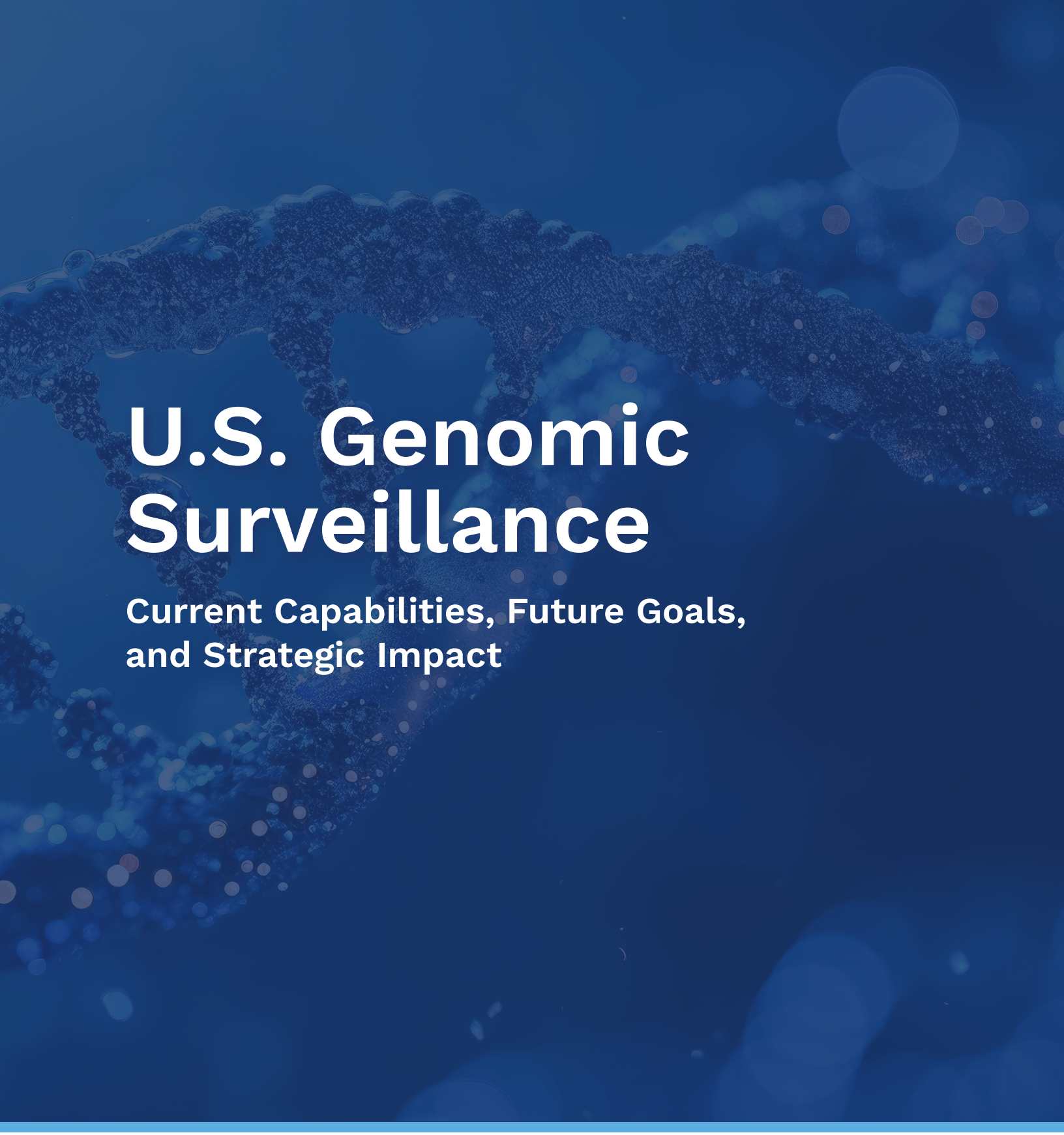

U.S. Genomic Surveillance

Current Capabilities, Future Goals, and Strategic Impact

JOHNS HOPKINS
BLOOMBERG SCHOOL
of PUBLIC HEALTH

Center for
Health Security

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Amesh Adalja, Anita Cicero, Augustin Martin, Tom Inglesby
Johns Hopkins Center for Health Security

Executive Summary

Existing genomic surveillance programs are valuable but can be strengthened

The United States has built a number of highly valuable genomic surveillance programs, but these efforts have developed largely independently and without an overarching national strategy. Existing programs vary in coverage, technical approaches, analytical standards, data-sharing practices, and long-term sustainability. Funding uncertainty threatens workforce retention, infrastructure maintenance, and future innovation. National priorities should be established that balance surveillance for routine public health threats and surveillance for novel, pandemic, or engineered biological threats.

The government should establish a clear strategy and ensure adequate funding

The report recommends that the federal government establish a comprehensive **National Strategy for Genomic Surveillance** that defines national goals, priority use cases, sample sources, governance structures, and performance metrics. The objective should be an enduring capability that supports routine public health operations while also strengthening national preparedness for pandemics and biological threats.

The report recommends restoring federal genomic surveillance funding to approximately the FY2020–FY2025 level of $360 million annually. At that funding level, CDC-supported programs were able to maintain approximately 1,500 surveillance sites covering roughly 45 percent of the U.S. population while also supporting airport surveillance programs, workforce development, and innovation efforts. Funding has declined substantially since, with FY2026 support falling to approximately $155 million and the FY2027 budget request proposing only $70 million. Sustained reductions at that level would significantly diminish national genomic surveillance capacity and geographic coverage. In addition, the federal government should establish clear privacy, data stewardship, analytic standards and oversight policies to ensure public trust as surveillance capabilities expand.

A durable system will strengthen public health and enhance biodefense

The United States has already invested substantially in genomic surveillance and demonstrated its practical value for outbreak detection, situational awareness, and public health response. These capabilities should be strengthened and integrated into a durable national system that strengthens public health, enhances biodefense, and provides earlier warning of both local outbreaks, as well as the next epidemic, pandemic, or engineered biological threat. With a clear national strategy, sustained funding, interoperable systems, and continued technological innovation, genomic surveillance can become a foundational element of U.S. health security for years ahead. This a program that should get faster, stronger and capable of using the latest innovations in technology to offer broad genomic surveillance protection against biological threats.

I. Purpose of the Report

The purpose of this report is to assess the current state of genomic surveillance in the U.S., the goals of various genomic surveillance programs, and potential future strategic options and directions for these systems. There is growing recognition in and out of government of the potential value of genomic surveillance to strengthen and accelerate early detection of both naturally occurring endemic and epidemic diseases, as well as deliberate, novel, engineered pathogens of concern.

On April 24, 2026, the Johns Hopkins Center for Health Security (CHS) convened a full-day expert meeting in Washington, D.C. titled "Genomic Surveillance: Current Capabilities, Future Goals, and Strategic Directions." The convening's key goals were to establish a shared understanding of the types of genomic surveillance systems currently in operation at the federal, state, and local levels, as well as those managed by private sector organizations and research organizations, and to provide expert input to policymakers responsible for funding and implementing genomic surveillance programs.

The meeting brought together a cross-sector group of 30 scientists, policymakers, and surveillance experts from federal agencies, state and local health departments, academic research institutions, and private disease surveillance companies. The meeting was held under Chatham House rule to allow candid exchange between those in and out of government.

This report synthesizes the meeting's key themes and makes a series of recommendations. It represents the views of the CHS team, as informed by the meeting discussion and advisory input of meeting attendees. It does not necessarily reflect the views of all individual meeting attendees on these issues.

II. Intended Audience of this Report

This report is intended for senior U.S. government decision-makers responsible for national health security policy, public health infrastructure, biodefense, and disease surveillance investments. This includes leadership and program offices within the Department of Health and Human Services (HHS), including the Centers for Disease Control and Prevention (CDC) and the Administration for Strategic Preparedness and Response (ASPR); the Department of War (DOW), including the office of the Assistant Secretary of War for Nuclear Deterrence, Chemical and Biological Defense Policy and Program and the Defense Health Agency and Military Health System components; the Department of Homeland Security (DHS), including the Countering Weapons of Mass Destruction (CWMD) Office and its BioWatch program; the White House Office of Science and Technology Policy (OSTP); and congressional authorizing and appropriations committees with jurisdiction over public health preparedness and biodefense.

While this report is intended to provide useful input to all federal agencies noted above, its focus is almost entirely on the civilian side genomic surveillance programs, as compared to those run out of the DOW. The DOW genomic surveillance programs are of high importance to international disease surveillance efforts and force protection, but this particular CHS expert meeting that provided input to this report yielded more detailed input and discussion on civilian programs.

III. Background: The Landscape of Genomic Surveillance

Genomic surveillance refers to the systematic sequencing and analysis of pathogen genetic material collected from environmental, clinical, or population-level sources to detect, characterize, and track infectious disease threats. Every virus has a unique genetic code, and sequencing is the process of reading that code. Genomic sequencing and surveillance encompass a spectrum of approaches. On one spectrum is the highly targeted PCR testing of specific known pathogens – this is simplest and has been historically less expensive that other approaches. On the other end of the spectrum is broad, metagenomic sequencing capable of detecting many or all pathogens, potentially including even novel organisms, including engineered threats. Historically this has been slower and more expensive, though costs have come down and the technology has become more widely available.

The field has expanded substantially since the early applications of wastewater poliovirus surveillance in the 1930s and the integration of PCR technology into routine surveillance in the 1990s. The COVID-19 pandemic served as a major accelerant, demonstrating the power of genomic surveillance to track SARS-CoV-2 variant emergence. More recent uses have included the discovery of measles circulating in a community days before the first clinical case is detected.

Wastewater genomic surveillance has increasingly demonstrated practical public health utility beyond theoretical early warning. During the COVID-19 pandemic, wastewater signals in major metropolitan areas frequently preceded increases in clinically diagnosed cases and provided population-level situational awareness when individual testing rates declined. Wastewater surveillance results guided medical countermeasure deployment as specific monoclonal antibodies were targeted to specific variants that were most dominant. More recent work has shown similar value for other pathogens. Wastewater detection of measles in Houston identified viral signal before reported cases emerged, underscoring the sensitivity of environmental surveillance even in low-incidence settings. The CASPER (Coalition for Agnostic Sequencing of Pathogens from Environmental Reservoirs) group has demonstrated detection of a single case of measles virus in wastewater associated with cases in Cook County, Illinois, highlighting the potential of wastewater surveillance to supplement traditional case-based reporting. Additional work, including analyses from New Mexico, has suggested that wastewater monitoring may provide earlier or complementary insight into measles transmission dynamics relative to clinical surveillance. Similar approaches have also been applied successfully to mpox, where wastewater detection tracked community transmission and demonstrated utility for monitoring outbreaks in populations that may be underrepresented in conventional testing systems. Collectively, these studies show that wastewater genomics is evolving from an experimental capability toward an operational public health tool capable of informing situational awareness, outbreak detection, and resource allocation across multiple pathogens.

While wastewater surveillance is the most broadly applied genomic surveillance approach in the U.S., it is also possible to use genomic surveillance approaches to analyze nasal swabs, bloodbank samples, hospital and airplane wastewater, hospital

air and other sources of genetic material, and there are existing programs or pilots using all of these approaches in one setting or another in the U.S.

What Genomic Surveillance Can Answer

A well-designed genomic surveillance system can help to answer a range of pressing questions, including:

- Is a pathogen of epidemiological significance present in a given community and necessitating serious public health attention? This includes detecting known threats such as poliovirus, measles, Ebola, or novel variants of circulating pathogens, as well as tracking antimicrobial resistance genes.
- Are standard clinical testing systems, like those used in hospitals, clinics, and labs, missing cases? Wastewater and environmental surveillance can provide an early-warning signal before individual diagnostic testing results realize there is an outbreak underway.
- Should treatment protocols or medical countermeasure strategies be updated because of resistance to locally circulating pathogens that have been detected through genomic surveillance? Genomic characterization of circulating strains—as demonstrated with COVID-19 variant surveillance informing monoclonal antibody use—can directly inform the most effective therapeutic decisions.
- What is the circulating level of different known diseases in different geographic communities or facilities? Hospital and college campuses could represent high-value sentinel sites for influenza, COVID, and other pathogens, with direct implications for institutional preparedness.
- Is a novel or unexpected high-consequence pathogen present that would not be detected by conventional surveillance methods looking for normally circulating "ordinary" infectious diseases? These kinds of novel new epidemic diseases have been called "Disease X" and diagnosing them via genomic approaches would probably require metagenomic techniques that sequence broadly rather than use of PCR which works best for confirming the presence or absence of a predetermined target (see below).

Technical Approaches and Trade-offs

Three broad sequencing strategies are currently used in genomic surveillance, each with distinct performance characteristics:

- Amplicon (PCR-based) sequencing is the most targeted approach. It offers the highest sensitivity with a low rate of false negatives. It also provides the fastest turnaround time but is limited to pathogens for which primers have been specifically designed in advance. It cannot detect novel or unexpected threats.
- Hybrid capture sequencing uses probe-based enrichment to selectively capture nucleic acids from a predefined but broad panel of pathogens. It offers a middle ground between sensitivity and breadth and is well-suited to surveillance programs that need to monitor many known pathogens simultaneously.

- Shotgun metagenomics sequences all nucleic acids present in a sample without prior selection. This approach has the theoretical capacity to detect unknown pathogens but has a higher cost and longer turnaround time that is typically at least a several days. This approach may raise privacy concerns given that it is technically capable of capturing individual genetic information — including sensitive human genomic data. Untargeted sequencing also creates obligations around select agent reporting if a select agent is detected in a sample.

Wastewater surveillance presents a particular technical challenge (as compared to other genomic surveillance samples like bloodbank and nasal swabs) because wastewater samples contain enormous quantities of background nucleic acids from bacteria, human cells, and environmental organisms. Depletion strategies—removing ribosomal RNA and host DNA prior to sequencing—improve signal-to-noise ratios but add cost and complexity.

How to balance these technical approaches, in terms of cost, turnaround time, analytical infrastructure, and threat detection breadth, is one of the central strategic questions for expanding local and national genomic surveillance programs.

Expanding Sample Diversity

Wastewater surveillance has received the greatest public profile, gaining national recognition during COVID-19. Wastewater surveillance has great potential value to meet a range of genomic surveillance goals. However, it represents only one sampling modality. Other sample types including nasopharyngeal swabs from sentinel clinical sites for passengers arriving from overseas, blood bank specimens, and hospital wastewater, air, and clinical effluent – could offer complementary or superior surveillance approaches to wastewater for different use cases. Different approaches have distinct advantages in terms of geographic resolution, population coverage, pathogen detectability, and linkage to clinical outcomes.

A strategic integrated national genomic surveillance system would establish and sustain sample analysis from a range of sample types and geographic sites around the country. An integrated system would do so in ways that maximize the ability to use it for both routine outbreak detection and response locally, as well as early warning for high threat pathogens or novel epidemics, be they naturally occurring or deliberately engineered and introduced into the U.S. This kind of expanded strategic approach of combining genomic surveillance of a range of samples should be a goal of a national program going forward. Such a national program would determine how different sample sources could best cover different parts of the country, what would be most cost effective, what combination of samples could best provide protection against novel major threats, et al.

One Health

Genomic surveillance systems have traditionally been designed with human health as the primary endpoint, but the animal-human-environment interface (One Health) represents a critical and underappreciated surveillance gap. The H5N1 avian influenza outbreak demonstrated this concretely: wastewater detection of H5N1 genetic material in milk products and dairy-related waste streams provided early signal

about viral spread through dairy herds before the full scope of human exposure was understood. A mature national genomic surveillance architecture should incorporate one-health principles that integrate human, animal and environmental surveillance data, including specifically data streams and analytical frameworks designed to detect and interpret signals that originate in animal populations before they manifest as human disease.

IV. Key Findings

Highly Valuable Programs but With Uncertain Futures

There are a number of U.S. federal, state, city and private sector wastewater genomic surveillance programs in place now that are providing early warning of infectious disease outbreaks. However many of these programs run entirely independently of each other and without a larger plan of coverage or geography. While many of the programs inform local decision-making, some are unconnected to local health officials who would be responsible for taking action to contain local outbreaks identified.

Most of these existing programs are federally funded through CDC, and many of these programs are dependent on either emergency supplemental funding that will soon expire, or, uncertain year to year grants in the local or research setting. This uncertainty affects workforce retention and recruitment for these programs.

While genomic surveillance programs arising independently and with differing technical approaches have fostered innovation around the field, they have also led to the creation of a patchwork around the country. They provide non-uniform coverage and use variable analytical standards.

From FY2020-FY2025 CDC spent approximately $360M a year on genomic surveillance programs across the country. This was supported mostly by emergency supplemental funding. The great majority of the funding was aimed at funding wastewater surveillance efforts at the state and local level, using either state and local providers and public health laboratories or the private sector as performers. Funding also supported airport surveillance programs – including genomic surveillance of nasal swabs from people traveling into the country who voluntarily agree to a swab, as well as surveillance of airplane wastewater. In total, a little more than 3% of the funds went to CDC to manage the genomic surveillance programs it supported around the country, to create national dashboards, integrate data streams, etc.

In FY2026 CDC received less than half of this funding — $155M — for national genomic surveillance programs, again largely supported by previously appropriated emergency supplemental funding. In the President's budget request for FY2027, $70M total is requested for genomic surveillance programs overall.

The prior CDC annual funding of $360M allowed genomic surveillance in 1500 sample sites around the country, representing some level of genomic surveillance of 45% of the population. That funding also supported traveler and airport surveillance programs as per above, as well as some level of research and innovation in Centers of Excellence in different parts of the country.

Use of Genomic Surveillance for Standard Outbreak Response (e.g. measles, influenza) vs. Early Warning for Serious Shocks (e.g. Ebola, pandemics, engineered deliberate events)

The majority of existing genomic surveillance programs are focused on expected, frequent threats to public health, like measles and influenza, hepatitis or others, with most of them using PCR methods. These programs use a targeted, cost-efficient approach to detection. A small subset of existing genomic surveillance programs are designed to detect novel or unexpected high consequence threats. These surveillance programs are the more broadly focused metagenomic approaches. No consensus framework currently advises or requires health departments or the private sector to set programs up for one set of outcomes or another. Different stakeholders prioritize these use cases differently depending on their mandate, funding or program goals. For example, a local health department is more likely to value measles genomic surveillance while a federal biodefense funded program will prioritize high consequence pathogens. Some research grant funded programs can identify pathogens across the spectrum of routine to novel and engineered.

Privacy, Ethical, and Governance Considerations

As genomic surveillance systems expand in scale and capability, they raise important privacy and ethical considerations. Untargeted metagenomic sequencing can capture human genetic material and pathogen-associated information beyond the original surveillance intent, creating potential risks related to inference of sensitive health conditions within communities, including HIV prevalence, sexually transmitted infections, or substance use patterns inferred through associated biomarkers or wastewater analyses. While most surveillance systems operate at aggregate population levels rather than identifying individuals, increasing analytical sophistication raises concern about the potential for stigmatization of specific communities, secondary use of data, and governance over sensitive findings.

Data Siloing is a Critical Challenge

Fragmentation of data across federal, state, and commercial systems is a fundamental challenge to having any kind of integrated national genomics surveillance picture. DOW and CDC operate largely parallel systems with limited interoperability, and federal programs are not well integrated with the public health enterprise. In at least some cases, the data being produced by airport screening programs is not routinely conveyed to cities that are closest to those airports. This fragmentation reduces the ability to synthesize a national picture and undermines the speed and quality of public health response. Similarly, some state and local programs share all data with the federal government, while some share in a much more limited way. The less clear that data sharing standards are followed, the greater the chance that important disease patterns will be missed and public health actions will be delayed.

Turnaround Time as a Performance Metric

The practical value of surveillance data is a function of how actionable it is and how quickly it reaches decision-makers. Current turnaround times vary substantially across programs and sample types. Explicit time targets would be valuable in driving utility of these programs: how long should it take to go from-sample-collection to getting lab results, and how long should it take to go from results to public health actions being taken – these are critical for driving, improving, measuring operational response.

Lack of Standardization Constrains the Field

Across federal, state, and commercial programs, the absence of common standards is a fundamental barrier to realizing the full potential of genomic surveillance. Programs currently operate under disparate sampling protocols, sequencing platforms, bioinformatics pipelines, and reporting formats, making it difficult to aggregate data across sites, compare signals across jurisdictions, or distinguish true signal from noise. A particular challenge is that catchment size varies enormously — a signal from a sewer shed serving ten thousand people carries very different epidemiological weight than the same signal from one serving a million — yet current standards do not provide a framework for interpreting that difference. Standardization does not require uniformity of technology but does require interoperability of outputs and a shared taxonomy for describing what is being detected and at what confidence level.

V. Recommendations for U.S. Government Action

Based on the expert meeting discussion and input and our analysis of the state of genomic surveillance in the U.S., we recommend the following:

1. Establish a National Strategy for Genomic Surveillance

The U.S. needs a guiding strategy that drives the goals, sample sources, technology, funding and implementation of a federally-funded national genomic surveillance program.

Goals

A national strategy for genomic surveillance should establish clear goals. Goals should include establishing enduring state and local genomic surveillance programs and networks of these programs that:

- provide actionable warnings of infectious disease outbreaks and rises in endemic disease;
- provide analysis of patterns of antimicrobial resistance that allow action to be taken to decrease antimicrobial infections at the state and local level;
- enable early warning of pathogens of potential epidemic consequences, including those that might be brought in by people traveling into the U.S.;

- are capable of early detection of bioengineered pathogens that could cause widespread harm in the population.

These goals should be pursued as a standing capability in the U.S., not one that is cobbled together only during emergencies. Genomic surveillance programs should be part of routine federal and state/local structures and programs that serve valuable routine purposes, even while they also serve the goals of providing warning of high consequence epidemics of deliberately engineered threats.

Routine genomic surveillance of infectious diseases including influenza (including avian influenza), respiratory syncytial virus, coronaviruses, measles, enteroviruses, antimicrobial-resistant organisms, and significant animal pathogens, should be the baseline expectation for state and local systems that are part of federally funded genomics surveillance programs. The infrastructure, workforce, bioinformatics pipelines, and reporting structures built to that routine baseline are precisely what would be leveraged and scaled in the event of an emerging or novel engineered threats.

The national federally funded strategy for genomic surveillance should not in any way interfere with non-federally funded programs that are occurring via research efforts, state and locally funded efforts, or private sector funded efforts that are not related directly to federal goals. But programs that are funded by CDC for the national genomic surveillance programs should directly relate to the goals as set by the national strategy.

Sample Sources

Wastewater surveillance has demonstrated high public health value and has the important advantage of detecting diseases from populations that may not engage with the healthcare system. However, wastewater has limitations: geographic resolution can be poor (a single sewer-shed may encompass hundreds of thousands of people), it cannot be linked to clinical outcomes at the individual or hospital institutional level, and its sensitivity for certain pathogens—particularly those shed inconsistently or at low levels in feces—is uncertain.

A national strategy meeting the above goals will combine wastewater surveillance with other sample sources. Nasopharyngeal and nasal swabs collected through both programs such as TGS and sentinel clinical networks, which provide sensitivity for respiratory pathogens and the potential of direct linkage to clinical data. Genomic surveillance of blood bank specimens can provide population-level seroprevalence and pathogen prevalence data. Hospital wastewater, air sampling, and clinical laboratory remnant specimens offer concentrated pathogen signal in high-risk settings.

Technological Approaches

A national strategy meeting the above goals will need to choose between available technological approaches for genomic surveillance. Technological approaches – e.g. PCR, hybrid capture, vs metagenomics – will need to balance maximizing the right kind of data collection, sensitivity to novel threats and very early detection, overall costs, and turnaround times.

For pathogen-specific surveillance of known priority organisms, PCR based approaches likely offer the best combination of sensitivity, cost, and speed and will be, in the near term, the likely default for many organizations. Hybrid capture approaches are likely more appropriate for programs monitoring a broad panel of known threats simultaneously, such as a hospital system or a high-volume wastewater node. Metagenomic approaches are most valuable for novel or unknown threat detection, where the higher cost and longer turnaround are justified by the expanded detection breadth. Further, as costs fall for metagenomics, it may supplant other methods.

Evaluation and Data Review

As decisions are now being made regarding national genomic surveillance goals, it will be critical to review the federally funded genomics surveillance data from the past 5 years to understand what outbreaks have been detected, and through what specific systems and technologies, and through what specific sample sources. That information should be aggregated and analyzed in order to make the best possible strategic decisions about deployment of funding and technologies going forward.

2. Reset Level of funding for Genomic Surveillance Programs to FY 20-25 Level

Resetting this level of genomics surveillance funding that had been previously provided to CDC for five years - $360M annually – would allow the agency to pursue all of the national genomics surveillance strategy goals set out above.

If this level of funding were provided, it would and should allow the continuation of state and local wastewater surveillance funding in existing sample sites around the country. Additional sites and geographic coverage could potentially be added (given this level of effort provided only 45% geographic coverage). If instead the president's budget request of $70M is what is provided for genomic surveillance programs in FY2027, there would need to be a major reduction in genomic surveillance across the country, drastically reducing the wastewater surveillance coverage for all purposes.

If $360M level of funding is provided, the national genomics surveillance program that could be sustained and strengthened going forward would allow sustained and expanded wastewater surveillance coverage. It could and should also include:

- A new component that provides pilot start-up funding for genomic surveillance on samples sources including bloodbanks and hospitals. The data coming out of these initiatives could be assessed for their potential contributions to a national genomics surveillance program.
- A pilot effort that assesses the potential contributions and feasibility of larger scale use of metagenomic surveillance approaches in a national genomics surveillance program. For example, a state-funded wastewater surveillance effort in Houston can do metagenomic wastewater surveillance testing for as little as $500 per sample. If this could be reproduced, performed twice weekly, this could conceivably cost something on the order of $52K per sewershed / per year. If that program is reproducible on larger scale, it could cover 100 sewersheds per

year for $5.2M, or 1000 sewersheds for $52M. This kind of metagenomic approach could provide detection of a very broad set of biological threats with substantial geographic coverage.

- A program that assesses the scientific feasibility and practical implementation of analyzing wastewater for bioengineered entirely novel threats. This kind of genomic surveillance is currently being pursued at very small scale, mostly as privately funded research efforts. It should be scaled up into actual operational use to provide broad geographic strategic warning of novel and engineered threats, whether or not this is part of such a larger scale national genomics strategy as detailed above.

3. Ensure Privacy Issues are Addressed

National federally funded genomic surveillance strategies need explicit policies regarding data stewardship, privacy protections, reporting thresholds, retention practices, and oversight mechanisms to ensure public trust while preserving surveillance utility.

4. Resolve Data Siloing and Turnaround Times Through Interoperability Standards and Governance

Genomic data that is collected by one federal agency is not necessarily shared with the other federal agencies, and genomic surveillance data collected at the state and local level is not always shared with federal agencies. This is not a technical problem. It is a governance and data stewardship problem. Federal department genomic surveillance data sharing needs to be resolved by a government interagency process likely emanating from the White House over time.

Additionally, given the zoonotic implications of such pathogens as avian and swine influenza, United States Department of Agriculture (USDA) activities should be integrated into this system.

The work of the Coalition for Agnostic Sequencing of Pathogens from Environmental Reservoirs (CASPER) is an example of collaboration between academic labs, government labs, and the private sector that has demonstrated real value and may provide the scaffolding for a more extensive system.

The current genomic surveillance landscape also operates under disparate sampling protocols, sequencing platforms, bioinformatics pipelines, quality thresholds, and reporting format. This heterogeneity makes it impossible now to aggregate data across sites and programs, compare findings across jurisdictions, or evaluate program performance consistently. It also creates barriers to entry for state and local health departments that lack the technical capacity to independently evaluate and adopt new methodologies. It is critical to work toward standard analytical approaches.

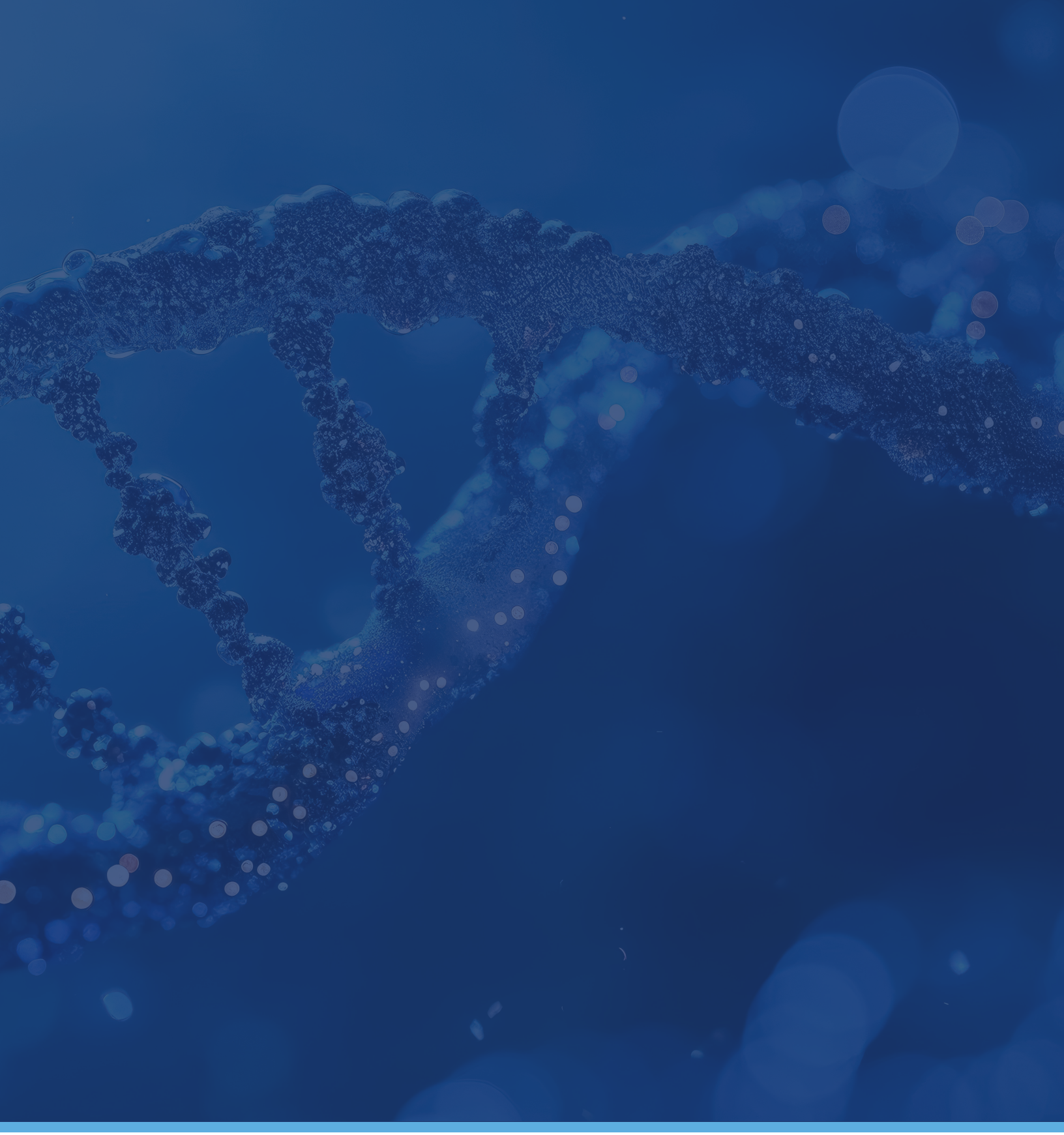
CDC, working with groups such as the Association of Public Health Laboratories (APHL) and relevant academic partners, should develop and publish minimum performance standards and data reporting formats for genomic surveillance programs seeking federal funding or contributing data to national systems. This should include

standards for sample collection and preservation, nucleic acid extraction, sequencing depth and coverage thresholds, bioinformatics reference databases, and the structure of submitted sequence data and associated metadata.

Conclusion

In summary, there is great promise in genomics surveillance strategies to rapidly detect and track a range of expected and common public health threats, and to provide early warning of novel, surprise epidemic and bioengineered threats. Much has been built and learned in recent years about the effectiveness and challenges around these programs. A strong, integrated, cutting-edge national genomics surveillance program should now be established on this foundation. To do this will require a combination of policymaker support, funding to reach national goals, and application of science and innovation to the program as it moves ahead.

We are excited to continue to help advance thinking and commitment to this nationally important effort.



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