

## **M.L. 2021 Minnesota Aquatic Invasive Species Research Center Subproject Abstract**

For the Period Ending June 30, 2025

**SUBPROJECT TITLE:** MAISRC Subproject 49: Practical field-based tools for detecting high priority microbes

**SUBPROJECT MANAGER:** Dr. Nicholas Phelps

**ORGANIZATION:** University of Minnesota

**COLLEGE/DEPARTMENT/DIVISION:** Department of Fisheries, Wildlife and Conservation Biology

**MAILING ADDRESS:** 135 Skok Hall, 2003 Upper Bufford Circle

**CITY/STATE/ZIP:** St. Paul, MN, 55108

**PHONE:** 612-624-7450

**E-MAIL:** phelp083@umn.edu

**WEBSITE:** <https://maisrc.umn.edu/research/49>

<https://z.umn.edu/phelpslab>

**FUNDING SOURCE:** Environment and Natural Resources Trust Fund (ENRTF)

**LEGAL CITATION:** M.L. 2021, First Special Session, Chp. 6, Art. 6, Sec. 2, Subd. 06e

**SUBPROJECT BUDGET AMOUNT:** \$210,904

**AMOUNT SPENT:** \$210,320

**AMOUNT REMAINING:** \$584

### **Sound bite of Project Outcomes and Results**

Field deployment of eDNA-based detection methods for AIS would provide significant advantages over current methods. We evaluated multiple sampling approaches for three harmful microbes and worked to validate field detection methods. Our results suggest that there is significant promise for this approach, however additional research is required to reliably scale.

### **Overall Subproject Outcome and Results**

Molecular tools to identify environmental DNA (eDNA) in water is an emerging approach for early detection and surveillance of aquatic invasive species. eDNA-based detection methods show significant promise for reducing costs and detection time, and increasing sensitivity, thereby improving managers' ability to rapidly respond. A key bottleneck in these methods remains the field deployability of the assays. Currently, samples are collected from the field and transported to a lab for analysis, adding cost and time. Our goal was to develop and validate methods that put the full testing pipeline in the field – from sample collection to actionable result. Our team focused this study on three high priority harmful microbes: largemouth bass virus (LMBV), viral hemorrhagic septicemia virus (VHSV), and *Didymosphenia geminata* (Didymo). We were successful in collecting field samples for LMBV (n=11 lakes) and Didymo (n=7 rivers), and conducting a laboratory exposure trial for VHSV (n=24 tanks). Due to persistent challenges with equipment, vendors, federal government spending restrictions, and sample inhibition, we were less successful validating the field deployable LAMP assays. Each microbe presented unique challenges that could not be overcome within the timeframe of the project. However, we were able to test most VHSV and Didymo samples by qPCR (lab-based assay) to demonstrate the effectiveness (or not) of various active and passive sample collection methods. eDNA detection from water was successful: for static water (i.e., lake; VHSV) the active filtration worked best, while passive sampling performed better for moving water (e.g., river; Didymo). We have concluded that there is significant need and promise for deploying eDNA detection methods in the field; however, the platforms and assay-specific reagents will need further optimization to reliably scale. Our team is committed to pursuing this work and will continue to collaborate closely with existing and new partners to bring our goals to fruition.

### **Subproject Results Use and Dissemination**

While we were not able to fully transfer a finalized protocol for the three targets, we did conduct outreach and demonstrations with two of our planned partners. With the Grand Portage Band of Lake Superior Chippewa, we collected water samples at Grand Portage Creek with tribal personnel and conducted a demonstration of the full point of use protocol using a previously validated LAMP assay as an example. We also trained personnel at Voyageurs National Park on the full point of use protocol.

Publications related to this project will be forthcoming. We aim to complete the testing of all collected samples in the coming months.

#### *Select Presentations*

- Kageyama, S., L. Sacco, N. Phelps, S.F. Spear, 2024, A Reverse Transcription-Loop-Mediated Isothermal Amplification Assay for Detecting Viral Hemorrhagic Septicemia Virus, Genotype IVb (VHSV-IVb), Government Working Group eDNA Workshop, Columbus, OH. Poster.
- Kageyama, S., T. Schreier, L. Sacco, M. Edlund, N. Phelps, S.F. Spear, 2024, Development of a rapid method for detecting *Didymosphenia geminata* in Lake Superior tributaries, Upper Midwest Invasive Species Conference (UMISC), Duluth, MN. Poster.