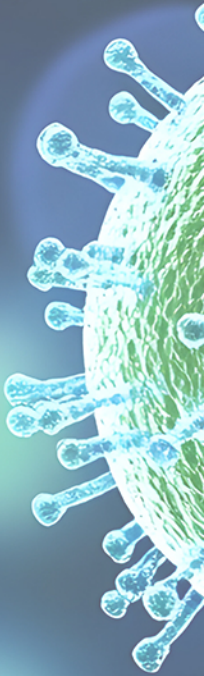
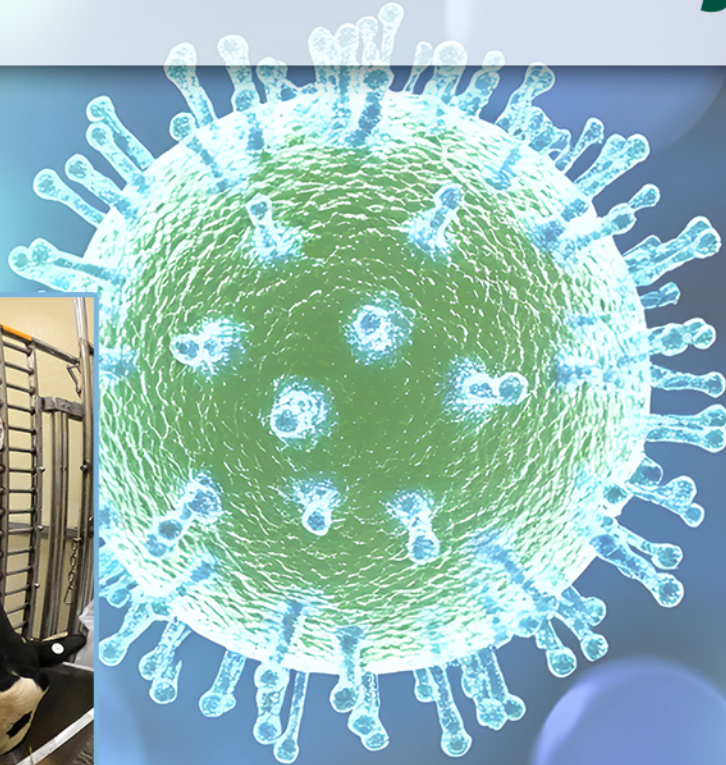




Animal and Plant Health Inspection Service
U.S. DEPARTMENT OF AGRICULTURE

FY2024 Cycle 5 NAHLN Farm Bill Funded Projects



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NAHLN Farm Bill Showcase

Presentations from 2023 (FY24, Cycle 5) NAHLN Farm Bill Funded Projects

Wednesday, January 7, 2026

12:00PM – 2:30PM CT

Moderator: Kelli Almes

12:00 PM	Welcome <i>Dr. Julie Wallin, NADPRP Program Director</i>	
12:05 PM	Establishment of Standardized NGS Sequencing, Data Analysis, and Reporting Protocols <i>Ganwu Li, Susan Sanchez, Ailam Lim, Kiril M. Dimitrov, Leyi Wang, Lifang Yan, Zhenyu Shen</i>	2
12:20 PM	Development of an Android/iOS Application and Enhancement of Existing Web-based Tools to Facilitate Accurate and Efficient Field Data Capture and Electronic Submission to NAHLN Laboratories by Means of a Standardized Order Message <i>Steve Smith, Greg Juda, Angela Pillatzki, Jon Greseth, Travis Clement, Yan Zhang, Alexandra Brower</i>	5
12:35 PM	Building Sequencing Capacity and Efficient Workflows to Enhance Capability for the Detection of Emerging Diseases <i>Ailam Lim</i>	7
12:50 PM	Building Workflow Efficiency and Testing Capacity in Preparedness for ASF Outbreak Response <i>Ailam Lim</i>	9
1:05 PM	Questions/Break	
1:15 PM	Evaluating a Hybrid Capture Approach for Next Generation Sequencing of Salmonid Viruses <i>Thomas Waltzek, Brandi Torrevillas, Becca Wolking, Kevin Snekvik</i>	11
1:30 PM	Broadening Expertise in Nanopore-based Sequencing for Pathogen Detection and Development of Bioinformatics Support Community <i>Kevin Lahmers</i>	13
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2:00 PM	Questions / Comments / Closing	

Establishment of Standardized NGS Sequencing, Data Analysis, and Reporting Protocols

Ganwu Li, Susan Sanchez, Ailam Lim, Kiril M. Dimitrov, Leyi Wang, Lifang Yan, Zhenyu Shen

Iowa State University Veterinary Diagnostic Laboratory
Ames, IA

Project objective:

1. Develop a standard NGS sequencing library preparation protocol for DNA and RNA viruses for the Illumina sequencing platform.
2. Develop a nearly automated bioinformatics analysis pipeline for DNA and RNA viral sequencing.
3. Develop a standardized reporting protocol. A standardized reporting protocol will ensure consistency and reliability in data interpretation.

Deliverables completed:

Wetlab

- To address the need for more methodological quality-based standards that laboratories could meet to demonstrate the analytical performance of any NGS test developed by individual laboratories, we have created and optimized protocols for standardized sequencing library preparation for viral genome sequencing, including sample processing and nucleic acid extraction, cDNA synthesis for target RNA viruses, and library preparation, normalization, and sequencing. These protocols have been developed and validated by the NGS section at ISU VDL. And for these protocols to be adopted by new users from other diagnostic laboratories, we have adapted and re-formatted them following AAVLD quality standards for procedure documentation.
- In these protocols, we have also provided technical metrics for specific steps of the workflow for the user to record information vital for assessing sample quality and to determine whether samples meet the minimum requirements for the next protocol.
- We also created a metrics table that users can use to record metadata about the samples, reagent information, and results after each step of the workflow.
- The original plan for creating online tools to assist users with multiple library calculations was replaced with the metrics table that includes built-in formulas for the user to auto-calculate sample concentrations for specific steps.
- Because our group had to upgrade our sequencing platform from the MiSeq to the MiSeq i100 Plus earlier this year, the protocols were modified to adapt to the updated version of the library preparation kit and the new platform.
- With the new sequencing platform, the protocols were tested on two types of clinical specimens (serum and lung) for a target RNA virus, Porcine Reproductive and Respiratory Syndrome Virus, with detected Ct values ranging from low Ct (15-20), mid-point Ct (24-25), and high Ct (27-30). The sequencing results generated from wetlab testing were then analyzed following the standardized bioinformatics protocols.

Bioinformatics

- We have designed a simplified, highly customizable automated bioinformatics pipeline using kraken2, ideally suited for small and medium-sized labs with limited programming capabilities. The pipeline serves as a foundational framework that can be readily extended and adapted by any laboratory eliminating the need to build a solution from scratch. This pipeline will serve clinical and research samples sequenced on Illumina's platforms for viral and shotgun metagenomic analysis. The pipeline

also provides a single command solution for the installation of the Micromamba based environment and kraken2 database of user's choice to be used in genome sequence assembly. This simplified pipeline has been developed and validated at the NGS section of ISU VDL. In its current beta version, the pipeline as well as the corresponding protocols (following AAVLD quality standards for procedure documentation) were presented and made available to the co-PIs for testing and feedback. Once the feedback is received, the simplified pipeline will be optimized further and released publicly.

- In addition, the existing bioinformatics analysis pipeline utilized at the NGS section of ISU VDL has been converted into an advanced, modular, nearly automated, highly parallelized and customizable pipeline and is used for routine diagnostics. Several important tools were identified to qualitatively analyze the intermediate and final output.
- Protocol for standardized report generation for metagenomic and viral samples, such as PRRSV, IAV, aMPV, PCV2, Rotavirus, etc. were also developed at NGS section at ISU VDL and used for routine cases. The report generation protocol along with templates and examples were shared with co-PIs.

Wetlab and bioinformatics

- The wetlab and bioinformatics protocols have been distributed to co-PIs of this grant for validation and testing.

Deliverables yet to be completed:

Wetlab

- Due to the recent purchase of a new sequencing platform, there was limited time to test samples with the updated workflows. Thus, we elected to first test RNA viruses with the updated workflows as these are commonly requested for sequencing compared to DNA viruses. However, the next test will be to test the workflows on DNA virus.

Wetlab and bioinformatics

- Information about the completed deliverables, including protocols and workflows, from this grant project will be presented at the upcoming AAVLD LTC committee meeting in October 2025.
- Videos that show a user going through each step of the protocols will be created and distributed to co-PIs of this grant to aid them in test validation, which will be conducted in spring 2026. During this validation period, co-PIs will give feedback on the protocols and provide any recommendations or improvements.
- After validation, protocols will then be finalized and available for distribution to NAHLN-participating laboratories by request.

Bioinformatics

- Create a webpage for small and medium-sized VDLs to give them access to submit samples for analysis through the advanced pipeline.
- Provide a web-based NGS request submission form to fill in along with sample analysis.
- Create a webpage for small and medium-sized VDLs to access NGS resources.
- Create FAQ page to answer most common questions from clients about timeline, how to submit requests, how to receive results, data retention policy, fees, contact information.
- Any special requests that can be handled will be listed on the FAQ page along with guidelines on what the report will entail.

How the project benefits NAHLN:

Though the primary goal of this project is to help bridge the knowledge gap for small and medium-sized labs in establishing NGS workflows, the standardized methods developed from this project can be used in large-sized VDL labs.

Because Illumina sequencing platforms have been widely adopted by labs of different capacities, these workflows and protocols were designed for Illumina sequencing technologies. In addition, we have created protocols that work for the latest platform, the MiSeq i100 Plus, which will replace the MiSeq instrument as this iSeq will no longer be supported after 2029.

The standardized protocols will ensure that strict quality control measures are in place throughout the NGS workflow, from sample preparation to data analysis. This guarantees the reliability and consistency of the generated data, minimizing technical variations and errors. Adhering to the standardized protocols ensures the production of results that are reproducible across different laboratories and cases, aids in meeting regulatory requirements and guidelines governing the use of NGS in different applications, such as clinical diagnostics and research, and provides a foundation for the continual advancement of NGS technologies and methodologies.

These protocols will allow labs to apply NGS technology for pathogen or viral variant discovery, outbreak investigation, and for routine surveillance for bacterial and viral pathogens.

These will also significantly bolster diagnostic capacities in VDLs of NAHLN in their ability to detect and manage emerging infectious diseases.

Lastly, the standardized NGS protocols will enable seamless collaboration and knowledge shared between NAHLN and other national and international laboratory networks. By fostering a culture of collaboration, this project will empower NAHLN to actively support and partner with other networks during animal health emergencies. This enhanced collaborative capacity will enable a more concerted and effective response, solidifying NAHLN's pivotal role in mitigating the impact of such crises.

Development of an Android/iOS Application and Enhancement of Existing Web-based Tools to Facilitate Accurate and Efficient Field Data Capture and Electronic Submission to NAHLN Laboratories by Means of a Standardized Order Message

Steve Smith, Greg Juda, Angela Pillatzki, Jon Greseth, Travis Clement, Yan Zhang, Alexandra Brower,
Connecticut Veterinary Medical Diagnostic Laboratory, Maryland Veterinary Diagnostic Laboratory

Montana Veterinary Diagnostic Laboratory
Bozeman, MT

Project objective:

There are five primary objectives for this proposal, each of which are detailed below:

1. Order Messaging. This objective furthers development and implementation of a standardized order message.
2. Mobile Device Application. This objective develops a mobile (android/iOS) application, to allow for integration with data capture systems (RFID readers, barcode scanners, etc.)(including offline use), data upload, and incorporation of field data into a standardized order message directed to any appropriately configured NAHLN lab. The application will also allow for direct authentication with specific VADDS laboratories in order to utilize lab-specific submission templates, take advantage of existing client data, and display previous results.
3. Generic Web-Based Submission Portal. This objective will create a generic web portal that allows for PC-based upload of submission data and generation of an order message that can be directed to any NAHLN laboratory configured to receive it.
4. Laboratory-Specific Web Portal Upgrades. This objective will enhance the existing functionality of laboratory-specific web portals for participating VADDS laboratories (MT, SD, AZ, CT, MD, WY), to ensure that participating laboratories are functioning at the highest possible level.
5. Development of Maintenance Functions in VADDS. This objective will develop the needed maintenance functionality for the new features being developed for both the mobile application and the enhanced laboratory-specific web submission portals.

Deliverables Completed:

Specific deliverables are discussed by objective, below:

1. Order Messaging (**complete**). The additional work to develop a standardized order message is now complete and in place for testing and subsequent development.
2. Mobile Device Application (**in progress**). An early version of the mobile app supporting generic submissions to the six participating laboratories is in place, and further testing and development of additional functionality is in progress.
3. Generic Web-Based Submission Portal (**complete**). A functional generic submission portal was developed. An enhanced copy of this portal is expected to undergo further development to serve as an official universal portal.
4. Laboratory-Specific Web Portal Upgrades (**complete**). Each of the six participating laboratories (MT, SD, AZ, CT, MD, WY) have received site-specific development work to enhance their existing web submission portals.
5. Development of Maintenance Functions in VADDS (**complete**). Each of the six participating laboratories (MT, SD, AZ, CT, MD, WY) have received site-specific development work to update and enhance their lab-specific internal LIMS maintenance functionality.

How the project benefits NAHLN:

This project benefits the NAHLN by developing and enhancing mechanisms for improved electronic submission of data to NAHLN laboratories. In particular, further development of a standardized order message and integration with a generic/universal submission portal and mobile application open the door for a brand new route of submission. Development in concert with NAHLN data requirements will ensure that submissions from both web and mobile platforms contain all of the appropriate data points for NAHLN results messaging, and will also facilitate improved data mining for animal health surveillance and monitoring. The universal, LIMS-agnostic aspect of both the mobile application and generic web portal ensure that any appropriately configured laboratory can receive the results electronically in an efficient manner. This improves the quality of the incoming information, and also significantly increases the efficiency of the receiving and accessioning process for the receiving laboratory.

Building Sequencing Capacity and Efficient Workflows to Enhance Capability for the Detection of Emerging Diseases

Ailam Lim

Wisconsin Veterinary Diagnostic Laboratory
Madison, WI

Project objective:

This project prioritizes the acquisition of laboratory equipment to support the enhancement of the National Animal Health Laboratory Network (NAHLN) through the development of next-generation sequencing (NGS) capacity, improved workflow efficiency at the Wisconsin Veterinary Diagnostic Laboratory (WVDL), and the sharing of knowledge with other veterinary diagnostic laboratories within the NAHLN and AAVLD networks.

Objective 1

Build WVDL's capacity to rapidly detect novel and emerging pathogens that pose a threat to livestock health by implementing a shotgun metagenomic sequencing approach.

Objective 2

Improve workflow efficiency and pathogen discovery using shotgun metagenomics by evaluating the effectiveness of various wet-lab methods for depleting host genomic material from diagnostic samples.

Objective 3

Facilitate knowledge sharing and standardization by disseminating project outcomes to other VDLs. This will include active leadership and participation in the AAVLD Laboratory Technology Committee, development of standardized quality parameters and metrics, and open-access sharing of protocols and training resources

Deliverables completed / Deliverables yet to be completed:

This project experienced significant delays due to Illumina's transition from the MiSeq to the MiSeq i100 platform. As a result, a one-year no-cost extension was granted to allow for project completion.

WVDL received the new MiSeq i100 instrument in August 2025, and training was completed in September 2025. Since then, limited sequencing runs have been implemented for the bacterial AMR whole genome sequencing project. The new MiSeq i100 offers substantial improvements over the previously used iSeq 100, with reagent costs reduced by 40% and run times shortened by 60%, all without compromising data quality.

The next phase of the project will focus on implementing a shotgun metagenomic sequencing approach for the rapid detection of novel and emerging pathogens that threaten livestock health.

The cost savings from purchasing the MiSeq i100 (instead of the original MiSeq model) also enabled WVDL to acquire an IndiMag 2 nucleic acid extraction platform. This equipment has already been validated and approved for Influenza A Virus (IAV) testing and is currently in use for routine processing of samples during the ongoing IAV outbreak.

In addition, a modified extraction protocol was validated using the IndiMag 2 platform to enable simultaneous extraction of nucleic acids from both Gram-positive and Gram-negative bacterial isolates for downstream AMR whole genome sequencing. This automated workflow offers significant time savings compared to the traditional spin column method, which was both time-consuming and labor-intensive. The new method has greatly improved efficiency in WVDL's sequencing workflows.

How the project benefits NAHLN:

WVDL actively participates in the NAHLN AMR whole genome sequencing (WGS) efforts, and the acquisition of new equipment will significantly enhance our capacity to deliver high-quality sequencing data in a timely manner.

The ability to rapidly sequence viruses during outbreaks or perform metagenomic sequencing on cases with unknown causes is critical for the early identification of new, emerging, or mutating infectious diseases that could have devastating impacts on animal health. Building this capacity at WVDL is essential, serving as a first line of defense for the region and the entire country, in alignment with the mission of NAHLN laboratories.

Building Workflow Efficiency and Testing Capacity in Preparedness for ASF Outbreak Response

Ailam Lim

Wisconsin Veterinary Diagnostic Laboratory
Madison, WI

Project objective:

The Wisconsin Veterinary Diagnostic Laboratory (WVDL) has identified critical opportunities to optimize daily workflow and surge testing capacity during high-consequence disease outbreaks. This project aimed to improve operational efficiency by integrating two centrifuges and two benchtop liquid handlers into WVDL's centralized serum processing workflow.

These additions are intended to support high-throughput African Swine Fever (ASF) serology and PCR testing, increasing processing speed and sample handling accuracy. The liquid handlers will also streamline whole blood sample pooling, enhancing ASF PCR testing efficiency.

This initiative supports WVDL's strategic goal of maximizing the use of non-microbiologist staff in sample processing, thereby expanding testing capacity for both routine diagnostics and National Animal Health Laboratory Network (NAHLN)-supported testing.

Objective 1:

Reduce sample processing time and increase the throughput capacity of the Sample Receiving section by utilizing new centrifuges to accelerate serum preparation, and implementing benchtop liquid handlers for automated serum transfer to testing plates for ASF serology.

Objective 2:

Enhance efficiency and capacity of the NAHLN testing unit by using benchtop liquid handlers to automate whole blood pooling for ASF PCR testing.

Deliverables completed / Deliverables yet to be completed:

Status: *Completed.*

WVDL successfully implemented the planned improvements to sample processing efficiency using benchtop liquid handlers and centrifuges. Building on this success, the same workflow has been adapted for use in milk surveillance for Highly Pathogenic Avian Influenza (HPAI). Equipment originally acquired for COVID-19 testing, along with devices purchased under this project, have been repurposed for this initiative. Staff have been trained, and the system is now actively supporting the National Milk Testing Program.

The sample pooling method for the Integra D-One liquid handler module has been validated for Bovine Viral Diarrhea (BVD) testing. This validated method is directly transferable to ASF PCR testing and will be implemented accordingly. Staff training for this procedure is currently ongoing, with full operational deployment anticipated upon completion of the training phase.

How the project benefits NAHLN:

This project enabled WVDL to implement a high-efficiency workflow that maximizes the use of multiple laboratory sections, increasing both testing capacity and overall productivity. It began with expanding the sample receiving area to include centrifugation of serum samples. This adjustment reduced the workload on the Serology section, allowing staff to focus on high-throughput testing. In the event of an ASF outbreak, this setup would enable serologists to dedicate their efforts to ASF-specific serology testing.

A similar strategy was applied to the IAV PCR assay, where milk samples were pipetted into a 96-well format. Combined with the use of prefilled RNA extraction kits, this change saved approximately 60 minutes per 96-well PCR run for proficiency-tested staff. This efficiency gain was especially impactful during large-scale herd-level testing (~5,400 herds) conducted as part of Wisconsin's National Milk Testing Surveillance Program. In an ASF outbreak, this model will allow microbiologists to concentrate on high-volume ASF PCR testing.

Overall, this project has significantly strengthened WVDL's outbreak preparedness. The streamlined workflow is easily transferable and adaptable for future NAHLN program disease outbreak responses.

Evaluating a Hybrid Capture Approach for Next Generation Sequencing of Salmonid Viruses

Thomas Waltzek, Brandi Torrevillas, Becca Wolking, Kevin Snekvik

Washington Animal Disease Diagnostic Laboratory
Pullman, WA

Project Objective:

The overarching goal is to build laboratory capacity through development and enhancement of Next Generation Sequencing technical expertise for the detection and genomic sequencing of emerging salmon viruses.

Deliverables completed:

Milestone 1.1: Design and test custom hybrid capture panel targeting salmonid viruses

We have succeeded in building a comprehensive hybrid capture (HC) panel for next-generation sequencing (NGS) of salmon viruses and creating a curated salmon virus database incorporating over 9,000 publicly available sequences and more than ten new salmon virus sequences generated from archived case materials. The inclusion of these previously unpublished genomes enhances the breadth and relevance of our custom salmon virome HC panel compared to currently available vertebrate pan-viral capture panels. The aforementioned new salmon virus genomes have been deposited into GenBank and manuscripts are in progress.

Furthermore, our salmon virome HC panel is predicted to improve the recovery of full genome sequences from samples with low viral loads as compared to agnostic metagenomic approaches.

Milestone 1.2: Compare metagenomic tissue sequencing with hybrid capture sequencing

We have completed the experimental design to test the new HC panel versus agnostic viral discovery sequencing workflows. Viral cultures and viral infested tissues have been collected from local case material or acquired from collaborators. Samples to be tested include known salmon viruses such as IHN, IPN, ISA, and VHS viruses. Priority will be given to samples for which both the viral culture and the infected source tissues are available.

Deliverables to be completed:

Milestone 1.2: Compare metagenomic tissue sequencing with hybrid capture sequencing

We have just received the HC salmon virome kit (9/30/25) and we will soon begin preparing libraries for sequencing to compare the targeted HC approach to the agnostic metagenomic approach. Afterward we will perform data analysis using newly developed bioinformatic workflows and establish a draft SOP for data aggregation, analysis, and result reporting.

Milestone 1.3: Summary

At the conclusion of the project, we will have an established SOP for sequencing salmon viruses by hybrid capture including downstream bioinformatic analyses. An associated cost benefit analysis will be generated to compare the HC approach to the agnostic metagenomic approach.

How the project benefits NAHLN:

This project aims to enhance laboratory capacity and expertise in NGS to improve the detection and genomic sequencing of emerging salmon viruses. Building on our previous work in identifying

uncharacterized fish viruses, this project will address critical gaps in sequencing speed and cost. We will compare agnostic metagenomic and hybrid capture approaches to determine the most effective method for obtaining full genome sequences of salmon viruses. The expected outcome is a robust testing strategy that NAHLN labs can implement to rapidly and accurately identify both existing and novel viral threats to salmon populations. This strategy will place NAHLN labs at the forefront of salmon virus detection, supporting timely response to potential biosecurity risks.

Broadening Expertise in Nanopore-based Sequencing for Pathogen Detection and Development of Bioinformatics Support Community

Kevin Lahmers

Virginia Tech Animal Laboratory Services
Blacksburg, VA

Project objective

- Goal 1: Expand technical and bioinformatic expertise in rapid next generation sequencing and confirmatory modalities.
 - Nanopore and Illumina-based sequencing of known disease samples with associated electron microscopy and *in situ* hybridization with training of 3 individuals
 - Compare GridION outputs with PromethION outputs
- Goal 2: Develop a bioinformatics support/training space and foster a bioinformatics community.
 - Develop a cloud-based, containerized workspace with ability to limit access
 - Promote diagnostic community involvement for bioinformatic support and training

Deliverables completed

- Nanopore-based sequencing of known and previously undescribed viruses.
 - Electron microscopy
 - In situ probe design
 - Comparison of GridION and PromethION outputs on bacterial sequencing.
- Promote diagnostic community involvement for bioinformatic support and training.

Deliverables to be completed

- ISH comparing whole genome designed probes vs. shotgun metagenomic based probes
- Training of additional individuals using the sequencing data obtained
- Additional shotgun sequencing

How the project benefits NAHLN

- Increased expertise in sequencing based pathogen discovery and characterization
- Expertise development in ISH confirmation of pathogen

Configurable Online Submission Forms to Improve Speed and Accuracy of Sample Submission Data

Amy Swinford ¹, Tammy Leimer ², Jamie Kidd ², Carlos Rodriguez ¹

¹ Texas A&M Veterinary Medical Diagnostic Laboratory, ² Trace First
College Station, TX

Project Objectives

Overview: Recent outbreaks of high-consequence diseases, such as Highly Pathogenic Avian Influenza, have demonstrated the essential role of National Animal Health Laboratory Network (NAHLN) laboratories testing and emergency response capabilities. Submissions that are incomplete or missing data have become a common issue, delaying testing and reporting while consuming valuable resources. To remedy, this project's objectives are:

- Enhance the field sample collection to laboratory processing workflow
- Ensure required data is captured and submitted properly
- Creation of a streamlined workflow to simplify the data entry process
- The project outcome should be scalable to support NAHLN throughout future changes.

The planned outcome of this project will result in the implementation of the Rapid Submission Form, enabling faster and more reliable submission of data for NAHLN testing and surveillance.

Deliverables Completed:

MS 1: Client portal enhancement to improve the speed and accuracy of submissions to our laboratory.

Develop a toolkit in CoreOne for Labs, enabling laboratories to create customized submission forms for NAHLN and other diseases.

1.1 Determine which submission types need specific online submission forms: We will develop a prioritized list of sample submission types (e.g. NAHLN testing, other high consequence disease testing) that would benefit from a specific submission form.

1.2 Analysis of the nature of the differences between specific submission forms: The approach is to create a toolkit which will allow NAHLN laboratories to define their own set of customized submission forms. This milestone will entail an analysis of the findings from 1.1 to determine what submission form components require the ability to be configured/customized.

1.3 Ability of labs to create and deploy custom client portal submission forms: Enhancements to our CoreOne for Labs laboratory information management system will be led by Trace First, our LIMS provider. These enhancements will see creation of a toolkit allowing any lab using CoreOne for Labs the ability to create customized submission forms in the portal. These forms will not be hard-coded, meaning that they can easily be amended in the event of changes to NAHLN messaging standards.

1.4 Testing of new submission options in client portal: Testing of the enhancements will first be conducted by Trace First support desk staff and then moved to the field for testing by those who will actually be submitting samples.

MS 2: Training materials (videos and user documentation) will be developed. Provide documentation and training materials for the submission form functionality in the LIMS. This documentation should be accessible to any user of the LIMS so that other labs using a given LIMS can also take advantage of submission from usage if need arises.

2.1 Training videos placed in Trace First University learning management system: Our LIMS vendor maintains a learning management system, Trace First University where an extensive library of videos on how to use CoreOne for Labs is maintained. Videos on the use of this configurable submission form will be created and posted. Trace First University is free to all CoreOne for Labs users.

2.2 User documentation placed in Trace First's online Knowledge Base Our LIMS vendor maintains an online Knowledge Base where user guides and other documentation are available to all CoreOne for Labs users. Documentation of this new feature will be developed and posted on the Knowledge Base.

Rapid Submission Form Overview:

The Rapid Submission Form is designed to simplify the process of submitting samples while accelerating the submission process. A new front-end screen allows for the listing of common Testing Submission Forms, allowing the users to quickly locate the form and create high-occurrence submissions.

Key Features

- Ease of Access: A front-end interface set to display a list of available Testing Submission Forms for easy selection.
- Enhanced Navigation: Depending on how the lab configures the submission form, a limited subset of tests, specimens, and taxons will be displayed, reducing the number of screens to navigate.
- Minimized Data Entry: Users can complete submissions rapidly by entering only essential information.

Submission Form Configuration:

Each laboratory can customize its Rapid Submission Form by providing the following configuration data to Trace First:

- Form Information
 - Form name
 - Description
 - Owner details
- Animal Information
 - Age
 - Unit of Measure (UOM)
 - Sex code
- Taxon
- Weight
 - Weight and UOM
- Specimen Information
 - Specimen name
 - Specimen type
 - Collection date
 - Specimen type description
- Attachments
- Veterinarian Information
- Receiving Laboratory
- Test Schedules

- Additional Data
- Additional Data Fields

Laboratory Customization Options:

- Show or hide specific fields within the submission form
- Mark specific fields as required for submission type

Example Use Case: Avian Influenza Matrix Test:

An example implementation of the Rapid Submission Form has been developed for the Avian Influenza Matrix Test:

- Configured for a single test submission
- Built specifically for the Avian Influenza Matrix Test, with all necessary data entry fields present to support quick submissions.

Training and Support:

To assist users in understanding the creation and utilization of Rapid Submission Forms, the following training resources are provided:

- Trace First University: Recorded demonstrations provide a step-by-step walkthrough of the submission process. The recordings are accessible through Trace First University.
- KnowledgeBase Access: The KnowledgeBase information platform provided by Trace First contains a walkthrough of the Rapid Submission process.

Conclusion:

The introduction of NAHLN Rapid Submission Forms through the Configurable Online Submission Forms Project aims to improve the accuracy and efficiency of disease surveillance and reporting. By enhancing the process of data collection and submission creation, the introduction of the Rapid Submission Form will strengthen NAHLN's ability to quickly respond to cases of threatening disease.

How the project benefits NAHLN:

To enhance these capabilities, this project aims to improve the speed, accuracy, and efficiency of data collection and submission processes for the range of received diagnostic and surveillance related samples. The introduction of Rapid Submission Forms would decrease the amount of incomplete submissions being received while streamlining the submission process.