



## Agency Recommendation Summary

The Department of Health request funds to enhance surveillance and epidemiological investigations with genomic data across conditions of public health importance (notifiable conditions). Support for pairing pathogen sequencing and epidemiological data will allow us to maintain staff to continue characterizing SARS-CoV-2 over time as well as scale these efforts to other notifiable conditions. Through this effort, we will support LHJs in the investigation of outbreaks, detect emerging variants, and improve preparedness. This improvement in synthesis, analysis, and use of genomic data across notifiable conditions will enable the public health system to better respond to infectious diseases of public health importance.

## Fiscal Summary

Fiscal Summary <i>Dollars in Thousands</i>	Fiscal Years		Biennial	Fiscal Years		Biennial
	2024	2025	2023-25	2026	2027	2025-27
<b>Staffing</b>						
FTEs	0.0	11.3	5.65	11.3	11.3	11.3
<b>Operating Expenditures</b>						
Fund 001 - 1	\$0	\$1,469	\$1,469	\$1,469	\$1,469	\$2,938
Total Expenditures	\$0	\$1,469	\$1,469	\$1,469	\$1,469	\$2,938

## Decision Package Description

There is a need to expand the integration of genomic data as a core component of the state’s public health system to ensure a rapid scale-up of response strategies in the event of an infectious disease emergency. The usefulness of pathogen genomic sequence data to support surveillance and epidemiological investigations is well-described. Some examples of its use include: detection and characterization of outbreaks, identification of spatiotemporal patterns of pathogen transmission, ascertainment of pathogen and disease severity, identification of pathogen with molecular markers of clinical significance, assessment of impact on host immune response, effectiveness of prophylactics and treatments, and analyze transmission dynamics. However, genomic data use depends on WA DOH maintaining the resources for integrating genomic and epidemiologic data while building capacity around data analysis and interpretation within our agency and the local health jurisdictions (LHJs). Presently, WA DOH has an opportunity to leverage the experience gained while responding to the COVID-19 pandemic to capitalize on the systems that were put in place and the tools that were developed to effectively manage and analyze genomic data to inform public health actions.

One key way the agency can improve infectious disease preparedness and control efforts is to expand the use of paired genomic and epidemiologic data, or to improve its use across condition areas. By expanding these efforts to other notifiable conditions, the Molecular Epidemiology Program will support public health preparedness efforts across notifiable infectious diseases in coordination with those program area leads. Funding the molecular epidemiology program ensures that existing capacity gains made in genomic data use during the SARS-CoV-2 pandemic are not lost so that this capacity can be leveraged to expand use of this rich data source to improve public health response across notifiable conditions. Below we highlight the infrastructure, processes, and data use that we stood up during the COVID-19 pandemic to demonstrate real world application and utility of these data.

### Data management and integration

The Molecular Epidemiology Program in collaboration with Data Science Support Unit (DSSU) and the Data Integration & Quality Assurance (DIQA) teams built and scaled a flexible data management system with multiple workflows to securely receive, harmonize, link, and integrate submissions that contain SARS-CoV-2 genomic sequencing information from a variety of laboratories into WA DOH’s surveillance database, see figure 1 attachment. This work included developing scripts to collate disparate submissions and creating algorithms using data science methods to systematically review and link sequencing results with case level data in the Washington Disease Reporting System (WDRS). Once sequencing results have been linked cases, the Molecular Epidemiology Program integrates the genomic data with epidemiological, clinical, biological, environmental, geospatial, behavioral, and social data to produce robust datasets that can be analyzed and used to inform public health efforts.

### Data use

WA DOH has successfully integrated SARS-CoV-2 sequencing results with epidemiological, clinical (vaccination status, hospitalization status), and geospatial (county, zip code, census blocs, and census tracks) data to inform outbreak investigations, conduct cluster detection, monitor variant spread at the county level, and assess the risk of hospitalization among SARS-CoV-2 variants. These are some examples of applied molecular epidemiology:

The Molecular Epidemiology Program works closely with LHJs to assist with genomic epidemiology and bioinformatics needs. During a time when SARS-CoV-2 coinfections were not fully understood, the Molecular Epidemiology Program teamed up with Public Health Seattle & King County (PHSKC) to confirm a coinfection case in Washington state. This work has been published in the CDC’s Morbidity and Mortality Weekly Report (MMWR)<sup>1</sup>.

The Molecular Epidemiology Program publishes a weekly SARS-CoV-2 Sequencing Report featuring information on SARS-CoV-2 lineages circulating in Washington state (left) as well as the proportion of variants in Washington state over time (right). This information is publicly available in the WA DOH website, see figure 2 attachment. Under this proposal similar reports could be produced for other notifiable conditions.

The Molecular Epidemiology Program maintains Nextstrain builds (phylogenetic analysis allowing visualization of genomic data) for near real-time tracking and surveillance of SARS-CoV-2. Nextstrain builds have been useful for understanding SARS-CoV-2 evolutionary relationships among WA state sequences, as well as for use in cluster detection and identification, see figure 3 attachment. Nextstrain builds are pathogen-specific and under this proposal they would be extended to other pathogens linked to notifiable conditions.

The Molecular Epidemiology Program worked in collaboration with Fred Hutchinson Cancer Research Institute and the Bill and Melinda Gates Foundation Institute for Disease Modeling on a study examining the impact of SARS-CoV-2 variants on disease severity. **The study had major implications for the scientific community and was cited by the World Health Organization in their SAR-CoV-2 variants report, see figure 4 attachment.** Under this proposal the Molecular Epidemiology Program will collaborate with other teams, LHJs, and Tribal partners to produce similar studies across notifiable conditions as processes are scaled.

<sup>1</sup>Roskosky M, Borah BF, DeJonge PM, et al. **Notes from the Field: SARS-CoV-2 Omicron Variant Infection in 10 Persons Within 90 Days of Previous SARS-CoV-2 Delta Variant Infection — Four States, October 2021–January 2022.**

MMWR Morb Mortal Wkly Rep 2022;71:524–526. DOI: <http://dx.doi.org/10.15585/mmwr.mm7114a2external> icon.

We are proposing funding for a total of **eight FTE positions**: 6 in the Molecular Epidemiology program and 2 in the Data Integration and Quality Assurance (DIQA) team. Funding these eight positions will support:

- Gathering lessons learned regarding genomic data integration, linkage, and use both from the SARS-CoV-2 response, as well as from programs currently using genomic data in varying capacity
- Outlining an approach, timeline, and plan of action to extend the collection, integration, and use of genomic data to other infectious notifiable conditions, and implementing this approach
- Collaborations with partners across the public health system including PHL, PHOCIS, OID, CDE, LHJs, and Tribes to inform data integration and use
- Ongoing genomic epidemiology capacity-building for state, local, and Tribal public health partners through Genomic Epi Office Hours and other training opportunities
- Academic collaborations to utilize linked genomic and epidemiologic data for public health studies and scientific gain
- Production and distribution of data visualization tools for partners and the public using linked genomic and epidemiologic data
- Development of data management systems to support the processing of genomic data
- Conducting data linkage and integration of genomic and epidemiologic data

Funding 6 positions in the Molecular Epidemiology Program:

Sr. Epidemiologist: Lead genomic epidemiology capacity within the agency and provide supervision to the program. Provide final oversight over epidemiologic study design, analysis, and reporting plans. Provide evidence-based recommendations to leadership to inform policies and procedures.

Bioinformatician (Epidemiologist 3): Produce phylogenetic trees for pathogen tracking and monitoring and outbreak investigation, sequence data quality review, clade assignment and lineage validation, technical subject matter expertise, bioinformatics support of LHJ, and Tribal partner's analyses.

Epidemiologist 3: Lead molecular epidemiology analysis, data interpretation and dissemination within the agency and with LHJs. Identify and pilot novel tools and methods for genomic epidemiology that can be used to inform public health actions.

Epidemiologist 2: Complete the landscape analysis of genomic data use across notifiable conditions, analyze the results, and coordinate with disease-specific program areas on next steps such as development of pathogen-specific roadmaps and data flows.

Epidemiologist 2: Conduct data pulls and data analysis in support of developing visualization tools for public audiences and public health partners. This could include dashboards to enable disease-specific program areas rapid access to data visualization and analytics.

HSC 2: Support newly established data systems, maintain molecular epidemiology training resources/website for LHJs, Tribes, and other public health partners.

Funding 2 positions in the DIQA team:

Epidemiologist 3 (supervisor) DIQA: Provide oversight on data linkage, support the integration of genomic and epidemiologic data, lead the development of data management systems to support the processing of genomic data, and support the production of genomic data sets to facilitate use of genomic data in epidemiological analysis.

Epidemiologist 2 DIQA: Conduct data linkage and integration of genomic data. Identify, refine, and repurpose reproducible data management methods and tools that can be repurposed from SARS-CoV-2 to process other genomic pathogen data. Support the integration of genomic and epidemiologic data to facilitate use of genomic data in epidemiological analysis. Lastly, disseminate documentation on data management methods via open-source repositories such as GitHub.

This proposal aligns with Communicable Disease Control, with foundational capabilities of assessment (including surveillance and epidemiology), emergency preparedness and response, communications, and policy development and support. The proposal to provide sustainable funding for the Molecular Epidemiology Program is the best option as it would improve the availability and use of sequencing data for multiple notifiable conditions and improve data analysis for public health decision-making.

A consequence of not funding this proposal is that sequencing data use will not be integrated for other notifiable conditions which do not have specific grant support for genomic data use and genomic and epidemiological data integration. At present, WA DOH has built capacity for genomic epidemiology that, with ongoing funding, could impact prevention and mitigation of other communicable diseases. Sustaining this capacity is a gain for public health in the control of communicable diseases.

Without adequate resources, WA DOH will not be able to ingest, analyze, or monitor pathogen-specific sequencing data produced by laboratories to answer questions of epidemiological and biological importance, such as disease severity, transmission, and infectivity. WA leaders, clinicians, and residents will not have awareness of circulating pathogens with molecular markers that could inform clinical therapy and public health decision-making.

Other alternatives that have been explored include smaller scale that would limit out capacity, which reduces our capacity for data integration and visualization development. Additionally, we are applying for federal funding sources to sustain the program, but at present have not identified funding. One such opportunity is the Center of Excellence in Pathogen Genomics grant (CoEPG), which will be announced at the end of

September, 2022. If awarded, this funding would cover 3.5 FTE outlined here (approximately 40% of this DP). While we have provided a strong application, it is important to highlight that the funding only covers part of the Molecular Epidemiology Program, the funding is limited to 5 years, and there is no guarantee that we will be awarded the CoEPG grant.

**Assumptions and Calculations**

**Expansion, Reduction, Elimination or Alteration of a current program or service:**

Overall, the current program size will be maintained through this funding, but the focus on COVID-19 will be reduced, and the focus on other notifiable conditions will be expanded.

**Detailed Assumptions and Calculations:**

The assumptions made to determine the need for 6 FTEs in the Molecular Epidemiology Program and the 2 FTEs in Data Integration and Quality Assurance include:

- Need for a program lead/supervisor (Senior Epi) – that this program cannot be absorbed into an existing program.
- Need for a bioinformatician (Epi 3) dedicated to monitoring case-level genomic data and supporting analyses across communicable disease conditions. If the demand on this position grows with the addition of notifiable conditions, additional FTE may be needed.
- Need for a data management/data analysis lead (Epi 3) – assuming the agency prioritizes partnership with academic partners and results publication.
- Need for assessment to help establish a workplan for expansion to additional notifiable conditions (Epi 2).
- Need for data sharing and production of visualizations for the public (Epi 2).
- Need for program and communications support (HSC2).
- Need for development and application of data linkage and integration into existing data systems (Epi 3 and Epi 2)

Overall, the current program size will be maintained through this funding, but the focus on COVID-19 will be reduced, and the focus on other notifiable conditions will be expanded. Estimated expenditures include salary, benefit, and related costs to assist with administrative workload activities. These activities include policy and legislative relations; information technology; budget and accounting services; human resources; contracts; procurement, risk management, and facilities management.

FY 2025 \$1,469,000 FTE 11.3  
 FY 2026 \$1,469,000 FTE 11.3  
 FY 2027 \$1,469,000 FTE 11.3

**Workforce Assumptions:**

Workforce Assumptions FY25 Projections Only					
FTE	Job Classification	Salary	Benefits	Startup Costs	FTE Related Costs
1.0	SENIOR EPIDEMIOLOGIST (NON-MEDICAL)	\$123,000.00	\$41,000.00	\$4,000.00	\$8,000.00
3.0	EPIDEMIOLOGIST 3 (NON-MEDICAL)	\$326,000.00	\$113,000.00	\$12,000.00	\$23,000.00
3.0	EPIDEMIOLOGIST 2 (NON-MEDICAL)	\$296,000.00	\$107,000.00	\$12,000.00	\$23,000.00
1.0	HEALTH SERVICES CONSULTANT 2	\$66,000.00	\$28,000.00	\$4,000.00	\$8,000.00
2.0	FISCAL ANALYST 2	\$108,000.00	\$52,000.00	\$0.00	\$0.00
1.3	HEALTH SERVICES CONSULTANT 1	\$66,000.00	\$32,000.00	\$0.00	\$0.00
<b>11.3</b>		<b>\$985,000.00</b>	<b>\$373,000.00</b>	<b>\$32,000.00</b>	<b>\$62,000.00</b>

Estimated expenditures include salary, benefit, and related costs to assist with administrative workload activities. These activities include policy and legislative relations; information technology; budget and accounting services; human resources; contracts; procurement; risk management, and facilities management.

## Strategic and Performance Outcomes

### **Strategic Framework:**

WA DOH seeks to be a national leader in the production and use of whole genome sequencing (WGS) data for public health action. The Molecular Epidemiology Program seeks to expand the integrated use of pathogen genomic sequence data to support surveillance and epidemiological investigations and inform public health decision-making in Washington state.

Funding the Molecular Epidemiology Program will help the agency achieve goal 4: Healthy and safe communities in the Governor's Results Washington and support the "data, information, and technology innovations" transformational area listed in the agency's strategic plan. Continuing expansion into other notifiable conditions ensures epidemiologist involvement in this work and enables scaling innovative processes and solutions. Additionally, the Molecular Epidemiology Program currently engages multiple external partners, including monthly meetings with the Bedford Laboratory and bi-weekly office hours to support LHJs, Tribal, and other public health partners. This request supports the Departments Transformational Plan:

GLOBAL AND ONE HEALTH All Washingtonians live in ever-connected environments that recognize and leverage the intersection of both global and domestic health as well as the connections of humans, animals, and the environment.

### **Performance Outcomes:**

Active engagement and coordination within the agency, LHJs, and Tribal partners

Expected outcome: increased participation in the use of genomic data

Complete genomic and epidemiological data landscape analysis across notifiable conditions

Expected outcome: identify gaps and opportunities in use of genomic epidemiology and associated bioinformatics needs

Develop pathogen-specific roadmaps and pipelines for the integration of genomic and epidemiological data

Expected outcome: Clear plans for the expansion of genomic data use to additional notifiable conditions

Implement pathogen-specific roadmaps for additional notifiable conditions

Expected outcome: Increase availability of integrated genomic and epidemiological data for multiple pathogens

Identify, pilot, and implement technologies and applications of genomic epidemiology for public health

Expected outcome: Increase access and adoption of genomic epidemiology tools

Produce datasets with genomic, epidemiologic, clinical, biological, environmental, geospatial, behavioral, and social components

Expected outcome: Increase availability of integrated genomic and epidemiological datasets

Build capacity and provide training opportunities within the agency, LHJs, Tribal partners, and epidemiologist candidates

Expected outcome: Increase capacity and expertise in genomic epidemiology and improved familiarity with genomic epidemiology tools and applications

## Equity Impacts

### **Community outreach and engagement:**

Sustainable funding for these positions will support the expansion of efforts to identify and engage with LHJs and tribal partners and other public health stakeholders to improve the use of genomic data to inform decision-making.

### **Disproportional Impact Considerations:**

No communities are expected to be marginalized or disproportionately impacted by this proposal.

### **Target Populations or Communities:**

The proposal to provide sustainable funding for the Molecular Epidemiology Program to establish and scale the use of integrated genomic and epidemiologic data across notifiable conditions would result in the production of robust data sets and visualization tools that include demographic and geographic information. Increasing access to comprehensive characterization of pathogens will facilitate the identification of populations and communities that are disproportionately affected by infectious diseases. This proposal has the potential to positively impact communities of color and other underserved communities which are disproportionately impacted by some notifiable conditions. For such conditions, tracking and data analysis could lead to targeted recommendations and health education efforts.

## Other Collateral Connections

### **Puget Sound Recovery:**

N/A

### **State Workforce Impacts:**

We do not anticipate impacts to existing collective bargaining agreements or statewide compensation and benefits policy.

### **Intergovernmental:**

The Molecular Epidemiology Program currently offers genomic epidemiology office hours, which extend to public health partners, including state, LHJs, and Tribal Public Health. These office hours seek to build capacity for genomic epidemiology and encourage use of pathogen genomic sequencing data at the local level. Support anticipated. Additionally, we will provide training opportunities within the agency, LHJs, Tribal partners on the use of genomic epidemiology tools, and support analysis, outbreak investigations, and other public health efforts.

### **Stakeholder Response:**

Through this proposal, the Molecular Epidemiology Program will be able to continue collaborations with academic partners such as the Bedford Lab which has been at the national forefront of developing genomic tools that have been essential for genomic epidemiology and real-time pathogen surveillance. Additionally, the results of the landscape analysis will support the expansion of efforts to identify and engage with other community partners and non-governmental stakeholders.

### **State Facilities Impacts:**

The FTE positions are mostly remote and we do not expect any impact to facilities and workplace needs.

### **Changes from Current Law:**

We do not anticipate any necessary changes to existing statutes, rules, or contracts.

### **Legal or Administrative Mandates:**

This proposal is not in response to litigation, an audit finding, executive order, or task force recommendations.

## Reference Documents

- [Boost Review of Notifiable Diseases figure 1-4.pdf ss.pdf](#)
- [Boost Review of Notifiable Diseases FNCal.xlsm](#)

## IT Addendum

### **Does this Decision Package include funding for any IT-related costs, including hardware, software, (including cloud-based services), contracts or IT staff?**

No

## Objects of Expenditure

Objects of Expenditure <i>Dollars in Thousands</i>	Fiscal Years		Biennial	Fiscal Years		Biennial
	2024	2025	2023-25	2026	2027	2025-27
Obj. A	\$0	\$986	<b>\$986</b>	\$986	\$986	<b>\$1,972</b>
Obj. B	\$0	\$373	<b>\$373</b>	\$373	\$373	<b>\$746</b>
Obj. E	\$0	\$50	<b>\$50</b>	\$50	\$50	<b>\$100</b>
Obj. T	\$0	\$60	<b>\$60</b>	\$60	\$60	<b>\$120</b>

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