 (2025): 175-180.
7. Molldrem, S., & Smith, A. K. "Reassessing the ethics of molecular HIV surveillance in the era of cluster detection and response: Toward HIV data justice." *The American Journal of Bioethics* 20.10 (2020): 10-23.
8. Molldrem, S., & Smith, A. K. "Health policy counterpublics: Enacting collective resistances to US molecular HIV surveillance and cluster detection and response programs." *Social Studies of Science* 54.3 (2024): 451-477.
9. Oster, A. M., France, A. M., McClung, R. P., Buchacz, K., Lyss, S. B., Peters, P. J., & Hernandez, A. L. "The CDC HIV outbreak coordination unit: developing a standardized, collaborative approach to HIV outbreak assessment and response." *Public Health Reports* 137.4 (2022): 643-648.
10. Oster, A. M., Lyss, S. B., McClung, R. P., Watson, M., Panneer, N., Hernandez, A. L., & France, A. M. "HIV cluster and outbreak detection and response: the science and experience." *American Journal of Preventive Medicine* 61.5 (2021): S130-S142.
11. Philpott, D. C., Curran, K. G., Russell, O. O., McClung, R. P., Hallmark, C. J., Pieczykolan, L. L., & France, A. M. "HIV clusters reported by state and local health departments in the United States, 2020–2022." *JAIDS Journal of Acquired Immune Deficiency Syndromes* (2022): 10-1097.
12. Quilter, L. A., Agnew-Brune, C., Broussard, D., Salmon, M., Bradley, H., Hogan, V., & Bernstein, K. "Establishing best practices in a response to an HIV cluster: an example from a surge response in West Virginia." *Sexually transmitted diseases* 48.3 (2021): e35-e40.
13. Schuster, A. L., Folta, A., Bollinger, J., Geller, G., Mehta, S. R., Little, S. J., & Bridges, J. F. "User experience with HIV molecular epidemiology in research, surveillance, and cluster detection and response: a needs assessment." *Current Medical Research and Opinion* 40.11 (2024): 1873-1883.
14. Shook, A. G., Buskin, S. E., Golden, M., Dombrowski, J. C., Herbeck, J., Lechtenberg, R. J., & Kerani, R. "Community and provider perspectives on molecular HIV surveillance and cluster detection and response for HIV prevention: qualitative findings from King County, Washington." *Journal of the Association of Nurses in AIDS Care* 33.3 (2022): 270-282.
15. Sizemore, L., Fill, M. M., Mathieson, S. A., Black, J., Brantley, M., Cooper, K., & Wester, C. "Using an established outbreak response plan and molecular epidemiology methods in an HIV transmission cluster investigation, Tennessee, January–June 2017." *Public Health Reports* 135.3 (2020): 329-333.

16. Watson, M., Michels, E., Spieldenner, A., Ortmann, L. W., & Barrett, D. H. "Stories, stigma and sequences: HIV cluster detection and response activities through a narrative ethics lens." *Narrative ethics in public health: The value of stories*. Cham: Springer International Publishing, 2022. 95-109.
17. Watson, M. "Perspectives on the Use of Molecular HIV Data for Public Health." (2023).

Source of support: Nil; **Conflict of interest:** Nil.

Cite this article as:

Ayo-ige, A. B. & Botwe, F. F. “Enhancing Rapid Response to HIV Outbreaks: Lessons from U.S. Cluster Detection and Contact-Tracing Models." *Sarcouncil Journal of Internal Medicine and Public Health* 5.1 (2026): pp 30-38.

Publisher: SARC Publisher