

A1. Title Page

**QUALITY ASSURANCE PROJECT PLAN
eDNA MONITORING OF BIGHEAD AND SILVER CARPS**

Prepared for:

**U.S. Fish and Wildlife Service
USFWS Midwest Region**



Bloomington, MN

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REVIEW CERTIFICATION SHEETS

Final Quality Assurance Project Plan for the
eDNA Monitoring of Bighead and Silver Carp

Approved by:

Aaron Woldt, Deputy Assistant Regional Director, Fisheries, USFWS Midwest Region

Kelly Baerwaldt, Asian Carp/eDNA Program Coordinator, USFWS Midwest Region

Teresa Lewis, Center Director, Midwest Fisheries Center

Emy Monroe, Project Leader, Whitney Genetics Lab, eDNA Processing Leader

Maren Tuttle-Lau, eDNA Processing QA Specialist, Whitney Genetics Lab

Katherine Bockrath, DNA Documentation & Reporting Specialist, Whitney Genetics Lab

Mark Holey, Project Leader, Green Bay Fish & Wildlife Conservation Office

Mark Brouder, Project Leader, Ashland Fish & Wildlife Conservation Office

Sam Finney, Project Leader, La Crosse Fish & Wildlife Conservation Office

Scott Koproski, Project Leader, Alpena Fish & Wildlife Conservation Office

Rob Simmonds, Project Leader, Cartersville, Fish & Wildlife Conservation Office

Jason Goeckler, Project Leader, Columbia, Fish & Wildlife Conservation Office

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A2.3 ACRONYMS/ABBREVIATIONS

Table 1 Common acronyms/abbreviations commonly referenced in this document.

Acronym/Abbreviation	Definition
COC	Chain of custody
CSO	combined sewer overflow
DI	deionized (water)
DNA	Deoxyribonucleic acid
dNTP	deoxyribonucleotide triphosphates, also known simply as nucleotides
eDNA	environmental Deoxyribonucleic acid
FWCO	Fish and Wildlife Conservation Office
GL	Great Lakes
GPS	Global Positioning System
LDB	left descending bank
MRWG	Monitoring and Response Work Group
SDS	Safety Data Sheets
PCR	polymerase chain reaction
QAPP	Quality Assurance Project Plan
RDB	right descending bank
Taq	Thermus aquaticus
USACE	United States Army Corps of Engineers
USFWS	United States Fish and Wildlife Service
UV	Ultraviolet light
WGL	Whitney Genetics Lab

SECTION 1 PROJECT DESCRIPTION AND PERSONNEL REQUIREMENTS

1.1 Background

Invasive aquatic nuisance species pose a major threat to aquatic ecosystems worldwide. Within Illinois, the manmade Chicago Sanitary & Ship Canal (CSSC), constructed in the early 1900s, provided an unnatural portal for invasive species dispersal between the geologically separated Mississippi River and Great Lakes drainage basins. In 2002, in an effort to curtail the spread of invasive species between the two basins, the U.S. Army Corps of Engineers (USACE), constructed a dispersal barrier system within the CSSC. The primary objective of the barrier system when initiated was to stop the dispersal of the invasive Round Goby into the Mississippi River basin; however, once the project was completed, it was found that the Round Goby had already surpassed the barrier. Since then, a new threat to the Great Lakes from the Mississippi River basin has become the primary objective of the dispersal barrier system. Invasive Asian carps, including Bighead Carp (*Hypophthalmichthys nobilis*) and Silver Carp (*H. molitrix*) have been steadily dispersing upstream through the Mississippi, Illinois, and Des Plaines rivers. Their potential dispersal through the dispersal barrier system within the CSSC poses a potential threat to the Great Lakes ecosystem.

In the past, traditional fishery techniques were used to detect the leading edge of the Asian carp population; however, this method was somewhat ineffective at targeting these species at low densities. The University of Notre Dame, with funding from the USACE, developed a method that detected “environmental” DNA (eDNA) left behind in the aquatic system by the targeted species. Environmental DNA enters the system through a variety of mechanisms, some of which include sloughing of external epidermal cells into the water, sloughing of internal epidermal cells into feces and into the water, and as tissue residues following injury or predation. The detection of eDNA in water samples is based on whole DNA extraction from particulate organic and inorganic matter found in the water and polymerase chain reaction (PCR) assays for species-specific mitochondrial DNA markers.

Use of this method is to provide detection of Asian carp at low densities and to serve as an early detection system of the spread of Asian carp into previously uninhabited areas. The original Quality Assurance Project Plan (QAPP) detailing the eDNA monitoring process, including methodologies and quality controls, was requested from the U.S. Army Engineer Research and Development Center (ERDC) as the USACE assumed eDNA monitoring responsibility from the University of Notre Dame. This modified QAPP will be followed by the U.S. Fish and Wildlife Service (USFWS) offices responsible for field sampling and lab processing of eDNA samples. Fish and Wildlife Conservation offices (FWCO) will handle field sampling and the Whitney Genetics Lab (WGL) at the La Crosse Fish Health Center will process eDNA samples since the USFWS assumed responsibility for monitoring Asian carp in the Chicago Area Waterway System (CAWS) and other water bodies in 2013.

This version of the QAPP has been modified to be a general guide to field and laboratory methods that should be employed during eDNA monitoring programs. Specific sampling plans and schedules for particular water bodies will be developed by regional sampling agencies and their partners, as well as overseeing governing bodies (such as the Asian Carp Regional Coordinating Committee and Great Lakes Fishery Commission). These plans are available online on various agency websites and will not be included in this document.

1.2 General Requirement

USFWS Midwest Region requires a Quality Assurance Project Plan (QAPP) for eDNA monitoring. Full-scale eDNA monitoring commenced in September 2010 by the USACE, and based on consultation with

experts in processing of litigable DNA evidence (which applies to eDNA monitoring), a final, comprehensive QAPP was not in place within that time frame. Instead a provisional QAPP was used during the first year of eDNA monitoring, to be followed later by a finalized version under a different scope of work. The USFWS will continue to maintain and update a QAPP for use in eDNA monitoring programs that allows for inclusion of any beneficial technical or strategic modifications that become apparent from past monitoring events, research conducted by the eDNA calibration research team, or research published in the literature and vetted by the eDNA calibration team or other USFWS genetics laboratories.

1.3 Project History

The University of Notre Dame, Department of Biological Sciences, Center for Aquatic Conservation, prepared a Standard Operating Procedure (SOP) in 2010. The SOP provided details regarding eDNA monitoring protocol and was given to USACE in May 2010 in compliance with Cooperative Ecosystem Study Unit agreement #W912HZ-08-2-0014, modification P00007. On 15 and 16 December 2009, a technical and quality systems audit of the Center for Aquatic Conservation Lodge Laboratory at the University of Notre Dame was conducted by the US Environmental Protection Agency. The laboratory audit report dated 5 February 2010 was provided to USACE in addition to the eDNA monitoring protocol. These documents served as the basis for the QAPP followed by ERDC. Additionally, USACE submitted the eDNA methodology for an Independent External Peer Review (IEPR), which is a requirement to examine decision documents and supporting work products where there are public safety concerns, significant controversy, a high level of complexity, or significant economic, environmental and social effects to the nation. Released fall of 2011, the eDNA IEPR report, conducted by objective panelists with technical expertise in genetics and population ecology, confirmed eDNA sampling and testing methodology is sound for detecting Silver and Bighead carp DNA but cannot indicate the source of Asian carp DNA (information on the size, gender, age and number of individuals present and cannot distinguish between pure Silver or Bighead carp and their hybrids). In 2013, the WGL received the QAPP and made changes so that it would be applicable to the new field sample processing and eDNA processing personnel and their specific locations. It was also modified according to results of the eDNA Calibration Studies (ECALS) and lab validations carried out by the interagency ECALS team. Annual modifications (see section 1.8) to the QAPP will be approved by regional field staff, the USFWS eDNA team, and leadership of USFWS Midwest Region. Changes to sample analysis will undergo peer-review by external experts and validation in specifically designed studies carried out in at least three different laboratories.

1.4 Objective

The objective of this QAPP is to provide detailed procedures for Asian carp eDNA sample collection, sample processing (including filtering, centrifuging, DNA extraction, PCR, biomarker analysis, DNA sequencing), data reporting, and quality control/quality assurance procedures to ensure that data are as technically defensible, consistent, and usable as possible. The specific goals and objectives of sampling plans for particular bodies of water are currently directed by the appropriate governing body. For example, the Chicago Area Waterway sampling plan has been issued by the Asian Carp Regional Coordinating Committee's Monitoring and Response Workgroup in the Monitoring and Response Plan. The Great Lakes, Ohio River, and Upper Mississippi River plans will be or have been issued by USFWS Midwest Region in conjunction with state and other partners.

Use of this QAPP for all aspects of eDNA monitoring for the early detection of Silver and Bighead carp is strongly encouraged if resource agencies would like to compare results to FWS results. Any samples processed that do not follow this protocol cannot be directly compared to FWS monitoring results.

1.5 Project Personnel

The eDNA monitoring project in USFWS Midwest Region has formed an eTeam, with members of the Regional Office, all field stations and the Whitney Genetics Lab. An official document defining roles and responsibilities is attached in Appendix A, and the names and contact numbers should be updated annually.

The eDNA monitoring program of USFWS Midwest Region must have personnel appointed to the following positions, and it is highly recommended for other agencies interested in eDNA monitoring:

Field sampling point of contact for each field station responsible for sampling and field processing. For each sampling trip, specific personnel will differ for each role as listed in the QAPP, but each role will be filled on each sampling trip

- eDNA Project Coordinator
- Field Operations Manager
- Sampling Leader
- Sampling Quality Assurance Specialist
- Sample Processing Leader
- Sample Processing Quality Assurance Specialist
- DNA Processing Leader
- DNA Processing Quality Assurance Specialist
- Data Documentation & Reporting Specialist
- Supporting Agency contacts

The minimal responsibilities of the above positions are detailed below. Specific personnel assigned to the project are listed in Appendix A.

Sampling and Sample Processing roles may NOT be filled by the same person and must each be filled on every sampling trip.

Prior to each trip, the eDNA Program Coordinator and the eDNA Processing Leader need the name and mobile phone number for the field sampling and sample processing leaders. After each trip, a brief summary report (Exhibit 16) covering quality assurance issues and any changes in personnel roles should be provided to the eDNA Program Coordinator.

These roles assume all staff are USFWS Midwest Region Staff who have the minimum requirements and have been trained in the QAPP methods. If other agency personnel are assisting in the field or lab, they must have read and understood the QAPP and have Exhibit 15 and their CV on file with the lead FWS office. When personnel from other agencies or volunteers do not meet the minimum requirements or have equivalent requirements (e.g. state boat operator training), this must be documented on Exhibit 16 as a deviation from the QAPP and a brief explanation provided that explains the situation.

eDNA Project Coordinator: USFWS Midwest Regional Office staff specialist responsible for development, coordination and implementation of the USFWS eDNA monitoring program for Asian carps. Assumes principal responsibilities for initiating, leading, facilitating, integrating, coordinating, and communicating necessary monitoring work and activities using eDNA of the Midwest Region's Fisheries Program through the cooperative conservation community. Provides guidance for implementing and utilizing eDNA activities at the field level. Provides technical leadership to plan, conduct and lead other biologists as well as coordinate activities to identify and coordinate surveillance areas in water bodies for

the early detection of Asian carp eDNA. Ensures the best scientific practices are used during the development and implementation of management plans to monitor, control, and eradicate Asian carp. Implements and coordinates the eDNA collection program; eDNA processing and interpretation of data; collection and dissemination of research information from institutions and research agencies on findings and new developments in eDNA collection and interpretation of data and the development and implementation of Asian carp management plans. Responsible for the overall QAPP and its implementation at the field and lab levels. Responsible for communication between the lab and Regional office. Integration with interagency ECALS team and other relevant entities.

Field Operations Manager: Serve as lead biologist to implement the eDNA monitoring program for the watersheds assigned to their respective field office. Under the supervision of the Project Leader, develops and implements eDNA sampling plans for waters assigned and serves as a point of contact, with their Project Leader, for partners to coordinate all eDNA field activities.

Sampling Leader: Responsible for obtaining water samples for eDNA monitoring and providing those to sample processing team. Responsible for reporting results to Sample Processing and DNA Processing Team Leaders, the eDNA Program Coordinator, as well as other designated USFWS personnel.

Sampling Quality Assurance Specialist: Responsible for knowing all quality assurance/quality control (QA/QC) measures for eDNA sampling efforts. Advises Sampling Leader on any potential QA/QC problems. Reviews procedures, field logs, data collection methodology; ensures that all agencies participating in sampling are conforming to procedures, and documents this after each sampling trip (Exhibit 16). Recommends corrective actions for non-conformities.

Sample Processing Leader: Responsible for filtering/centrifuging water samples for eDNA monitoring and providing those processed samples to eDNA Processing team. Responsible for reporting results to Sampling and DNA Processing Team Leaders, the eDNA Program Coordinator, as well as other designated USFWS personnel.

Sample Processing Quality Assurance Specialist: Responsible for knowing all QA/QC measures for filtering/centrifuging efforts. Advises Sample Processing Leader on any potential QA/QC problems. Reviews procedures, laboratory logs, and documentation for processing; ensures all personnel are conforming to procedures, and documents this after each sampling trip (Exhibit 16). Recommends corrective actions for non-conformities.

DNA Processing Leader: Responsible for processing eDNA samples through DNA extraction, PCR, and sequencing. Responsible for reporting results to eDNA Program Coordinator, as well as other designated USFWS personnel.

DNA Processing Quality Assurance Specialist: Responsible for knowing all QA/QC measures for eDNA processing efforts. Advises eDNA Processing Leader on any potential QA/QC problems. Reviews procedures, laboratory logs, and documentation for DNA processing; ensures all personnel are conforming to procedures. Recommends corrective actions for non-conformities.

Data Documentation & Reporting Specialist: Assists DNA Processing Leader in maintaining laboratory database for eDNA sample processing. Performs data completeness and data verification checks, and ensures that all data are documented completely.

Assigned Project Leaders and Specialists: Others serving on the project may include researchers, technicians, and budgetary personnel. Sampling may employ personnel from other agencies in coordinated efforts. All personnel must meet a minimum standard for training and/or experience before

independently conducting any portion of the eDNA monitoring protocol. Each station's lead eDNA personnel will attend an annual QAPP review training (train the trainer). These lead eDNA staff will then train any other staff assisting with eDNA work. The supporting agency contacts are given in Appendix A. Minimum personnel training requirements are given below.

Personnel Training Requirements

Minimum training and/or experience requirements for the different major components of the eDNA monitoring protocol are detailed below.

Boat Operator:

- Must meet USFWS boat operator requirements as a minimum.

Sampling:

- A BA/BS degree or its equivalent in biology or related field of study, or
- At least 2 years of specialized postsecondary training or an associate degree in applied science or science-related technology, or
- A high school diploma or its equivalent and a minimum of 2 years professional experience in biology-related field.
- First aid and/or boating safety course.
- Minimum 1 year experience in collecting field samples for biological analyses.

Sample Processing:

- A BA/BS degree or its equivalent in biology or related field of study, or
- At least 2 years of specialized postsecondary training or an associate degree in applied science or science-related technology, or
- A high school diploma or its equivalent and a minimum of 2 years professional experience in biology-related field.
- First aid training.
- Facility-specific safety training.
- Minimum one semester college level laboratory experience, plus eDNA-specific training.

DNA Processing:

- A minimum BA/BS degree or its equivalent in biology or related area and successful completion of college course work (graduate or undergraduate level) covering the subject areas of biochemistry, genetics, and molecular biology (molecular genetics, recombinant DNA technology) or other subjects that provide a basic understanding of the foundation of DNA analysis, as well as course work and/or training in PCR amplification as it applies to eDNA analysis.
- A minimum of 6 months of general DNA laboratory experience, including experience with DNA extraction and PCR. Additionally, 2 weeks of training on Asian carp eDNA protocols.
- Successful completion of a qualifying test demonstrating effective execution of eDNA-type assays before beginning independent work on the project.

1.6 Reporting:

- All agencies, need to submit resumes (Curriculum Vitae) for proposed staff to the eDNA Program Coordinator, to be reviewed and approved by the eDNA Program Coordinator. As new personnel are acquired and trained, their resumes must be filed with the eDNA Program Coordinator. Those documents will be kept with the project file. This paperwork should be updated each time the QAPP is updated.

- For each sampling event, a pre-trip summary of the sampling sites, dates, personnel roles, and contact information should be supplied to the eDNA Program Coordinator, other USFWS personnel as needed, and partner agencies as appropriate.
- Specific staff member names conducting the various activities must be documented on all official data sheets (e.g., on the field sampling log).
- Pre-trip communications with eDNA Program Coordinator may be via email or text.
- Upon completion of all sampling events, the trip completion report (Exhibit 16) must be filled out and filed with the eDNA Program Coordinator. This form includes areas to clearly list case numbers, sample numbers, sampling locations, personnel, and ensures that the Sampling and Sample Processing Quality Assurance Leads confirm adherence to the QAPP.
- The lab will file weekly reports with the eDNA Program Coordinator that contain up-to-date information on the progress of samples within each case.
- The lab will update the eDNA Program Coordinator with information regarding presumptive positive samples so that timely handling of final results can be mapped and communicated internally and with other offices and partners as needed.
- The lab will file final reports for each case that contains all of the processing information and final positive and negative results with the eDNA Program Coordinator.
- The eDNA Program Coordinator will track eDNA sampling events and processing in a master case file that will be shared with USFWS personnel and partner agencies.

1.7 Case number assignment and management:

All eDNA field and lab data will be collated and housed in a geo-referenced database maintained at the Regional Office. The database is organized around a unique reference ID for each individual sample, thus a unique identifier is required for each eDNA sample.

- Each sampling event is centered around a specific water body, and will be assigned a case number consisting of a 5-digit integer (00000). Sample ID numbers within cases will be in consecutive numerical order, and will consist of a 3-digit integer (000). Each sample will be identified by the 8-digit number consisting of the case **and** sample ID number, without spaces or punctuation (00000000).
- WGL will create a master case list each season and assign case numbers as needed to each FWCO. FWCOs will assign case numbers to sampling events so that the lab remains blind for sample processing.
- A table of case numbers will be provided by WGL to the eDNA Project Coordinator so that case numbers will never be repeated among sampling years.
- Sampling priority will be finalized by the eDNA Project Coordinator and appropriate FWS and partner personnel.
- Lab processing priority (which may differ from sampling priority) will be finalized by the eDNA Project Coordinator and appropriate USFWS and partner personnel.

1.8 QAPP maintenance and modifications

Early detection of aquatic species by eDNA is a new technique that is simultaneously undergoing extensive development on the research front as it is applied on the ground in monitoring efforts. These

results in rapid advancement of the technique that should be applied to monitoring efforts to not only improve use of the tool in management applications, but also to improve efficiency.

- The USFWS works closely with collaborating agencies such as the USGS and the USACE to keep up with current research so that the eDNA monitoring program can be updated regularly.
- The QAPP will be updated annually to reflect advancements in eDNA research as well as to improve efficiency in field and lab efforts based on lessons learned from the previous year of implementation.
- Annual updates to the QAPP may be implemented by two mechanisms.
 - Changes to field methods and anti-contamination measures by the eTeam. In 2014 USFWS FWCOs, WGL, and the Midwest Regional Office formed an eDNA team (eTeam, see Appendix A) to work on maintaining the QAPP.
 - These changes are suggested by field staff, and reviewed by the eTeam, and upon approval, implemented into the QAPP. In general, these changes are to accommodate a more-widely implemented monitoring program spatially to include a much greater area than the CAWS. It also accommodates implementation by several different FWCO offices, instead of a fairly limited crew used in the CAWS.
 - None of these changes reduce the level or rigorousness of quality control measures so that the QAPP maintains the high level of quality control that was approved by several external reviews.
 - Changes to lab methods as recommended by collaborating research agencies such as the USGS or USACE or lab staff. New techniques and products must be validated through rigorous studies conducted in at least two labs, preferably three labs.
 - Again, these changes incorporate the same level of rigorous quality control as the original QAPP.
- Other agencies that would like to contract with other labs for eDNA monitoring may want to use the QAPP are encouraged to do so. However it is likely that partnering with other labs will lead to procedures that are not covered in the QAPP. In this case, it is up to each agency to decide on their own requirements needed for eDNA sampling and lab processing.
 - The USFWS recommends a minimum of following closely sections 1-4, 6-10 to ensure rigorous quality control and sample integrity.
 - Use of other labs should be carefully reviewed by the contracting agency staff and each agency should ensure that labs are validated and can process samples with at least the same level of quality control and in lab situations that minimize contamination in highly sensitive PCR applications.
 - It is likely that other labs will use assays with different PCR markers and even different PCR techniques such as digital PCR. It is up to the management agency contracting the work to ensure that these assays have been rigorously tested and validated for use in sensitive eDNA monitoring programs. At a minimum, the assay methods should be published or validated in a rigorous, round-robin lab study.
- List of updates to QAPP
 - 2013
 - Section 2.1.5 added guidance for expanding sampling into Great Lakes tributaries.
 - Section 2.1.6 added for eDNA processing trailer maintenance and cleaning.
 - Section 2.4 added guidance for wading and non-motorized sampling procedures.
 - Section 3.3 added detailed procedures for centrifuging samples as an alternative to filtering. Filtering was the only method allowed when objectives were early

detection and surveillance for Asian carp. Centrifugation was allowed in special cases when approved by Region 3 RO staff.

- Section 5.5.5 added extraction procedures for using the Qiagen DNeasy Blood and Tissue kit. All official 2013 monitoring samples were processed with the Qiagen kit. The original Power water kit methods were moved to appendix H in 2015.
 - A blind, round-robin validation study was conducted in three laboratories to ensure the Qiagen kits performed as well as or better than the Power Water kits (Amberg, J.J., S.G. McCalla, E. Monroe, R. Lance, K. Baerwaldt, and M.P. Gaikowski. 2015. Improving Efficiency and Reliability of Environmental DNA Analysis for Silver Carp. Accepted. Journal of Great Lakes Research. doi:10.1016/j.jglr.2015.02.009.).
- All exhibits were updated with customization for Whitney Genetics Lab
- Appendices A-G were added or updated to function within the US Fish and Wildlife Service.
- 2014
 - Section 5.6, 5.7 and 5.8 were updated with new qPCR markers, new methods for determining presumptive positive and confirmed positive results, and protocols for data reporting and management. Markers published in: Farrington, H.L., C.E. Edwards, X. Guan, M.R. Carr, and R.F. Lance. 2015. Mitochondrial Genome Sequencing and Development of Genetic Markers for the Detection of DNA of Invasive Bighead and Silver Carp (*Hypophthalmichthys nobilis* and *H. molitrix*) in Environmental Water Samples from the United States. PLoS ONE 10(2): e0117803. doi: 10.1371/journal.pone.0117803. A blind, round-robin validation study was conducted in three laboratories to document marker performance. Final report and publication to follow. All 2014 samples were screened with these new markers.
 - Original sections regarding amplification with old cPCR markers, and methods for determining results were moved to appendix G.
- 2015
 - Section 1.5 had an additional role added for field stations, Field Operations Manager.
 - Section 3.3 Centrifugation was approved for use in all eDNA applications based on results of WGL study, Validation of centrifugation vs. filtering for eDNA sample collection (Appendix K). Report filed with Regional Office. Filtering methods were moved to appendix H. References to bottles in other sections were either moved to Appendix H or changed to reflect centrifuging materials and methods.
 - Section 5.5.6 IBI Scientific gMAX Kit Procedure for centrifuged samples was validated (Appendix I) and added as an alternative to the Qiagen DNeasy Blood and Tissue kit for sample DNA extraction.
 - Section 5.6-8 were enhanced with the addition of methods using an internal positive control to assess and measure inhibition of PCRs.
 - Section 5.6.5 added details regarding quantitative PCR standard control materials and methods.

1.9 eDNA Security Plan(s)

- A detailed eDNA security plan for the Midwest Fisheries Center has been developed due to the co-location of the La Crosse FWCO and the WGL. Staff in the FWCO often work in Asian carp contaminated waters and conduct field work where Asian Carp are directly handled. Thus, this plan includes detailed procedures for decontaminating field equipment as well as boats, trailers,

and trucks used for all field work including eDNA sample collection. It is a stand-alone document included as Appendix G.

- A DNA security plan for each field or lab station involved in eDNA sampling or processing should be developed using the Midwest Fisheries Center eDNA security plan as a model, but adapted for each station's unique situation. This plan should be kept on file at the regional office. The documents should be signed by all personnel at the field or lab station and approved by the eDNA Project Coordinator(s).

SECTION 2 SAMPLE COLLECTION

Prior to any field sampling work, all field employees must review this QAPP and acknowledge the procedures and processes to be followed for every sample and every event. Field employees will acknowledge their understanding and intent to comply by signing the certification form given as Exhibit 15. Field employees will also review the sampling safety plan (separate station-specific document) and participate in a safety briefing.

Prior to any sample processing or analysis work, all laboratory employees must review this QAPP and acknowledge the procedures and processes to be followed for every sample and every event. Laboratory employees will acknowledge their understanding and intent to comply by signing the certification form given as Exhibit 15. Laboratory employees will also review the laboratory safety plan (separate station-specific document) and participate in a safety briefing.

2.1 Pre-Trip Planning and Site Selection

Refer to the internet for annual monitoring plans issued by the agency responsible for each particular body of water. For example, the CAWS monitoring plan can be found at www.asiancarp.us.

2.1.1 Purpose

Accurate planning of a general collection site is necessary to effectively manage the time of crews collecting samples, as well as to ensure complete and correct sampling procedures are used.

2.1.2 Pre-trip Planning Procedure

Refer to the annual monitoring plans to properly plan for sampling. The sampling agency should use interactive aerial imagery software (i.e., Google Earth) to scope out reaches to be sampled, placement of samples, and unique features that should be targeted during sampling.

- (1) Aerial maps should be detailed enough to show unique features (e.g., barge slips, factory, bridge pilings etc.) that can be identified in the field and used as markers for location when sampling. The recommended minimum scale is 1':500', if that is not available, use the best scale possible.
- (2) Aerial maps should be marked with sample locations and should ensure spatial coverage and overall representativeness of the sample area.
- (3) Target specific areas (backwaters, island side channels, pooled areas, below and around structures, confluence of tributaries) as well as integrating transect plots in the sampling plan.
- (4) Print map(s) with detailed sample plan.
 - Locate access points for boat launch and acquire permission to use if necessary. If sampling around locks, or if sampling will require lockage, notify the Lockmaster at least 1 day before sampling.
- (5) Coordinate sample plan with sampling crew, eDNA Program Coordinator, or any partner agency.
 - Sampling crew should comprise three people at a minimum: one boat operator, one lead sampler, and one sampling assistant.
 - Processing crews should consist of two people. All crew members must have their resume (CV) on file with the USFWS (section 1.6), prior to the sampling event.

- All participants must have read this QAPP and must have a signed certification statement (Exhibit 15) on file with the USFWS, prior to the sampling event. All participants, including partner agency employees and any volunteers, involved in the sampling must meet the minimum qualifications given for their role in Section 1.3 of this document.
 - A field equipment checklist and datasheets (Exhibits 1&2) should be printed prior to each sampling trip on Rite-in-the-Rain® paper or other waterproof paper. Datasheets may be printed on front and back.
 - Check river stage and weather forecast.
 - File pre-trip plan with sampling sites, launches, personnel in designated QAPP roles, and field contact information with eDNA Project Coordinator and other appropriate FWS and partner contacts. This can be done via email or text.
 - Prior to each trip, the eDNA Program Coordinator and the eDNA Processing Leader need the name and mobile phone number for the field sampling and sample processing leaders.
- (6) In the event of a significant rainfall event (more than 1.5 inches in a 24-hr period), the Field Operations Manager must assess the situation and determine if sampling should be pursued. The first consideration is crew safety. Once it is determined that sampling can occur safely, sampling may be pursued. However, because effects of high rain fall events will differ among systems, it is important for experienced field staff to weigh in on the discussions to avoid unnecessary travel if the high water would prevent sampling. If it is deemed safe for sampling to occur, the sampling crew and eDNA Program Coordinator need to discuss the effects of high water on the ability to detect eDNA. In some cases, the rising limb of a hydrograph may stimulate spawning of the target species, thus it may be advantageous to sample. In other cases, increased run-off could dilute the signal, and thus decrease the chances of detecting target DNA. This call must be made on a case-by-case basis. In the CAWS, sampling should be avoided within 3 days of a combined sewer overflow (CSO) event, due to adverse health effects from raw sewage in the CAWS. Weather data and river stage for the area to be sampled can be checked at: <http://waterdata.usgs.gov/nwis>. The occurrence of a CSO event can be verified by contacting the FWCO contact for that particular sampling event listed in Appendix A
- (7) In general sampling should be avoided in water that has obvious disturbance from the sampling vessel that increases the turbidity and suspended sediments in the water. If possible, those areas should be avoided for sampling and care should be taken to prevent sediment disturbances as much as possible. This is because eDNA can be stored in sediments for long time periods, which confounds early detection monitoring goals.

2.1.3 Field equipment list

(procedures are in section 2.2; to be provided by sampling office/agency)

- (1) Waterbody-appropriate vessel. If possible, vessel and associated equipment should be dedicated to eDNA collections to minimize risk of DNA contamination of samples from other sources. If boat dedication is not possible, or eDNA collection occurred in known carp positive waters, procedures for decontaminating boats and equipment are included in Section 2.2.4. These procedures will also work for converting a previous carp sampling boat to a dedicated eDNA sample collection vessel.
- a. eDNA-only dedicated personal flotation devices (PFD) for each crew member, using the type of devices listed in the safety plan. Minimum PFD requirements are Type I within the Safety Zone near the existing electric barrier (on the Chicago Sanitary and Ship Canal) or Type II for other areas. NOTE: In some cases, eDNA sampling may occur in Asian carp-infested waters,

avoid using clean eDNA dedicated field gear for these trips to prevent contamination for later use in non-infested waters.

- b. It may be necessary to sample eDNA in carp-infested waters. In this case, crews should carefully consider which personal protective gear should be used. It may be prudent to avoid exposing clean eDNA gear to carp-infested waters and instead other “relatively” clean gear should be used instead. If there is uncertainty or questions, call the eDNA Program Coordinator.
- (2) If centrifuging: enough 100-qt coolers capable of holding 5 50-ml centrifuge tubes per planned field sample. See Appendix D for tube handling plan.
 - (3) If centrifuging: Sterile, chemical-free polypropylene 50-ml centrifuge tubes, that are rated to withstand 6000 x g, labeled by sampling agency. Tubes will not be re-used, but WGL will return shipping containers to be re-used by sampling agencies if requested.
 - (4) 3-gallon sprayer (low pressure hand sprayer for spraying down boats in the field), hot water pressure sprayer (for decontaminating boats where water and electrical hookups are available) or cold water high pressure sprayer with low pressure detergent injection (may be portable for use in the field). Car washing brushes or mops may be used in lieu of low pressure hand sprayer for chemical decontaminant applications.
 - (5) Habitat measurement equipment (Global Positioning System [GPS], Digital Depth Sounder).
 - (6) Field Collection Summary sheets (Exhibit 1) and Field Datasheets (Exhibit 2).
 - (7) Chain-of-custody form (Exhibit 3).
 - (8) Sharpie® permanent marker in black.
 - (9) Powderless nitrile or latex gloves.
 - (10) Ice for coolers with samples.
 - (11) Drinking water for crew.
 - (12) Safety plan – the USFWS plan represents minimum requirements; agency-specific alternative plans are allowable as long as all hazards are addressed and minimum requirements are met.
 - (13) Bleach (any commercially available brand or strength), detergent for use with cold water pressure sprayer, or Virkon Aquatic: decontamination chemicals will only decontaminate clean surfaces, thus clean any solid surface well to completely remove any film or biological build up before application of decontaminating agents. If using cold water pressure sprayer to apply detergent in lieu of hot water pressure sprayer or bleach/Virkon, surfaces must be pre-cleaned before application of the detergent (3-5 min contact time) with a 10-second high pressure rinse.
 - a. Bleach may be mixed in two strengths: 10% solutions require 10-minute contact time but 20% solutions require 5-10 second contact time.
 - b. The oxidative feature of bleach deteriorates with exposure to organic material and over time, so bleach solutions must be made fresh daily in order to decontaminate DNA.
 - c. Virkon must be applied in a 2% solution for DNA decontamination or reduction methods. Equipment must be fully submersed in a 2% Virkon solution for 30 minutes for complete decontamination. A 2% Virkon spray or swab application for a 10-minute contact will reduce DNA to negligible levels. Virkon mixed in solution is good for one week.
 - (14) Water sources: water used to mix bleach or Virkon solutions can be any source of potable water, it does not have to be DI water. Tap water may be used to wipe down surfaces or to rinse equipment

such as filter funnels after bleach soak. DI water is only required when the water used will come into contact with a filter that will be processed in the lab.

(15) Garbage bags

2.1.4 Lotic System Site Selection Procedure (in the field)

Specific eDNA monitoring plans that explicitly explain where and how many eDNA samples will be collected for particular water bodies will be created each year by the sampling office or agency in coordination with state partners and other agencies. These plans will contain specific sampling locations, numbers of samples, temporal and spatial sampling details. These plans are outside the scope of this document, however, there are some critical considerations that should be followed.

- (1) In lotic systems, sampling should occur in a downstream to upstream direction to minimize the potential for surface water disturbance caused by the vessels wake within the sample reach. The only exception where sampling may occur in an upstream to downstream direction would be if the nearest boat launch is upstream of the reach to be sampled or if it is not feasible to sample a system in an upstream direction (for example by kayak). Sample direction should be noted on the Field Collection Summary datasheet (Exhibit 1).
- (2) Samples should be collected in two ways – transect and targeted sampling.
 - (a) Transect: Location of transects will be determined by the USFWS prior to the start of a sampling event. The first transect will be set across the downstream end of the reach to be sampled with subsequent transects set 500 m apart heading upstream (see exception to protocol above (1)). Transects will run perpendicular to flow, and three samples will be collected along each transect using the following scheme: one collected near the left descending bank (LDB), one in mid-channel (MC), and one near the right descending bank (RDB). Where samples are collected should be recorded in the “Habitat” column of the Sampling datasheet (Exhibit 2). Samples should be collected on the upstream side of the boat or off the bow.
 - When collecting samples near the bank, be observant of wake-disturbed surfaces. To compensate for the wake created by a passing boat, samples may need to be collected 2–3 ft off the bank to obtain displaced surface film.
 - (b) Targeted sampling is collecting samples in the most probable places of eDNA accumulation, such as (but not limited to):
 - Backwater areas
 - Island side channels
 - Confluences of tributary waters
 - Effluent areas
 - Eddies or pooled areas
 - Near structures that create slack-water (e.g., sunken barges)
 - Bays
 - Below Lock and Dam structures
 - Wind driven scumlines
 - Other areas where organic material has accumulated on the water surface

Avoid taking samples from directly in the middle of such areas and target the perimeter to lessen the likelihood of overwhelming the sample filter. Avoid sampling under or

downstream of bird rookeries or storm sewer outflows since these have been shown to be vectors of eDNA from sources other than a live fish.

2.1.5 Lentic System Site Selection Procedure (in the field)

- (1) Lake and bay samples will be selected using a blocked random sampling design including targeted collections within each block. The sampling strategy will incorporate potential focus areas based on introduction vector probability, attraction (food and habitat) and proximity to the CAWS.
- (2) Once focus areas have been identified and boundaries defined, each hotspot will be divided into 8 equal sized blocks. Block size will be dependent on the hotspot boundaries, concentrating around highest productivity area. These will then be numbered and 4 of the 8 randomly chosen for sampling.
- (3) When using the filtering method, 25 water samples (2L) will be collected (100 total) for each block. Using the centrifuge method 125 water samples (50 ml centrifuge tubes) will be collected for each block. Water collection will follow a probabilistic sampling design targeting areas throughout the entire block where eDNA will accumulate.
- (4) Targeted areas include backwaters, island side channels, pooled areas, below and around structures, confluences of tributaries as well as any areas where floating debris accumulates. Juvenile and age-0 Asian carp prefer shallow, productive areas like those adjacent to and within wetlands. Areas to be considered for sample collection include those with locally high productivity, such as sewage system effluents.

2.1.6 eDNA Trailer Preparation and Field Considerations

Routine trailer maintenance is covered in Appendix F. Prior to departure the trailer should be cleaned, decontaminated and then stocked with all supplies needed for field sampling and lab processing.

- (1) Decontaminate surfaces and floors with a 10% bleach solution, allow it to soak for 10 minutes, then rinse to prevent build-up of bleach salts.
- (2) Ensure all supplies needed for the field and sample processing are stocked and secure for travel.
- (3) UV lights can be used for 30 minutes at the beginning of each day.

Upon arrival at the sample processing site, select an area to park the trailer that has limited risk for contamination from other activities on-going in the area. For example, avoid parking next to boat washing stations where commercial carp fishing boats will be sprayed clean.

2.2 Equipment Preparation

2.2.1 Purpose

In order to perform laboratory molecular analyses to detect eDNA, vessels and equipment must be decontaminated in accordance with the following protocols to eliminate introduction of outside DNA sources in the sampling regime. Bleach will only decontaminate clean surfaces, so be sure to clean any solid surface well to completely remove any film or biological build up so the bleach can destroy any DNA.

Cautions: Precautions should be made to avoid direct skin contact with bleach; bleach solution may also stain clothing or other materials. Be aware of pollutants in the aquatic environment and related health hazards.

Water used for bleach solutions may be any source of clean, potable water. Water used to rinse equipment, such as the filtering funnels or sample container interior that comes into contact with the actual eDNA sample should be DI water to avoid introducing any inhibitors to the samples.

2.2.2 Equipment Procedure for Coolers

- (1) A 10% bleach solution with water will be prepared in a 3-gallon low-pressure sprayer that is dedicated to the project. The bleach solution must be prepared immediately prior to use, and each time decontamination activities will be occurring.
- (2) Remove mud and other biological residues from surfaces by rinsing and scrubbing. Equipment surfaces must be free of debris and other material before decontaminating.
- (3) Sample transport coolers will be decontaminated with freshly made 10% bleach solution in the low pressure sprayer. Use the low-pressure sprayer to thoroughly cover the inside and outside surfaces. Allow 10 min of contact time before rinsing with water. Coolers may be left to air dry, or dried using clean paper towels while wearing clean gloves.
- (4) Purchase sterile, chemical-free disposable 50-ml polypropylene tubes with maximum RCF of at least 6,000 x g. Even sterile tubes can still have traces of the chemical used to free the plastic tubes from the metal forms during production. Some manufacturers sell sterile tubes that do not have this residual chemical in them, and these should be used to avoid introducing PCR-inhibitors from the sample tube.
- (5) Sample labels can be printed by the sampling agency. Sample containers will be labeled with a unique barcode ID or agency generated code (Section 1.7 for case and sample numbering) that does not indicate location (to allow blind processing). Labels will be printed on Rite-N-Rain® or some type of waterproof labels and affixed to the outside of the sample tubes.
- (6) Once tubes have been labeled, they will be placed in the sterilized sample coolers in numerical order. Sample containers will be stored in the sterilized coolers until use, and will be transported only in the coolers. Although the sample ID number of the samples is not relevant except for identification purposes, collecting in consecutive order will aid in determining where samples were taken in case of a recording error.
- (7) A minimum of 10% of the number of samples collected should be field blanks. For offices working with the WGL, all field blanks must be filled by WGL. For other agencies, blanks may be filled with any city-provided tap water (If water source is a well or you are unsure of the source, use distilled or deionized water). Note, if the sampling design for your particular body of water requires a specific sample size in order to meet a precise detection probability, then containers for control samples to meet the 10% will be added to the total number of sample containers dictated by your sampling plan.

2.2.3 Boat and Field Equipment

This section applies to all motorized or hand-powered boats, paddles, and any associated field equipment used to collect eDNA.

- (1) A set of field equipment used by staff collecting eDNA such as personal flotation devices, rain gear, hats, sunglasses, etc., should be dedicated for eDNA field work only, to avoid contamination risks. This is especially important if the same staff are involved in field work in rivers with well-

established populations of Asian Carp, or if staff conduct field work where they come into direct contact with Asian Carp. This dedicated gear should be stored and transported in designated containers (such as totes) so that contamination from trucks or boats contaminated with Carp DNA is avoided. After the trip, gear and transport containers should be decontaminated according to section 2.2.4.

- (2) It is preferable to have designated vessels, trailers, and trucks set aside for eDNA work if possible. Even if there is designated equipment, because eDNA can be moved among sites on vessels, boats and equipment must be decontaminated prior to sampling, and between sampling sites. If complete decontamination cannot be performed between cases while in the field, choose the most preferred method of DNA reduction available in between cases (Appendix E). Upon return to the field station office, a complete DNA contamination for all associated equipment must be performed before returning to the field.

2.2.4 Boat and Equipment Decontamination Procedure

Follow steps 1-12 for decontamination or reduction of DNA on equipment surfaces before and between collections of eDNA samples from any site. Refer to Appendix E for a list of recommended decontaminants. Use personal protective equipment (PPE) and read MSDS before use with any product. Follow equipment safety instructions and read equipment manual before using an industrial hot water pressure washer:

- (1) Put on appropriate PPE. Decontamination PPE should be designated, stored separately and decontaminated after each use to prevent reintroduction of DNA to equipment, and transfer of splashed DNA around your facility.
- (2) Remove equipment from boats, trucks, etc. and lay them out separately so that all surfaces of equipment will be exposed to treatment. Treat one side and then flip if necessary.
- (3) Remove any environmental debris such as plant material, mud, or fish slime with brushes or gloves. If possible, perform this step at the sampling site to leave as much DNA material behind as possible. Buckets and brushes or a water pump can help rinse boat surfaces of blood and slime before leaving the water.
- (4) Rinse surfaces with the highest pressure water available for the location. Surfaces must be clean for decontaminant/DNA reducers to work.

Choose a decontamination method that is appropriate for the equipment, location and services available (Proceed to steps 5, 6, 7 or 8). If equipment has been exposed to Asian carp DNA use one high pressure sprayer method ***in conjunction*** with one chemical method (steps 5 or 6 ***and*** 7 or 8) for decontamination:

- (5) Use an industrial hot water pressure washer set at 212 F to decontaminate appropriate surfaces. Minimum exposure time for decontamination is 10 seconds.
- (6) Apply detergent at low pressure to saturate surfaces with an industrial cold water pressure sprayer with detergent injector. Wait 3 to 5 minutes, then rinse at high pressure for 10 seconds.
- (7) Mix a 10% solution of household bleach (5-8% sodium hypochlorite before mixing) in tap water in a hand pressure sprayer (low pressure saturation) or large tub (immersion bath). Spray or swab to saturate at low pressure or immerse all appropriate surfaces. Exposure time for complete decontamination is 10 minutes. Rinse with fresh water and allow surfaces to dry. Mixed solution good for one day.

- a. As an alternative to step 6 for smaller items, prepare a 20% bleach solution in a small tub and completely immerse items for 10 seconds. Rinse and allow surfaces to dry.
- (8) Immerse smaller equipment in a 2% Virkon bath for 30 minutes. Metals should be immersed no longer than 10 minutes. For larger equipment, prepare a 2% Virkon solution in a low-pressure sprayer or swab and saturate surfaces. Minimum exposure time is 10 minutes. Rinse with fresh water and allow surfaces to dry. Caution: Do not aerosolize this product. Use at the largest droplet setting to avoid respiratory exposure. Mixed solution good for one week.

In absence of availability of methods for decontamination previously mentioned in this document, rinse equipment with copious amounts of water at the highest pressure available and allow to dry. Exposure to the sun or UV radiation and heat will help reduce residual DNA. Follow complete decontamination procedures beginning at step 1 upon return to field station office or at first availability.

Upon completion of methods above, follow steps 10-12 to complete eDNA clean-up:

- (9) Use DNA Away and paper towels to decontaminate pens, hats, notebook surfaces, electronic equipment surfaces, truck interior and other non-saturable equipment.
- (10) Contain any equipment that was not treated in bags or totes for later decontamination.
- (11) Wash hands, launder or change soiled clothing.
- (12) Remove PPE and decontaminate before storing separately for next use.

2.3 Motorized Sample Collection Procedure

2.3.1 Purpose

In order to perform laboratory molecular analyses to detect eDNA, samples must first be collected from the appropriate aquatic environment in accordance with the following protocols. Each morning prior to sampling, collection staff and filtering staff prior to departing will have a morning briefing that will discuss where and how the sampling is occurring. At this time a float plan and GAR model will be filed with the boat operator and collection crew and processing lead. Once the meeting is complete the processing lead will email those documents to the lead agency's main office project leader and any other necessary personnel.

Cautions: Lifejackets must be worn at all times in transport vessels (boats). Additionally, disposable powder-free latex or nitrile gloves must be worn when collecting water samples and measuring water depth and temperature. Be aware of pollutants in the aquatic environment and related health hazards. Field crews should have separate and designated field gear and outerwear that is for eDNA sampling only. This gear should be stored separately from other field gear that may come in contact with Asian carp biological material. Gear should be transported in a clean eDNA gear box so that it is not contaminated in vehicles, boats, or trailers. Follow Boat and Equipment Decontamination Procedures (above section 2.2.3) between sampling sites.

Gear (such as PFDs and hats) should be decontaminated between sampling events according to section 2.2.3. However, if any gear is compromised during sampling (accidentally falling in, or a spill, etc.) and staff feel that it may contribute to contamination of the samples, the gear should be decontaminated as soon as possible at the end of the work day, or replaced with new gear as soon as possible.

2.3.2 Water Collection Procedure

- (1) Prior to launch, crew members will have reviewed this QAPP, will have signed the QAPP certification form (Exhibit 15), and will understand their assigned roles in the sample collection

procedure. All sampler identification information and other field data will be recorded on the Field Collection Summary (Exhibit 1).

- (2) The transport vessel will be launched from an appropriate area that allows access to the reaches to be sampled.
- (3) Sampling will commence at the first transect located at the downstream end of the reach to be sampled and will proceed in an upstream direction. The only exception to this protocol is when the boat launch is located upstream of the sampling reach. Then sampling will commence at the first transect located at the upstream end of the reach to be sampled and will proceed in an downstream direction. The direction traveled for sampling should be recorded on the Field Collection Summary (Exhibit 1).
- (4) It is imperative to avoid disturbing sediments, and avoid collecting samples where the sediments have been stirred up. If sediments are accidentally disturbed by the boat motor, it is required that the driver, re-position the boat in a new area without disturbing sediments. The data recorder must make a note on the data sheet and record actual GPS coordinates where the sample was taken. (Sediments add to the inhibition load of the sample and could increase the rate of false negative results for both filtered or centrifuged samples).
- (5) When arriving at a sample location (within either a transect or targeted area), the lead sampler and sampling assistant will put on new gloves (powderless latex or nitrile). **REMINDER – Gloves must be changed before each new transect is taken to prevent cross contamination. The same gloves may be worn when collecting blank samples in tandem with a regular sample in a transect.**
- (6) Going in consecutive numerical order based on the tube labels, the lead sampler will remove a labeled sample tube from the sample cooler.
- (7) Just prior to collecting the sample, the lead sampler will unscrew and remove the lid(s) from the sample containers. Do not under any circumstances touch the interior of a sample container, even with a clean glove. Lids should be held in hand and kept clean, or placed in a container designated for holding lids while water is collected. To remove lids from holding container, dump them into a clean gloved hand, do not reach into the container to remove the lids.
- (8) The lead sampler will then reach over the upstream side or the bow of the transport vessel with the sample container and fill the tube by skimming the surface of the field water. The sample container must not be submerged or dipped beyond the upper 2 inches of the surface water for sample collection, since the intent of the sampling is to collect floating organic matter that is on the water surface. Avoid collecting large organic debris such as twigs, leaves, seeds, etc., because they cause problems in extraction. A small amount of duckweed is fine. To avoid contamination, the individual collecting the sample should avoid touching any other surfaces with the clean gloves (i.e. the gunwhale) and should only handle the sample container and cap.

Note: Centrifuge samples for early detection and monitoring are comprised of 5 replicate 50-mL tubes, which may be collected in two ways: 1) to minimize variation among offices, a sampling device may be use to collect all 5 tubes at once, as long as there is a clean place to store five caps while sampling is occurring. 2) to collect samples across a larger accumulation zone, tubes may be collected one at a time across a larger sample area within the accumulation area or along a transect,

or spaced around a block, to increase detection probability. This option should be covered in the specific site plan, where specific guidance on the methods should be explicit for field crews.

Centrifuge samples may also be collected in already carp-infested waters to detect or confirm spawning events, or to find areas where carp congregate to be used in control efforts. In these applications, samples are a single 50-ml tube.

- (9) Once the sample container is filled, the lead sampler will screw the lid back on until it is tight. The closed container will then be returned to the sample cooler from which it was removed. Tubes may be filled all the way, there is no reason to measure water, and as long as all tubes are filled the same, they will be safe to use in the centrifuge.
- (10) While the lead sampler is collecting the water sample, the sampling assistant will take and record habitat measurements: water temperature, depth, GPS coordinates in Decimal Degrees, time of sample, location (e.g., left-bank descending (LBD), center, right-bank descending (RBD), and record the information on the datasheet next to the appropriate sample ID. Be sure to save the GPS coordinates with the way-point feature of your device and to note the waypoint ID on the field datasheet.
- (11) If the lead sampler pulls a field blank (water filled prior to trip) from the cooler, the sampler will unscrew the lid and remove to expose the container contents to the atmosphere for 5 sec, reseal the container, fully submerge the container in the field water, and return the container to the sample cooler from which it was removed. The lead sampler should relay to sampling assistant responsible for data recording that the sample was a blank, so that it can be recorded on the data sheet next to the appropriate ID. **BLANKS ARE TAKEN IN TANDEM WITH THE NEXT ACTUAL SAMPLE AND DO NOT REPLACE A SAMPLE IN THAT LOCATION.** If a blank has been pulled, the boat will remain at the same location and an actual sample will be taken.
- (12) Steps 1 through 10 will be repeated at each sampling location until sampling has been completed for the targeted reach.
- (13) Once a cooler is full, add ice to completely cover all containers. Replace ice as it melts, removing excess water only as needed, since ice water will provide better cooling than ice alone.
- (14) Chain-of-custody (COC) forms (Exhibit 3) will be completed for every sample and every cooler. All samples, including blanks, will be logged onto COC forms. The forms will be collected and signed whenever the coolers are transferred between parties. If you must split samples into different configurations than listed on the original COC, make an entry for those samples on the original COC and create a new COC for any new transfer or shipping containers. Be sure that each container has its own COC that has records for exactly and only the samples contained within.

2.4 Wading and Non-motorized Sample Collection Procedure

2.4.1 Purpose

Collection of water samples for eDNA analysis may be conducted in areas not accessible by motorized watercraft and alternative means must be employed. In order to provide accurate and creditable eDNA results, watercraft and equipment must be decontaminated in accordance following section 2.2.3 protocols to eliminate introduction of outside DNA.

Cautions: Precautions should be made to avoid direct skin contact with bleach solution which may also stain clothing or other materials. Be aware of pollutants in the aquatic environment and related health hazards. When canoeing or kayaking two people must be together either in separate kayaks or in one canoe with PFD's worn at all times and a float plan and GAR model on file with sample lead, processing lead, sample quality lead and processing quality lead and sampling agency's main office. If wading PFD's must be worn.

2.4.2 Wading Water Collection Procedure

- (1) Collection of water samples while wading should commence at the most downstream accessible sampling site and proceed upstream. Carefully approach each sampling site slowly to avoid disrupting sediments and accumulation areas. When taking the sample the collector's position should always be down current of the targeted area.
- (2) When there is no access to the downstream most site except from an upstream location field crew may enter at that point and proceed downstream carefully. Sampling will commence at the downstream most site of the reach to be sampled and proceed upstream. The entire sampling route, including direction, should be recorded on the Field Collection Summary (Exhibit 1). When traveling downstream stay out of the water as much as possible and avoid disturbing any areas of accumulation or sampling sites.
- (3) The sample collector will put on clean gloves, remove the first container from the cooler and wade to an area of accumulation to collect the first sample. After the sample is taken, the collector will return to shore and replace the sealed container to the cooler. Do not under any circumstances touch the interior of a sample container, even with a clean glove. If you cannot grasp the container with one hand, use both hands to hold the container. Since the lid should not be set down, either hand the lid to the sampling assistant or hold the lid with the inside toward the container along side the container as you collect the sample, keeping the lid out of the water.
- (4) When approaching an accumulation area moving downstream make a "J" like approach to disturb the water and sediment as little as possible. If approaching an accumulation area moving up stream make an "L" like approach to not disturb sediment along the bank.
- (5) Change gloves and remove the next sample number going in consecutive order and proceed to the next accumulation area repeating steps 1 and 2.
- (6) If sampling in a remote location a backpack container may be used. The backpack should be either a hard plastic pack/trapper's basket or a frame pack with a hard plastic storage container attached. Any backpack containers used must be able to withstand the bleach decontamination protocols and not absorb/retain water. Clean sampling container should be placed in a large plastic bag (i.e., heavy duty garbage bag) and closed prior to loading into the backpack. Another plastic bag placed in the backpack will be for full water samples. The person wearing the back pack will serve as the data recorder if a third person is not available. The collector will put on new gloves prior to opening and removing a sample container from the clean bag. Ensure the clean bag is sealed after removing a container. After collection, place the container in the bag designated for water samples, seal the bag, and remove contaminated gloves. The box of clean gloves should be sealed in a plastic bag/container between uses. Place used gloves in a separate waste bag. Place water samples on ice as soon as possible and within two hours or less of collection.

Note: Centrifuge samples are comprised of 5 replicate 50-mL tubes, which may be collected in two ways: 1) to minimize variation among offices, a sampling device may be use to collect all 5 tubes at once, as long as there is a clean place to store five caps while sampling is occurring. 2) to collect

samples across a larger accumulation zone, tubes may be collected one at a time across a larger sample area within the accumulation area or along a transect, or spaced around a block, to increase detection probability. This option should be covered in the specific site plan, where specific guidance on the methods should be explicit for field crews.

2.4.3 Non-motorized Water Collection Procedure

- (1) Kayaking/Canoeing will commence at the most upstream site (collecting samples in an upstream to downstream fashion). As you are moving downriver, try to maintain a reasonable distance from the shoreline to reduce wave action to the shoreline and accumulation areas.
- (2) Clean sampling containers (up to seven) can be placed either loosely within the boat or in a plastic trash bag depending on type and design of craft. Sample numbers of containers should be in consecutive order and collected in order.
- (3) When approaching an accumulation area moving downstream kayak #1 will make a “J” like approach not to disturb the water and sediment as little as possible. After the sample is collected and kayak #1 has moved from the collection spot kayak #2 will move into the spot to record depth, water temperature and GPS coordinates. Do not under any circumstances touch the interior of a sample container, even with a clean glove. If you cannot grasp the container with one hand, use both hands to hold the container. Since the lid should not be set down, either hand the lid to the sampling assistant or hold the lid with the inside toward the container along side the container as you collect the sample, keeping the lid out of the water.
- (4) After 5-7 containers have been collected kayak #1 will switch roles with Kayak #2 (i.e., kayak #2 is the collector and kayak #1 is the data recorder). The eDNA trailer or a filter staff member will meet the kayakers at a location downstream that is accessible to place collected water samples into a cooler with ice.
- (5) At this time the kayakers will take the last of the containers in the cooler and continue collecting within the collection reach repeating steps four and five as needed until all locations are sampled.
- (6) If sampling location is in slow or no current areas (e.g., impoundments, shallow channels, etc.) sampling collection protocols should follow the lentic procedures in section 2.4.2. Craft may proceed upstream and also should collect from downwind to upwind if possible and approach all accumulation sites with minimal to no disturbance.

SECTION 3 SAMPLE PROCESSING (FILTERING or CENTRIFUGING)

3.1 Purpose

In order to isolate eDNA from water samples collected in the field, particulate matter must be concentrated. It can be filtered from the sample using a vacuum filtration system, or concentrated by centrifugation. As of March 2015, centrifuging will be used by the USFWS. Filtering methods have been moved to appendix H.

Centrifugation of water samples collects matter at the bottom of the tubes, which can be collected on sterile cotton swabs and eDNA can be extracted from the swab. Validation of this method has shown that a maximum of five tubes can be swabbed with a single swab.

Cautions: Wear powder-free latex or nitrile gloves when handling samples (a glove change is required for each sample). Be careful to avoid unintentional punctures of gloves when using forceps. Punctured gloves must be changed immediately. Be careful not to touch commonly used items in the laboratory when wearing sample gloves (i.e., writing utensils, stationary lab equipment). If in doubt, change your gloves!

3.2 Centrifuging Procedure

Water samples collected in the field need to be centrifuged within 12–16 hours after the last field sample is collected.

Equipment needed:

- Sterile, chemical-free centrifuge tubes (Midwest Scientific #TP91050) made of polypropylene that can withstand 6000 xg with caps and labels (recommended Avery laser white weatherproof address labels #5520).
- Paper towels
- 95% ethanol or 70% isopropyl alcohol (mix prior to trip with purchased molecular grade water)
- A reusable bottle-top re-pipettor for dispensing alcohol
- Black permanent markers (e.g., Sharpie®)
- Powderless latex or nitrile gloves
- Refrigerated centrifuge(s) with rotors and adaptors for 50-ml tubes (Fisher item # listed for: Sorvall Legend XTR centrifuge; rotor GS25F7087G item #75-033-607; 750 ml round bucket GS25F7087G item #75-003-608; 50-ml tube adaptors item #75-003-638)
- Bleach
- 10% bleach bath for decontaminating plastic centrifuge tube adaptors *Bleach destroys DNA, so take care to avoid contaminating samples with dripping bleach.
- 20% bleach bath for decontaminating centrifuge tubes before processing *Bleach destroys DNA, so take care to avoid contaminating samples with dripping bleach.
- Rinse bath of water to rinse containers before processing
- Dedicated lab equipment cleaning sink
- Waste water disposal location such as nonspecified-use sink
- Clean bench paper or clean paper towels
- Dedicated water bottles: one for DI water; one for bleach solution
- Washbin for centrifuge adaptors and buckets, such as a dedicated 10 qt plastic tub

3.2.1 Laboratory Preparation

- (1) Hands must be washed thoroughly prior to starting. A dedicated plastic wash bottle with 10% bleach solution should be prepared for wiping down lab tables and other surfaces prior to processing samples. All equipment must be sterilized and all supplies collected prior to starting.
- (2) Each workstation must be rinsed with bleach solution and the surface covered with one or more clean paper towels or bench paper prior to beginning the centrifuging process. Paper must be switched between each batch of sampling sites. New powder-free latex or nitrile gloves must be worn for processing each batch. Prior to centrifuging samples, each work station should have pre-printed labels or one black, waterproof permanent marker for labeling sample tubes, a wastewater container (with lid), and a dedicated wash bottle with 10% bleach solution, and a dedicated alcohol bottle with 95% ethanol or 70% isopropanol. At least a 10-qt plastic tub (e.g., Rubbermaid® plastic storage bin) should be filled with 20% bleach solution for the sterilization bath inside the lab.
- (3) At each workstation a refrigerated centrifuge set at 4⁰ C. If in mobile trailer, check horizontal alignment, trailer should be as level as possible.
- (4) A decontamination station with a 20% bleach bath to decontaminate racks and tubes prior to processing.
- (5) Centrifuge tube racks should be available for organizing and working with sample tubes. One set of racks can be used with samples prior to decontamination, and a second set of racks should be decontaminated by dipping in the 20% bleach bath and rinsing with tap water. Take care to place only decontaminated tubes in the clean racks. Be sure tubes are dried well after their sanitizing dip to avoid any contamination of the samples during processing.

3.2.2 Sample Preparation

New powder-free latex or nitrile gloves must be worn prior to handling each sample set. Process tubes in sets of replicates, until a full centrifuge batch is prepared.

A centrifuge equipment control comprised of 50 ml of tap water should be included with each batch of tubes in each centrifuge. It should be labeled with the range of sample numbers included in the batch. For example, centrifuge equipment control sample number 1000001-1000005 was included in the centrifuge with field samples 1 through 5 from case number 10000. This equipment control is in addition to the field control, and should be made by the sampling office or agency while processing samples in the trailer.

3.2.3 Centrifuging the Samples

- (1) 50-ml tubes should be removed from the transport cooler and caps checked and tightened. Sample containers should be submerged to the bottom of the cap in the 20% bleach for 10 seconds and then completely dried before being moved into the processing area. *It is imperative that bleach not be allowed under the caps or to come in contact with the sample, since bleach destroys DNA.
- (2) Place the 50ml tubes that have been cleaned and dried in the refrigerated centrifuge set at 4 °C. Tubes must be evenly distributed within the centrifuge to maintain the rotor balance. NOTE: Always follow the manufacturer's guidelines for centrifuge operation. Remember to include one equipment control tube with each full centrifuge. It is also important to keep replicate tubes for each sample together in batches. Do not split a sample between batches, otherwise it is too difficult to trace equipment control results through the lab.

- (3) Once 50 ml tubes are in position, close and secure centrifuge lid. Set centrifuge to spin the samples for 30 min at max speed (~4500-5000 xg) and begin centrifuging the samples. During this period the other tubes may be decontaminated and placed on a sterilized surface or rack. **DO NOT PLACE DECONTAMINATED TUBES ON ANY SURFACE OR RACK THAT HAS NOT BEEN STERILIZED.**
- (4) Once samples have been centrifuged the eDNA will be on the bottom of the tube. Wearing a new pair of gloves for each set of tubes comprising one sample, carefully remove cap and GENTLY pour off water into a wastewater container. It is imperative to decant as much water as possible while ensuring pellet retention. A carboy is useful to prevent splashing, or a plain bucket with bleach in the bottom will also work. Change gloves after each sample set.
- (5) Add ~10 ml of 95% ethanol or 70% isopropanol to the tube. The alcohol is required to stabilize the eDNA, and if too little is used, the DNA will degrade before it is detected. Replace cap and swirl alcohol around tube covering the entire internal wall. Centrifuge the samples with alcohol for 10 minutes (or more as needed if pellet is too loose) at max speed (~4500-5000 xg).
- (6) Decant excess alcohol until the level of the alcohol is within the conical end of the tube. Place tubes back into a sterilized rack, keeping samples organized by sample number and ensure control samples are labeled so that they can be paired with their processing batches. Change gloves between sample sets.
- (7) When racks are full, put them in plastic bags so that the tubes are secured in the rack. Tape bags closed and sign across the tape where it overlaps. Place in box to be shipped. NOTE: If a stabilizing solution (i.e., ethanol) is not used eDNA samples must be frozen (traditional commercial freezer or -20 °C freezer) or placed in cold storage. To conserve dry ice, samples may be placed in a cooler filled with ice during the working day. At the end of the day, quickly transfer all samples into a dry ice cooler for long-term storage. Be sure to monitor temperature twice a day and replenish dry ice as needed.
- (8) Prior to centrifuging the next batch of 50 ml samples remove the 50 ml tube adaptor inserts and examine for any water or debris. If anything is found, place in 10% bleach bath for 10 minutes, rinse well to remove all residual bleach, dry with new paper towels, and replace. If adaptor inserts are clean and dry only perform this step during daily lab cleanup. (It may be helpful to have two full sets of inserts so that processing can proceed while any dirty inserts are being cleaned).
- (9) On the field datasheet next to the appropriate sample ID, record the time of centrifuge completion and the initials of the person that processed the sample.

Steps 1–9 should be repeated until all samples have been processed. As always, gloves must be changed and the workstation sterilized between batches.

When the wastewater collection carboy is full, it should be disposed of in a sink separate from the one used to bleach equipment. If a second sink is not available, dispose of the wastewater in any drain that is connected to a sewage treatment facility or system.

If a sample is accidentally spoiled during the centrifuging process (e.g., the pellet was lost during decanting, bleach was squirted into a tube, or cross-contamination is suspected), it should immediately be thrown away. Record on the corresponding datasheet the appropriate sample ID as well as the reason for the ruined sample.

If any deviations from this QAPP occurred during water sample collection in the field or during processing of samples, clearly describe the deviations on Exhibit 16. If deviations will affect lab processing, the eDNA Program Coordinator will contact the eDNA Processing Leader. **Even if there were no deviations from the QAPP, Exhibit 16 forms should be sent to the eDNA Project Coordinator**

following a sampling event to satisfy reporting requirements in section 1.6. Be sure to note any changes in personnel from the pre-trip plan on Exhibit 16 when the report is filed.

SECTION 4 SAMPLE SHIPMENT

4.1 Purpose

Samples must be maintained accordingly depending on sample type. Non-preserved centrifuge samples must be on dry ice or in a -80 freezer until they can be shipped to the DNA processing lab (WGL lab in Onalaska, WI) as soon as possible. Temperature should be recorded twice a day during sample storage and immediately prior to sealing the shipping container (Exhibit 7). If samples were centrifuged, samples do not need to be cooled. All samples should be shipped as soon as logistics in the field allow. There is no longer a 24-hour maximum time limit on shipping, but that does not mean that several cases may be saved up to be delivered or shipped at one time. Since the lab has to open and account for each individual sample and equipment control, samples should be shipped in no more than 400 total samples (unless a single case is larger than this, then ship by case). The Processing Leader is responsible for ensuring that samples are properly packed and shipped according to the procedure below.

There will be no air shipments accepted on Fridays at WGL. Experience in the past with the rare failure of FedEx to deliver on Friday has resulted in loss of samples. If samples cannot be shipped by Wednesday, then they must be held, with temperatures recorded, by the sampling agency (according to step 3.3.3 (7)) until the following week. If shipping flammable samples by ground, WGL will accept Friday deliveries, since these samples are preserved.

Please note: the COC forms are as important as the samples themselves. If COC forms are not filled out properly, then sample integrity is lost and the samples will not be processed because their custody cannot be accounted for. Therefore, please be sure to accurately and completely fill out the COC forms. If you have questions, do not hesitate to call the eDNA Program Coordinator or the eDNA laboratory.

Cautions: Wear gloves and use caution when working with dry ice.

4.2 Shipping Procedure for samples on dry ice (WGL will NOT accept deliveries on Friday since dry ice would melt over a weekend if shipping were delayed)

- (1) Centrifuge tubes must be shipped organized in racks, secured in plastic bags that will keep tubes in the racks, and shipped in containers that will hold the tubes and prevent damage to the tubes.

Be sure tubes are securely closed to prevent leaking. If necessary, twist caps counter-clockwise to properly seat the threads indicated with a “click”. Tighten. If tubes have been chilled, lids may become loose, so double-and triple-check before packing. Place tubes back into the rack in numerical order. Place the rack of tubes back into a plastic bag, seal or wrap it tight to keep tubes from falling out, tape it closed, stapling or signing across the tape. Pack racks of tubes into boxes, using packing material to keep them from shifting.

- (2) Fill out a COC form for each shipping container where the most recent listing lists exactly and only the samples shipped in that particular container (equipment controls are separate samples from the field samples, so they must be accounted for on COC forms in the containers in which they are shipped). The individual employee packing and sealing the containers should list their name in the “from” line, be sure to include agency and print clearly. The container should be packed and released on the same date. Sign and place COC forms (Exhibit 3) in a clean 1-gal resealable bag, place evidence tape across the seal, and place the bag on top of the cooler before closing the corrugated shipping box and sealing with packing tape. **Each box MUST** have a separate signed COC form included to document the specific samples included therein. If you must split samples

into different configurations than listed on the original COC, make a new entry for those samples going into one container on the original COC and create a new COC for any new shipping containers.

- (3) Fill out a Federal Express (FedEx) air bill shipping label with appropriate information. Be sure to affix a dry ice warning label (can be purchased in rolls from FedEx, or printed from the internet) with the amount of dry ice in each cooler on the cardboard shipping container. On the label be sure to designate FedEx Overnight Express (delivery is usually the following day between 8 and 10 AM) as well as to identify the weight of the dry ice in the package. When ready, drop off at FedEx or call FedEx (1-800-463-3339) for pickup. Be sure to tell the operator that the package contains dry ice and ask for an approximate pickup time. Be sure to record tracking numbers for all boxes being shipped.
- (4) Items will be shipped to the following address:

Whitney Genetics Lab
555 Lester Avenue
Onalaska, WI 54650
608-783-8444

4.3 Shipping Procedure for samples preserved with 70% isopropyl or 95% ethanol

NOTE: WGL will ONLY accept FedEx Ground packages with flammable liquids. We did extensive research with management at FedEx, read the CFR, and we expect all shipments to meet the CFR. The guidelines here and on the handout provided at our annual training meet the required code. Shipping flammable liquids via air require different labeling and a hazard label, EVEN for limited quantities (CFR 173.150).

- (1) Centrifuge tubes must be shipped organized in racks, secured in plastic bags that will keep tubes in the racks, and shipped in containers that will hold the tubes and prevent damage to the tubes, as well as meeting regulations for shipping “small quantities” of flammable liquids according to 49 CFR 173.4. Note, these samples may only be shipped ground, and if using FedEx, you must call for pickup, they will NOT accept drop-offs at any office.
- (2) Be sure tubes are securely closed to prevent leaking. If necessary, twist caps counter-clockwise to properly seat the threads indicated with a “click”. Tighten. Use a single piece of tape to secure the lid to the tube. Place tubes back into the rack in numerical order. Place the rack of tubes back into a plastic bag, seal or wrap it tight to keep tubes from falling out, tape it closed, signing across the tape.
- (3) Construct shipping box, double-taping all seams. Box must meet federal guidelines, two options can be purchased from Uline: model #S-4798 (holds 120 samples or 600 tubes) or model #S16458 (holds 90 samples or 450 tubes).
- (4) Use two sections of absorbent material (BLU-102 from newpig.com) and make a cross over the box. Push the center of the cross into the bottom of the box, making sure to press the matting into the bottom corners.
- (5) On top of the matting, place a 24x24x48 gusseted bag.
- (6) Place racks in a 3x2 configuration (3 layers high) for a 22x18x16 box. They only fit like this one way. 18 racks in total. A 22x22x22 box will be able to add another layer, for 4 layers of 3x2 racks. Add more matting or use spare zip bags to fill in the side space left by the larger box.

- (7) Twist tie shut the 24x24x48 gusseted bag to fully enclose all the tube racks. Use tamper tape to lay the twist knot as flat as possible. You can tuck most of it into the space created where two racks meet.
- (8) Fold tag ends of matting onto each other to fully enclose the top of the box with matting.
- (9) Place a 20x20 divider on top of everything to make a flat surface.
- (10) Fill out a COC form for each shipping container where the most recent listing lists exactly and only the samples shipped in that particular container (equipment controls are separate samples from the field samples, so they must be accounted for on COC forms in the containers in which they are shipped). The individual employee packing and sealing the containers should list their name in the “from” line, be sure to include agency and print clearly. The container should be packed and released on the same date. Sign and place COC forms (Exhibit 3) in a clean 1-gal resealable bag, place evidence tape across the seal, and place the bag on top of the divider before closing the corrugated shipping box and sealing with packing tape. **Each box MUST** have a separate signed COC form included to document the specific samples included therein. If you must split samples into different configurations than listed on the original COC, make a new entry for those samples going into one container on the original COC and create a new COC for any new shipping containers.
- (11) Finally, double tape the top seams to close the box. Clearly write “This package conforms to 49 CFR 173.4 for domestic highway or rail transport only” on one side of the box. Be sure to draw arrows on all sides of the box, indicating which side is the top of the box.
- (12) Fill out a Federal Express (FedEx) GROUND shipping label with appropriate information and request a pick-up. FedEx will only ship flammables if you request a pick up, you will not be allowed to drop boxes off at FedEx.
- (13) Items will be shipped to the following address:

Whitney Genetics Lab
555 Lester Avenue
Onalaska, WI 54650
608-783-8444

4.4 WGL contacts

- (1) Once items have been shipped, at least one person at WGL must be contacted and notified of approximate delivery date and time. At least one of the following personnel should be contacted via telephone and email regarding shipment, continue calling down the list until you speak with a human on the phone. Following shipment, email approximate delivery time, date and tracking numbers to the person you talked with and the WGL Project Leader (emy_monroe@fws.gov) who will be receiving the delivery at WGL:

Nick Berndt
Phone: 608-783-8419
Email: Nicholas_Berndt@fws.gov
Kyle Von Ruden
Phone: 608-783-8411
Email: Kyle_VonRuden@fws.gov
Maren Tuttle-Lau

Phone: 608-783-8403

Email: maren_tuttle-lau@fws.gov

Nick Grueneis

Phone: 608-783-8404

Email: Nikolas_Grueneis@fws.gov

Erica Mize

Phone: 608-783-8449

Email: Erica_Mize@fws.gov

Katherine Bockrath

Phone: 608-783-8442

Email: Katherine_Bockrath@fws.gov

Zeb Woiak

Phone: 608-783-8424

Email: Zebadiah_Woiak@fws.gov

- (2) Upon receipt of the samples at WGL, if the samples were shipped with dry ice, the inside temperature of all the coolers must be taken and recorded. Samples shipped with dry ice that have remained at room temperature (approximately 20°C) for more than 24 hours will be discarded, and the sample names and reason(s) for discarding will be noted in the laboratory log. Samples that are shipped at ambient temperature do not need a temperature recorded upon receipt.
- (3) Personnel receiving the shipment must immediately sign the COC form, scan it and email it back to the sender of the COC and that station's Field Operations Manager. Make sure to cc the Data Reporting Specialist, the eDNA Processing Coordinator and the eDNA Project Coordinator so that proper documentation can be recorded. Receiving personnel should also call the sender and sampling leader if they do not have email access in the field.

SECTION 5 DNA ASSAYS

5.1 General Quality Assurance and Chain-of-Custody Considerations

Any change to described DNA handling, storage, or processing procedures must not result in reduction of eDNA sensitivity relative to current values and must be cleared with the eDNA Processing Leader. The original protocol produced the following results at different concentrations of purified DNA amplicons ¹ in sterile water:

Table 2. Different concentrations of purified DNA amplicons ¹ in sterile water for Bighead and Silver Carp.

Species	Purified DNA amplicon (copies/ μ l water)	Purified DNA amplicon (ng/ μ l water)
Bighead Carp	207	3.30×10^{-8}
Silver Carp	7	7.25×10^{-10}

New markers developed and then tested and verified via the Marker Validation Study were found to be more sensitive than the original markers:

Table 3. Marker copies per/ μ l water and marker length (bp) for both Silver and Bighead Carp individually, as well as combined.

Marker (species)	Copies/ μ l water	Marker length (bp)
ACTM 1 (both, cannot differentiate)	3	145
ACTM 3 (both, cannot differentiate)	3	133
SCTM 4 (Silver)	3	168
SCTM 5 (Silver)	3	98
BHTM 1 (Bighead)	3	144
BHTM 2 (Bighead)	3	96

The new markers are located throughout the mitochondrial (mt) DNA loop (figure 1), and a suite of markers will be used to detect and confirm the presence of carp DNA in the water samples, rather than a single locus per species. Each pair of markers can be analyzed in duplex, or a single reaction, and when positive for markers, indicate 2 loci within the mt genome are present. The initial screening reaction will detect the presence of two loci within the cytochrome oxidase 1 (COI) gene in the mtDNA of both Silver and Bighead carp. This locus is particularly powerful, as it is used as the universal barcode of life, a region of mtDNA used to identify specimens to species for the entire animal kingdom. In order to be deemed presumptive positive, both of the COI loci must be detected in at least one replicate reaction, but they do not have to be the same replicate. The confirmation of each species will then be demonstrated by detecting at least one additional locus on the mtDNA genome. For Silver carp, two markers are in the ND2 and ND6 gene subunits, and for Bighead carp in the ND2 and ND4 gene subunits. The presence of one or the other locus in at least one replicate will confirm the presence of either Silver or Bighead carp DNA in the sample.

¹ As reported in Jerde et al., 2012. Response to Casey et al.'s sensitivity of detecting environmental DNA comment. Conservation Letters 0:1-2.

Detecting at least three different loci within the mt genome provides confidence in the detection of carp DNA in the water sample, and sequencing is not required since the entire amplicon (marker length in table above) is required to match the primers and probe indicating high specificity.



Figure 1. Map of entire Asian carp mitochondrial genome which was determined at ERDC with 33 bighead carp and 29 silver carp collected from across the United States (Farrington et al. in review²). Marker locations are indicated with arrows. The original markers are located within the control region (D loop). The ACTM 1 and 3 markers are on either end of the COI gene. Bighead markers BHTM 1 and 2 are in the ND4 and ND6 regions, and Silver markers SCTM 4 and 5 are in the ND6 and ND2 regions, respectively.

²Farrington, H.L., C.E. Edwards, X. Guan, M.R. Carr, and R.F. Lance. 2015. Mitochondrial Genome Sequencing and Development of Genetic Markers for the Detection of DNA of Invasive Bighead and Silver Carp (*Hypophthalmichthys nobilis* and *H. molitrix*) in Environmental Water Samples from the United States. PLoS ONE 10(2): e0117803. doi: 10.1371/journal.pone.0117803

- Each stage of eDNA genetic processing procedures (eDNA sample extraction, PCR setup, and post-PCR processes) should be performed in a separate room in order to minimize the risk of sample cross-contamination. If separate rooms are not available, extractions and PCR set up can be combined in one room, ONLY if PCRs are set up in a PCR hood with a hepa filter and UV light. All post-PCR processing *must* be in a separate room.
- Every effort should be made to ensure that equipment, work areas, and solutions are free from DNA contamination. All surfaces should be wiped clean with 10% bleach solution (or commercial DNA eliminating solution such as DNA Away) before and after use. If equipped with UV lamps, clean lab rooms or PCR hoods should be irradiated with UV light 30 minutes at the beginning and end of the work day.
- Non-sterile, non-PCR ready microcentrifuge tubes (MCT) and glassware used in the lab must be autoclaved at 121°C for 20 min before being used. Any re-used items must be soaked in a freshly made 10% bleach solution for 10 minutes followed by a thorough rinse. (Sterile, certified DNA-free MCT do not need to be autoclaved prior to use).

- Good housekeeping policy should be practiced at all times. Reagents that have passed expiration dates should not be used, nor should any reagents that have been kept at incorrect storage temperatures for a significant length of time. All reagents, reaction tubes, etc., must be clearly labeled. Records of batch numbers of all reagents used in individual assays should be made whenever reagents are signed out from the designated freezer. The temperatures of cold storage units must be monitored once a day, using the forms given in Exhibits 7-8.
- Positive and/or negative reactions should be used to test all new batches of critical components prior to or concurrent with their application to eDNA samples.
- Standard sterile techniques should be used in the DNA laboratory to prevent the unintended transfer of DNA between surfaces, and to prevent cross-contamination between samples. Contamination can adversely affect the outcome of a case; therefore, it is essential that the laboratory have procedures in place to limit, recognize, and address contamination.
- Gloves (e.g., powder-free nitrile or latex) must be worn throughout sample processing. At a minimum, gloves should be changed at the completion of each step of the process. If gloves become contaminated or if contamination is suspected, discard them and replace them with new ones. For example, gloves should not be worn when using or handling keyboards, notebooks, pens, telephones, etc. and must be replaced immediately before recommencing bench work.
- Centrifuge tubes before opening the reagents. Uncap and close tubes carefully to prevent aerosol contamination.
- Ensure that centrifuges are always balanced when centrifuging samples.
- Ensure that all equipment, including paper, pens, and lab coats, are dedicated for use only in that particular laboratory (e.g., laboratory coat for each stage of procedure rooms. Workbooks that have been in contaminated areas shall not be taken into clean PCR areas. A Project Lab Book should be kept in a room separate from the DNA Extraction Room and DNA PCR Room. Each room (Extraction, PCR, Post-PCR) should have note-taking materials (e.g., loose-leaf paper, networked tablet PCs) that can be transported or viewed for consolidation in the Project Lab Book. Other solutions for preventing contamination of sensitive areas via lab notes may be used following approval by the eDNA Processing Leader. Any changes should be incorporated into a revised QAPP. Laboratory notes/notebooks should:
 - Be written or printed on tamper-proof paper (e.g., does not exactly photocopy).
 - Have lab book identification, with consecutive numbering, dates, and signatures (of the note-taker) on each page.
 - Be made using permanent ink. Special pens may be required for certain paper types.
 - Have any changes to notebooks be dated and initialed by the person who made the change. Any incorrect information should have a single line drawn through it and not be completely obscured.
 - Contain all data images (e.g., gel photographs, denaturing curves, DNA sequence electropherograms). Images should be permanently affixed to the notebook and signed across both the edge of the insert and the page.
 - Be kept in a locked drawer or cabinet with restricted access when not in use.
- A log of all batches of critical components should be kept. This log should include material safety data sheets (MSDS) and product information sheets. Dates of receipt, opening, testing, and disposal for each component should be recorded in the log.

5.2 Quality Control for Sample Custodian Procedure and Storage

- An internal log book should be kept for all samples. Tamper-proof paper should be used. The log book should be kept in a locked drawer or cabinet when not in use.
- Separate freezers should be designated for storage of (a) concentrated water samples, (b) DNA extracts, (c) PCR and sequencing product, and (d) PCR, cloning, and sequencing kit components. A dedicated refrigerator should also be maintained for any PCR, gel electrophoresis, cloning, and sequencing kit components that require 4°C storage.
- Maps or other designations of the location of samples within freezers should be maintained.
- All items in freezers should have indelible ink identifications.
- All freezers should have non-universal locks or marine brackets attached that can be used with keyed locks, or be housed in a secure facility.
- All samples placed into or removed from freezers should be signed for on freezer log or ambient storage log (see Exhibits 7, 8, and 9).

5.3 Physical Separation of Pre-PCR and Post-PCR Assay Stages

5.3.1 The eDNA Extraction Room

- Extraction of DNA must be performed where PCR products and stocks of cloned material are not handled.
- A PCR hood with a built-in ultraviolet (UV) light and HEPA filter may be used to further isolate DNA extraction kit solutions and elutes from ambient DNA.
- A complete separate set of necessary laboratory equipment, consumables, and laboratory coats should be dedicated for use in DNA extraction.

5.3.2 Pre-PCR Room

- To prevent carry-over of amplified DNA sequences, PCR reactions should be set up in a separate room from that used for post-PCR manipulations.
- A completely separate set of necessary laboratory equipment, consumables, and laboratory coats should be dedicated for the specific use of pre-PCR manipulations.
- Reagents and supplies should be taken directly from clean storage into the PCR area and should never be taken or shared with areas in which post-PCR analyses are being performed. Equipment such as pipettes should never be taken to the post-PCR area after use with amplified material.
- A sign-in log system should be implemented for use of the thermal cyclers (PCR machines), including the run name, plate orientation, and the number of thermal cycler heads.

5.3.3 PCR Product Analysis Room

This is the post-PCR Room where post-PCR manipulations are performed, including agarose gel electrophoresis of products and sequencing of presumptive positives.

- This room is a contaminated area; therefore, **no** reagents, equipment, laboratory coats, etc. from this room should be used in any of the other lab areas.
- A biological or PCR-type hood may be used for setting up cloning or sequencing reactions.

5.4 Receipt of Tubes

5.4.1 Source

Water samples have been taken in the field according to Section 2 and centrifuged according to Section 3. Samples have been shipped to WGL and personnel assigned to the WGL eDNA Team have received packages from the overnight service. NOTE: alcohol-preserved centrifuged samples are shipped at ambient temperature.

- (1) Upon receipt of samples from the eDNA sample filtering team, the shipped box(es) should be opened and if shipment was on dry ice, the temperature inside each box recorded. The general condition of the box(es) should also be recorded.
- (2) If samples were shipped on dry ice only: measure temperature upon opening the box, either (a) place a glass thermometer inside the Styrofoam container, replace lid, and leave the thermometer in place for at least 2 min before removing it and immediately recording temperature or (b) immediately aim an infrared laser thermometer at the samples and press the MEASURE button to record the temperature inside the cooler.
- (3) Place all samples in sample storage freezer (-80°C) and log samples on freezer sheet (Exhibit 8). If centrifuged samples are to be processed within a week, it is permissible to place tubes in ambient sample storage (shelves) and log samples on bench-top log sheet (Exhibit 9).
- (4) Sign and date the COC forms that accompanied the samples. Place them in a designated file; a copy should also be provided to sampling agency. If the forms were inside sealed bags, slit the bag to remove the COC forms. Note any condition issues (broken tape or seals, damaged containers or containers, etc.) with the samples on the COC forms. Note any samples that must be discarded due to condition issues and the reason for discard.
- (5) Enter sample data into internal sample log book (or LIMS), including noting any samples that are being discarded and that should not be analyzed, and create new WGL COC form for samples. Note any observations about samples such as condition issues. Store COC forms in a secure area.
- (6) Alert Sampling and Processing Leaders that samples have been received. Use e-mail addresses with return/receipt requested and directly contact via telephone; team contacts are listed in Appendix A. This reporting must be done within 1 hour of completing sample check-in. Be sure to scan and send COCs according to 4.2 (10).

5.5 DNA Extraction from Tubes

5.5.1 Source

Tubes from eDNA sampling have been received by WGL eDNA Team and logged. Centrifuged sample tubes may be in ambient storage or if they are not preserved with alcohol in designated -80°C freezer.

5.5.2 DNA Extraction Quality Assurance and Chain-of-custody

At this stage, a critical component of quality control should be to correctly label all sample extraction processing tubes so that there is no question about the origin of samples.

- (1) Bench areas in DNA extraction laboratory and PCR-type hood (if used) should be wiped before and after use with 10% bleach. Validated, commercially available sterilization reagents, such as LookOut® DNA Erase®, may be preferred. Extraction rooms should be irradiated with UV lights for 30 minutes prior to use.
- (2) After an item or surface is cleaned with bleach, it must be rinsed with purified water or alcohol to prevent the build-up of sodium hypochlorite crystals. Instruments or equipment cleaned with bleach must be rinsed to avoid corrosion.
- (3) It is common practice for moisture barrier paper towels to be placed on the bench top while processing samples to act as a barrier. The paper barriers must be changed and the bench top cleaned between sample batches.
- (4) Centrifuges, thermal cycler, tube racks, pipettes, and any other equipment used for the extraction process should be cleaned before and after each use.
- (5) Instruments such as forceps and scissors should be cleaned just prior to use. Sterile disposable equipment should be opened just prior to sample processing and discarded after one use.
- (6) When using pipettors, use filtered tips and never allow the liquid in a pipette tip to rise up to the barrier.
 - Do not rest the pipette on a dirty surface.
 - Avoid cross-contamination by changing pipette tips after each use.
 - Watch that the tip, and only the tip, is allowed to go into a bottle of reagent, never the pipette itself.
- (7) Record all solution batch/lot numbers used for reactions in lab notes.
- (8) Always mix tubes by vortex or finger flicking, and then briefly spin down tubes before opening.
- (9) No deviations to the DNA extraction protocol are allowed without written approval by the eDNA Processing Leader. Any errors in processing should be noted in the laboratory log. Samples affected by errors in the extraction protocol should be clearly identified.

5.5.3 Alcohol evaporation from centrifuged samples procedure

- (1) Centrifuged samples may need to be re-spun to re-concentrate sample at the bottom of the tube after shipping. Swirl liquid to re-capture any observable debris from the side of the tube wall.
- (2) Centrifuge at max speed for 5 minutes. This entire procedure can be done in advance, and samples stored at -80 until ready for processing.
- (3) Centrifuged samples preserved with alcohol must have the alcohol evaporated away before extracting the samples. Prepare laminar flow hood by wiping down the work surface with 10% bleach or DNA away and/or use the UV lamp for 15 minutes.
- (4) Remove samples from freezer or ambient storage; note on freezer/storage and sample log (see Exhibits 7-9).
- (5) Move samples in tube racks to the laminar flow hood. Carefully remove tube lids and place in the same order as the samples next to each rack. Turn on the air flow and leave the samples to dry until all traces of ethanol or isopropanol smell are gone, because these are both PCR inhibitors. Do not let

samples sit at room temperature longer than overnight, and never over a weekend. If working in advance, evaporated samples should be stored at -80 until extraction.

- (6) Include a hood negative control sample for each hood or case of samples set out to dry. Negative hood controls will be ran only if there are any positive results for silver or bighead carp or if there is a contamination issue. Make a negative hood control by placing an empty, sterile centrifuge tube in the racks with the lid removed alongside the field samples.
- (7) Positive and negative extraction controls should be added to each eDNA extraction procedure batch.
 - Before proceeding with extraction, a positive control swab is prepared by pipetting 100 µl of Silver and Bighead carp cell lines or tissue slurry directly onto a sterile swab in 1.5-ml MCT. Alternative species (e.g. sturgeon or bluegill) may be used as the positive control to reduce risk of sample contamination from carp tissue. Alternative species must have PCR primers that do not cross-react with carp DNA. A batch of extraction positives can be prepared ahead of time and frozen at -20°C.
 - Additionally, an extraction negative control sample should be prepared by pipetting 100 µl of sterile lab DI water onto a sterile swab in a 1.5-ml MCT. A batch of extraction blanks can be prepared in advance and kept frozen at -20°C
 - For every extraction batch of filter samples or centrifuged samples processed, conduct DNA extraction (below) on one frozen, sterile extraction negative control and one prepared positive control.
- (8) For all samples and cooler, equipment, and extraction controls, follow the DNA extraction protocol detailed below.

Cautions: As with all components of eDNA processing, quality control and sterilization procedures must be carefully followed in order to avoid contamination of downstream procedures.

5.5.4 Centrifuged samples shipped on dry ice procedure

Centrifuged samples may need to be re-spun to re-concentrate sample at the bottom of the tube after shipping. Thaw 5 samples of tubes, and work quickly to avoid DNA decomposition. When that set of 5 samples is finished, place them back into the freezer and take out the next five samples. Since samples are being placed back into the freezer, do not worry about entering this action into the freezer log. Only fill out the freezer log when samples are removed to extraction.

- (1) Swirl water to re-capture any observable debris from the side of the tube wall. Consolidate pellets into a single tube, rinse sides with additional water if needed, using a squirt bottle, and taking care to avoid contaminating the tip. Be sure to change gloves between samples.
- (2) Centrifuge at max speed for 5 minutes. Decant as much of the water as possible so that the entire sample can be extracted, including the remnant water.
- (3) This entire procedure can be done in advance, and samples stored at -80 until ready for processing.
- (4) Remove samples from freezer, note on freezer log (see Exhibits 7-9).
- (5) Samples frozen with water can be directly extracted.
- (6) Positive and negative extraction controls should be added to each eDNA extraction procedure batch.
 - Before proceeding with extraction, a positive control swab is prepared by pipetting 100 µl of Silver and Bighead carp cell lines or tissue slurry directly onto a sterile swab in 1.5-ml MCT. Alternative species (e.g. sturgeon or bluegill) may be used as the positive control to reduce risk

of sample contamination from carp tissue. Alternative species must have PCR primers that do not cross-react with carp DNA. A batch of extraction positives can be prepared ahead of time and frozen at -20°C.

- Additionally, an extraction negative control sample should be prepared by pipetting 100 µl of sterile lab DI water onto a sterile swab in a 1.5-ml MCT. A batch of extraction blanks can be prepared in advance and kept frozen at -20°C
- For every extraction batch of filter samples or centrifuged samples processed, conduct DNA extraction (below) on one frozen, sterile extraction negative control and one prepared positive control.

(7) For all samples and cooler, equipment, and extraction controls, follow the DNA extraction protocol detailed below.

Cautions: As with all components of eDNA processing, quality control and sterilization procedures must be carefully followed in order to avoid contamination of downstream procedures.

5.5.5 Qiagen DNeasy Kit² (or equivalent kit) Procedure for centrifuged samples

- (1) Obtain one **lyse and spin** kit per sample to be extracted, open packages and organize tubes in rack. Label both caps of each sample. You will have time to label the rest (3 lab-supplied 1.5-mL MCT, 1 Qiagen spin tube, and 3 Qiagen collection tubes) during the 1-hour incubation. Be sure you have added positive and negative extraction controls to each eDNA extraction procedure batch.
- (2) Add 370 μL **ATL** to the top of each basket tube.
- (3) Add 30 μL **proteinase K** to the **ATL**.
- (4) Remove sterile **swabs** from pack and place one swab into each tube of ATL/proteinase K mix.
- (5) Move dried samples in centrifuge tubes to the extraction room. Use the moistened swab to swab the bottom of each tube included in the field sample (e.g. if there are 5 tubes per sample, swab the bottom of all 5 tubes with the moistened swab). If the swab becomes covered with debris, rinse swab in ATL solution for that sample in the extraction tube and proceed swabbing the rest of the replicates. Be careful to avoid cross-contamination at this step.
- (6) Place the swab back into the **ATL** mixture, break the wooden stick and close the tube.
- (7) Incubate at 55°C for 1 hour. Label the rest of the tubes and print final archive labels for filters and extracts.
- (8) Remove from incubator and centrifuge at $\geq 18,000 \times g$ for 1 minute. Remove the assembly and dispose swab in the basket if all liquid has been spun out. If very little or no liquid is in the collection tube repeat centrifuge step or pipet liquid from swab and lyse and spin basket and place in collection tube.
- (9) Add 400 μL Buffer **AL**.
- (10) Add 400 μL **ethanol** (96–100%, molecular grade). Mix thoroughly by vortexing. If liquid collects around the cap, spin briefly before opening to reduce contamination risk.
- (11) Transfer about half of the mixture by pipet into a DNeasy Mini spin column placed in a 2 mL collection tube. Centrifuge at $\geq 6000 \times g$ for 1 minute. Discard flow-through and collection tube.
- (12) Transfer the remaining mixture by pipet onto the same spin column and place in a new 2 mL collection tube. Centrifuge again at $\geq 6000 \times g$ for 1 minute. Discard flow-through and collection tube.
- (13) Place spin column in a new 2 mL collection tube. Add 500 μL Buffer **AW1**. Centrifuge at 6000 $\times g$ for 1 minute. Discard flow-through and collection tube.
- (14) Place spin column in a new 2 mL collection tube.
- (14) Add 500 μL Buffer **AW2**. Centrifuge at 18,000 $\times g$ for 3 minutes. Discard flow-through and collection tube.
- (15) Transfer the spin column to a new 1.5 mL or 2 mL MCT.
- (16) Add 200 μL Buffer **AE** to the center of the spin column membrane. Incubate for 1 minute at room temperature (15 - 25°C). Centrifuge at $\geq 6000 \times g$ for 1 minute. (17) Discard the spin column and store the eluted DNA samples at -20°C. If DNA is to be immediately used for PCR, keep on ice.

²Amberg, J.J., S.G. McCalla, E. Monroe, R. Lance, K. Baerwaldt, and M.P. Gaikowski. 2015. Improving Efficiency and Reliability of Environmental DNA Analysis for Silver Carp. 2015. Journal of Great Lakes Research. doi:10.1016/j.jglr.2015.02.009.

5.5.6 IBI Scientific gMAX Kit Procedure for centrifuged samples

- (1) Obtain one Qiagen **lyse and spin** kit per sample to be extracted, open packages and organize tubes in rack. Label both caps of each sample. You will have time to label the rest (1 lab-supplied 1.5-mL MCT, 1 GD spin column, and 3 IBI collection tubes) during the 30 minute incubation. Be sure you have added positive and negative extraction controls to each eDNA extraction procedure batch.
- (2) Add 350 μL **GSB** to each lyse and spin basket tube. If precipitate has formed in GSB buffer, dissolve by incubating at 60°C for 10 minutes.
- (3) Add 35 μL **proteinase K** to the GSB.
- (4) Move dried samples in 50ml centrifuge tubes to the extraction room. Make sure each tube is dry.
- (5) Remove a sterile swab from pack, and dip it into a numbered tube of GSB/proteinase K mix. Use the moistened swab to swab the bottom of each tube included in the field sample (e.g. there is 5 tubes per sample, swab the bottom of all 5 tubes with the moistened swab). If the swab becomes covered with debris, rinse swab in tube of GSB/proteinase K solution for that sample, and proceed swabbing the rest of the replicates. Be careful to avoid cross-contamination at this step.
- (6) Place the swab back into the GSB mixture, break the wooden stick as close to the swab as possible, and close the tube. Change gloves between samples.
- (7) Incubate at 60°C for 30 minutes. Label the rest of the tubes, place GD spin columns in your tube rack (same amount as your sample size), and print final archive labels for swabs and extracts. Also during this time place the Elution Buffer into the 60°C bead bath.
- (8) Remove lyse and spin tube from incubator and centrifuge at $\geq 16,000 \times g$ for 1 minute. If all liquid has spun out remove spin basket with swab and discard. If liquid remains in basket recentrifuge or transfer liquid with pipette.
- (9) Add 500 μL **ethanol** (96 – 100%, molecular grade) to the flow through of the lyse and spin tube. Mix thoroughly by vortexing. If liquid collects around the cap, spin briefly before opening to reduce contamination risk.
- (10) Transfer up to 740 μL of the mixture by pipet into a GD spin column placed in a 2 mL collection tube. Centrifuge at $\geq 16000 \times g$ for 1 minute. Discard flow-through and collection tube.
- (11) Transfer any remaining mixture by pipet onto the same spin column and place in a new 2 mL collection tube. Centrifuge again at $\geq 16000 \times g$ for 1 minute. Discard flow-through and collection tube.
- (12) Place GD spin column in a new 2ml collection tube. Add 400 μL Buffer **W1**. Centrifuge at 16000 $\times g$ for 30seconds. Discard flow-through and collection tube.
- (13) Place spin column in a new 2 mL collection tube. Add 600 μL **Wash Buffer**. Centrifuge at 16000 $\times g$ for 3 minutes. Discard flow-through and collection tube.
- (14) Transfer the spin column to a new 1.5 mL MCT.
- (15) Add 200 μL of the pre-heated **Elution buffer** to the center of the spin column membrane. Incubate for 1 minute at room temperature (15 - 25°C). Centrifuge at $\geq 16000 \times g$ for 30 seconds.
- (16) Discard the spin column and store the eluted DNA samples at -20°C. If DNA is to be immediately used for PCR, keep in 4°refridgerator.

5.6 PCR Amplification of eDNA Samples

5.6.1 Purpose

In order to determine if the DNA of a specific species is present in the concentrated water samples taken in the field, the total DNA extracted from the filtered samples must be amplified using species-specific primers. New in 2014, real-time PCR markers will be used for detecting presumptive positive samples as well as confirming Silver or Bighead carp DNA. All samples will be first assayed with two general Asian carp markers that detect two loci within the cytochrome oxidase I gene of both Silver and Bighead carp mitochondria (ACTM 1 and ACTM 3). Any sample that has at least one replicate PCR positive for both loci will be considered presumptive positive.

5.6.2 Source

eDNA samples have been received by WGL eDNA Team and DNA has been extracted. DNA elutes from samples should either be located in designated -20°C freezer or carried from the DNA extraction room to PCR room. Be sure the room is irradiated with UV light for 30 minutes prior to use. Ensure thermal cyclers are available before mixing the master mix. Master mix with or without template DNA cannot sit longer than it takes to prepare the samples for cycling. While preparing samples prepared master mix should be kept in a cool box or in the refrigerator.

5.6.3 PCR Quality Assurance and Chain-of-custody

This stage of DNA processing is particularly susceptible to contamination and, subsequently, inaccurate results. Carefully follow quality control and COC steps listed below:

- (1) PCR-type hood bench should be wiped before and after use with 10% bleach. Validated commercially available sterilization reagent such as LookOut[®] DNA Erase[®] may be preferred. PCR room should be sterilized using a built-in UV lights if available.
- (2) After an item or surface is cleaned with bleach, it must be rinsed with purified water or alcohol to prevent the build-up of sodium hypochlorite crystals. Instruments or equipment cleaned with bleach should be rinsed to avoid corrosion.
- (3) Centrifuges, thermal cycler, tube racks, pipettes, and any other equipment used for PCR amplification should be cleaned before and after each use.
- (4) Use autoclaved, filtered, or commercially sterile molecular grade water prior to use for setting up PCR reactions.
- (5) Aerosol-resistant pipette tips should be used. Place the sterile tip on the pipette immediately prior to use. If the pipette is set down with the tip on, discard the tip. A new pipette tip must be used for the addition of each reagent to a sample tube.
- (6) Use autoclaved sample tubes for PCR master mix.
- (7) Close each tube immediately after labeling and after the addition of sample or reagents to prevent cross-contamination.
- (8) Be sure to only touch the tip of the MCT cap or use a tube opener, clean Kimwipe[®], or other suitable barrier to open MCT.

- (9) Record all solution batch numbers used for reactions in lab notes.
- (10) PCR reagents should be aliquoted (a portion of the original stock) to avoid excessive freeze-thawing and to protect stock reagents if contamination occurs.
- (11) Lightly vortex (quick touch, because vigorous vortexing can damage *Taq*) to mix sample and quick-spin/centrifuge tubes before opening the reagents to avoid splashes or drips from cap when opening. Uncap and close tubes carefully to prevent aerosol contamination.
- (12) Any revisions to the DNA amplification protocol must be approved by the eDNA Project Leader and documented in writing.

Cautions: Wear powder-free latex or nitrile gloves throughout the DNA amplification and gel electrophoresis procedures. Ethidium bromide, used in DNA gel electrophoresis to visualize DNA, is a known mutagen that affects biological processes.

Note for exhibit 13: Plate maps have been included for scenarios most processed at WGL. 384-well plate sheets with inhibitor PCR components are included for initial screening of each case, but 96-well plate sheets are also included for processing any equipment controls for confirmed positive samples. Likewise, 96-well sheets are included for confirmation assays using silver and bighead PCR components, but if needed, 384-well sheets may be used instead.

5.6.4 Procedure

- (1) If DNA samples (extraction elutes) are removed from freezer, note on freezer/ambient log (see Exhibits 7-9). Also note on sample log (Exhibit 6).
- (2) Use preprinted plate map (Exhibits 12-13) or build plate map in LIMS to determine which samples will be pipetted into which wells. Clearly mark plate identification on bottom edge skirt of plate. Write plate identification information (ddMONyy_initials_ASSAY_case(sample#-sample#)_Plate#) in lab notes.
- (3) Make sure sample map for each plate is entered into the LIMS or attached to lab notes and a signature is written across the map and lab book page.
- (4) Follow DNA amplification protocol detailed below.
- (5) Primers for two loci (ACTM 1 and ACTM 3) within the cytochrome oxidase I gene of the mitochondrial genome will detect either *Hypophthalmichthys molitrix* (Silver Carp) or *H. nobilis* (Bighead Carp), or both to screen eDNA samples and detect DNA present in the eDNA samples by PCR. The PCR programs used to amplify the extracted DNA are the same for all three pairs of duplex real-time markers. The PCR protocol has been optimized to utilize TaqMan Environmental Master Mix 2.0 (Life Technologies, Carlsbad, CA) in the eDNA screening. If other brands of real-time PCR master mixes are used, optimization of the recipe and thermal profiles must be executed. Eight reactions are set up for each sample, in addition to negative (DNA blank) and positive (DNA extracted from cell lines or tissue) controls for each master mix. The PCR reactions are prepared as follows:
- (6) Wipe lab bench area with 10% bleach, 75% Ethanol, or commercial DNA sterilization wipes. Also wipe down work area in PCR hood. Use built-in UV lamps to radiate clean room for 30 min prior to PCR set-up.
- (7) Electronic pipettors should be wiped down with one of the solutions or wipes listed in Step 1.
- (8) In the clean reagent room, obtain all PCR master mix reagents (using only those that have not expired and that have been tested and found viable).
 - a. TaqMan Environmental Master Mix 2.0

- b. One tube with two forward and two reverse primers at 10 μM working dilution.
 - c. One tube with a FAM-labeled probe for ACTM 1 and one HEX-labeled (or another appropriate fluorophore for your instrument) probe for ACTM 3 diluted to 2.5 μM . (we prefer double-quenched probes that include a ZEN quencher located about 9 basepairs from the fluorophore as well as an Iowa Blackhole Quencher on the 3' end of the probe, but regular TAMRA-quenched probes may also be used).
 - d. Sterile molecular grade water (commercially sterile or Millipore filtered, autoclaved)
- (9) Allow reagents to thaw. Do not vortex primers or Taq too violently. Briefly spin down tubes to minimize aerosolization.
- (10) Record in lab notebook the lot number of all reagents used.
- (11) Prepare PCR master mixes in clean reagent room. The master mix volume can be adjusted according to the number of samples to be processed. In order to make sure that master mix does not run out prior to supplying all the desired reactions (this may occur as a result of minor errors or variations in pipetting volumes), it is generally helpful to make more than enough master mix than is needed for the desired number of reactions. For example, make enough master mix for 100 reactions when actually preparing for 96 reactions. NOTE: If positive extraction controls consist of a different species of DNA, be sure to make a small separate master mix for those samples and use primers specific to the content of the control sample. Negative extraction controls should be amplified with the Asian carp master mix.

Each Initial PCR 1X reaction should contain:

- 10.0 μL TaqMan Environmental Master Mix 2.0
- 1.0 μL primer mix (10 μM each, working dilution)
- 1.0 μL probe mix (2.5 μM each, working dilution)
- 5.0 μL sterile water (*7.0 μL in standard curve mix)
- 3.0 μL sample extract as template (*1.0 μL gblock template in standards)

NOTE: The TaqMan Environmental Master Mix is very viscous, and requires careful pipetting to ensure accuracy. The maximum size pipet allowed is the 1000- μL pipet, and a new tip should be used for each aliquot removed. The tip must be left in the mix for a few seconds after aspiration to ensure complete aspiration of the desired volume, and upon dispensing, a pause is required to allow the mix to pool in the tip before the final plunge to dispense the last drop of mix. If this mix is pipetted too quickly, there will be too little volume to fill the required wells.

- (12) Mix master mix well by slowly inverting the tube 17 times. Avoid shaking or inverting too quickly to prevent creating bubbles. Move prepared mix from reagent room into PCR room.
- (13) Remove DNA extracts from freezer or fridge (fill out logs as needed), vortex (quick touch) and quick-spin down the extract tubes. Take them into the PCR room. Place the 96-well PCR plate onto a clean surface, positioned from left to right.
- (14) NOTE: WGL now has automated liquid handling robots that will fill plates for cycling. If these are unavailable, detailed directions for loading plates follows. Fill all plate wells with 17 μL PCR mix. To avoid creating bubbles, which interferes with data collection, place the pipette tip gently in the very bottom of the wells. Fill wells from the bottom up. Do not dispense air into the mix.
- (15) Carefully pipette 3 μL of each extract (or 1 μL gblock in standards) to be screened onto the side of each well of a column, changing the pipette tip between each sample. Again, placement of the tip is important to avoid creating bubbles, so set the tip against the side of the well, above the level of master mix, and then deposit the aliquot of template.
- (16) Each column of eight wells should be filled with the same sample (i.e., eight replicates per sample to be tested). The first 10 columns of the PCR plate can test 10 different samples. Use the 11th 12th

columns for PCR negative and positive controls and standard curve dilutions. Pipette 3 μL of water into wells G and H to serve as PCR negative samples. Five-point, five-fold standard curves with 10, 50, 250, 1250, and 6250 copies/ μL will be used. The highest standard should be placed in well B followed by the next lowest standards through well E. Place a mixed sample of both Silver and Bighead carp cell extract into well A to serve as PCR positive samples. (See Exhibit 13 for plate maps)

- (17) Extraction negatives will be run as they were extracted within the sample batch.
- (18) Extraction positives will be removed and run on separate plates with a bluegill marker assay (Takahara et al. 2013).

³Takahara T., T. Minamoto, and H. Yamanaka, H. Doi, and Z. Kawabata. 2012. Estimation of fish biomass using environmental DNA. PLoS ONE 7:e35868.

Each Bluegill PCR 1X reaction should contain:

- 13.4 μL TaqMan Environmental Master Mix 2.0
- 1.8 μL forward primer (10 μM each, working dilution)
- 1.8 μL reverse primer (10 μM each, working dilution)
- 1.0 μL probe (2.5 μM , working dilution)
- 2.0 μL of extraction positive extract as template.

- (19) A new tip should be used for each template or standard delivered in each well. Carefully observe the volume of liquid in the pipette tip is accurate. All templates or standard material is delivered on the side of the well, as described in (15).
- (20) Before the PCR plate is sealed, check every well for bubbles. Bubbles disrupt the accuracy of the camera detecting fluorophores and need to be removed before the plate is sealed and put into the machine. To remove bubbles, remove the straw from an isopropanol bottle and use the fumes from the alcohol to break the surface tension of the bubble. If a bubble is trapped in the bottom of the well, seal the plate and spin for an extended period of time. Use care to avoid touching tip to any surface of the plate or wells.
- (21) Place PCR film over the PCR plate and use an automatic plate sealer to ensure the edges of all wells are sealed. Spin down the plate in the plate spinner to ensure all DNA is down in the master mix.
- (22) WGL has a BioRad brand plate sealer. Use the seal guard to keep the seal from shifting. Turn on the sealer and ensure it is up to temp. Seal 96 well plates at 180⁰C for 3 seconds and 384 well plates at 167⁰C for 3 seconds. Inspect the seal to ensure it is not loose, and all wells are sealed. If necessary to obtain reliable seals, temperature and time may be adjusted.
- (23) If you do not have a plate sealer, use a plate roller or paddle to ensure a good seal. It is imperative to have a good seal to prevent evaporation which will prevent data collection, and potentially contaminate the lab with amplified DNA.
- (24) Place the PCR plate in the thermal cycler, close and secure lid, and select the appropriate PCR thermal program. The thermal programs for the ACTM 1 & 3 duplex reaction is:
- (25) Initial denaturation at 95⁰C for 10 min
Followed by 40 cycles of:
95⁰C for 15 sec
60⁰C 1 min
- (26) Record the plate ID, thermal cycler unit or head, plate orientation, and run times for the PCR plate in the PCR log (Exhibit 10).
- (27) Place cycled PCR plates and product in trash can without opening the seal. Remove plates promptly.

- (28) Under no circumstances should you open or uncover PCR plates that have been cycled in the PCR room.

5.6.5 Standard curve material, preparation and storage

The use of standard curves in quantitative PCR applications allows for calculation of the initial starting copy number of target DNA in the aliquot of template used in each reaction. Standard curve materials will be synthetic strands of DNA purchased from a reliable production company. WGL will purchase G-block product from Integrated DNA Technologies, but other suitable vendors are allowed. To get reproducible and high quality standard curve data, it is important to store materials properly, and make serial dilutions fresh each week. Storing longer produces inaccurate results.

- (1) gblock standard curves
 - a. gblock is purchased so that it contains all 6 qPCR marker targets.
- (2) gblock is hydrated with TE buffer to make an initial dilution that is 1.00 E+10 copies per microliter. (an excel stock dilution calculator spreadsheet is on the shared drive at WGL).
 - a. Volume TE to add = $fmoles * 0.0000000000000001 * 6.022E+23 / 1.00E+10$
 - i. Mix well. Do not freeze this stock.
- (3) Use initial stock to make 10X freezer stock in several aliquots. Use screw-cap tubes with O-rings to prevent evaporation in the freezer.
 - a. Add 1.0 μ l of initial stock to 31.0 μ l 100ng/ μ l yeast tRNA in water. This 10X stock has 312,500 copies/ μ l.
- (4) Serial dilutions for use in assays should be made fresh weekly with the 10X stock and 100 ng/ μ l tRNA as a diluent. They may be stored frozen and thawed as needed throughout the week.
 - a. A **new** pipet tip **is required for each** dilution for accurate results.
 - b. After each addition, use the pipette to mix a **minimum** of 17 times.
 - c. Currently, a 5X curve is used at WGL.
 - i. 30 μ l working stock into 270 μ l tRNA. Mix 17 times = 31,250 copies
 - ii. 60 μ l of 31,250 mix into 240 μ l tRNA, mix 17 times = 6250 copies.
 - iii. 60 μ l of 6250 mix into 240 μ l tRNA, mix 17 times = 1250 copies
 - iv. 60 μ l of 1250 mix into 240 μ l tRNA, mix 17 times = 250 copies
 - v. 60 μ l of 250 mix into 240 μ l tRNA, mix 17 times = 50 copies
 - vi. 60 μ l of 50 mix into 240 μ l tRNA, mix 17 times = 10 copies

5.6.6 Internal Positive Control (for indicating inhibition)

The use of internal positive controls in qPCR is the most commonly used method to detect inhibition in laboratories spanning from clinical diagnostic settings, forensic settings to environmental research. WGL will use a novel mouse gene, HemT, which encodes for a hematopoietic cell-specific transcript. Known numbers of the HemT will be spiked into each well of the plate containing field samples, which will then be quantified using standard curves for that target. If fewer copies of the spike are measured in a sample, inhibition is assumed, and the extract will be cleaned up with a PCR clean-up kit (OneStep Inhibitor Removal kit by Zymo Research, Irvine, CA), and re-amplified. Samples will then continue through the eDNA workflow. This method will not determine what particular inhibitor may be present, and will only test for inhibition due to blockage of taq activity.

- (1) At WGL, all primers, probes, and the target ultramer will be purchased from Integrated DNA Technologies, but other providers may be used.
 - a. HemT Forward Primer = 5' TCTGAGTGTCCCTCGAATCT 3'
 - b. HemT Reverse Primer = 5' GCAGTCCTTGAGAACATAGAGC 3'

- c. HemT Probe = 5' Cy5/ZEN TGA CAG TCT CCT TTC GTG TGA ACA TTC G 3' IBQ
- d. Hem T Ultramer = 5' CTA CAT AAG TAA CAC CTT CTC ATG TCC AAA GCT CTC TGA GTG TCC CTC GAA TCT CAG ACG CTG TAT GAC AGT CTC CTT TCG TGT GAA CAT TCG GCT GCT CTA TGT TCT CAA GGA CTG CAC 3'

- (2) HemT primers should be hydrated, diluted to 5.0 μ M, and stored in small aliquots in the reagent room freezer.
- (3) The HemT probe should be diluted to 2.5 μ M and stored in small aliquots in the reagent room freezer.
- (4) HemT standard curves will be run on each plate, with the ACTM1 and 3 markers, but this will be a 10X curve. The table below indicates standard curve dilutions to be used. See Exhibit 13, page 1 for the PCR datasheet.

Standard dilution copy number of HemT IPC	Standard dilution copy number of ACTM 1 and ACTM 3 gBlock
10 ⁵	6250
10 ⁴	1250
10 ³	250
10 ²	50
10 ¹	10

- (5) The PCR cocktail recipe for the ACTM 1 and 3 assays have been adjusted to account for the spike. All unknown field samples and the PCR negative and PCR no template control samples will be made from master mixes including 100 copies of HemT per reaction. The recipe per reaction follows:
 - a. TaqMan Environmental Master Mix 2.0 = 10.0 μ L
 - b. HemT Primer Mix (5.0 μ M) = 1.0 μ L
 - c. HemT Probe (2.5 μ M) = 0.75 μ L
 - d. AC TM1/3 Primer Mix (10 μ M) = 1.0 μ L
 - e. AC TM1/3 Probe (2.5 μ M) = 1.0 μ L
 - f. IPC spike template (10²) = 1.0 μ L
 - g. ddH₂O = 2.25 μ L
- (6) 3.0 μ L of template is added to each reaction.
- (7) The PCR cocktail recipe for the standard curve samples differs because it does not include the IPC spiked sample. Only 1.0 μ L of each G-block standard dilution is used in these reactions.
 - a. TaqMan Environmental Master Mix 2.0 = 10.0 μ L
 - b. HemT Primer Mix (5.0 μ M) = 1.0 μ L
 - c. HemT Probe (2.5 μ M) = 0.75 μ L
 - d. AC TM1/3 Primer Mix (10 μ M) = 1.0 μ L
 - e. AC TM1/3 Probe (2.5 μ M) = 1.0 μ L
 - f. ddH₂O = 4.25 μ L
- (8) Analysis of results
 - a. The standard curve of the IPC must meet efficiency of 80-100% and R² >0.95.
 - b. The difference between the minimum and maximum C_q values of the PCR negatives, PCR no template controls, and the 10² standard dilutions will be used to define the expected C_q for the IPC in the samples.
 - c. Inhibition will be defined as any field sample with a C_q for the IPC that is greater than the reference C_q average by more than the range of C_qs used in the reference calculation or at least 1cycle if the range is less than one.

- d. The entire remaining extract of samples determined to be inhibited will be cleaned up with the PCR inhibitor clean up kit according to the manufacturer's directions and re-assayed with the ACTM1 and 3 markers.
- e. Uninhibited results will enter the normal workflow, negative results reported, and presumptive positive results screened with the confirmation assays.

5.7 Presumptive positive determination, confirmation positive determination and data management

5.7.1 Purpose

Once real-time data has been collected, the results must be documented, interpreted (i.e., scored), and archived.

5.7.2 Source

Following cycling, data files can be exported from the cyclers, analyzed with R-statistical package code, and results confirmed by visual examination of the trace data. Following data processing, samples determined as presumptive positive must be assayed with two additional reactions, one each for Silver and Bighead confirmation.

5.7.3 Presumptive Call Documentation and Storage Assurance

- (1) Assay quality must be assessed before data is accepted. Data must be exported as a *.txt file and saved into a folder named with the case number. File names must be carefully entered without any mistakes in spacing or coding. File names will follow this format: ddMONyy_initials_ASSAY_case#(sample#-sample#)_Plate#_cyclerSN. There should not be any spaces. Sample range should be integers separated with a dash. Plate numbers are designated as P1, P2, P3.....and no plate numbers should be repeated within an analysis day. Therefore, if there are 3 rounds of PCR, plate numbers should go from 1 to 24. Dates must be as depicted with a two-digit day, three letter CAP month, and two digit year. Initials are not case sensitive, but assay MUST BE CAPS.
- (2) Once text files are in the folder, the program R should be used to analyze the data. Output will include the following:
 - a. Summary statistics (StandardCurves.csv) on assay quality including the efficiency (E) and R^2 of the duplicate standard curves on each plate. Minimum requirements for accepting the data are $E=80-120\%$ and $R^2 \geq 0.95$. If necessary, errant standard curve points may be dropped to recover curve statistics, but there must be at least one 3-point curve remaining. This is acceptable, since the standard curves are for assessing assay performance only, and not for quantification of starting copy number. If the standard curves fail, the plate must be re-amplified.
 - b. Summary data for the total number of negative controls that were clean and the total number of positive controls that were positive, sorted into extraction vs PCR controls (AnalysisLog.txt). If there are any issues, the samples and controls must be re-processed at the step of failure. For example, if an extraction positive fails to amplify, all of the samples and controls must be re-extracted along with two new extraction controls and then re-amplified. If PCR controls fail, the plate must be re-amplified. If the problem is resolved with the re-do, the re-run data

should be used. If the problem still persists, then the data should be rejected and not reported. Document failed analyses on the data sheets and in the case log file.

- i. Rerun data should be exported as a txt file with the same naming convention, but saved within a folder nested within the folder with case results. The folder with re-run data must be named “reruns”, all lowercase one word.
 - c. A list of samples that had cycle thresholds less than or equal to 15 cycles that were changed to negative.
 - d. A list of presumptive positive samples (Presumptives.csv).
 - e. A table of data including the number of octets positive per sample and the average and standard deviation copy number for positive samples (DataSummary1.csv).
- (3) Enter the quality control summary data into the database in an Excel file and on the data sheet in the laboratory notebook, or in LIMS.
 - a. Notify the eDNA Processing Leader immediately of any cases with presumptive positive results.
- (4) All reports will reviewed by the eDNA Processing Leader before being reported.
- (5) A paper copy of the report should be held in the files for 5 years.
- (6) Electronic copies of all reports should be held for 5 years or longer, as space permits.
- (7) Any substantive revisions to the DNA amplification protocol must be approved by the eDNA Processing Leader and approved by the eDNA Coordinator. Any such changes must be incorporated into a revised QAPP.

5.7.4 Confirmation of Presumptive Positive Samples

- (1) Repeat section 5.6.4 for only the presumptive positive samples with the SCTM markers and with the BHTM markers. Recipes for the master mix are the same, except substitute the appropriate primers and probes. The PCR program is the same as well. Be sure to use silver carp positives for the SCTM marker and bighead positives for the BHTM marker assay.
- (2) Repeat section 5.7.3. to assess assay quality before accepting data.
- (3) All equipment controls for confirmed positive samples must be extracted with the same method as the samples, and assayed with ACTM 1 and 3, and as in section 5.6.4. If any equipment controls test positive, the result for that sample will not be included.
- (4) Final confirmed results are in the output file: DataSummary2.csv. This file is formatted so that if sorted by sample ID, the results may be copied and pasted into the case log file. Be sure to proof alignment of the paste by checking sample ID numbers randomly the full length of the case.
- (5) Notify the eDNA Processing Leader immediately of any cases with confirmed positive results.
- (6) Ensure that all raw data, output files from the thermocyclers and data analysis are in the case folder on the LIMS computer.

5.8 Communication of eDNA Assay Results and field data from WGL to USFWS Midwest Region Leadership

5.8.1 Purpose

To convey to Service designated personnel the progress and results of eDNA assays.

5.8.2 Source

WGL keeps a record of each samples progress through the eDNA assay procedure. These records are summarized for each batch for reporting to the eDNA Coordinator in USFWS Midwest Region.

Each field sampling agency keeps a record of field data. These records are summarized and reported to the eDNA Coordinator in USFWS Midwest Region via the eDNA database.

The eDNA Coordinator in USFWS Midwest Region collates field and lab data for reporting results to partners and the public.

5.8.3 Quality Control

The WGL eDNA Processing Leader will provide updates and reports to the USFWS Midwest Region eDNA Coordinator. At this time, Emy Monroe is the WGL eDNA Processing Leader and Kelly Baerwaldt is the USFWS Midwest Region eDNA Coordinator. Any permanent or temporary changes to either position should be communicated immediately to the assigned USFWS senior executive. Any permanent changes should be incorporated into a revised QAPP.

Any revisions to the reporting procedures must be approved by the eDNA Processing Leader and approved by the assigned USFWS senior executive. Any such changes should be incorporated into a revised QAPP.

5.8.4 General Procedure (for details see Appendix E for SOP)

The USFWS eDNA Processing Leader should, on every Friday during the period over which the WGL eDNA Team is processing samples, provide updates on all sample batches to the USFWS eDNA Coordinator. Reports should be organized by case and should consist of spreadsheets showing the stage of processing for each sample. Additionally, following approval by the eDNA Processing Leader, the WGL PRR should convey final results for each case (all samples confirmed as positive or negative for AC eDNA) within 24 hours of completion of processing for the last sample within a case.

The USFWS eDNA Coordinator may request updates from the eDNA processing leader at any point. The WGL eDNA Processing Leader is expected to respond as soon as possible during normal working hours.

SECTION 6 INTERNAL QUALITY CONTROL CHECKS

Details on quality control are found within each of the various protocol sections. In summary, however, quality control relative to sample contamination is covered by the transport (or cooler), equipment, DNA extraction, PCR, and sequencing blanks or negative controls. Quality control for efficacy of methodology, solutions, etc. is covered by positive controls for each sample handling step (extraction, PCR, and sequencing) of the eDNA protocol. Furthermore, each new solution or kit to be used in eDNA processing will be tested with positive and negative controls before or during the first use.

The WGL eDNA processing facility and protocols was reviewed by an ERDC audit shortly after completion of the transition plan and full deployment of Asian carp eDNA dedicated equipment.

6.1 Laboratory Quality Control Evaluation Criteria

Quality control is measured in two ways:

- If transport, filtering, centrifuge, hood, extraction, PCR, and DNA sequencing negative controls show product (e.g., bands in PCR or DNA sequence), the associated positive data are negated and, when possible, samples are reprocessed. Contamination of DNA extract will require that any positive samples be removed from consideration. If all other samples are negative, contamination was only an issue in the controls, and negative results may be reported.
- Positive controls are currently employed for extraction, PCR, and sequencing. If the positive controls fail to behave as expected, any sample showing an apparent lack of results will be rerun at the same time or following rerunning of the positive controls. This will be done until all positive controls produce the expected results.
- We incorporate two types of positive controls during sequencing. One positive control PCR products from positive control reactions and one sequencing reaction per plate with a standard DNA sequencing template (pGem) provided by the manufacturer. If less than a full plate is sequenced, one pGEM per batch of sequencing master mix made, and a minimum of one per plate eDNA samples that are sequenced. In the case that any of these fail, any samples that fail to produce sequence data that were run at the same time will be rerun at the same time as positive controls are rerun.
- In cases where fewer than 16 eDNA samples are sequenced, both types of positive sequence controls are still run.

SECTION 7 SPECIFIC ROUTINE PROCEDURES TO ASSESS DATA PRECISION, ACCURACY, AND COMPLETENESS

7.1 Field Methods and Laboratory Data

Use of quantitative PCR techniques provides regular and on-going assessment of accuracy and precision of laboratory analyses. The integrity of each plate analyzed is confirmed when the standard curves pass minimum requirements in 5.7.3.2a. Each standard curve represents a 5-fold dilution of carp DNA down to 10 copies.

Thus, the following 3 month assay no longer needs to be executed to document quality of data produced in the lab.

SECTION 8 CORRECTIVE ACTIONS

Corrective actions may be required for two classes of problems: analytical/equipment problems and noncompliance problems. Analytical and equipment-related problems may develop during sampling and sample handling, sample preparation, laboratory instrumental analysis, and data review. Noncompliance issues arise when eDNA sampling, processing or lab procedure execution deviates from procedures described in the QAPP.

In the case of analytical/equipment problems or deviations from set procedures (as outlined in QAPP), the responsible lead will determine if the problem or deviation will impact the accuracy of the resulting data. If it is determined that the problem or deviation does impact data accuracy, two courses of action may be followed:

- (1) If possible, the procedure is repeated until it is performed without any problem or deviation, or
- (2) The sample or samples are removed and not processed any further.

In either case, a corrective action report must be completed (Exhibit 16). Careful notes of any corrective actions and what incident led to them, as well as the resolution or preventative measure(s) identified will be carefully noted in the corrective action report, which must be provided electronically to all Leaders (Project Leader, Sampling Leader, etc.) as an after action report. The paper copy of the corrective action report will be maintained in the project file as a long-term record.

In the case that the responsible lead determines that data accuracy is not affected by the analytical/equipment problem or deviation from procedure, the sample or samples may continue to be processed. The responsible lead will make careful note of the incident in project records and include the rationale for continuing processing.

SECTION 9 PREVENTATIVE MAINTENANCE PROCEDURES

9.1 Field Equipment/Instruments

Hand-held or console installed sonar: Batteries will be changed at least once a month in hand-held units (if not required sooner) to ensure accurate readings of the instrument. In addition, reading accuracy should be checked prior to sampling season for all units. Depth readings may be checked by filling a container of a known depth with water and submerging the instrumentation. Temperature readings of the sonar may be checked against a thermometer. These records should be kept in ink in a bound notebook, where the originals are kept on site in a secure location and copies are sent to the eDNA Coordinator at the end of each sampling season.

GPS equipment: Batteries will be changed at least once a month (if not required sooner) to ensure accurate readings of the instrument. In addition, coordinate accuracy will be checked against known benchmarks.

DI equipment in the Trailer: Keep a bound hard-copy notebook in the trailer to record the total dissolved solids present each day the trailer is used. It should read zero.

Centrifuges: Annual service is a good idea if they are heavily used.

If filtering:

Plastic 2L sample bottles: After bleaching and autoclaving, bottles will be inspected for dents and/or warping of the material. Any bottle failing inspection will be disposed of and replaced.

Forceps: Forceps will be inspected monthly, and those exhibiting large amounts of rust will be disposed of and replaced.

Carboys: Carboys will be inspected monthly for cracks in the glass that could pose a safety hazard to filtering personnel. Any carboy failing inspection will be disposed of and replaced.

Plastic tubing: Plastic tubing used to connect the carboy to the manifold will be inspected monthly for cracks in the plastic. Any plastic tubing failing inspection will be disposed of and replaced.

All other laboratory equipment will be inspected monthly and undergo proper maintenance to maintain their ideal working condition. Any equipment not performing accurately or to established standards will be disposed of and replaced.

9.2 Laboratory Instruments

Pipettes: Annually all pipettes will be inspected, calibrated, and certified. Any pipette failing inspection and certification will be disposed of and replaced.

Any thermal-cycler head that fails the manufacturers self-test upon instrument startup will be removed and replaced with the manufacturer's certified replacement part.

Equipment maintenance contracts, with annual maintenance check-ups, will be used for any appropriate equipment (i.e., DNA sequencer).

SECTION 10 PERFORMANCE AND SYSTEM AUDITS

10.1 Field Audits

Internal audits of field crew performance and quality controls for sampling and filtering will be made semi-annually by the FWCO field staff to make sure that all procedures in the sample collection portions of the QAPP are being followed. On sampling trips where more than two FWCO offices are on the team, the visiting FWCO eDNA leader will serve as the sampling auditor. A brief report will be made to the eDNA Program Coordinator of audit findings, including a signed checklist of audited procedures (Exhibit 16). If there are no trips with coordinating offices, then the representative on the eTeam for USFWS Midwest Region may serve as the auditor for their office.

10.2 Laboratory Audits

Internal audits of WGL laboratory performance and quality controls will be made semi-annually by the DNA Processing Lead to make sure that all procedures in the DNA processing portions of the QAPP are being followed. A brief report will be made to the eDNA Program Coordinator of audit findings, including a signed checklist of audited procedures. Participation in validation studies by the lab may suffice as internal audits, and reports of such studies may be substituted and filed with the eDNA Program Coordinator. Every 2 years an external review of WGL eDNA processing will be undertaken. The review panel or consultant(s) will be selected by the Project Lead. The DNA Processing Lead may assist the Program Coordinator in identifying one or more potential reviewers.

SECTION 11 EXHIBITS

Exhibit 1. Field Collection Summary

Case Number _____	Sample Date _____	
Sampling Lead _____	Sampling QA/QC _____	Data Recorder _____
Location _____	Prep List (Initial and Date)	
Samples (range) _____	Blanks (CI) _____	Centrifuge tubes _____
Boat Ramp (lat, long) _____	Coolers bleached _____	
Water Collection Personnel	Tubes loaded _____	
Boat Operator _____	Blanks loaded _____	
Other Personnel _____	Boat cleaned _____	
	Boat cleaned _____	
Water Processing Personnel		
FWS Lead _____	FWS QA/QC _____	
Other Personnel _____		
Time Frame		
Start _____ End _____		
Tubes Iced _____		
Return to Lab/Filtering Trailer _____		
Other Notes: _____		
Map Attached		

Figure 2. A template for the Field Collection Summary. Its main purpose is to collect metadata and other important information for the sampling event.

Field Collection Supply List

Field Collection Supply List	Exhibit 1 page 2
Coolers	<input type="checkbox"/> sunglasses
<input type="checkbox"/> Labeled <u>containers</u>	
<input type="checkbox"/> Field blanks	Devices
Clipboard	<input type="checkbox"/> Charged GNSS Receiver
<input type="checkbox"/> pencils/pens	<input type="checkbox"/> Charged iPad(s)
<input type="checkbox"/> Data sheets	<input type="checkbox"/> Car/USB Charger for iPad and Receiver
<input type="checkbox"/> GPS	
<input type="checkbox"/> Extra batteries for GPS	Drinking water
<input type="checkbox"/> Maps	
<input type="checkbox"/> Hard Copy of ArcGIS Collector App Instructional Manual	
<input type="checkbox"/> Drybag	
<input type="checkbox"/> Gloves	
<input type="checkbox"/> Depth/temp device	
<input type="checkbox"/> Wet Wipes	
<input type="checkbox"/> Sunblock	
Others	
<input type="checkbox"/> bleach	
<input type="checkbox"/> mop	
<input type="checkbox"/> bucket	
<input type="checkbox"/> camera	
<input type="checkbox"/> <u>ipass</u>	
<input type="checkbox"/> Life jackets	
<input type="checkbox"/> Filed float <u>plan</u>	

Figure 3. The Field Collection Supply List is page 2 of Exhibit 1. A checklist of recommended items for eDNA sampling according to QAPP procedures.

Exhibit 2. Field Collection Data Sheet

CASE NUMBER _____ DATE _____ NAME _____ START TIME _____ Volume: 2L or 5x50ml SHEET ___ of ___

Sample ID	Wind Direction	Way-point	Latitude (dec.degrees)	Longitude (dec.degrees)	Temp (C/F)	Depth (m/ft)	Blank (B)	Habitat (LDB/MC/RDB /BAY/TRB)	Collect time	Processing time	Processor Initials

Notes/comments:

Figure 4. A template for the Field Collect Data Sheet. Each sample should have all the corresponding metadata fields filled out at the time and location in which the sample is taken.

Exhibit 3. Chain-of-custody Form

US Fish & Wildlife Service		<u>CHAIN-OF-CUSTODY RECORD</u>		
Date and time of collection:		Collected by (first and last names):		
Notes:				
Case Number:				
All control samples must also be listed and accounted for. The chain of signatures should be continuous.				
Sample Numbers	From: (Print name, Agency)	Release signature:	Release Date:	Delivered via: • FedEx • In Person • Other:
	To: (Print name, Agency)	Receipt signature:	Receipt Date:	
Sample Numbers	From: (Print name, Agency)	Release signature:	Release Date:	Delivered via: • FedEx • In Person • Other:
	To: (Print name, Agency)	Receipt signature:	Receipt Date:	
Sample Numbers	From: (Print name, Agency)	Release signature:	Release Date:	Delivered via: • FedEx • In Person • Other:
	To: (Print name, Agency)	Receipt signature:	Receipt Date:	
Sample Numbers	From: (Print name, Agency)	Release signature:	Release Date:	Delivered via: • FedEx • In Person • Other:
	To: (Print name, Agency)	Receipt signature:	Receipt Date:	
Sample Numbers	From: (Print name, Agency)	Release signature:	Release Date:	Delivered via: • FedEx • In Person • Other:
	To: (Print name, Agency)	Receipt signature:	Receipt Date:	
Sample Numbers	From: (Print name, Agency)	Release signature:	Release Date:	Delivered via: • FedEx • In Person • Other:
	To: (Print name, Agency)	Receipt signature:	Receipt Date:	
Sample Numbers	From: (Print name, Agency)	Release signature:	Release Date:	Delivered via: • FedEx • In Person • Other:
	To: (Print name, Agency)	Receipt signature:	Receipt Date:	

Figure 5. A template of the Chain of Custody Form. This form should be updated throughout the progression of the case and completed for each case of samples. The main purpose of this form is to document the exchange of samples via shipping or drop off.

Exhibit 4. USFWS WGL Sample Receipt Checklist

Case Number:	Receipt Date:
Other:	Rec'd by:
Were samples shipped? Yes, FEDEX/UPS/Other No, Courier pickup/ <u>hand</u> delivered	Comments:
Cooler temp upon arrival C/NA	
Chain-of-custody (COC) present? Yes/ <u>no</u> Complete? Yes/no	
Custody seals present on <u>cooler</u> ? Yes/no Samples? Yes/no	
Were sample containers intact? Yes/no	
Samples and COC match? Yes/no	
If any problems, was project manager notified? Yes/no By whom? _____	
Appropriate sample containers? Yes/no	
Date/time of collection on COC Yes/no	
Location and ID of sample storage: Freezer _____ Refrigerator _____	
Temperature log updated for <u>storage</u> ? Yes/no	

Figure 6. A template of the USFWS WGL Sample Receipt Checklist. This document serves as a record of the condition of samples when they are received into the lab and as a record of receipt into WGL custody.

Exhibit 5. Screen Capture of Excel Log File, First Worksheet

Priority	Case Number	Number of Samples	Check-in Date	Sample progress	Status (Open/)	Confirmed Positives (number of samples)		Quality Control Success (Y/N)			
						Silver Carp	Bighead Carp	Extraction Control	PCR Control	# Inhibited	Equip Control
1	10104	23	19-Mar-15	complete	OPEN	0	0	Y	Y	0	0
2						#REF!	#REF!	#REF!	#REF!		#REF!
3						#REF!	#REF!	#REF!	#REF!		#REF!
4						#REF!	#REF!	#REF!	#REF!		#REF!
5						#REF!	#REF!	#REF!	#REF!		#REF!
6						#REF!	#REF!	#REF!	#REF!		#REF!
7						#REF!	#REF!	#REF!	#REF!		#REF!
8						#REF!	#REF!	#REF!	#REF!		#REF!
9						#REF!	#REF!	#REF!	#REF!		#REF!
10						#REF!	#REF!	#REF!	#REF!		#REF!
11						#REF!	#REF!	#REF!	#REF!		#REF!
12						#REF!	#REF!	#REF!	#REF!		#REF!
13						#REF!	#REF!	#REF!	#REF!		#REF!
14						#REF!	#REF!	#REF!	#REF!		#REF!
15						#REF!	#REF!	#REF!	#REF!		#REF!
16						#REF!	#REF!	#REF!	#REF!		#REF!
17						#REF!	#REF!	#REF!	#REF!		#REF!
18						#REF!	#REF!	#REF!	#REF!		#REF!
19						#REF!	#REF!	#REF!	#REF!		#REF!
20						#REF!	#REF!	#REF!	#REF!		#REF!
21						#REF!	#REF!	#REF!	#REF!		#REF!
22						#REF!	#REF!	#REF!	#REF!		#REF!
23						#REF!	#REF!	#REF!	#REF!		#REF!
24						#REF!	#REF!	#REF!	#REF!		#REF!
25						#REF!	#REF!	#REF!	#REF!		#REF!
26						#REF!	#REF!	#REF!	#REF!		#REF!
27						#REF!	#REF!	#REF!	#REF!		#REF!
28						#REF!	#REF!	#REF!	#REF!		#REF!
29						#REF!	#REF!	#REF!	#REF!		#REF!
30						#REF!	#REF!	#REF!	#REF!		#REF!
31						#REF!	#REF!	#REF!	#REF!		#REF!
32						#REF!	#REF!	#REF!	#REF!		#REF!
33						#REF!	#REF!	#REF!	#REF!		#REF!
34						#REF!	#REF!	#REF!	#REF!		#REF!
35						#REF!	#REF!	#REF!	#REF!		#REF!
36						#REF!	#REF!	#REF!	#REF!		#REF!
37						#REF!	#REF!	#REF!	#REF!		#REF!
38						#REF!	#REF!	#REF!	#REF!		#REF!
39						#REF!	#REF!	#REF!	#REF!		#REF!
40						#REF!	#REF!	#REF!	#REF!		#REF!
41						#REF!	#REF!	#REF!	#REF!		#REF!
42						#REF!	#REF!	#REF!	#REF!		#REF!

Figure 7. Screen capture of Excel log file. First worksheet in workbook outlines log for all sampling events or cases which correspond to samples from a particular system. Subsequent worksheets are created for each case and allow for sample tracking through the eDNA lab. This will be used until a Laboratory Information System (LIMS) is adopted. "REF" in cells is due to formulae already entered into the form, which will work once data are entered.

Exhibit 6. Screen Capture of Excel Log File, Sample Log Open

Case #:		Samples		Equipment Control Result		Totals		Quality Control pass (y/n)		Enter data for QC in the line corresponding to the last sample in the processing batch. Extraction batches are 48 samples, but multiple filters will affect total sample batch size. A PCR batch corresponds to the total number of reactions mixed in one master mix. If enough mix was made for two plates, that Be sure to enter "-" in cells that don't need data entered.															
Case #:		Samples		Equipment Control Result		Presumptive +		Quality Control pass (y/n)		For EC use 1 or 0															
Case #:		Samples		Equipment Control Result		Presumptive +		Quality Control pass (y/n)		Quality Control Checks															
Sample ID	Date of Receipt	Initials	Extraction Date	Initials	sample	PCR 1 Date	Initials	Presumptive +	PCR Date	Initials	Confirmed +	PCR Date	Initials	Confirmed +	Run Equipment	Equipment	Initials	EXT - control	Centrifuge -	Hood -	EXT - control	Sample Range	PCR + control	PCR + control	PCR + control
case	smpl						per1	AC	BHC	BHC	BHC	SVC	SVC	SVC	Control (y or n)	Control Result		#-s of 8 reps	Control Range	Control Range	#-s of 8 reps	for EXT controls	#-s of 2 reps	#-s of 2 reps	#-s of 2 reps
0 001															n	-	-	-	-	-	-	-	-	-	-
0 002															n	-	-	-	-	-	-	-	-	-	-
0 003															n	-	-	-	-	-	-	-	-	-	-
0 004															n	-	-	-	-	-	-	-	-	-	-
0 005															n	-	-	-	-	-	-	-	-	-	-
0 006															n	-	-	-	-	-	-	-	-	-	-
0 007															n	-	-	-	-	-	-	-	-	-	-
0 008															n	-	-	-	-	-	-	-	-	-	-
0 009															n	-	-	-	-	-	-	-	-	-	-
0 010															n	-	-	-	-	-	-	-	-	-	-
0 011															n	-	-	-	-	-	-	-	-	-	-
0 012															n	-	-	-	-	-	-	-	-	-	-
0 013															n	-	-	-	-	-	-	-	-	-	-
0 014															n	-	-	-	-	-	-	-	-	-	-
0 015															n	-	-	-	-	-	-	-	-	-	-
0 016															n	-	-	-	-	-	-	-	-	-	-
0 017															n	-	-	-	-	-	-	-	-	-	-
0 018															n	-	-	-	-	-	-	-	-	-	-
0 019															n	-	-	-	-	-	-	-	-	-	-
0 020															n	-	-	-	-	-	-	-	-	-	-
0 021															n	-	-	-	-	-	-	-	-	-	-
0 022															n	-	-	-	-	-	-	-	-	-	-
0 023															n	-	-	-	-	-	-	-	-	-	-
0 024															n	-	-	-	-	-	-	-	-	-	-
0 025															n	-	-	-	-	-	-	-	-	-	-
0 026															n	-	-	-	-	-	-	-	-	-	-
0 027															n	-	-	-	-	-	-	-	-	-	-
0 028															n	-	-	-	-	-	-	-	-	-	-
0 029															n	-	-	-	-	-	-	-	-	-	-
0 030															n	-	-	-	-	-	-	-	-	-	-
0 031															n	-	-	-	-	-	-	-	-	-	-
0 032															n	-	-	-	-	-	-	-	-	-	-
0 033															n	-	-	-	-	-	-	-	-	-	-
0 034															n	-	-	-	-	-	-	-	-	-	-
0 035															n	-	-	-	-	-	-	-	-	-	-
0 036															n	-	-	-	-	-	-	-	-	-	-
0 037															n	-	-	-	-	-	-	-	-	-	-
0 038															n	-	-	-	-	-	-	-	-	-	-
0 039															n	-	-	-	-	-	-	-	-	-	-
0 040															n	-	-	-	-	-	-	-	-	-	-
0 041															n	-	-	-	-	-	-	-	-	-	-
0 042															n	-	-	-	-	-	-	-	-	-	-
0 043															n	-	-	-	-	-	-	-	-	-	-
0 044															n	-	-	-	-	-	-	-	-	-	-
0 045															n	-	-	-	-	-	-	-	-	-	-
0 046															n	-	-	-	-	-	-	-	-	-	-
0 047															n	-	-	-	-	-	-	-	-	-	-
0 048															n	-	-	-	-	-	-	-	-	-	-
0 049															n	-	-	-	-	-	-	-	-	-	-

Figure 8. Screen capture of Excel log file with the first case sample log open. Samples are tracked by date and process step through the lab. Corresponding quality control results by extraction batch and PCR batch are reported with sample results. Quality control columns continue to right, to include all markers tested through confirmation.

Exhibit 7. Example of -20 Freezer Temperature Log

Freezer Temperature Log

Month: _____ Year: _____

Freezer ID: _____ Freezer Location: _____

Day	Displayed Temp	Date	Initials	Maintenance (Y/N)
1				
2				
3				
4				
5				
6				
7				
8				
9				
10				
11				
12				
13				
14				
15				
16				
17				
18				
19				
20				
21				
22				
23				
24				
25				
26				
27				
28				
29				
30				
31				

78

Temperature should be between -23 and -17 °C for recording.

Figure 9. A template for the daily -20 freezer temperature log. Temperature should be between -23 and -17 C for recording.

Exhibit 8. Daily log for cold storage coolers, used in processing trailers to keep samples cold until shipment to WGL.

Cooler Temperature Log

Case#: _____

Sample IDs	Date	Time (am/pm)	Displayed Temp	Initials

Figure 10. A template for the daily log for storage coolers.

Exhibit 9. Example of -80 Freezer Temperature and Sample Storage Log

Example of -80 freezer temperature and sample storage log. All cold storage appliances that store samples after receipt but before extraction, or store archived extracts have a temperature log and a sample log. The temperature log is filled out daily and the sample log each time samples are removed or stored.

Ultra Low Freezer Temperature Log

Month: _____ Year: _____

Freezer ID: _____ Freezer Location: _____

Day	Temp in range (Y/N)	Date	Initials	Maintenance (Y/N)
1				
2				
3				
4				
5				
6				
7				
8				
9				
10				

Figure 11. A template of the Ultra Low Freezer Temperature Log.

-80 °C Sample Log

Freezer ID and Location: _____

Line Number	Case # and sample numbers CHECKED IN	Sample number range, state action taken (ex: extraction). Date and Initial CHECKED OUT.			

Figure 12. A template of the -80 °C Sample log.

Exhibit 10. Example of Ambient Temperature Sample Storage Log

Bench-top Shelving Log

Room _____

Line Number	Case # and sample numbers CHECKED IN	Sample number range, state action taken (ex: extraction). Date and Initial CHECKED OUT.			

Figure 13. Example of ambient temperature (alcohol-preserved centrifuge samples only) sample storage log. The sample log is filled out each time samples are removed or stored.

Exhibit 11. Thermocycler log

PCR Log

Month: _____ Year: _____

Machine ID: _____ Machine Location: _____

Plate ID	PCR Machine ID	Plate Orientation	PCR Program	Run Start Time	Run Finish Time	Date/Initials

Figure 14. A template of a PCR Thermocycle log. It should be filled out at the start of a PCR run and completed at the conclusion of a PCR run.

Exhibit 12. Extraction Data Sheet

Extraction data sheet: to be filled out and taped into Extraction room data [book](#)

"copy" watermark is grey on original.

Analyst _____ Room# _____ Date _____ Sample batch _____

Reagents used: note lot ID and expiration date for kit [components](#)

Reagent/tubes	Lot #	Expiration date
GSB buffer		
Proteinase K		
Ethanol		
W1 buffer		
Wash buffer		
Elution buffer (at 60°C)		
Spin filter		

Start time _____

Tube ID	Sample ID	Tube ID	Sample ID
1		25	
2		26	
3		27	
4		28	
5		29	
6		30	
7		31	
8		32	
9		33	
10		34	
11		35	
12		36	
13		37	
14		38	
15		39	
16		40	
17		41	
18		42	
19		43	
20		44	
21		45	
22		46	
23		47	Extraction Negative
24		48	Extraction Positive

Write notes for any deviations from QAPP or lab blunders on facing page of lab book.

Figure 15. A template data sheet for a IBI extraction. This should be completed for each extraction event.

Exhibit 13. 384 well plate Asican Carp General qPCR data sheet

ERDC AC TM1/3 IPC qPCR data sheet: to be filled out and taped into PCR room data book

Analyst _____ date _____ Kit or sample batch _____

Reagents and recipe: note batch (for diluted working primers), or lot ID and expiration date

SAMPLE PLATE MM

Reagent name	Volume per rxn	Volume for ___ rxns	Lot or ID #	Expiration date
TM Env. Master Mix	10.0 µl	µl		
HemT Primer Mix (5.0 µM)	1.0 µl	µl		
HemT Probe (2.5 µM)	0.75 µl	µl		
AC TM1/3 Primer Mix (10 µM)	1.0 µl	µl		
AC TM1/3 Probe (2.5 µM)	1.0 µl	µl		
IPC spike template (10 ³)	1.0 µl	µl		
ddH ₂ O	2.25 µl	µl		

3.0ul template

STANDARD MM

Reagent name	Volume per rxn	Volume for ___ rxns	Lot or ID #	Expiration date
TM Env. Master Mix	10.0 µl	µl	SEE ABOVE FOR LOTS AND EXPIRATIONS	
HemT Primer Mix (5.0 µM)	1.0 µl	µl		
HemT Probe (2.5 µM)	0.75 µl	µl		
AC TM1/3 Primer Mix (10 µM)	1.0 µl	µl		
AC TM1/3 Probe (2.5 µM)	1.0 µl	µl		
ddH ₂ O	4.25 µl	µl		

1 µl ERDC g-block and 1µl IPC standard

Plate Name _____

ddMONyy Initials ASSAY case(sample#-sample#) P#

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	
A																								POS	
B																									6250 10 ⁴
C																									1250 10 ⁴
D																									250 10 ⁴
E																									50 10 ⁴
F																									10 10
G																									NTC
H																									NEG
I																									POS
J																									6250 10 ⁴
K																									1250 10 ⁴
L																									250 10 ⁴
M																									50 10 ⁴
N																									10 10
O																									NTC
P																									NEG

Cycler ID _____

Did cycle complete Y N

Time started _____

Time removed _____

Figure 16. Page 1 of 2 of a template for a data sheet used during qPCR with a 384 -well plate for Asian Carp.

384-well Plate Asian carp general qPCR data sheet, page 2

Plate Name _____
ddMONyy_Initials_ASSAY_case(sample#-sample#)_P#

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	
A																								POS	
B																									6250 10 ⁶
C																									1250 10 ⁵
D																									250 10 ⁴
E																									50 10 ³
F																									10 10
G																									NTC
H																									NEG
I																									POS
J																									6250 10 ⁶
K																									1250 10 ⁵
L																									250 10 ⁴
M																									50 10 ³
N																									10 10
O																									NTC
P																									NEG

Cycler ID _____ Did cycle complete Y N
 Time started _____ Time removed _____

Plate Name _____

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	
A																									POS
B																									6250 10 ⁶
C																									1250 10 ⁵
D																									250 10 ⁴
E																									50 10 ³
F																									10 10
G																									NTC
H																									NEG
I																									POS
J																									6250 10 ⁶
K																									1250 10 ⁵
L																									250 10 ⁴
M																									50 10 ³
N																									10 10
O																									NTC
P																									NEG

Cycler ID _____ Did cycle complete Y N
 Time started _____ Time removed _____

Figure 17. Page 2 of 2 of a template data sheet used during qPCR with a 384 well plate for Asian carp.

Exhibit 14. 96-well Plate Asian carp general qPCR data sheet

ERDC AC TM1/3 qPCR data sheet: to be filled out and taped into PCR room data book

Analyst _____ date _____ Kit or sample batch _____

Reagents and recipe: note batch (for diluted working primers), or lot ID and expiration date

SAMPLE PLATE MM

Reagent name	Volume per rxn	Volume for rxns	Lot or ID #	Expiration date
TM Eny. Master Mix	10.0 µl	_____ µl		
AC TM1/3 Primer Mix(10 µM)	1.0 µl	_____ µl		
AC 1/3 Probes (2.5 µM)	1.0 µl	_____ µl		
ddH ₂ O	5.0 µl	_____ µl		

3.0 µl template

STANDARD MM

Reagent name	Volume per rxn	Volume for rxns	Lot or ID #	Expiration date
TM Eny. Master Mix	10.0 µl	_____ µl	SEE ABOVE FOR LOTS AND EXPIRATIONS	
AC TM1/3 Primer Mix(10 µM)	1.0 µl	_____ µl		
AC 1/3 Probes(2.5 µM)	1.0 µl	_____ µl		
ddH ₂ O	7.0 µl	_____ µl		

1.0 µl g-block standard

Plate Name _____

ddMONyy_Initials_ASSAY_case(sample#-sample#)_P#

	1	2	3	4	5	6	7	8	9	10	11	12
A											POS	POS
B											6250 10 ⁵	6250 10 ⁵
C											1250 10 ⁴	1250 10 ⁴
D											250 10 ³	250 10 ³
E											50 10 ²	50 10 ²
F											10 10	10 10
G											NTC	NTC
H											NEG	NEG

Notes for any lab blunders or deviations from protocol:

Cycler ID _____ Did cycle complete Y N

Time started _____ Time removed _____

Figure 18. A template data sheet used during qPCR with a 96 well plate for Asian Carp.

Exhibit 15. 96-well Silver carp qPCR plate for confirmation of presumptive positive samples

ERDC SC TM4/5 qPCR data sheet: to be filled out and taped into PCR room data book

Analyst _____ date _____ Kit or sample batch _____

Reagents and recipe: note batch (for diluted working primers), or lot ID and expiration date

SAMPLE PLATE MM

Reagent name	Volume per rxn	Volume for ___ rxns	Lot or ID #	Expiration date
TM Env. Master Mix	10 µl	µl		
SCTM 4 Primers (10 µM)	1.0 µl	µl		
SCTM 5 Primers (10 µM)				
SCTM 4/5 Probes (2.5µM)	1.0 µl	µl		
ddH ₂ O	5 µl	µl		

3 µl template

STANDARD MM

Reagent name	Volume per rxn	Volume for ___ rxns	Lot or ID #	Expiration date
TM Env. Master Mix	10.0 µl	µl	SEE ABOVE FOR LOTS AND EXPIRATIONS	
SCTM 4 Primers (10 µM)	1.0 µl	µl		
SCTM 5 Primers(10µM)				
SC TM 4/5 Probe (2.5 µM)	1.0 µl	µl		
ddH ₂ O	7 µl	µl		

1 µl ERDC g-block

Plate Name _____

ddMONyy_Initials_ASSAY_case(sample#-sample#)_P#

	1	2	3	4	5	6	7	8	9	10	11	12
A											POS	POS
B											6250	6250
C											1250	1250
D											250	250
E											50	50
F											10	10
G											NTC	NTC
H											NEG	NEG

Notes for any lab blunders or deviations from protocol:

Cycler ID _____ Did cycle complete Y N
 Time started _____ Time removed _____

Figure 19. A template data sheet used during qPCR with a 96 well plate for Silver Carp.

Exhibit 16. 96-well Bighead carp qPCR plate for confirmation of presumptive positive samples

ERDC BH TM1/2 qPCR data sheet: to be filled out and taped into PCR room data book

Analyst _____ date _____ Kit or sample batch _____

Reagents and recipe: note batch (for diluted working primers), or lot ID and expiration date

SAMPLE PLATE MM

Reagent name	Volume per rxn	Volume for _____ rxns	Lot or ID #	Expiration date
TM <u>Envy</u> Master Mix	10 µl	_____ µl		
BH TM1 Primers (10 µM)	1.0 µl	_____ µl		
BH TM2 Primers (10 µM)				
BH TM 1/2 Probes (2.5µM)	1.0 µl	_____ µl		
ddH ₂ O	5 µl	_____ µl		

3 µl template

STANDARD MM

Reagent name	Volume per rxn	Volume for _____ rxns	Lot or ID #	Expiration date
TM <u>Envy</u> Master Mix	10.0 µl	_____ µl	SEE ABOVE FOR LOTS AND EXPIRATIONS	
BH TM1 Primers (10 µM)	1.0 µl	_____ µl		
BH TM2 Primers (10 µM)				
BH TM 1/2 Probe (2.5 µM)	1.0 µl	_____ µl		
ddH ₂ O	7 µl	_____ µl		

1 µl ERDC g-block

Plate Name _____

ddMONyy. Initials. ASSAY. case(sample#-sample#). P#

	1	2	3	4	5	6	7	8	9	10	11	12
A											POS	POS
B											6250	6250
C											1250	1250
D											250	250
E											50	50
F											10	10
G											NTC	NTC
H											NEG	NEG

Notes for any lab blunders or deviations from protocol:

Cycler ID _____ Did cycle complete Y N

Time started _____ Time removed _____

Plate Name _____

Figure 20. . A template data sheet used during qPCR with a 96 well plate for Bighead Carp.

Exhibit 17. 384-well Bluegill qPCR plate for positive extraction controls

Bluegill qPCR data sheet: to be filled out and taped into PCR room data book

Analyst _____ Date _____ Samples _____

Reagents and recipe: note batch (for diluted working primers), or lot ID and expiration date

Reagent name	Volume per rxn	Volume for _____ rxns	Lot or ID #	Expiration date
TaqMan Env. Master Mix	13.4 µl	µl		
Forward Primer 10µM	1.8 µl	µl		
Reverse Primer 10µM	1.8 µl	µl		
Probe (2.5µM)	1.0 µl	µl		

2 µl template

Plate Name _____

ddMONyy_Initials_ASSAY_case(sample#-sample#)_P#

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	
A																								POS	
B																									18750
C																									3750
D																									750
E																									150
F																									30
G																									NTC
H																									NEG
I																									POS
J																									18750
K																									3750
L																									750
M																									150
N																									30
O																									NTC
P																									NEG

Notes for any lab blunders or deviations from protocol:

Cycler ID _____ Did cycle complete Y N
 Time started _____ Time removed _____

Figure 21. A template data sheet used during qPCR with a 384 well plate for Bluegill positive extraction controls.

Exhibit 18. 96-well Bluegill qPCR plate for positive extraction controls

Bluegill qPCR data sheet: to be filled out and taped into PCR room data book

Analyst _____ Date _____ Samples _____

Reagents and recipe: note batch (for diluted working primers), or lot ID and expiration date

Reagent name	Volume per rxn	Volume for ___ rxns	Lot or ID #	Expiration date
TagMan Env. Master Mix	13.4 µl	µl		
Forward Primer 10µM	1.8 µl	µl		
Reverse Primer 10µM	1.8 µl	µl		
Probe (2.5µM)	1.0 µl	µl		

2 µl template

Plate Name _____

ddMONyy_Initials_ASSAY_case(sample#-sample#)_P#

	1	2	3	4	5	6	7	8	9	10	11	12
A											POS	POS
B											18750	18750
C											3750	3750
D											750	750
E											150	150
F											30	30
G											NTC	NTC
H											NEG	NEG

Notes for any lab blunders or deviations from protocol:

Cycler ID _____

Did cycle complete Y N

Time started _____

Time removed _____

Figure 22. A template data sheet used during qPCR with a 96 well plate for Bluegill positive extraction controls

Exhibit 19. Quality Assurance Project Plan Certification Statement

I, the undersigned, certify that I have read and that I understand the Quality Assurance Project Plan (QAPP) for the eDNA monitoring of Invasive Asian Carp. I further certify that I will follow the procedures listed in this QAPP.

Signed:

Name
Agency
Date

Exhibit 20. Quality Control Audit Checklist for Field Sampling and Water Processing

This must be filled out after each trip and sent to the eDNA Program Coordinator along with your post trip report highlighting any differences between actual executed work and the pre-trip field plan.

I, _____ Sampling Quality Lead _____, observed sampling processing for case# _____ collected on _____, from the following locations: _____, by the following personnel _____.

During this time, I compared the actions of the crew to the QAPP and witnessed adherence to the QAPP in the following: A check indicates compliance with the QAPP. An X indicates the QAPP was not followed and a short explanation follows. If more space is needed, attach a written report.

Contamination Prevention:

Boat and equipment preparation _____

Sample collection and navigation _____

I, _____ Processing Quality Lead _____, observed sampling processing for case# _____ collected on _____, from the following locations: _____, by the following personnel _____.

During this time, I compared the actions of the crew to the QAPP and witnessed adherence to the QAPP in the following: A check indicates compliance with the QAPP. An X indicates the QAPP was not followed and a short explanation follows. If more space is needed, attach a written report.

Contamination Prevention:

Sample processing equipment _____

Sample processing procedures _____

Explanation for deviation(s) from the QAPP: _____

SECTION 12. APPENDICES

Appendix A. Roles and Responsibilities And Annual Staff Assignments

As of September 2014, the following staff are assigned to the eDNA monitoring project.

eDNA Program Coordinator: Kelly Baerwaldt, USFWS, 309-429-1442

eDNA Processing Leader: Emy Monroe, WGL, 608-783-8402

DNA Processing Quality Assurance Specialist: Maren Tuttle-Lau, WGL, 608-783-8403

Data Documentation & Reporting Specialist: Nikolas Greuneis, WGL, 608-783-8404

Fish and Wildlife Conservation Office Points of Contact:

La Crosse: Ann Runstrom, 608-783-8433

Columbia: Patty Herman, 573-234-2132 x 170

Cartersville: Sam Finney, 618-997-6869 x 17

Green Bay: Mark Holey, 920-866-1760

Ashland: Mark Brouder, 715-682-6185 x11

Alpena: Scott Koproski, 989-356-3052 x 1023

USFWS Midwest and Northeast Region
eDNA Roles and Responsibilities
September 2014

ROLES

Regional Office

Region 3 Deputy RD/National Asian Carp Lead: Charlie Wooley
Fisheries ARD: Todd Turner
Deputy ARD/FWS National Asian Carp Plan Coordinator: Aaron Woldt
R3 AIS Coordinator: Mike Hoff
R5 AIS Coordinator: Sandra Keppner
R3 Asian Carp/eDNA Coordinator: Kelly Baerwaldt
R3 FWCO Program Supervisor: Brian Elkington

Midwest Fisheries Center

Center Director: Teresa Lewis

Whitney Genetics Lab

Supervisory Molecular Geneticist: (acting) Emy Monroe

Fish and Wildlife Conservation Offices

Project Leaders: Mark Holey, Mark Brouder, Jason Goeckler, Scott Koproski, Rob Simmonds, Sam Finney, Kofi Fynn-Aikins

eDNA Point Of Contact's: Alpena: Chris Olds; Green Bay: Tim Strakosh; Ashland: Mark Brouder (or designee); Carterville: Jeff Stewart; Columbia: Emily Pherigo; LaCrosse: Jenna Merry; Lower Great Lakes (Region 5): Sandy Keppner

RESPONSIBILITIES

Deputy ARD/National Asian Carp Plan Coordinator:

Regional oversight of all Asian carp and eDNA activities. Senior level authority on all decisions on eDNA sampling program.

Region 3/5 Aquatic Invasive Species Coordinators:

National Aquatic Invasive Species Subject Matter Expert on development and implementation of processes and strategies for aquatic invasive species (AIS) management, providing regional project leadership on DOI initiatives addressing AIS management. Provides technical assistance for development and application of new scientifically based concepts and improved technology in AIS prevention and control. Leads interagency and interregional efforts to develop and implement programs for early detection and rapid response processes.

Region 3 Asian Carp/eDNA Coordinator:

Regional Office staff specialist responsible for development, coordination and implementation of the Midwest Region's eDNA monitoring program for Asian carps. Reports to the Deputy Assistant Regional Director. Assumes principal responsibility for initiating, leading, facilitating, integrating, coordinating, and communicating necessary monitoring work and activities using eDNA of the Midwest Region's Fisheries eDNA Program through the cooperative conservation community. Provides guidance for implementing and utilizing eDNA activities at the field level. Provides technical leadership to plan, conduct and lead other biologists as well as coordinate activities to identify and coordinate selection of surveillance areas in water bodies for the early detection of Asian carp eDNA. Ensures the best scientific practices are used during the development and implementation of management plans to monitor, control, and eradicate Asian carp. Implements and coordinates the Regional eDNA collection program; eDNA processing and interpretation of data; collection and dissemination of research information from institutions and research agencies on findings and new developments in eDNA collection and interpretation of data

and the development of Asian carp management plans. Responsible for the QAPP and coordinating its implementation with the FWCOs and lab, as well as ensures that field offices and laboratory staff receive proper training to adhere to the procedures identified within. Responsible for communication between the lab field offices, and Regional office. Integration with interagency ECALS team and other relevant entities (Academia, etc). Responsible for external communication with partners regarding eDNA programmatic changes (eg. Marker development, extraction techniques), collections, and results. Regularly communicates with the FWCO Program Supervisor, Supervisory Molecular Geneticist, and Center Director to ensure a high level of quality and scientific rigor with respect to field operations.

Region 3 FWCO Program Supervisor:

Responsible for the implementation and delivery of the FWS fisheries program through the Fish and Wildlife Conservation field offices of the Midwest region. Direct supervisor of the Project Leaders of FWCOs and Midwest Fisheries Center. Responsible for developing overall program direction and budget needs for FWCOs. In addition to managing the assigned field stations, serves the role of coordinating and integrating their operations with other Fishery Program operations, and ensuring cooperative and productive partnerships with the Upper Midwest and Great Lakes, Eastern Tallgrass Prairie and Big Rivers, Plains and Prairie Potholes, and Ozark Plateau Landscape Conservation Cooperatives and between the Midwest and Northeast Regions.

Midwest Fisheries Center Director:

Responsible for overseeing the delivery implementation of the eDNA program at Whitney Genetics Lab which includes: sample receipt and processing and reporting of results to the eDNA Program Coordinator. Will report any eDNA related issues/questions to Asian carp/eDNA coordinator and/or National Asian Carp coordinator.

Supervisory Molecular Geneticist, Whitney Genetics Lab:

Responsible for planning and implementing operations of the Whitney Genetics Lab (WGL) and provides lab services to federal and state entities nationwide. Reports to the Midwest Fisheries Center Director. Supervises a WGL staff of geneticists, fish biologists, and technicians performing a variety of procedures in support of early detection and monitoring of aquatic species and in meeting fisheries management objectives. Responsible for all processing of eDNA samples and reporting of results to eDNA coordinator and supervisor. Primary author and editor of all processing related portions of the QAPP. Regularly communicates with the Region 3 Asian Carp/eDNA Coordinator to ensure a high level of quality and scientific rigor.

FWCO Project Leaders

Responsible for overseeing the delivery implementation of the eDNA program at FWS aquatic conservation, management, and aquatic invasive species programs within the field level which includes: collection, processing (filtering or centrifuging), and shipping samples waters assigned to their station. Responsible for and supervises all aspects of administration of the Aquatic Nuisance Species Act in the states or geographic area of responsibility assigned to the respective office. Will report any eDNA related issues/questions to Asian carp/eDNA coordinator and/or National Asian Carp coordinator.

eDNA POC's

Serve as lead biologist to implement the eDNA program for the watersheds assigned to their respective field office. Under the supervision of the project leader, develops and implements eDNA sampling plans for waters assigned and serves as a point of contact, with their PL, for partners to coordinate eDNA activities. Serves as the representative of their respective office on the eTeam.

STRUCTURE AND FUNCTION OF THE eTEAM (eDNA Team)

Purpose:

1. Review and refine the QAPP as needed.
2. Facilitate communication among FWCO field staff responsible for eDNA sampling in a structured forum, in order to improve scientific quality of sampling.
3. Provide a forum for FWCO field staff to communicate with RO staff responsible for Asian carp surveillance activities.

Members:

eDNA Coordinator (Kelly Baerwaldt) - chair

Whitney Genetics Lab Leader (Emy Monroe)

FWCO eDNA POC's (Alpena: Chris Olds; Green Bay: Tim Strakosh; Ashland: Mark Brouder; Carterville: Jeff Stewart; Columbia: Patty Herman; LaCrosse: Jenna Merry; Lower Great Lakes: Sandy Keppner)

Asian Carp Coordinator (Aaron Woldt)

Regional FWCO Program Supervisor (Brian Elkington)

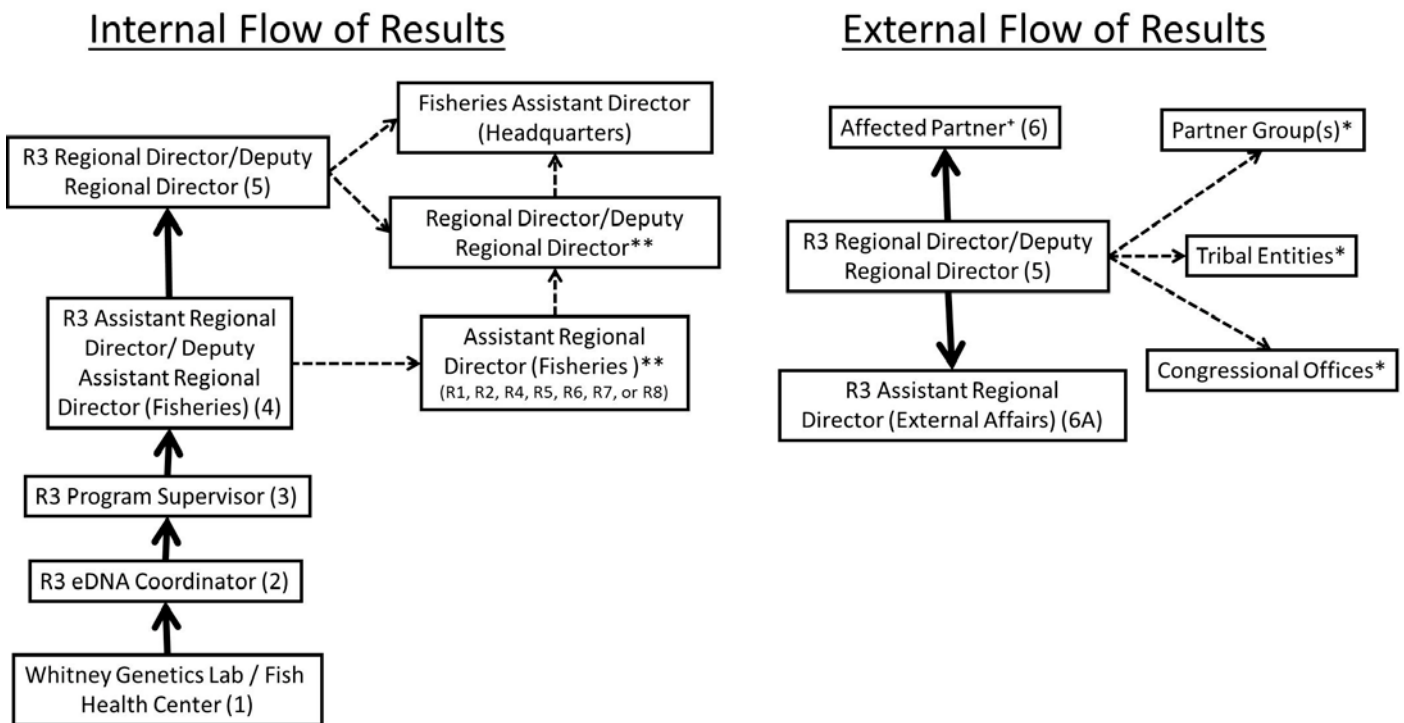
Goal of eTeam: Improve scientific rigor through improved field-level communication and cross-FWCO education. Facilitate communication regarding the field implementation and execution of the QAPP for eDNA between the FWCOs and the RO leadership.

Responsible for reviewing and recommending changes to the field sampling portions of the QAPP for eDNA. Responsible for keeping respective Project Leaders apprised of team progress. Responsible for developing site specific sampling plans in coordination with state partners. Responsible for developing, standardizing, and executing training of field staff. Will meet regularly or as needed to discuss field issues, recommended resolutions, and lessons learned regarding field sampling of eDNA.

eTeam will be chaired by the Regional Asian Carp Coordinator. All recommendations from the team will be communicated to the FWS National Asian Carp Coordinator for decision.

Appendix B. Internal Communication of Results SOP

This Standard Operating Procedure (SOP) is intended to guide U.S. Fish and Wildlife Service (Service) employees involved in the sampling and analysis of environmental DNA (eDNA) as they disseminate the results of early detection and monitoring for Bighead and Silver carp genetic surveillance. Included is a flowchart (Figure 1) depicting how information will be transmitted through the Midwest Region, as well as specific guidance relating to the format and types of information that will be crucial to include as eDNA results are communicated. Further guidance regarding Service eDNA sampling can be found in the Asian Carp Regional Coordinating Committee’s Monitoring and Response Plan and other regionally specific plans. All eDNA sampling should be completed in accordance with the *Quality Assurance Project Plan; eDNA Monitoring of Bighead and Silver Carp*.



*Affected Partner refers to an entity, such as a state, province, or tribe, who has management authority of the body of water being sampled.
 *Partners Group(s), Tribal Entities, and Congressional Offices communication will be carried out as determined appropriate by the Region 3 (R3) Regional Director/Deputy Regional Director. See “Post Analysis Coordination” section for further detail.
 **Information sharing cross regionally within the Service, communication will be carried out as determined appropriate by the R3 Assistant Regional Director and R3 Regional Director/Deputy Regional Director.
 - - - Dashed lines indicate situation dependent lines of communication based on case specific information.

Figure 1: The flow of information from the Whitney Genetics Lab (WGL) / Fish Health Center (FHC) within the Service to the Regional Director (RD), and then from the RD externally to our affected partner. Numeric order of the primary flow of results information noted at each step.

Data sharing from FWCO’s and Service Whitney Genetics Laboratory (WGL)

- Once sample processing is complete and positives identified, results will be communicated

through the flowchart (Figure 1) within Region 3 (R3) Fisheries to the Assistant Regional Director (ARD) level. Reporting internally to the eDNA Coordinator level as the results are determined by the Whitney Genetics Lab (WGL) will help streamline the process and allow time for the eDNA Coordinator to prepare for disseminating the results up and out to the affected partner

- All eDNA results information is to be kept confidential, being transmitted as shown in the flow chart (figure 1). Any potential communication with partner groups or other entities outside the Service will not occur prior to informing the affected partner. For further information on the dissemination of results to others, see the “Post Analysis Coordination” Section below.
- eDNA results information will be formatted as described in the Results Procedure Section (below) by the eDNA Coordinator and prepared as a briefing for the Fisheries Deputy Assistant Regional Director (DARD), and ARD.
- Once briefed, the R3 Fisheries ARD will brief the R3 Regional Director (RD), or Deputy Regional Director (DRD), which will allow the RD or DRD to provide input and disseminate the results as appropriate to affected partner and partner group(s) as outlined in the Post Analysis Coordination Section (below).
- The communication and briefing process from eDNA Coordinator to RD and/or DRD should occur quickly. This will allow R3 to disseminate results promptly and maintain our responsiveness to affected partner and partner group(s).
- When communications are made which transmit results or data from one step to the next in the flowchart (Figure 1), the person sending it must confirm receipt of the information via email response to ensure the message was received and maintain a record of the exchange.
- Communication of results beyond the eDNA Coordinator will only be made once all samples from the sampling event are fully analyzed.

Results Procedure:

- The sampling event data will be packaged together by the eDNA Coordinator in a uniform template to be used to inform the affected partner. Sampling events are defined by the geographic boundaries sampled or by the number of samples taken.
- Data and maps related to the sampling event will be provided to the eDNA Coordinator from each respective Fish and Wildlife Conservation Office (FWCO) upon their completion.
- The analysis results associated with each sampling event will be provided to the eDNA Coordinator by the WGL once processing at the lab is completed.
- The eDNA Coordinator, as part of gathering this information, will compare the datasets provided by the WGL and the FWCO to ensure the data matches each other, i.e. labeling and unique identifiers match, and combine them to create the final data package to be sent to the affected partner.
- The data package to be sent to the affected partner will include:
 - Geo-referenced map indicating all sites eDNA samples were taken, highlighting those sights that were determined to be positive for eDNA (Example included as Appendix A). This map will be formatted as a .jpeg file indicating positive results as red triangles (silver carp), blue squares (bighead carp) and negative results as yellow circles.
 - Digital Excel file with each sample uniquely identified. Data columns will include: Sample ID, Latitude and Longitude in decimal degrees, Date of Collection, Water Body Name, Silver Carp Results, and Bighead Carp Results.

- A transmission memo from R3 Fisheries ARD to the affected partner relating a summary of the information that has been collected and our proposed next steps (Memo template attached as Appendix B). This memo will be sent via email for timeliness as well as in hard copy.
- A press release template with eDNA specific language will also be included in the transmission to assist the affected partner as needed (Appendix C).

Post Analysis Coordination

- The data package of results will be emailed from the Deputy Regional Director (delegated to Assistant Regional Director or Deputy Assistant Regional Director as appropriate) directly to the affected partner point of contact (as determined by the affected partner). The Deputy Assistant Regional Director will follow up with secondary communication via telephone and/or email to the affected partner point of contact to ensure the data was received.
- Following transmission of the data package to the affected partner we will be prepared to work with them, to assist in interpreting the results or supporting further sampling if possible, understanding that in some cases the affected partner may not decide to carry out follow up investigation. We will also assist as requested in a partner led press release sharing the results with the general public.
- When notifying the affected partner, the data package will also be transmitted via email to our website manager and External Affairs Office. The Service External Affairs team will be prepared to assist the affected partner with outreach or press release materials upon request. This transmission will start a 5 business day waiting period at the end of which the results will be posted to a Service website. However, upon written request from an affected partner, the Service will extend the timeframe for up to an additional 5 business days. The request will specify the reason(s) for the extension (e.g. new geographic area of eDNA detection, high number of positive results, etc.), the name and position of the requesting official, and the number of additional days requested. See appendix D for further information regarding Service External Affairs role in eDNA results notification process.
- The website manager will review the materials and format them as needed to prepare them for posting on the FWS public website: www.fws.gov/midwest/fisheries/eDNA.html
- The results will be posted concurrent with any press releases issued by affected partner, **OR** by 3 PM CST on the third business day after delivery of the data package to the affected partner, whichever comes first. This is to ensure transparency in the system and to not restrict information sharing.
- Immediately upon posting the results online, the website manager will inform the ARD/DARD, who will then inform the affected partner via confirmed email.
- In addition, Partner Groups, Tribal Entities and Congressional Member Offices will be notified on a case dependent basis.
 - Partner Groups – Groups, such as the Asian Carp Regional Coordinating Committee, the Council of Great Lakes Fisheries Agencies, the Affected Great Lakes Fishery Commission Lake Committee, the Mississippi River Interstate Cooperative Resource Association, etc. will be notified via email and/or phone call from the DRD (delegated to ARD as appropriate) to their chairperson upon issuance of a press release by the affected partner.
 - Tribal Entities – Notifications will be made to each Tribe’s leadership respectively as an affected partner when sampling has taken place within or in direct proximity to tribal

lands. In this case, they will receive the same data package via email as any other affected partner (See Results Procedure section). If the samples were taken in treaty waters, but not in proximity to tribal lands, their leadership will be notified via email and/or phone call from the DRD (delegated to ARD as appropriate) either upon issuance of a press release by the affected partner or when the results are posted on the FWS website.

- Congressional Member Offices – Congressional Office contacts will be notified upon issuance of a press release by the affected partner on their behalf. Notification will be made via email and/or phone call from DRD (delegated to ARD as appropriate).

Example geo-referenced map of negative results, although none occur on this example, positive Silver carp results should be highlighted as red triangles and positive Bighead carp results should be highlighted as blue squares.



Figure 23. Map of of negative results, although none occur on this example, positive Silver carp results should be highlighted as red triangles and positive Bighead carp results should be highlighted as blue squares

Dear (Insert name of Partner),

Enclosed with this letter you will find the U.S. Fish and Wildlife Service (Service) Whitney Genetics Lab results relating to the recent Environmental DNA (eDNA) sampling which occurred in (Enter Name of Sampling Location or Water Body). These results are presented geographically to provide an overview of the locations where each individual sample was collected, as well as indicating those that were found to be positive for Asian Carp eDNA (include if positives are found). Additionally, there is a table provided which identifies each individual sample collected by unique identifier and its corresponding data.

If one or more samples were positive for Asian carp eDNA, use this paragraph:

Of the X samples taken, positive results were found in X samples. Of those, X were positive for silver carp and/or X were positive for bighead carp. Working with you as our partner, we would recommend that...

If no samples were positive for Asian carp eDNA, use this paragraph:

After reviewing the data, you will see that none of the water samples collected in this effort were found to be positive for Asian carp eDNA. We will keep you apprised as further information is collected through future sampling efforts.

Please be aware that these results will be posted on our public website no later than (Enter approximate time (noon) and date of posting if no press release if issued), 3 business days after the transmission of this message. Upon your request, we will work with you to interpret these results and issue a press release.

Include if more than one affected partner:

This information has also been sent to (Enter names of other affected partner) as affected partners. Please work together with the Service and the other affected partners to coordinate next steps in responding to these results and providing information to the public to ensure a clear and consistent message.

Please contact eDNA Coordinator XXXX at (Phone and email) if you have any questions.

FOR IMMEDIATE RELEASE

Month **XX, XXXX** Contact(s):

Name of Agency, Contact Name, Phone Number

Name of Partner Agency, Contact Name, Phone Number

MAIN TITLE

Subtitle

Analysis of water samples taken from **[insert water body]** on **[insert date]** have tested positive for the presence of Asian carp environmental DNA, also known as eDNA. Out of **[insert total number of water samples]** water samples collected by the **[insert agency]**, **[insert number]** have traces of genetic material from **[insert Asian carp species, e.g. bighead and/or silver]**.

The eDNA samples were collected as part of an extensive monitoring effort in **[insert all water bodies sampled]**. The samples were processed by the U.S. Fish and Wildlife Service's Whitney Genetics Lab in La Crosse, Wisconsin.

[Insert agency VIP quote explaining what the positive eDNA findings mean]

In response to the positive findings **[insert next steps]**.

eDNA can be left in the environment in the form of scales, cells, feces or mucus. At present, eDNA evidence cannot verify whether live Asian carp are present, whether the DNA may have come from a dead fish, or whether water containing Asian carp DNA may have been transported from other sources such as bilge water, storm sewers or fish-eating birds. The U.S. Fish and Wildlife Service, U.S. Army Corps of Engineers and the U.S. Geological Survey are leading a multi year Asian Carp Environmental DNA Calibration Study (ECALS), funded through the Great Lakes Restoration Initiative, to improve the understanding and interpretation of Asian carp eDNA results.

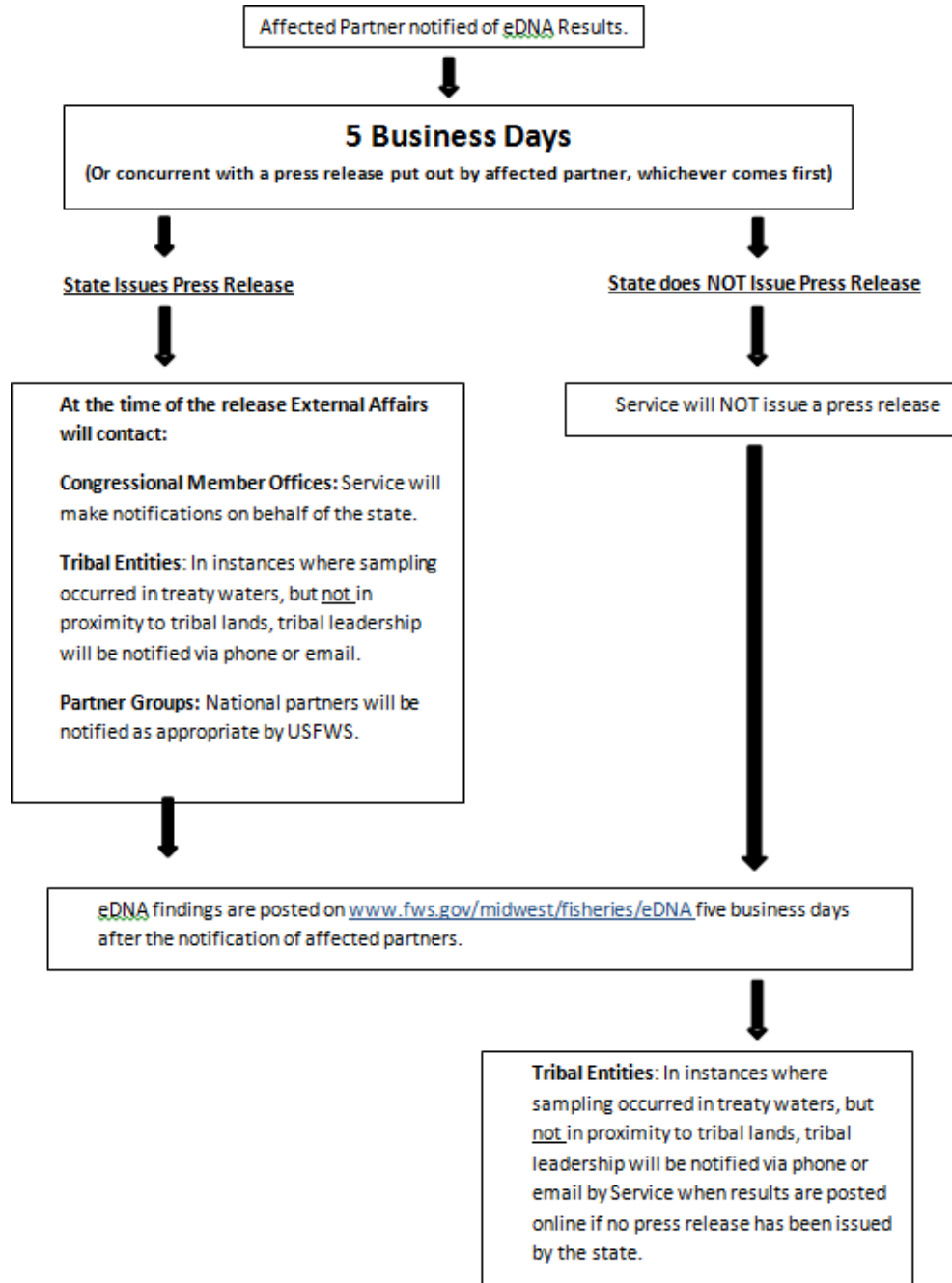
For more information on ECALS, please visit www.asiancarp.us/ecals.

eDNA results from this sampling event can be viewed at: www.fws.gov/midwest/fisheries/eDNA.html

For more information on the science of eDNA in the fight against Asian carp, watch the video at: <http://youtu.be/xXwply6ahQ8>.

[Insert agency boiler plate]

U.S. Fish and Wildlife Service External Affairs Flow Chart



This plan is available on: <http://www.fws.gov/midwest/fisheries/eDNA.html>

Figure 24. A flow chart describing the flow of eDNA results through U.S Fish and Wildlife External Affairs

Appendix C. Data Management

1. Purpose

In order to keep accurate records of eDNA sample collections, personnel associated with sampling and processing of collections, and data associated with a specific collection sample, datasheets associated with sample collections must be kept in accordance with the following protocols for quick reference and to prevent loss. This appendix describes procedures for data reporting and data management specific to USFWS.

2. Data management

(1) Field data and data sheets are the responsibility of the FWCO.

- a. FWCO staff are responsible for entering field data, proofing data and maintaining data at their location. Hard copy and electronic data should be backed up regularly.
- b. Field data sheets should be scanned and saved in a PDF with all of the data sheets for a particular location/case in one document. The filename should include sampling dates and location information, and should be saved on the station's shared drive as well as attached to the database described in #3.
- c. Original COC forms are sent to WGL with the samples. FWCOs will receive a scanned COC that should be printed and filed in a project binder and the electronic copy saved with electronic field data and scanned data sheets.
 - i. The original COC forms are kept in a project binder at WGL, and will be given to the eDNA Project Coordinator at the end of each sampling year.

(2) Lab data and data sheets are the responsibility of WGL.

- a. WGL will maintain hard copies of laboratory notebooks and the electronic project data file cataloging each case in an excel file. Gel photos are printed and placed into lab notebooks, and electronic files of the images are also saved on the lab network, which is backed up. Lab notebooks will be stored in a fireproof file cabinet. Sequence data will be saved electronically on the station's server.
- b. WGL will scan data notebooks into PDFs by cases and these will be saved on the lab networked computer with a back-up as well as on the station's shared drive which is also backed up by IT staff.
- c. Eventually an electronic Laboratory Information Management System will be utilized to track cases and samples through the lab workflow. The LIMS will be backed up a minimum of 4 times on separate hard drives.
 - i. Final reports will be generated as each case is completed, sent to the eDNA Program Coordinator as well as saved electronically in the lab network and on the station's shared drive.
 - ii. The PDFs of the scanned field COC as well as the gel images and sequencing results will be maintained in electronic copy on site with back-up.

(3) Collated field and lab data in geo-referenced database managed at the Regional Office

- a. FWCOs are responsible for entering and proofing field data. If possible, FWCOs should have data uploaded into the database within 5 business days after

collection. If other field work prevents uploading to the database, FWCOs may email the proofed excel file to the eDNA Program Coordinator within 5 business days, and the Coordinator will upload the data to the database.

- b. WGL is responsible for filing final case reports of results with the eDNA Program Coordinator within 24 hours of result confirmation.
- c. USFWS Midwest Region will maintain a database complete with field and lab data as well as electronic copies of reports provided to partner agencies and the public.

Fisheries Sampling Site Data Management Plan

Developed by Gabe DeAlessio and R3 Fisheries Program

Updated June 27, 2014

Purpose: The Fisheries Sampling data is collected by multiple field stations and needs to be reported and consolidated into a single location for archiving and centralizing mapping needs. Using ArcGIS Server (SDE) will create a simplified workflow and repository for the data.

User Descriptions:

Fisheries Field Users – these users are responsible for collecting the samples, quality control of the data, and inputting the sampling data into the system. They will have editing permission for the eDNA_SAMPLE table and read permission to the eDNA_SAMPLE_RESULTS feature class. This designation will include one employee from each FWCO as listed below:

Alpena FWCO – Chris Olds

Ashland FWCO – Mark Brouder

Cartersville FWCO – Jeff Stewart/Sam Finney

Columbia FWCO – Patty Herman

LaCrosse FWCO – Ann Runstrom/Jenna Merry

Green Bay FWCO – Tim Strakosh

Lower Great Lakes FWCO – Sandra Keppner/Scott Sanders

Fisheries Data Steward – This person (and their backup) will work with RO GIS Staff (see below) and be responsible for updating the eDNA_RESULTS data and joining the eDNA_RESULTS table to the eDNA_SAMPLE_RESULTS feature class. This person and their backup will have editing permission for the RESULTS table, the eDNA_SAMPLE feature class, and the eDNA_SAMPLE_RESULTS feature class. Also, the Data Steward will be the primary contact for field stations on assistance with training, troubleshooting, data review and management as needed, and day to day operations.

Primary – Kelly Baerwaldt / Brian Elkington

Backup – Karla Bartelt

eDNA Coordinator - This person will work with the Whitney Genetics Lab (WGL) to receive results and transmit them to the Fisheries Data Steward. The eDNA Coordinator will also assist in Coordinating FWCO eDNA sampling for the Region. This person will not have access to the SDE initially but may be added as a Primary Fisheries Data Steward in the future dependent on work flow and overall efficiency of the system.

Primary – Kelly Baerwaldt

RO GIS – Responsible for initial data loading, managing user permissions and server side issues. The RO GIS staff will advise the Fisheries Data Steward on database creation and editing (including design, implementation and training) but is not responsible for day to day updating of the database. Once in production mode, the RO staff will assist Field Users only if the Fisheries Data Steward is unable to resolve the issue.

Primary – Gabe DeAlessio

Workflow Overview:

Sample data is collected by field stations. The data are collected and recorded as outlined in the Quality Assurance Project Plan (QAPP), with the addition of the Regional Unique Identifier. While the physical samples are sent to the Whitney Genetics Lab (WGL) for analysis, the Fisheries Field Users are responsible for digitizing their raw data, ensuring data accuracy, and loading that data into the eDNA_SAMPLE feature class in the ArcGIS Server (SDE) using an excel file template provided by the Fisheries Data Steward. All data will be error checked prior to loading (See data upload instructions below) and will be loaded no more than 2 weeks post sampling event by the Fisheries Field Users to ensure it is entered prior to when results arrive at the RO from the WGL.

Upon receiving the results data from the WGL, via the eDNA Coordinator, the Fisheries Data Steward (or their backup) will load the results data into the eDNA_RESULTS table. Once the data is loaded, the Fisheries Data Steward will produce the necessary maps to be used to inform the affected partner.

Concurrent with website posting, the Fisheries Data Steward will join the eDNA_RESULTS table with the eDNA_SAMPLE feature class. This join will add the results and sampling data to the eDNA_SAMPLE_RESULTS feature class (read only for Fisheries Field Users) and delete the results and sampling data from the eDNA_RESULTS table and eDNA_SAMPLE feature class. The eDNA_SAMPLE_RESULTS feature class will be considered the long term data archive for future reference as needed.

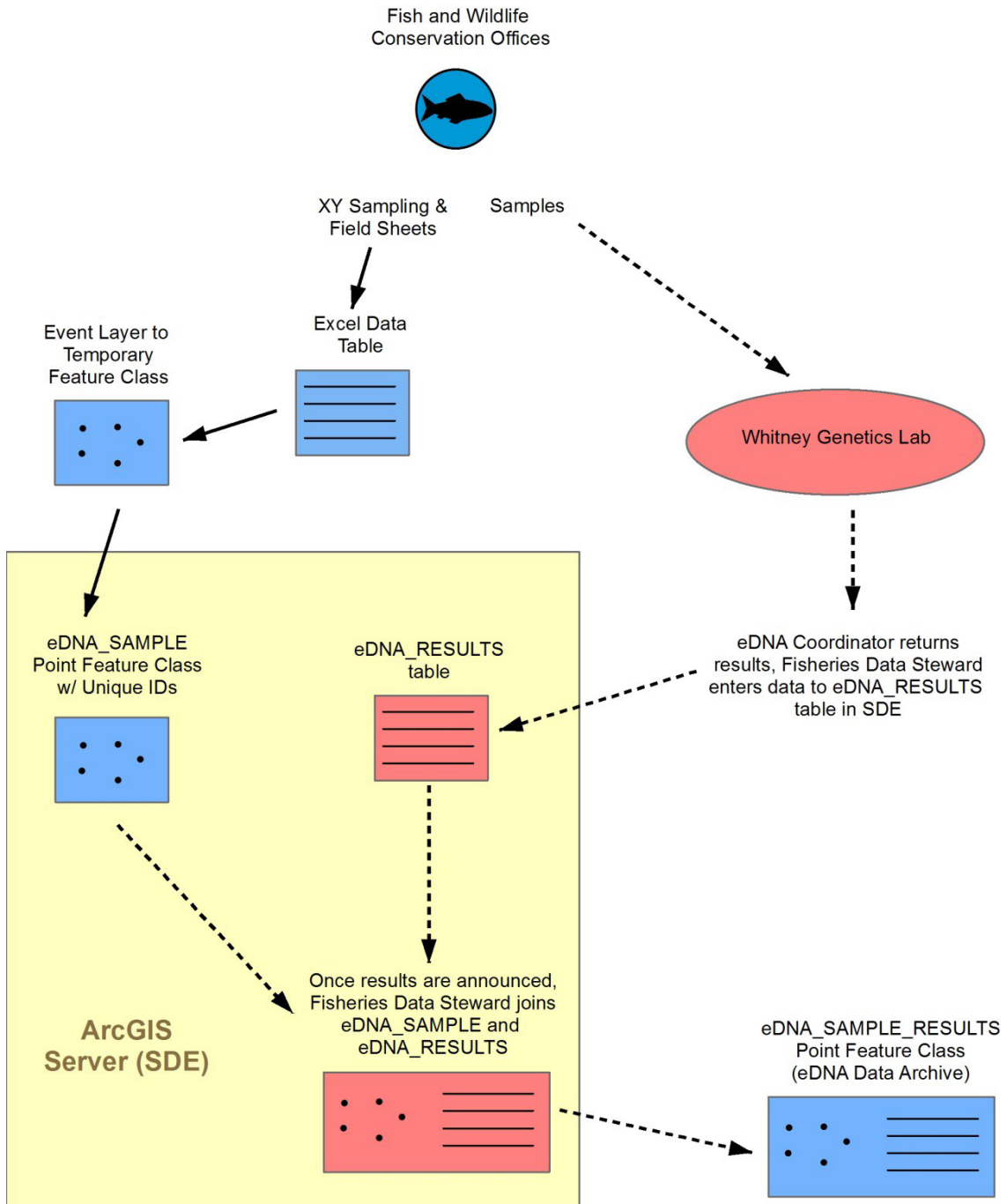


Figure 1. Workflow of eDNA sampling and results data into the Regional ArcGIS Server (SDE). The sampling data is entered by FWCO staff into the eDNA_SAMPLE point feature class, which contains all appropriate and standardized data fields (guidance provided in the Quality Assurance Project Plan (QAPP)). Corresponding results data is entered into a separate eDNA_RESULTS table once received from FHC and ultimately joined with the sampling data to create the eDNA_SAMPLE_RESULTS point feature class, a long term Regional eDNA data archive.

Table 1. Field descriptions for the eDNA_Sample point feature class.

Field Name	Alias	Type	Length	Description
RUID	Regional Unique ID	Long Integer	n/a (8)	Composite number that has a 5-digit “case” number (a series of unique numbers assigned by the WGL to each FWCO at the start of the sampling year and provided for each individual planned sampling event followed by a 3 digit sample ID number assigned by the FWCO numerically as they take samples in the field (no punctuation, #####))
FWCO_ID	Sampling Station ID code	Text	3	Alpena FWCO – ALP Ashland FWCO – ASH Carterville FWCO – CAR Columbia FWCO – COL Green Bay FWCO – GRB LaCrosse FWCO - LAX
STATE	State	Text	2	Two letter state code in which samples were taken.
BASIN	Basin	Text	4	LH = Lake Huron LM = Lake Michigan LE = Lake Erie LS = Lake Superior LO = Lake Ontario CAWS = Chicago Area Waterway System UMR=Upper Miss River OHR=Ohio river -Other designations to be added as needed by Fisheries Data Steward
WATERBODY	Waterbody	Text	100	Waterbody name
DATE_COLL	Collection Date	Date		Date of collection (MMDDYYYY)
WIND_DIR	Wind Direction	Text	20	Abbreviated wind direction, “Calm”, “Variable”, or shorthand (NE, NW, SE, SW, N, S, E, W) and wind speed if available.
LATITUDE		Double	n/a	WGS 84 Decimal Degrees, 5 decimals

LONGITUDE		Double	n/a	WGS 84 Decimal Degrees, 5 decimals
TEMP_F		Double	n/a	Temperature in degrees Fahrenheit (1 decimal)
DEPTH		Double	n/a	Depth where sample was taken in Feet (1 decimal)
DOUBLE_SAMPLE		Text	5	Yes/No
BLANK		Text	5	Yes/No
HABITAT		Text	30	Habitat type where sample was taken, i.e. LDB, RDB, MC, Bay, Lake, Confluence, etc.
COLLECT_TIME	Collection Time	Long Integer	4	Time stamp in military time, no punctuation
FILTER_TIME	Filter Time	Long Integer	4	Time stamp in military time, no punctuation
PROCESSOR		Text	3	Initials of person who filtered the sample
COMMENTS		Text	255	General notes, issues, or observations while sampling

Table 2. Field descriptions for eDNA_Results table.

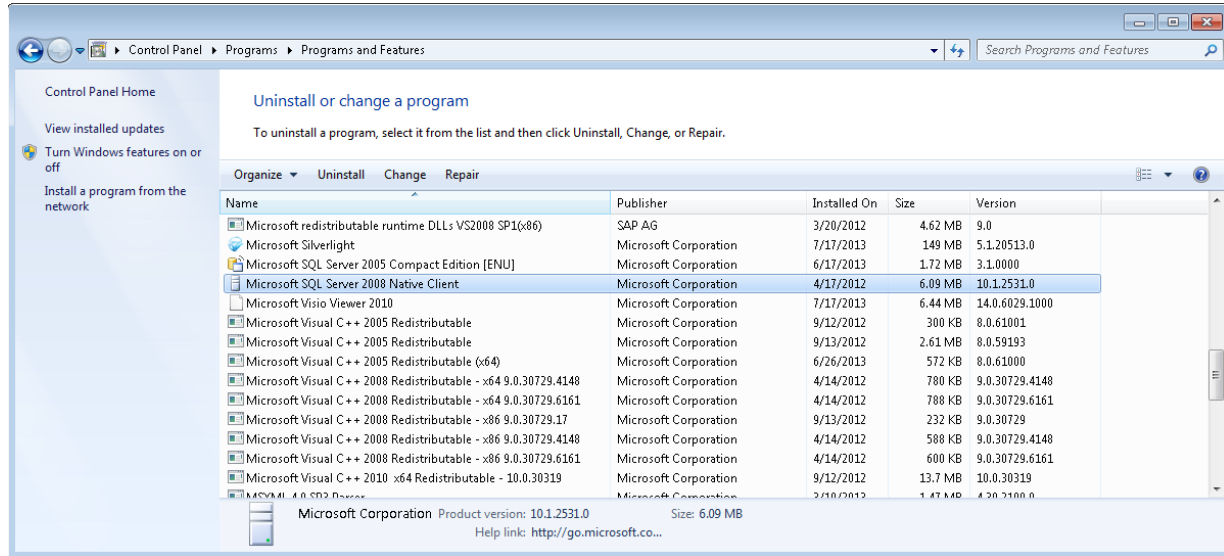
Field Name	Alias	Type	Length	Description
RUID	Regional Unique ID	Long Integer	n/a (8)	Composite number that has a 5-digit "case" number (a series of unique numbers assigned by the WGL to each FWCO at the start of the sampling year and provided for each individual planned sampling event followed by a 3 digit sample ID number assigned by the FWCO numerically as they take samples in the field (no punctuation, #####))
BIGHEAD		Text	5	Yes/No
SILVER		Text	5	Yes/No
MARKER_NAME		Text	25	Name of the specific markers used at the Whitney Genetics Lab to test the sample

System Requirements:

ArcGIS 10.1, SP1. This is available from “FWS Apps to Go” and doesn’t require elevated privileges to install. Contact IT with any problems.

SQL Server 2008 Native Client – This allows ArcGIS to connect to ArcGIS Server (SQL Server).

Look in Program Files to see if it’s installed (screenshot below). If not, contact IT (x5115) to get it installed prior to connecting.

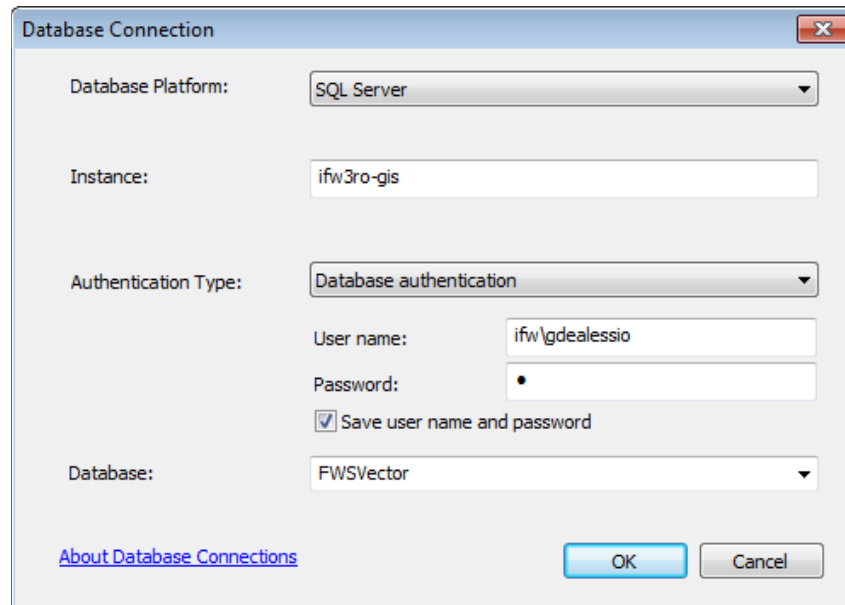


Establishing a Connection to the Region 3 ArcGIS Server:

Go to ArcCatalog. Scroll down in the Table of Contents to Database Connections Click Add Database Connection.

Set up as following, replacing the User Name with your Active Directory Short Name. (Generally IFW\first initial last name)

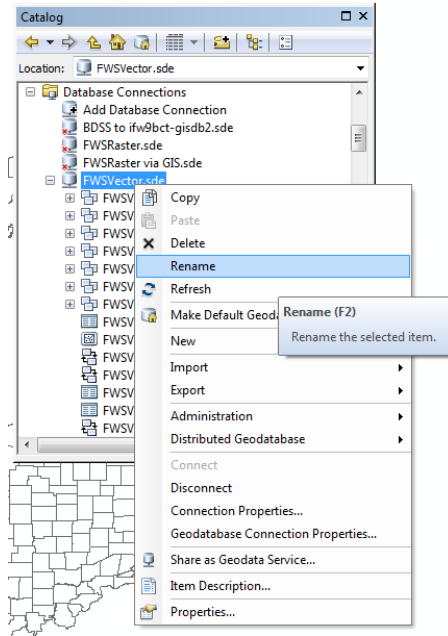
Set the Password to "a" (it cannot be left blank). Note that the software is actually passing your Windows Login password, the "a" is just a placeholder.



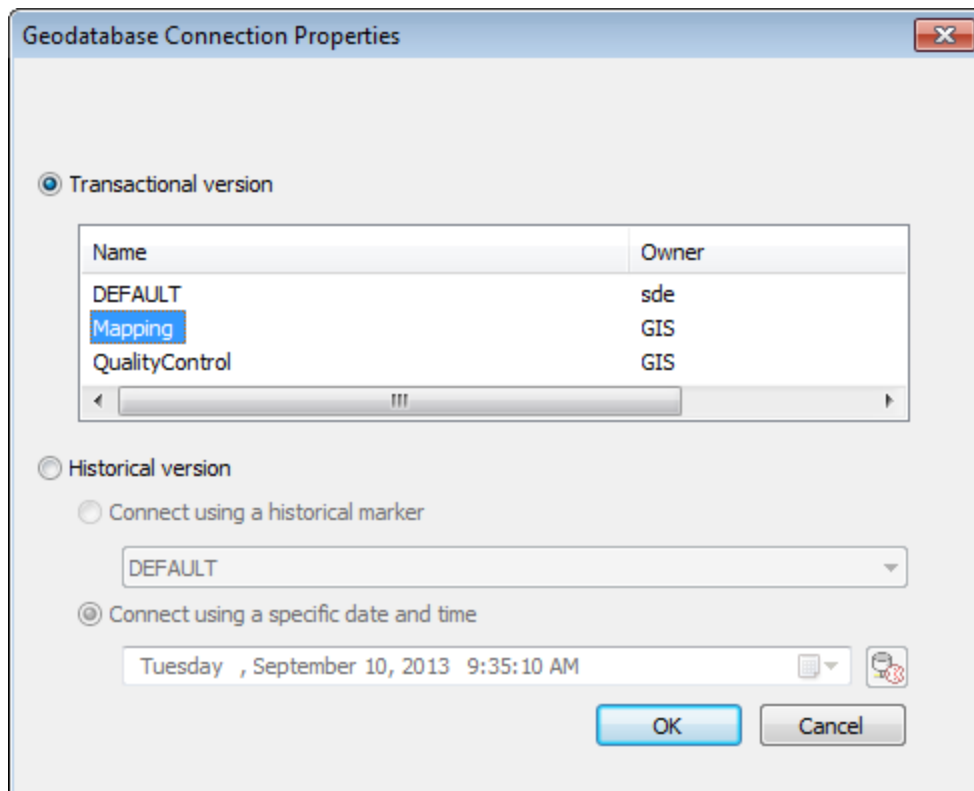
Click OK. You should be able to open the connection and see the various datasets.

Troubleshooting - if the connection fails, it is likely one of the following:

1. Double check your shortname and be sure all the parameters are correct.
2. You have not been granted permission to the database yet. Contact the RO GIS Staff (Gabe).
3. The SQL Server 2008 Native Client is not installed (see System Requirements). Once the database connection is made, you should be able to see the many datasets. Right click on the connection and choose RENAME. Change the name to FWSVector.



Lastly, we want to connect to the working version of the database. Right Click on the newly named FWSVector and choose Geodatabase Connection Properties.



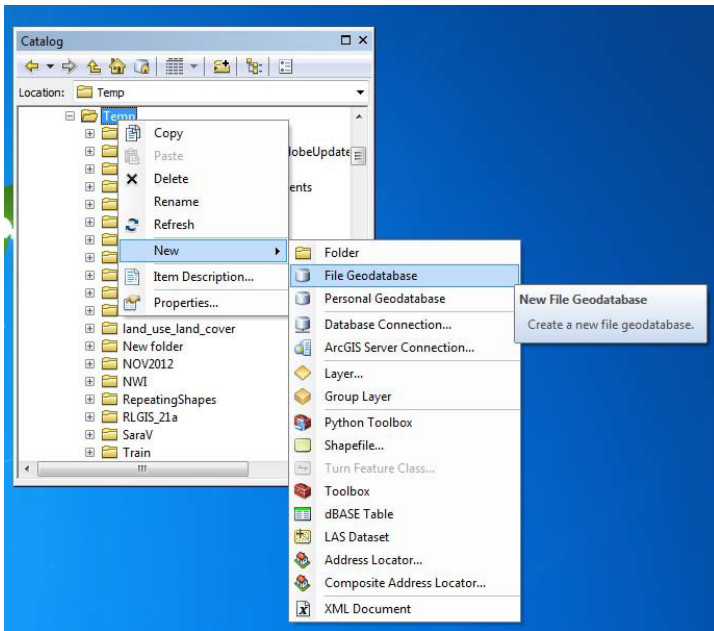
Select the Transactional version to Mapping and click OK.

Field User Instructions:

This section will guide you through the initial ArcMap set up and data loading process. Some of these steps can be done once as long as you save and reuse the ArcMap project for future data loads.

1. Create an empty geodatabase to store temporary data.

In ArcCatalog, select a location (suggested location > C:\TEMP) and **right click** and choose **New > File Geodatabase**



Rename the geodatabase: **Sample_Temp_Data.gdb**

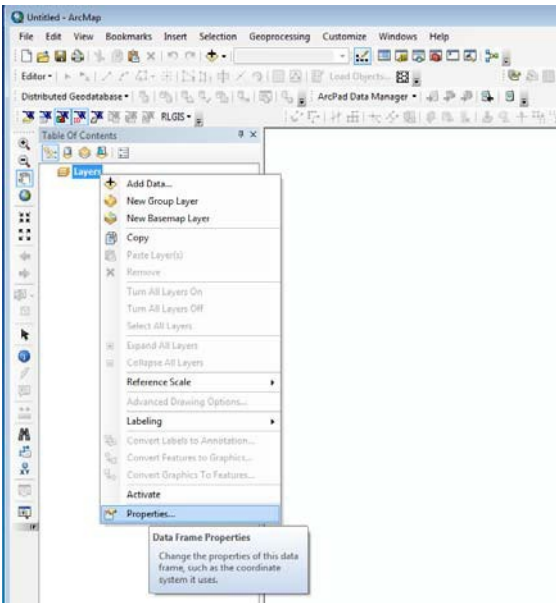
2. Be sure your data is loaded into the field data MS Excel eDNA_SAMPLE datasheet.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
	RUID	FWCO ID	River	Date	Collector	Wind_Direction	Waypoint	Latitude	Longitude	Temp	Depth	Double	Blank	Habitat	Collect_Time	Filter_Time	Signature	Comment
2	GRB20130255	1004-001	Muskegon	5/13/2013	Strakosh	Variable	255	43.42337	-85.67512	53.7	4.6			RVR	1134	1310	CMO	
3	GRB20130256	1004-002	Muskegon	5/13/2013	Strakosh	Variable	256	43.42422	-85.67521	53.7	4.6			RVR	1136	1312	SG	
4	GRB20130257	1004-003	Muskegon	5/13/2013	Strakosh	Variable	257	43.42522	-85.67530	53.7	2			RVR	1138	1315		
5	GRB20130258	1004-004	Muskegon	5/13/2013	Strakosh	Variable	258	43.42565	-85.67551	53.7	2.7			RVR	1139	1317		
6	GRB20130259	1004-005	Muskegon	5/13/2013	Strakosh	Variable	259	43.42598	-85.67561	53.7	3.9			RVR	1140	1328	CMO	
7	GRB20130260	1004-006	Muskegon	5/13/2013	Strakosh	Variable	260	43.42622	-85.67566	53.5	1.5			RVR	1141	1332	CMO	
8	GRB20130261	1004-007	Muskegon	5/13/2013	Strakosh	Variable	261	43.42652	-85.67570	53.5	2.2			RVR	1142	1336	SG	
9	GRB20130262	1004-008	Muskegon	5/13/2013	Strakosh	Variable	262	43.42686	-85.67577	53.5	4.9			RVR	1143	1345		

3. Open new ArcMap project.

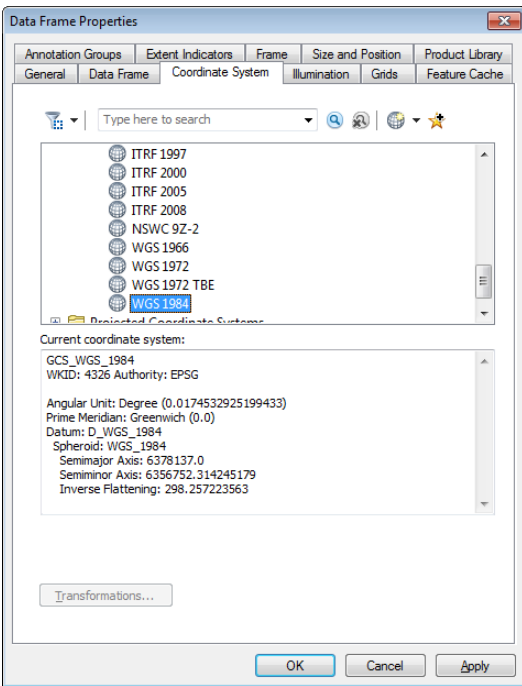
Right click on **Layers > Data Frame Properties**.

4. Choose the Coordinate System tab



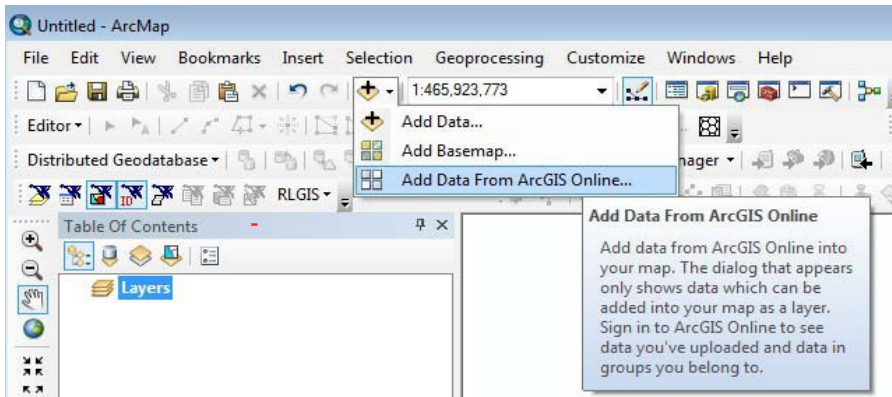
Select **Geographic Coordinate Systems >World > WGS 1984**.

5. **Click OK**. This sets your ArcMap project to the coordinate system your XY data is in (Decimal Degrees - Lat/Long).

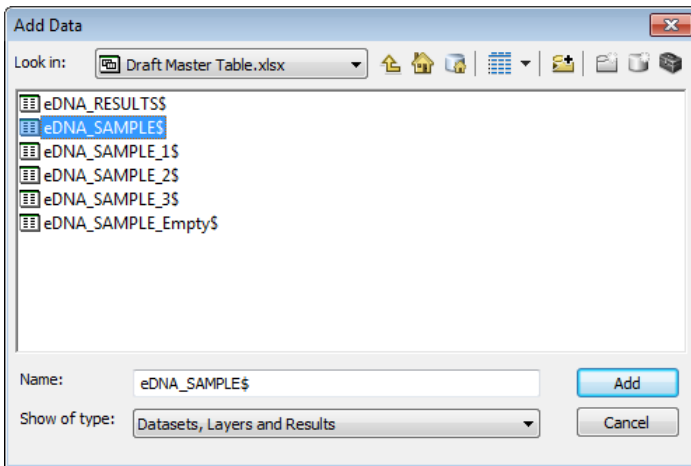


6. Next, add a basemap to your work area. If you have a local copy of a topographic or aerial, browse to that and add.

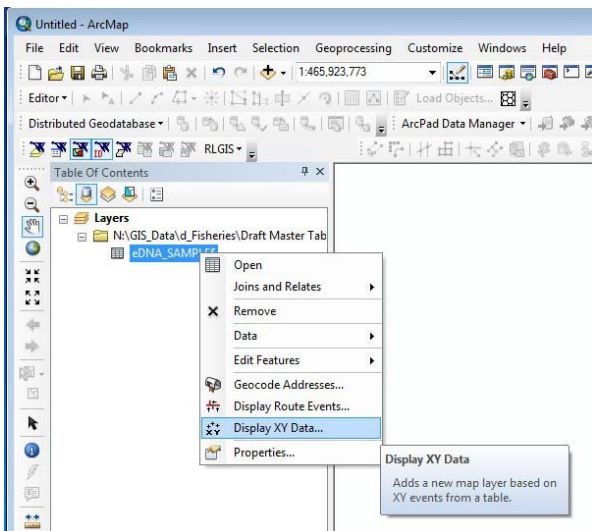
If not, you can use the **Add Data Dropdown** to choose **Add Data from ArcGIS Online** and type “Image” to locate a worldwide image set. (Note that slow internet speeds may be very slow to work with ‘live’ data.)



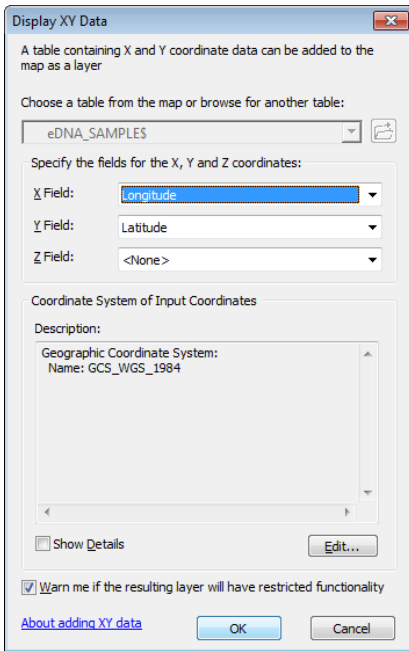
7. Use **Add Data** to bring the **eDNA_SAMPLE** datasheet into the Table of Contents.



8. **Right Click** on the table and choose, **Display XY Data**.

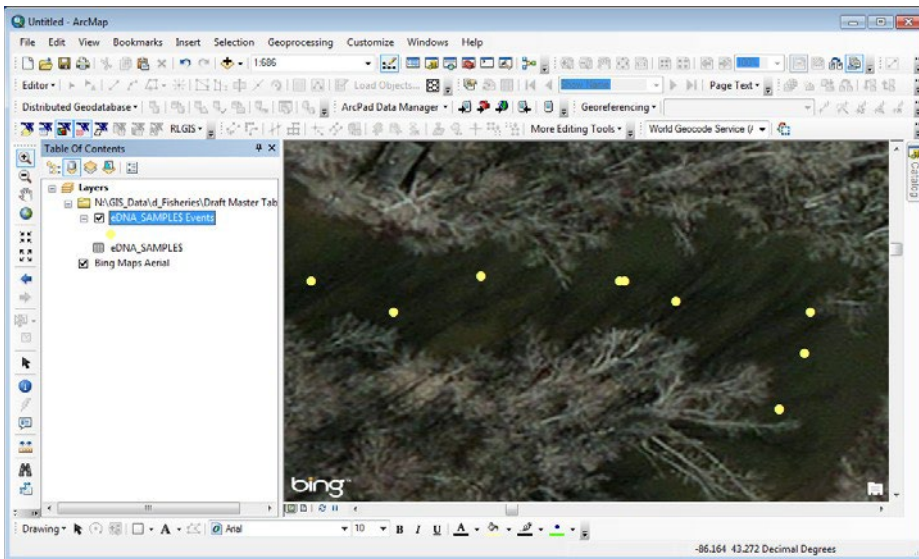


9. Latitude and Longitude will autopopulate. **Click OK**.

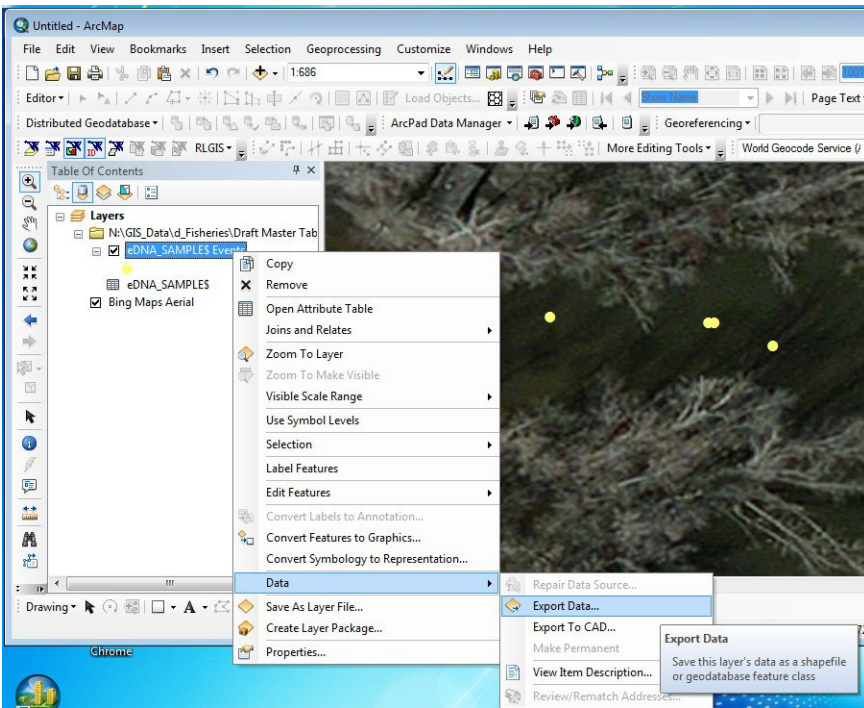


You will get a warning message regarding an Object ID field, **Click OK**.

10. Field users should Quality Check the data now. Review both positional accuracy as well as verifying all the required attributes are present and correct.

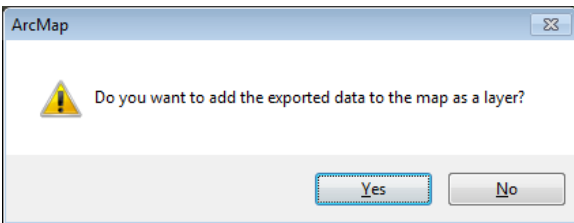


11. Once field QC is complete, right click on the Events layer and choose **Data > Export Data**



12. Browse to your Sample_Temp_Data.gdb and name the data SampleX. Click OK.

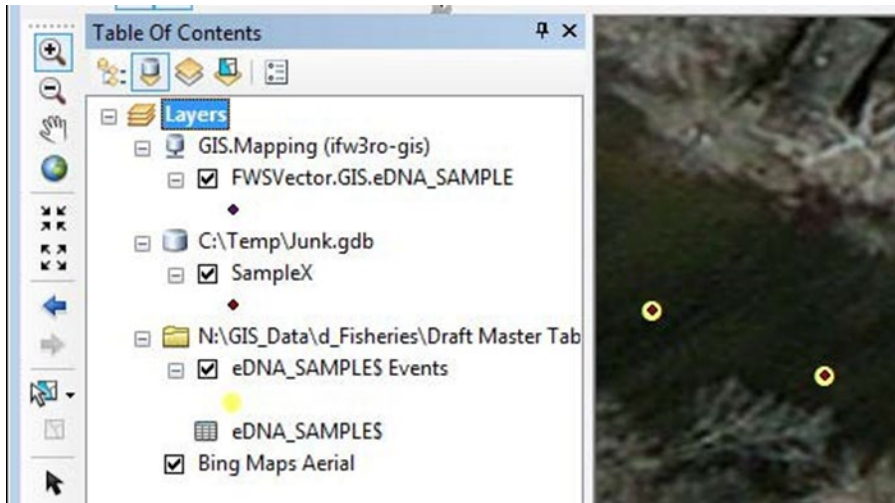
When asked if you want to add the data to the map, click Yes.



13. Add the eDNA_SAMPLE point feature class from the SDE server.

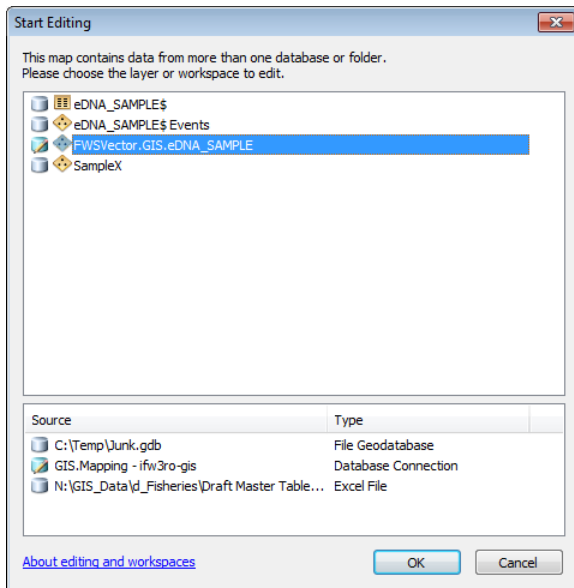
Click **Add Data**, then browse to **Database Connections > FWSVector.sde>eDNA_SAMPLE** Click **Add**

14. Confirm the table of contents looks like the following, showing the GIS.Mapping version of the eDNA_SAMPLE point feature class.



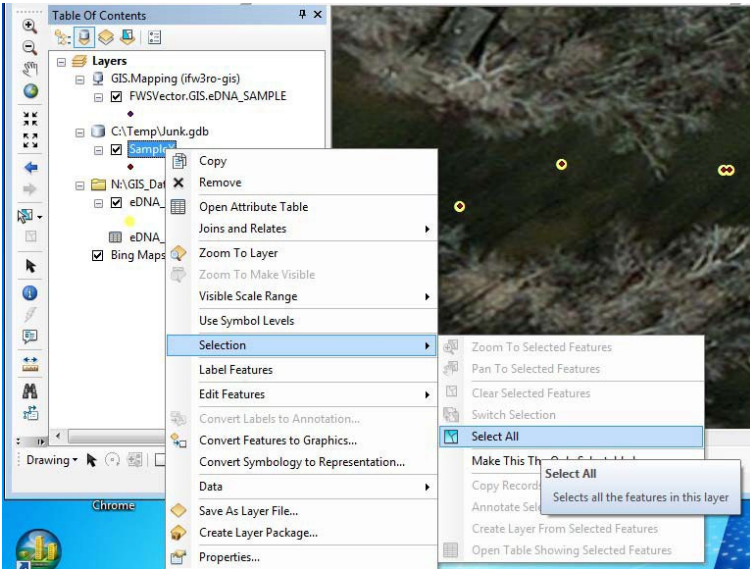
Make sure the Editor Toolbar is open. If it is not, go to **Customize>Toolbars>Editor**. Dock the toolbar where you prefer.

15. Click **Editor > Start Editing**. Choose the FWSVector.GIS.eDNA_SAMPLE layer.

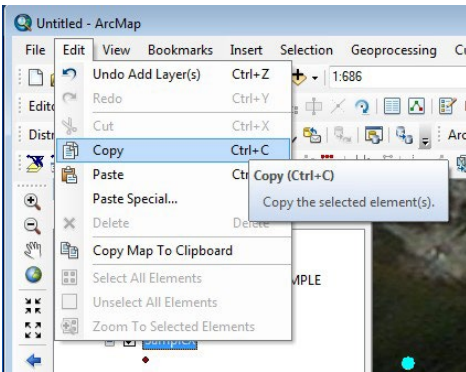


Click OK.

16. **Right click** on the SampleX layer. Choose **Selection > Select All**.



17. On the Main Menu, choose **Edit > Copy**. (or Ctrl + C)



18. Next choose **Edit > Paste**. (or Ctrl + V)

Be sure your target dataset is the **eDNA_SAMPLE** point feature class.



Click OK.

19. **Turn off** the SampleX and Event point data in table of content.

Zoom to the newly added data, and review that the attributes pasted correctly.

20. On the Editor Toolbar, **Save** edits and **Stop Editing**.

21. You can **right click** and **Remove** the SampleX, Event data and the Excel eDNA_SAMPLE table.

Your project is ready for the next data loading.

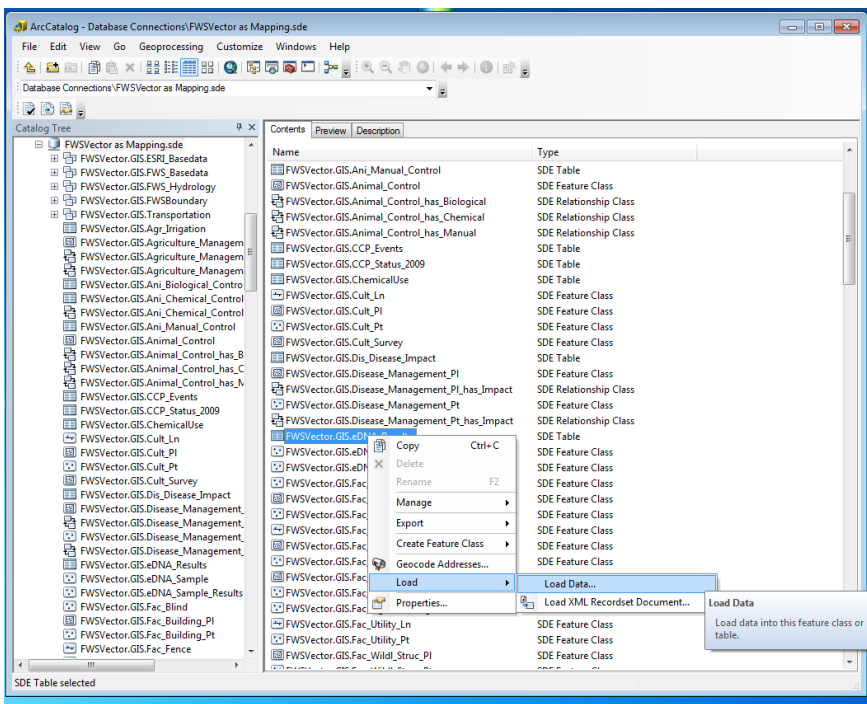
22. Go to **File > Save** to save the ArcMap project for reuse later. Note that you will now start on step 9 and skip steps 15 – 17 in future data loads if you use this .mxd.

Fisheries Data Steward Instructions:

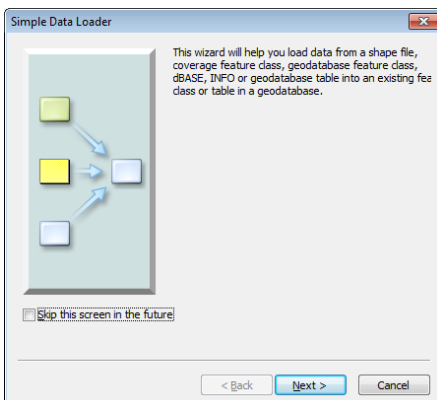
Fisheries eDNA Data Steward Guide

Describes the steps for the eDNA Data Steward to receive the results data and link it with the field-provided sample data to create maps.

- 1) Review data from the Fish Health Center. The data will come in Excel form. Make sure the fields are filled out correctly and match the required properties as set forth in the Data Standards document.
- 2) Convert the .XLS data to .CSV format. (Due to Excel and ArcGIS not communicating Long Integer values correctly, this step is necessary to load the RUIDs properly.)
- 3) Connect to ArcCatalog via the Mapping Version. Right click on the the eDNA_Results table and choose Load Data to open the Simple Data Loader wizard.



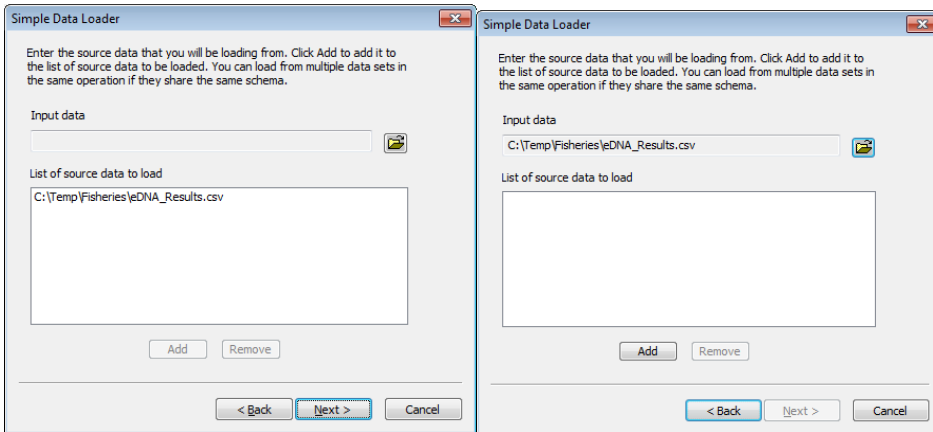
- 4) Click Next through the Simple Data Loader introduction screen (you can check the box to disable it for future runs.)



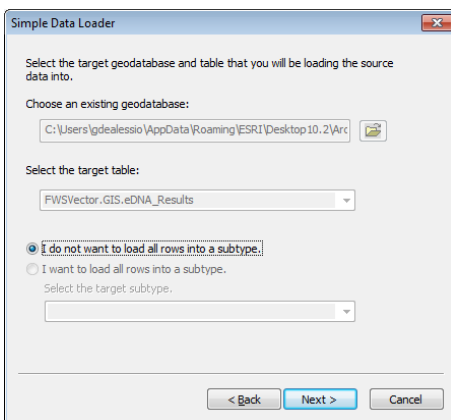
5) Click on the folder icon and browse to the .CSV file that was created in Step 2.

Click Add to move the .CSV to the List.

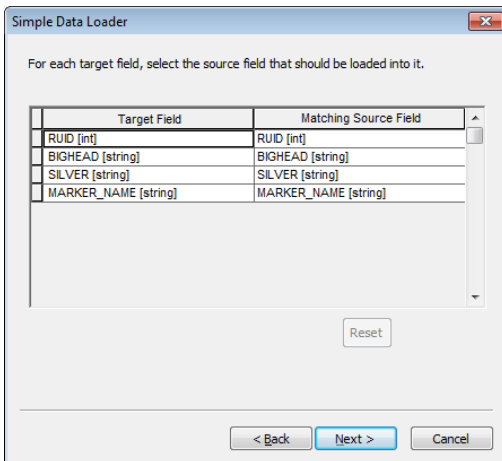
Click Next.



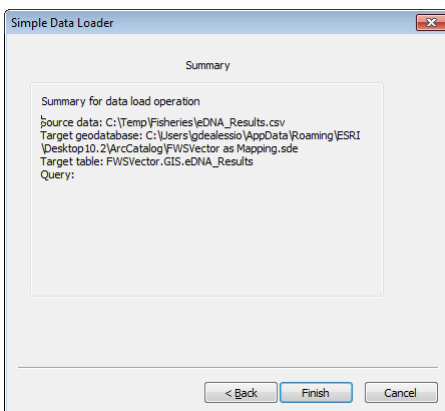
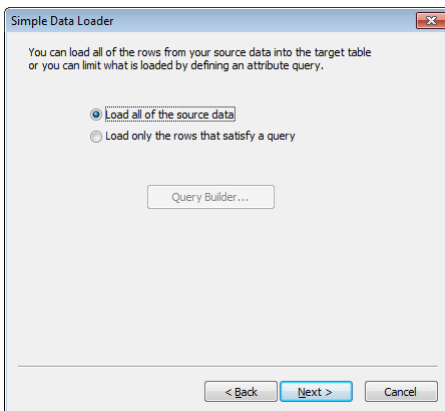
6) We aren't dealing with Subtypes, Click Next.



7) Make sure that each of the 4 RESULTS “Matching Source Field” correctly align with their respective “Target Field”.

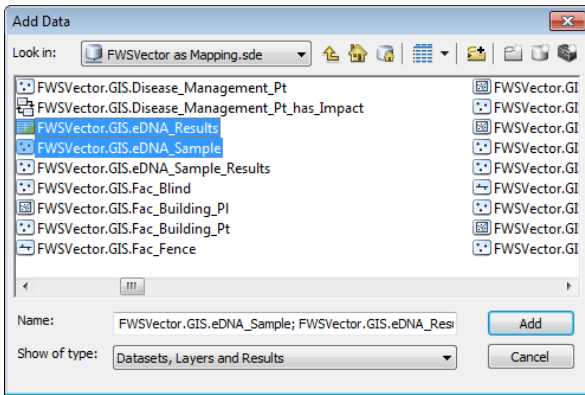


8) Assuming you aren't dealing with querying data while loading, click Next.



Review the Summary and click Finish to load the data.

Working with the eDNA data in ArcMap.



To produce the reviewer maps, the sample (XY location) data must be joined with the results data. This is done in ArcMap and then the map is created by adding a basemap, collateral data and whatever cartographic elements are required.

9) Open ArcMap.

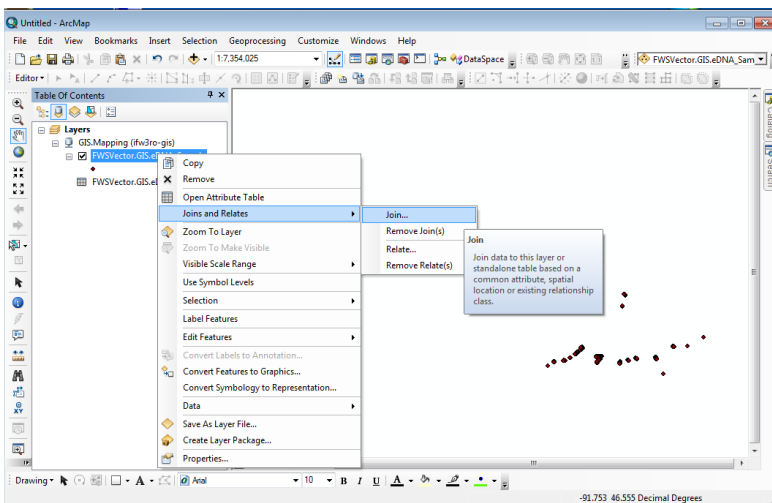
Click Add Data.

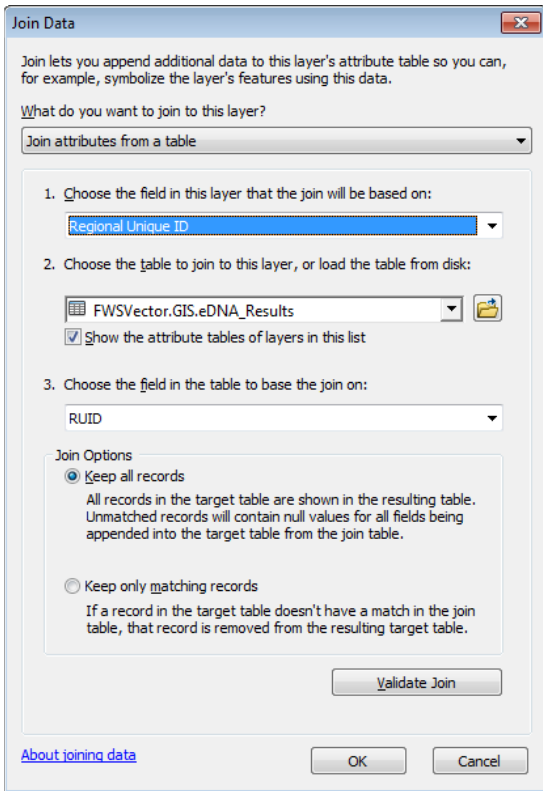
Browse to and highlight the eDNA_Results (table) and eDNA_Sample (point feature class).

Click Add.

10) You will see both the point data and the table added in the Source view of the Table of Contents.

On the eDNA_Sample data, right click and choose Joins and Relates, Join.





11) In the Join Data wizard, choose the “Regional Unique ID” field for #1.

For #2, the eDNA_Results should autopopulate, if not select it from the dropdown or browse to it (if it’s not already in your map.)

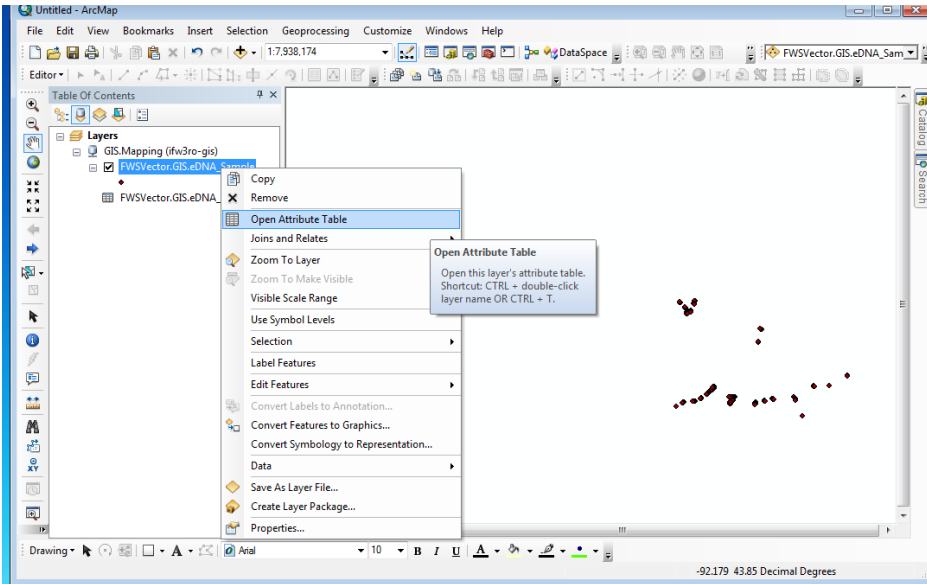
Be sure #3 is the RUID field (this is derived from the eDNA_Results table in #2.)

You do not have to Validate Join.

Click OK.

If you get the “Message from Join”, choose the “Perform Join Now Without Index” option.

12) To confirm your Join was successful, right click on the eDNA_Sample point feature class in the Table of Contents, and Open Attribute Table.



13) Scroll to the far right of the attribute table. Right click on the RUID field, and choose “Sort Descending”. This force the successfully joined data to the top of the attribute table.

BLANK	HABITAT	Collection Time	Filter Time	PROCESSOR	COMMENTS	SHAPE	OBJECTID *	RUID	BIGHEAD	SILVER	MARKER_NAME
NO	LDB	1242	1714	SAG	<Null>	Point	2538	10040	NO	NO	<Null>
NO	LDB	1243	1721	ERS	<Null>	Point	2539	10040	NO	NO	<Null>
NO	LDB	1244	1723	KGK	<Null>	Point	2540	10040	NO	NO	<Null>
NO	LDB	1245	1733	SAG	<Null>	Point	2541	10040	NO	NO	<Null>
NO	LDB	1246	1734	SAG	<Null>	Point	2542	10040	NO	NO	<Null>
NO	LDB	1247	1738	ERS	<Null>	Point	2543	10040	NO	NO	<Null>
NO	LDB	1248	1743	KGK	<Null>	Point	2544	10040	NO	NO	<Null>
NO	LDB	1249	1758	ERS	<Null>	Point	2545	10040	NO	NO	<Null>
YES	LDB	1250	1751	SAG	<Null>	Point	2546	10040	NO	NO	<Null>
NO	LDB	1250	1757	SAG	<Null>	Point	2547	10040	NO	NO	<Null>
NO	LDB	1252	1623	KGK	<Null>	Point	2548	10040	NO	NO	<Null>
NO	LDB	1253	1805	KGK	<Null>	Point	2549	10040	NO	NO	<Null>
NO	LDB	1255	1817	SAG	<Null>	Point	2550	10040	NO	NO	<Null>
NO	LDB	1256	1810	SAG	<Null>	Point	2551	10040	NO	NO	<Null>

14) Now it's time to make your Review Maps.

Appendix D. Centrifuge Tube Management Plan

New in 2015, samples will now be collected in 50-ml centrifuge tubes and concentrated in the field via centrifugation. Even though tubes come sterile and ready to use, the Regional Office has decided that WGL will serve as the single preparation facility for creating field blanks used in the Asian carp eDNA monitoring program.

WGL will fill new, sterile centrifuge tubes, package them in racks to be secured in a clean plastic sleeve, and then either deliver or ship them to field offices as needed.

field blankfield blankCooler (field) blanks:

- (1) Plastic bags fit to racks of filled tubes will be purchased by WGL
- (2) Filled tubes will be securely closed, and placed in the bag.
- (3) Bags will be twisted closed with wire closures or tape.
- (4) Filled tubes will be distributed at the annual field training meeting so that each field station will start out the season with the total estimated number of field blanks needed for the sampling season.
- (5) Field stations can store these prepared field blanks as long as needed, ideally in the field trailers. Bags should be re-sealed after removal of blanks to keep contamination risk low.
- (6) Field stations will prepare coolers according to the QAPP, in as clean of an area as possible at the station.
 - a. Anytime boxes are opened, staff should be in clean clothes and use a new pair of clean gloves for actually handling the tubes. For example, you may open the box with ungloved hands. Then, put on gloves to open the bag and touch the tubes.
- (7) Once clean coolers are ready, boxes may be opened, tubes labeled, and placed into clean coolers.
- (8) After use, field staff should return the racks to WGL, but dispose of all used tubes

A note on labels: We've found some great labels that withstand all sorts of abuse and are available on GSA. Avery laser white weatherproof address labels #5520.

Appendix E. Methods for Elimination and Reduction of eDNA on Boats and Equipment

Recommended methods for reduction of residual or environmental DNA on boats and other equipment associated with environmental conservation work in the field. For boats and equipment that have been previously exposed to carp DNA, choose one high pressure sprayer method *in conjunction* with one chemical method to reduce DNA levels to negligible or below LOD. Read MSDS and Use personal protective equipment (PPE). Read job hazard assessment (JHA) for applicable methods.

Method	Active Ingredient	Contact Time	Advantages	Disadvantages	Cautions
Steam + Pressure Washer @ 212 F	Pressure, Heat and Water	10 sec	Environmental safety	Need electrical and water hookups Can melt or tear materials	Use PPE – need proper safety training, can cause burns, cuts, air embolisms
10 % Household Bleach Low Pressure Saturation	Sodium hypochlorite (5-8% before mixing)	10 min	No hookups necessary – can use off station	Not preferred for environmental safety Single day use in solution	Use PPE and avoid breathing fumes
20 % Household Bleach Immersion Bath	Sodium hypochlorite (5-8% before mixing)	10 sec	No hookups necessary – can use off station	Not preferred for environmental safety Single day use in solution	Use PPE and avoid breathing fumes
2% Virkon Immersion Bath	Potassium Peroxymonosulfate and Sodium Chloride	30 min	Lasts 1 week in solution Environmental safety	Corrosive to metals when exposed longer than 10 min	Use PPE – wear a dust mask when mixing powder
2% Virkon Low Pressure Saturation	Potassium Peroxymonosulfate and Sodium Chloride	10 min	Lasts 1 week in solution Environmental safety	Not quite as effective as bleach in laboratory study; equal or better than bleach in field (boat) equipment study	Use PPE – wear a dust mask when mixing powder. Do Not Aerosolize! Use a low pressure dispenser (hose attachment sprayer at largest droplet setting)



Preventing the Spread of Pathogens, Bacteria and Invasives on/in Boats, Motors, Trailers and Equipment
 Developed by the U.S. Fish and Wildlife Service Midwest Region

Disinfection Techniques and Options:

Boat, motor, trailer, and gear must have all aquatic vegetation, visible organisms/animals, soil, and water drained and removed BEFORE TRANSPORT. Upon leaving a water-body possibly infected with pathogens or invasive species, a proper disinfection must be completed before re-use of boat, motor, trailer, and any exposed gear in another waterway. **Contact time** is crucial for complete disinfection. **Contact time** reflects exposure of air, water, or disinfectant to a specific area, and not the total amount of time spent disinfecting. For example, if you are using 50C water to disinfect your boat, you must apply 50C water to each area for ten minutes or longer (see options and procedures below). **Read MSDS, wear personal protective gear (ppg), and comply with federal and state regulations.**

Disinfection is MANDATORY for all exposed equipment and gear!

Methods	Procedures	Positives	Negatives
Heat + Air (Drying in hot sun/air)	30C (86 F) 24 hours minimum (time at temp contact period crucial) (exposure to hot sun/ air while dry)	Chemical free Effective, but only if properly done under ideal conditions	Time consuming Weather/Temperature criteria critical to reliable results.
Heat + Water Spray &/or Immerse	50C (122 F) contact time 10 minutes (time and temp contact crucial) (source of very hot water needed)	Chemical free Same as above	Must maintain high water temp/contact; hotter than normal tap or carwash. Use personal protective gear (ppg).
Steam Spray <small>*(approved for eDNA decontamination)</small>	100C (212 F) contact time 10 seconds (time and temp contact crucial) (steamer washer/ sprayer needed)	Chemical free Same as above	Must maintain veryhigh water temp/contact; (i.e. steamer washer/sprayer). Risk of burns use ppg.
Virkon Aquatic <small>*(approved for eDNA decontamination in a 2% solution for 10 - 30 min)</small>	Follow product directions for proper mixture and minimum contact time (apply directly, maintain saturation and rinse thoroughly)	Environmentally friendly Designed for aquatic use Quick inactivation time Sewer compatible	Follow MSDS directions for health risks and use ppg when mixing. Chemical based. Corrosive in concentrate form.
Quaternary Ammonium + Water (family of products)	Follow product directions for proper mixture and minimum contact time (apply directly, maintain saturation and rinse thoroughly)	Effective, user friendly Low health risks Sewer compatible	Follow MSDS directions for health risks and use ppg. Chemical based.
Sodium Hypochlorite + Water <small>*(approved for eDNA decontamination)</small>	200 ppm for pathogens; 5000 ppm for eDNA - contact time: 10 minutes (apply directly, maintain saturation and rinse thoroughly)	Widely available Effective	Follow MSDS directions for health risks and use ppg. Highly Corrosive.

USFWS Contacts: Corey Puzach, Fish Health Center: corey_puzach@fws.gov, Dave Wedan, Watercraft Safety Coordinator: dave_wedan@fws.gov

*for eDNA decontamination details contact Jen Bailey, Whitney GeneticsLab: jennifer_bailey@fws.gov

updated: April 2014

Appendix F. Mobile eDNA Trailer Maintenance and Use Manual

Mobile eDNA Trailer Maintenance and Use Manual

Purpose

In order to process water samples collected in the field, a sterile work environment is required to filter/centrifuge water while preventing any field contamination. The eDNA trailer is designed to be mobile while maintaining the highest level of quality assurance and quality control that would be found in any lab environment.

This is done in part by keeping all dry consumable equipment (filters, paper towel, gloves) in locked cabinets within the dry lab area. All equipment that requires decontamination between uses (filter funnels, carboys, filter manifolds) are stored under the work bench in the wet lab.

The eDNA trailer is equipped with two sinks, both of which are in the wet lab. The aft sink should be considered contaminated and the forward sink should be considered clean (non-contaminated). The forward sink has two faucets; one for deionized (DI) water and one for regular tap water.

Placement of the eDNA Trailer is important in optimizing its capabilities and improving the efficiency of sample processing. The eDNA trailer should be set up near an access point to the body of water being sampled, preferably upriver of where collections begin.

Cautions:

- Park eDNA trailer on level hard surface to prevent getting stuck and to keep filtering/centrifuging equipment functioning properly.
- Park eDNA trailer so exhaust from generator is blown away from eDNA trailer (if possible).
- If eDNA trailer is equipped with a dry ice cooler, turn on ceiling fan in dry lab to remove any carbon dioxide gas once trailer is set up and running.
- When the ultra-violet (UV) system is in operation, no staff should be in the wet lab.

If eDNA trailer will be set up at the same place for an extended period of time, disconnect from tow vehicle. If eDNA trailer will be located at a particular site for the day, it is acceptable to leave it connected to tow vehicle provided staff still go through the leveling procedures (see set up procedures section).

Tools Needed:

- Leveling jack socket
- Level
- Wheel chocks
- Four blocks of wood (2x4-12" long) to be placed under leveling jacks.

eDNA Trailer Set Up Procedure

1. Park eDNA trailer on flat hard surface. If using external water source, ensure there is enough water hose to reach water connection.
2. Place wheel chocks in front of and behind trailer tires.
3. Leveling the eDNA trailer.
 - a. Use the power jack on tongue of eDNA trailer to visually level trailer.

- b. Using a leveling jack socket, lower the four leveling jacks to the ground. Place blocks of wood under leveling jack pads. (leveling jacks are located at the four corners of the trailer).
 - c. Enter the eDNA trailer and place level on wet lab counter top to identify if eDNA trailer needs any further leveling (accomplished by putting weight down with leveling jacks located on all four corners of the trailer).
 - d. The four leveling jacks are used for making fine adjustments. The bulk of the leveling procedure should be accomplished with the power jack located on the tongue of the eDNA trailer.
4. Connecting power source (ensure all operating system switches are in the off position).
 - a. Operating from shore power.
 - i. Make sure to use 220v, with a 30 amp minimum service, but it cannot exceed a 50 amp service. If the proper shore power requirements are not available use on-board generator.
 - ii. First connect the extension cord to the eDNA trailer, then plug into the power source.
 - iii. Once the shore power is properly connect, switches for operating systems can be turned on.
 - b. Operating generator (ensure all operating system switches are in the off position).
 - i. To start generator, hold down generator starter in the priming position for 30-60 seconds.
 - ii. Push generator starter switch to the on position until generator starts.
 - iii. Once the generator is running, switches for the operating systems can be turned on.
 5. Connecting water source (fill internal water tank before heading into field).
 - a. If using external water source, connect hose to eDNA trailer and water source. Once the connection is made, turn on the water source to pressurize the water line to the trailer.
 - b. If using internal water source, turn on water pump.

Operating Systems

1. Supplies
 - a. All consumables (gloves, filters, paper towels) are stored in the dry lab.
 - b. All filtering equipment is stored in wet lab in side cabinets.
 - i. Filter manifolds, carboys, forceps, tubing, funnels are to be kept in the wet lab at all times.
2. Lighting
 - a. Light switches for wet lab are located in wet lab.
 - b. The ultra violet light (UV) on/off switch is located in dry lab with a flip-up plastic lid to prevent accidental use.
 - i. When UV system is on, a warning indicator light in wet lab will alert anyone working in wet lab that UV system is in on.
3. HVAC
 - a. Heating/ Cooling: Adjust thermostat to desired temperature for working conditions
 - b. Dry Lab Ceiling Fan: Set thermostat to turn on the fan.

CAUTION: DRY LAB CEILING FAN SHOULD ALWAYS BE ON WHEN DRY ICE IS KEPT IN DRY ICE COOLER.

4. Vacuum System

CAUTION: DO NOT LET VACUUM PUMP RUN MORE THAN 60 SECONDS WITHOUT an OPEN VALVE.

- a. Vacuum pumps are located in a cabinet in dry lab.
- b. To turn on vacuum pump, locate the switch in the wet lab and move to “on” position.
 - i. Each pump is set to operate each filter line on each side of trailer.
 - ii. Two shutoff valves located next to forward sink controls which vacuum lines are activated.
 - iii. Once filtering is complete, open several valves and allow the vacuum pump to operate without pressure for at least 5 minutes before shutting off.
- c. DI/water heater (if using internal water source turn on water pump).
- d. Water heater
 - i. On/off switch located in dry lab next to thermostat.
 - ii. Water heater should be turned on once filtering begins to ensure water is hot.
 - iii. When red indicator light turns off water is hot.
 - iv. Front sink left handle produces hot water.
- e. DI system
 - i. Front sink right handle produces DI water.
 - ii. DI water should be tested using TDS meter to ensure water quality is met.
 - iii. When DI water TDS is above 15ppm change resin in tank 1 and tank 2.

5. Refrigerator

- a. Runs off propane/electric

Laboratory Decontamination

After trailer has been leveled and set up, decontaminate the interior of the trailer at the beginning of each day:

1. Mix up a 10% bleach solution in bleach bath container.
2. Wipe down all counters and cabinets with bleach solution.
3. Wipe down all counters and cabinets with tap water to remove bleach residue.
4. Sweep the floor to remove any debris brought in on boots or coolers.
5. Mop floor with 10% bleach solution and rinse with water to remove any bleach residue.
6. Lock back door and dividing door of the wet/dry lab. Turn on the UV lights for 30 minutes.
7. After UV lights have been turned off, unlock trailer doors and begin setting up the wet lab for filtering/centrifuging.

Filtering/ Centrifuging Procedures

See QAPP 2014

eDNA Trailer Shutdown Procedure

Centrifuging:

1. Store centrifuging equipment in curb side cabinets.
2. Wipe out centrifuges with dry paper towel.

3. Secure centrifuges for travelling.

Filtering:

1. Once the last sample is filtered, disconnect all carboys from vacuum line. Completely open four or more valves and let vacuum pump run for 5 or more minutes. Doing so will remove any moisture in vacuum line, preventing long term damage to vacuum pump.
2. Store filtering equipment in curb side cabinets.

Towing Preparations

1. Remove garbage from inside eDNA trailer and place in nearest receptacle.
2. Thoroughly wipe down all countertops with water. (Any bleach residue will discolor and rust counter top).
3. Shut down all operating systems.
 - a. Turn off
 - i. Vacuum pumps
 - ii. Lighting
 - iii. Water pump
 - iv. Water heater
 - v. HVAC/ refrigerator
 - vi. Ceiling fan (make sure roof vent is closed)
4. Disconnect water source.
5. Disconnect power source.
 - a. If running generator, allow generator to run without load for 5 minutes before shutting down.
6. Raise leveling jacks
7. Connect eDNA trailer to truck (if needed).
 - a. Connect/check safety chains.
 - b. Raise power jack high enough to avoid rubbing ground.
 - c. Connect/check trailer lights and ensure they are functioning properly.
8. Remove tire chocks.
9. Take final walk in and around eDNA trailer.
 - a. Ensure eDNA trailer is ready for traveling.
 - i. Secure all equipment
 - ii. Close all windows and cabinet doors.
 - iii. Lock all doors including lab dividing door.
 - iv. Put caps on holding tanks.
 - v. Raise steps.

Trailer Maintenance

1. Before departing on each trip check tire pressure and tread wear.
2. Check hour meter on generator and service as prescribed in owner's manual.

3. Check propane cylinders to ensure they are still properly secured and inspect propane lines for cracking.
4. Ensure DI system is working properly, if necessary, replace resin.
5. Periodically check MSDS sheets, med kits, and fire extinguishers to ensure they are all update
 - a. One safety item to keep in the trailer is kitty litter to place on any diesel spilled on the ground.

Appendix G. eDNA Security Plan for Co-Located La Crosse FWCO and WGL

Standard Operating Procedure for Minimizing Risk of Invasive Carp DNA Contamination within the Midwest Fisheries Center

eDNA Security Team: Jenna Merry, Nick Grueneis, Mark Steingraeber

Project Leaders: Sam Finney, Ken Phillips, Emy Monroe

Safety Officers: Mark Steingraeber, Nikolas Grueneis, Terrence Ott

Effective Date: April 20, 2014

Review Date (annually): April 2015

Purpose: The shared location of three U.S. Fish and Wildlife Service (USFWS) Offices, La Crosse Fish and Wildlife Conservation Office (LFWCO), La Crosse Fish Health Center (LFHC), and Whitney Genetics Laboratory (WGL) presents a unique challenge to the USFWS Environmental DNA (eDNA) Monitoring Program. eDNA sample processing is a sensitive process, inherently susceptible to contamination from outside sources. Processing of eDNA samples requires strict adherence to laboratory hygiene and specific protocols for reduction of risk factors that could cause contamination of samples. Sample analysis for the entire eDNA monitoring program, currently including samples from the Great Lakes and Mississippi River basins, is performed at the Whitney Genetics Laboratory. Laboratory staff minimizes risk by following procedures designed to reduce introduction of DNA to the laboratory that may be on surfaces of sample packages, sample bottles, clothing and footwear. To compound risk factors, a mission of the co-located LFWCO is to monitor invasive carp populations directly, which includes collection of invasive carp and invasive carp tissue samples, as well as collecting water samples for eDNA analysis at WGL. Cross-contamination between eDNA samples and gear and carp sampling gear could be very likely if protocols were not in place to help staff address contamination challenges. The co-located La Crosse Fish Health Center occasionally receives whole carps and/or carp tissue samples for diagnostic fish health cases, and maintains several invasive carp tissue cell lines for research purposes as part of its mission. Midwest Fisheries Center staff, collaborators, volunteers, and associated sample containers, laboratory and field equipment have a large potential for acting as vectors of contamination by carrying invasive carp DNA to and within the co-located field station and indirectly to WGL. Due to the unique challenges that co-location of these offices presents, stringent protocols must be followed to prevent contamination of water samples during collection, sample receipt, movement through the building and shared spaces, and sample processing. Following these isolation and decontamination protocols will reduce unintentional transfer of invasive carp DNA to facilities, sampling gear, eDNA water samples and sample containers, field and lab personnel, and other surfaces.

Scope: This document identifies high risk zones for movement of personnel, collaborators, volunteers, visitors and fish or tissue samples throughout the facility, sets up communication practices for personnel to help contain known contamination risks so that they may be isolated and eliminated, and provides directions for the isolation and decontamination of field and laboratory equipment, samples, and packages.

Responsibilities: USFWS employees, collaborators and volunteers are responsible for following procedures outlined in this document and reviewing updates to this document annually. Visitors will be notified of procedures applying to the specific activities of their visit.

Definitions:

Invasive carp = silver and bighead carp.

Established invasive carp populations = waters where silver carp are observed jumping, or a commercial harvest is occurring.

Risk Zones: The facility is divided into zones of contamination risk for personnel or equipment dependent on the activities that may take place within (Figure 1).

- Zone A is the area of highest contamination risk. This area includes the gated outdoor area directly in front of the three south garage bays bordered by fences to the south and east, and a path from the entry gate to this area. Direct contact boats, vehicles, sampling gear, and nets may be stored in this area. This zone will also serve as the decontamination area for all traditional sampling gear and equipment.
- Zone B is the area with a moderate or periodic risk of contamination present. Areas with continuous moderate risk include the virology laboratory, the three LFWCO garage bays, the fisheries laboratory, and the woodshop. Invasive carp tissue cells are cultured in the virology laboratory and present a continuous risk. Aseptic techniques are applied to methods in all tissue cell culture procedures, which will minimize risk for escape of DNA from this laboratory. In addition to these practices, 10% bleach or DNA away will be applied as needed to equipment and laboratory surfaces when working with invasive carp tissue cells. Predominately decontaminated equipment and gear will be housed in the garage area, fisheries laboratory, and the woodshop, although in special circumstances direct contact gear, direct contact equipment, and invasive carp or their parts may be present. Specific protocols are in place to reduce contamination threats from these sources. Areas with periodic risk of contamination are the front door and reception area where fish and/or tissue samples may arrive for fish health diagnostic cases or research purposes. In this case diagnosticians will remove sample packages to the LFHC histology laboratory for processing. Specific protocols are in place to contain contamination threats and to communicate risks to building staff. In the rare case that a partner or member of the public in possession of an invasive carp brings carcass(es) into the building through the front entrance for reporting, Center staff will contain the risk and notify building personnel of the specific contamination potential associated with each individual case.
- Zone C is the area with a low contamination risk. This area includes the interior of the LFWCO, LFHC, the office and hallway space of WGL, the north garage bay, and the remainder of the gated parking lot aside from Zone A. Predominately only decontaminated personnel, equipment, and gear will be housed in this zone. Under special circumstances, contaminated data sheets, personnel, and invasive carp or their parts may be present. Specific protocols are in place to reduce contamination threats from these sources.
- Zone D is the area where there is a very small risk of outside contamination. This area includes the laboratories of WGL. Personnel and equipment entering Zone D must adhere to strict protocols prior to and upon entry or exit to reduce the potential of outside contamination into the laboratory.

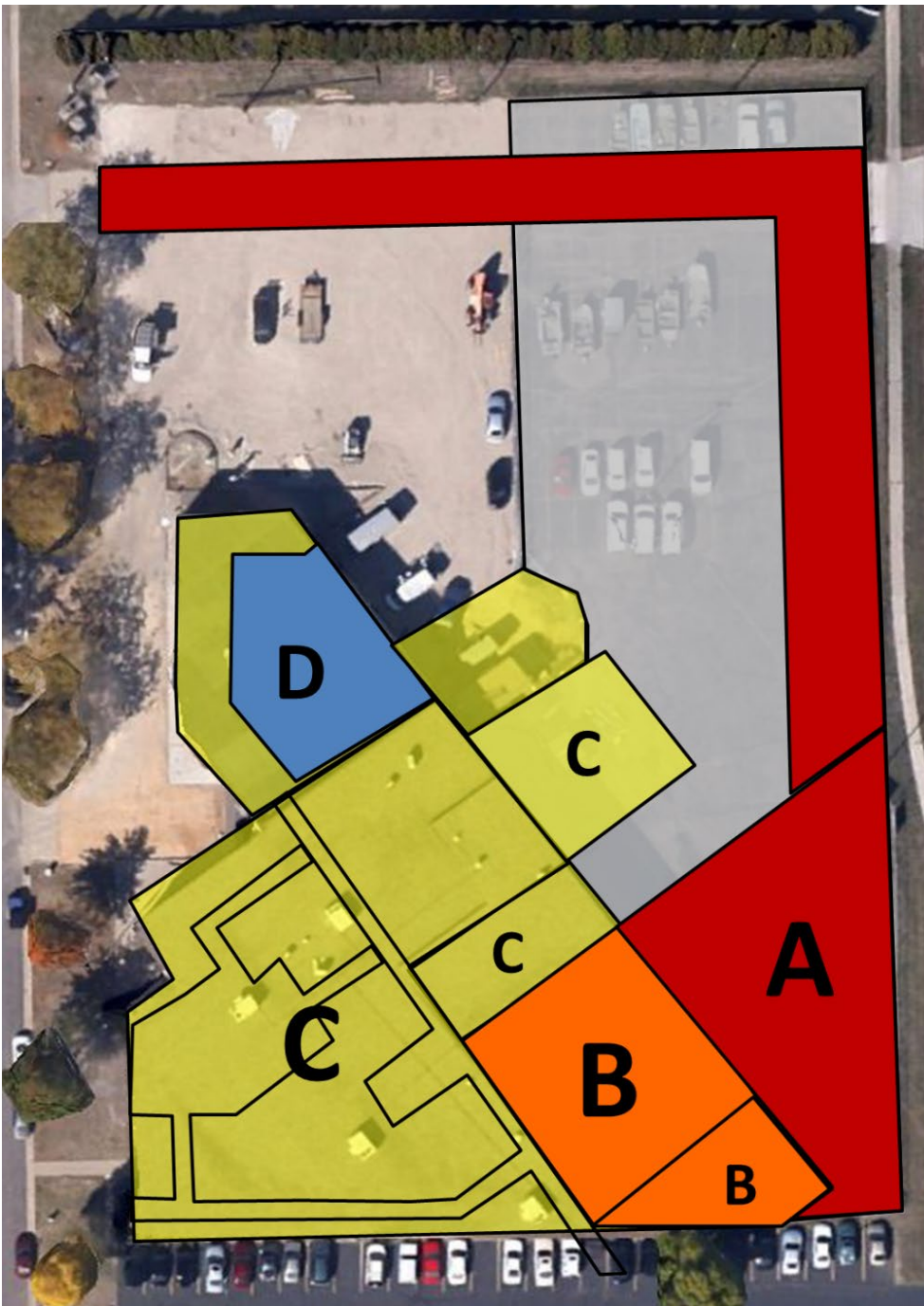


Figure 1. Zone map of the Midwest Fisheries Center Facility. Zones indicate the likelihood of invasive carp DNA being present, from A (red) the highest to D (blue) the lowest.

Movement of samples, equipment and people: Each office has outlined specific procedures to minimize contamination threats for tasks that occur within respective programs and may not carry over to the other co-located offices (see procedure details below). However, many times tasks and group projects are shared or overlap between offices, so staff, volunteers, and collaborators must have procedures in place that encompass a wide variety of tasks and projects that fall into gray or shared areas. All participants must be aware of decontamination or risk minimization procedures that apply to daily duties as well as shared or overlapping duties. All staff, collaborators and volunteers are responsible for knowing Risk Zones and procedures that apply to entering each risk zone. Staff is also

responsible for making collaborators, volunteers and visitors aware of procedures that apply to them and their corresponding activities. If staff or volunteers from one office will be working in the workspace of another office, or collaborating with another office, they must be familiar with SOP's pertaining to the work they are performing. Samples and equipment must be handled according to protocols, no matter who receives samples or packages, or which staff member is using the equipment. Much of the equipment in use for the Center is shared. Be aware of procedures to follow when borrowing or using shared equipment.

Decontamination Gear and PPE: There will be two separate decontamination zones, with dedicated equipment to remain in each zone. One zone will be for medium to low risk gear, and one for high risk gear. Clean sets of personal protective equipment (PPE) will be stored in cabinets in each zone (or nearby) that include boot covers, Tyvek suits, lab coats, and decontamination chemicals (Virkon, etc). This PPE should be worn while decontaminating gear, and then removed before reentry into low risk areas. In Zone C of the garage, a "clean" cold water pressure washer with attachments for degreasing detergent will be installed for use by Center staff to decontaminate medium to low risk field equipment and gear such as eDNA boats and equipment and boats and equipment used in Wild Fish Health Survey sample collections where invasive carp populations are not established. A duplicate set of decontamination equipment and PPE for use with highly contaminated boats, equipment, etc will be kept near the hot Zone A. Do not use this equipment for low-contamination equipment. This equipment and associated PPE will stay in Zone A. Keep "clean" and "dirty" equipment separate and do not move outside of their appropriate Risk Zones. Boot covers and Tyvek suits will be kept at entrances and transition areas for use as needed to prevent transfer of DNA on surfaces, boots, and employees.

Communications: Specific communications protocols for certain tasks are outlined in SOP's (below), but many communications are essential for maintaining the integrity of Risk Zones, samples, packages, and shared spaces. Please inform Center staff of risks they may become involved in to make sure they are aware and follow appropriate procedures to minimize risk. Inform Project Leaders and the eDNA and Biosecurity Team members (Nicholas Bloomfield, Ken Phillips, Jen Bailey, Mark Steingraeber) of known or unusual risks that are not covered in Procedures listed below. Inform staff members who will be working with equipment, samples, or in areas that may become affected of any procedures they may follow to reduce DNA contamination and prevent spread throughout the building. If this may also include a safety risk, inform Safety Officers (Nick Grueneis, Mark Steingraeber, Terry Ott) as well.

La Crosse Fish Health Center Standard Operating Procedures: The La Crosse Fish Health Center (FHC) follows guidelines established in the American Fisheries Society Fish Health Section Bluebook, Section 3: Quality Assurance/Quality Control, which establishes procedures for handling samples. The section provides basic guidance to prevent contamination in the laboratory and between samples.

Although not typical, the La Crosse FHC occasionally receives whole invasive carps and/or tissue samples from invasive carps as diagnostic cases. The La Crosse FHC also maintains several invasive carp tissue cell lines for research purposes. To minimize the spread within the Midwest Fisheries Center building of DNA from invasive carps, the La Crosse FHC has adopted additional procedures for handling invasive carps, tissue samples from invasive carps, and invasive carp tissue cultures. Procedures to be followed in addition to those described in Section 3 of the AFS-FHS Bluebook are:

1. La Crosse FHC staff will provide notification to Whitney Genetics laboratory staff that invasive carps and/or tissues are being worked with. WGL staff will take appropriate precautions.

2. Any whole invasive carps or tissue samples from invasive carps received at the La Crosse FHC will be in a sealed container. The external surface of the container will be coated with an appropriate decontaminant (10 % bleach or DNA away) for a minimum of 10 minutes prior to opening. Isopropanol and quaternary ammonium products (Lysol Professional, Extra) are not acceptable decontaminants for eliminating DNA).
3. Whole invasive carps will be dissected/processed within the Histology Laboratory (Room 10) at the La Crosse FHC. Processed tissue samples will be distributed to the appropriate laboratory(s) for pathogen screening.
4. La Crosse FHC staff will don appropriate PPE when working with invasive carps, invasive carp tissues, or invasive carp tissue cell culture. Appropriate PPE will be rain gear, Tyvek, or other designated clothing, and boots when dissecting invasive carps or processing tissues from invasive carps. Laboratory coats are considered minimum PPE and are only allowed for tissue cell culture work, or other laboratory work involving processed samples (histopathology samples, bacterial isolates, etc.). Laboratory coats and other PPE that may be contaminated with invasive carp DNA should not leave the laboratory until they have been washed, decontaminated or disposed of.
5. Immediately following completion of work involving invasive carps or their tissues, La Crosse FHC staff shall treat all laboratory surfaces, equipment and tools with an appropriate decontaminant (10 % bleach or DNA away) for a minimum of 10 minutes.
6. PPE shall be removed and placed in appropriate locations for disposal or cleaning. Employees shall thoroughly wash their hands with soap and water.
7. Any La Crosse FHC employee that worked directly with invasive carps and/or tissues from invasive carps, or may have potentially been exposed to invasive carp DNA, shall not enter Zone D until the following day.

La Crosse Fish and Wildlife Conservation Office Standard Operating Procedures: The following procedures are specific to La Crosse Fish and Wildlife Conservation Office programs and projects.

Separation of Field Equipment: To reduce the threat of contamination, field crews will maintain two separate sets of personal field sampling gear including at a minimum PFD's and rain gear: 1) eDNA sampling gear and 2) Any other traditional field applications. Equipment used for eDNA sampling versus traditional sampling will also be maintained separately: 1) One vehicle and one boat with the necessary associated equipment (oars, fuel tanks, tool box, etc.) will be dedicated to eDNA sampling and 2) Remaining boats, vehicles, and other gear will be designated for any other use. All eDNA field equipment (boat, vehicle, PFD's, rain gear, etc.) and supplies (gloves, filters, centrifuge tubes, etc.) will be housed at a separate storage location. Contaminated traditional sampling equipment will be predominately staged or stored in Zone A. Equipment that has been decontaminated and decontamination supplies will be housed in Zone B.

Decontamination Equipment List:

This decontamination equipment will be maintained separately between eDNA sampling and traditional sampling

- Brushes
- Water pump and/or buckets
- DNA Away or equivalent

- Paper Towels
- Garden Hose
- Garden Sprayer
- Pressure washer with steam option
- Virkon Aquatic
- >30 gallon decontamination tubs
- Personal Protective Equipment (PPE)

Decontamination Procedures:

Procedure A- Decontamination of eDNA sampling gear and equipment: This procedure refers to actions taken prior to leaving and upon returning to the station for collection of eDNA samples in the field. Equipment designated for eDNA gear and equipment decontamination will be used to perform any functions related to eDNA sampling. This equipment will be housed in Zone C of the garage. This procedure does not preclude additional protocols outlined in the Quality Assurance Project Plan (QAPP) performed prior to eDNA sampling. Due to the sensitivity of eDNA sampling, this must be done before and after each eDNA sampling trip.

1. Prior to leaving on a collection trip, use DNA Away or equivalent to decontaminate any personal items that will be used on the trip (watches, sunglasses, etc.)
2. Park truck and boat in Zone C.
3. Use pressure washer to rinse truck (including floor mats), boat, and any associated equipment capable of withstanding a high pressure rinse (oars, fuel tanks, tool box, totes, etc.). This could include PFD's, rain gear, or boots if they were heavily soiled.
4. Fill a pump sprayer with 2% Virkon Aquatic.
5. Spray all surfaces of truck, boat, and other equipment until all surfaces are completely soaked. These surfaces must be coated for at least 20 minutes. Rinse when complete.
6. Mix a batch of 2% Virkon Aquatic according to recommendations in the decontamination tub.
7. Dip PFD's, rain gear, boots, floor mats, oars, or any equipment capable of withstanding a prolonged submergence without damage. Allow to soak for 20 minutes.
8. Allow equipment to air dry on the designated drying racks prior to returning all eDNA equipment to the off-site facility.

Procedure B- Minimize Invasive Carp Residue Transport to Station: This procedure refers to returning from sampling that has occurred in waters with any reported invasive carp observations.

1. Prior to returning to the station, use water pump, buckets, and brushes to remove as much blood, slime, scales, sediments, etc. from the boat, equipment, and gear as possible.

Procedure C- Storage or Decontamination of Traditional Sampling Gear and Equipment: This procedure refers to returning from sampling that has occurred in water with any observed invasive carp. Equipment designated for traditional sampling gear and equipment decontamination will be used to perform any functions. This equipment will be housed in Zone B of the garage. Boats, vehicles, gear and non-enclosed equipment that will be stored inside the facility will be decontaminated. Note: Gear and equipment from non-invasive carp infested waters are still subject to disinfection standards prior to entering a different body of water.

1. Park vehicle and boat in Zone A. These and any gear or equipment may remain in Zone A without decontamination.
2. Personnel wearing direct contact clothes or shoes/boots should not proceed beyond Zone B.

3. Gill/trammel nets will be laid out to dry within Zone A. After drying, these will be stored in Zone A or enclosed with lids if storing in Zone B. Prior to entry to Zone B, the outside of the container will be decontaminated in step 6 of this procedure. Fyke/mini-fyke nets will be decontaminated in step 6 of this procedure prior to storage in Zone B.
4. Use hot pressure washer to rinse truck (including floor mats), boat, and any associated equipment capable of withstanding a high pressure steam rinse (oars, fuel tanks, tool box, totes, etc.). This could include PFD's, rain gear, or boots if they were heavily soiled.
5. Mix a batch of 2% Virkon Aquatic according to recommendations in the decontamination tub.
6. Dip PFD's, rain gear, boots, floor mats, oars, or any equipment capable of withstanding a prolonged submergence without damage. Allow to soak for 20 minutes. Rinse when complete.
7. Allow equipment to air dry on the designated drying racks.
8. Decontaminate cleaning supplies in tub and replace in Zone B
9. Data sheets and clipboards will be kept in an enclosed container within FWCO offices when not in use or in the FWCO lab. After handling sheets for data entry or verification, replace into enclosed container, clean work area with DNA Away or equivalent, and wash hands.

Procedure D- Net Mending: This procedure refers to mending gill nets, trammel nets, and fyke/mini-fyke nets that have been used in waters with any known invasive carp observations.

1. Prior to handling nets, personnel will don appropriate PPE (rain gear, Tyvex, or designated clothing and boots).
2. When possible, mending will take place in Zone A. When necessary, mending will take place within the woodshop section of Zone B. When working in Zone B, area will be sectioned off and labeled as a DNA hot zone.
3. Nets will be decontaminated via Procedure C-8 in the southern garage section of Zone B.
4. Prior to entering Zone C, any PPE will be removed and stored within the labeled hot zone and hands will be washed.
5. Upon completion of net mending, PPE and net mending tools will be decontaminated via Procedure C-8.
6. Remove any solids (leaves, scales, algae, etc.) that have accumulated on the floor.
7. Prepare a solution of decontaminate and mop floor.

Procedure E- Reduce Transport of DNA Contamination between Zones: This procedure refers to movement of personnel, gear, and equipment throughout the facility. Specific protocols must be followed to reduce the likelihood of spreading invasive carp DNA into zones of lower risk and ultimately WGL.

1. Personnel working with direct contact contaminated gear in Zone A or B will wear appropriate PPE. PPE will be removed and hands washed prior to re-entry into Zone C.
2. Personnel entering Zone D from Zone C will at minimum wash hands prior to entry.
3. It is recommended that personnel working in Zone D do not enter Zone A or B. If it is necessary, they will wear PPE to cover footwear and clothing prior to entering Zone A or B and remove upon exit.
4. Any potentially contaminated gear will be decontaminated via procedures above or enclosed prior to entry to Zone C or D.

Whitney Genetics Laboratory Standard Operating Procedures: Most of the procedures performed at Whitney Genetics Laboratory are specifically for eDNA monitoring of invasive carps and are incorporated into the Quality Assurance Project Plan (QAPP). Occasionally, duties are performed either in addition to or in support of the QAPP, or for programs not related to the QAPP such as flow cytometric analysis of

grass and black carp samples. Samples are also occasionally processed at Whitney Genetics Laboratory in support of research and development of the QAPP, or for other USFWS programs. The following procedures will be followed in addition to QAPP procedures while in support of the eDNA program, performing research, or during development of new programs.

1. Any staff, collaborators, volunteers, or visitors to the WGL who are wearing clothing or footwear that has been exposed to any water where invasive carp are known to exist must wear Tyvek suits, lab coats, gloves or boot covers as appropriate before entering the lab. These are provided at the two main entrances at WGL. Any WGL staff or associated member who is leaving the laboratory for an area of known contamination should bring PPE with them to minimize risk of becoming contaminated while outside the lab. Dispose of contaminated gear before re-entry to the lab. Change footwear if possible.
2. When receiving samples, equipment, or packages that may be contaminated with invasive carp DNA, wear appropriate PPE to help contain contamination and dispose of PPE, gloves, and boot covers after each use. Stay in receiving room and don't remove samples or associated equipment to another room until all surfaces have been decontaminated.
3. Spray surfaces of containers or equipment with 10% bleach (10 min exposure) or DNA Away and wipe surfaces with paper towels. Remove to storage or to work area within the receiving room for processing.
4. When working with tissue samples from grass carp or black carp (i.e., not silver carp or bighead carp) use bench paper to define working space and keep associated laboratory instruments, etc, confined to workspace. After task is complete, decontaminate instruments with 10% bleach (10 min) or DNA Away and wipe entire area with either decontaminant. Contain contaminated waste products in a sealed waste bag and remove to trash bin.
5. Decontaminate surfaces of any sample containers saved for storage in WGL before removing to storage or other sample processing rooms.
6. Direct work with invasive carp tissue cells is important for preparation of extraction control samples for the eDNA monitoring program and sometimes for other purposes. If at all possible, perform this work in borrowed laboratory space from LFHC or another appropriate space. Wear protective gear to contain DNA contamination during sample processing, use 10% bleach or DNA Away before, during, and after processing procedures, and dispose of contaminated PPE. Follow all procedures outlined for the laboratory space you are working in.

In addition to step-by-step procedures, it is pertinent for all WGL employees to follow immaculate laboratory hygiene practices:

- Dedicate footwear to laboratory space. This footwear should not be worn in Risk Zones A or B and should be worn only in Risk Zone D if possible. If you must enter Risk Zone C during times of known contamination, wear boot covers while working in that area and dispose of later.
- Clothing or attire should not have been exposed to any potential contamination risks without laundering before entering WGL. This applies to hats, jackets, boots, shoes and regular clothing. Any attire that has been worn in areas of potential risk must be laundered using detergent or decontaminated with DNA Away before returning to the lab. If you have been sampling for the eDNA program, volunteering with other programs, recreating in areas of known contamination, or performing research duties do not return to the lab wearing the same clothes.
- Wash hands with copious amounts of soap and water if you have been exposed to invasive carp DNA.
- Be aware of any potential risks that may not be covered in these protocols and inform teammates of any concerns.

Appendix H. Original Methods from previous versions of QAPP

Old 2.2 Equipment Procedure for Coolers and Sample Bottles

- (1) A 10% bleach solution with water will be prepared in a 3-gallon low-pressure sprayer that is dedicated to the project. The bleach solution must be prepared immediately prior to use, and each time decontamination activities will be occurring.
- (2) Remove mud and other biological residues from surfaces by rinsing and scrubbing. Equipment surfaces must be free of debris and other material before decontaminating.
- (3) Sample transport coolers will be decontaminated with freshly made 10% bleach solution in the low pressure sprayer. Use the low-pressure sprayer to thoroughly cover the inside and outside surfaces. Allow 10 min of contact time before rinsing with water. Coolers may be left to air dry, or dried using clean paper towels while wearing clean gloves.
- (4) If filtering: Sterilized disposable 2L bottles may be used for sample collection or 2L autoclavable reusable bottles sterilized in the following way may be used:
 - (a) NEW 2L bottles may be used straight from the manufacturer. For subsequent sampling events, send bottles to the WGL for cleaning, and WGL will return clean bottles (refer to Appendix D). For sampling agencies not working with the WGL, follow procedures b-c to properly decontaminate bottles between uses
 - (b) If there is no autoclave available, use a 10% bleach bath to decontaminate sample bottles.
 1. In an area free of carp-contamination prepare a 10% bleach solution and soak bottles and caps for a minimum of 10 minutes. It is important to ensure that there are no air bubbles inside bottles or caps, which may require two 10-minute soaks, one with the bottle upright on each end of the closed bottle.
 2. Rinse each bottle by partially filling with water and shaking vigorously so that all areas of the bottle are rinsed, repeat a minimum of three times per bottle, but be sure to rinse until there are no traces of bleach.
 3. Air dry, cap, and place in sanitized coolers. NOTE: It is essential to rinse well since residual bleach would destroy any DNA collected and is a PCR inhibitor.
 - (c) If you have access to an autoclave, bottles need to be rinsed well with clean tap water and autoclaved.
 1. Rinse bottles by partially filling with clean water, shaking vigorously with the cap loosely held over the opening. Empty and repeat a minimum of two times.
 2. Place the threaded caps on the bottles and lightly screw on cap (cap will not be able to come off, but will still be able to move).
 3. Place into autoclave and set cycle for 1 hour at 121°C (15 psig or 1 bar).
 4. Once the autoclave cycle is complete, carefully remove bottles and allow them to cool to room temperature before fully tightening caps. If caps are tightened before allowing the bottles to cool, the bottles will warp and collapse.

If centrifuging: purchase sterile, chemical-free disposable 50-ml polypropylene tubes with maximum RCF of at least 6,000 x g. Even sterile tubes can still have traces of the chemical used to free the plastic tubes from the metal forms during production. Some manufacturers sell sterile

tubes that do not have this residual chemical in them, and these should be used to avoid introducing PCR-inhibitors from the sample tube.

- (5) Once all 2L bottles have been sanitized, sample labels can be printed by the sampling agency. Sample containers will be labeled with a unique barcode ID or agency generated code (Section 1.7 for case and sample numbering) that does not indicate location (to allow blind processing). Labels will be printed on Rite-N-Rain® or some type of waterproof labels and affixed to the outside of the sample bottles/tubes.
- (6) Once bottles/tubes have been labeled, they will be placed in the sterilized sample coolers in numerical order. Sample containers will be stored in the sterilized coolers until use, and will be transported only in the coolers. Although the sample ID number of the samples is not relevant except for identification purposes, collecting in consecutive order will aid in determining where samples were taken in case of a recording error.
- (7) A minimum of 10% of the total number of samples collected should be field blanks. For offices working with the WGL, all field blanks must be filled by WGL. For other agencies, blanks may be filled with any city-provided tap water (If water source is a well or you are unsure of the source, use distilled or deionized water). If filtering, a minimum of one blank per cooler is required, but more may be included. If centrifuging, collect blanks to meet 10% of total number of samples collected. Note, if the sampling design for your particular body of water requires a specific sample size in order to meet a precise detection probability, then containers for control samples to meet the 10% minimum will have to be added to the total number of sample containers dictated by your sampling plan.

Old 3.2 Filtering Procedure

Water samples collected in the field need to be filtered within 12–16 hours after the last field sample is collected.

Equipment needed:

- Manifolds (Millipore 3-place stainless steel Hyrrosol Manifold, item #XX2504735)
- Magnetic 500-ml filter funnels (Pall item #4238; VWR item #28150-496)
- Glass fiber filters, 1.5 micron, 5.5 cm diameter glass fiber filter paper (Type 934-AH; Fisher item #1827-055)
- Forceps (microforceps) – at least two pair, labeled with different colors or other identifier
- Carboy (3.5 gal or larger), for wastewater generated during filtering
- Rubber vacuum tubing (14-176-24, 1.25 in. inner diameter), double hole stopper (Fisher item #14-140P) that fits carboy opening, and glass connectors or plastic connectors (Fisher item #509557177) for connecting manifold to carboy and manifold to vacuum line
- Vacuum trap flask to protect vacuum pumps (plastic is fine), single hole stopper to fit flask and tubing to fit flask vent
- Sterile conical tubes (50mL) with caps and labels
- Sterile conical tubes (15mL) with caps and labels
- Paper towels
- Black permanent markers (e.g., Sharpie®)
- Powderless latex or nitrile gloves
- Vacuum system capable of –75 kPa vacuum

- Bleach
- 10% Bleach bath to sanitize filter funnels (use any clean, potable water source to mix bath)
- Dedicated lab equipment cleaning sink
- Waste water disposal location such as nonspecified-use sink
- Sterile bench paper
- Dedicated water bottles, one for bleach solution, one for DI water
- DI water for equipment blanks only
- Washbin for manifolds, such as a dedicated 10 qt plastic tub
- Plastic sealable bags (e.g. Ziplock®)

3.2.1 Laboratory Preparation

- (1) Wash hands thoroughly prior to starting. Prepare a dedicated plastic wash bottle with 10% bleach solution for wiping down lab tables and manifold surfaces prior to processing samples. Sanitize all equipment, in freshly made 10% bleach solution, prior to starting. Collect all supplies.
- (2) Rinse down each workstation with bleach solution prior to beginning the filtration process. Cover each workstation surface with sterile bench paper or clean paper towels. Bench paper must be changed between samples.
- (3) Put on new powder-free latex or nitrile gloves. Prior to filtering a sample, each work station should have one black waterproof permanent marker for labeling sample tubes (or pre-printed labels), one sterile 50-mL and one sterile 15-mL plastic conical tube, sterile filter paper, one set of sterile forceps for placing filter paper on filter apparatus, one set of forceps for handling used filter paper, dedicated wash bottle with freshly made 10% bleach solution.
- (4) At each workstation, connect a 3-place stainless steel filter funnel manifold to a large carboy bottle using rubber vacuum tubing, two-hole stopper, and plastic tubing connector. Connect carboy bottle to a trap flask, and the trap flask to the vacuum line with second piece of rubber tubing. Glass connectors may be used instead if available. Note, a trap flask should be between the carboy and vacuum to protect the pump from damage should the carboy get too full.
- (5) Sample containers should be dried to remove all external water so that nothing will drip when the sample is being filtered or they can also thoroughly rinsed and dried completely before being brought into the trailer. Ensure there is no water trapped in the grooves between the caps and bottles by tipping bottles and drying away any water dripping out.

3.2.2 Sample Preparation

- (1) Put on new powder-free latex or nitrile gloves prior to handling each sample.
- (2) Remove first sample from cooler of cleaned sample bottles and make sure it is dry.
- (3) Label one sterile 15-mL conical tube and one sterile 50-mL conical tube with sample number; indicate that the filter to be stored in the 15-mL tube is the equipment control by labeling this tube with a "C". Ensure gloves that come into contact with labeling marker are not used again for handling other samples. Alternatively, labels may be preprinted and used for each tube.

3.2.3 Filtering the Equipment Control

- (1) Put on new powder-free latex or nitrile exam gloves prior to processing each new sample.

- (2) Place bottom portion of sterile (section 3.2.6) magnetic filter funnel equipped with rubber stopper on manifold and open vacuum line.
- (3) Take designated forceps for handling clean filter paper, remove one filter and place on bottom portion of sterile magnetic filter funnel. Once the filter paper is positioned on the magnetic filter funnel, attach the upper portion of the magnetic filter funnel (i.e., the funnel) to the bottom portion.
- (4) A sterile and clean magnetic filter funnel must be used for each sample. The cleaning process is described under the Equipment and Work Area Cleaning section 3.2.5.
- (5) Once the magnetic filter funnel top is secured to the bottom portion, pour 500 mL of DI water the magnetic filter funnel top as a control. In order to capture any potential contaminant DNA in the funnel, be sure to pour the DI water quickly so as to immerse all the internal surfaces of the magnetic filter funnel top with DI water. Once the DI water has been poured into the filter funnel top, turn the vacuum on to draw the water down quickly and filter the material as quickly as possible. Repeat with 500 mL.
- (6) Once the DI water has been filtered through the funnel, remove the filter funnel top, place it on clean bench paper dedicated for that sample. Take the forceps designated for that sample's used filter paper and grasp the edge of the filter paper. Roll or fold the filter paper until it is of a size to fit into the 15mL conical tube labeled as a control for the appropriate sample ID.
- (7) Place the control filter paper into the 15mL tube, screw on top, and place tube with control sample filter paper into cold storage. If work is at a laboratory, use a -20°C non-frost-free freezer, if work is in a mobile trailer, place tubes into a cooler filled with ice during the work day. If using a cooler, be sure to use a clean sealable bag designated for control samples only to keep equipment control samples separated from field samples to avoid any contamination while in cold storage. Seal the plastic bag after each new sample is added. At the end of the day, transfer all of the tubes to a cooler lined with dry ice (replaced as needed to keep samples frozen). The freezer or cooler should be secured (i.e., locked) if samples are left for any period of time unattended.

3.2.4 Filtering the Sample

- (3) Take designated forceps for handling clean filters, remove one filter and place on bottom portion of sterile magnetic filter funnel. Once the filter paper is positioned on the magnetic filter funnel, attach the upper portion of the magnetic filter funnel (i.e., the funnel) to the bottom portion. Avoid touching the funnel base with clean forceps. If forceps accidentally touch the base, get a new pair of forceps for handling clean filter paper. These designated clean forceps and the box of filters must be kept in a location far enough away from the filtering area to prevent them from becoming contaminated during filtering. If at any time water is spilled or splashed near the filters or forceps, get a new box of filters and a new pair of forceps.
- (4) Take the sample bottle and gently shake to distribute the contents within the sample evenly.
- (5) Once the magnetic filter funnel top is secured to the bottom portion, turn on the vacuum and then pour approximately one-third of the sample into the magnetic filter funnel top.
- (6) Once the one-third portion of the sample has been filtered through the funnel, *continue filtering until the filter is nearly dry*. Remove the filter funnel top. Take the forceps designated for used filter paper and grasp the edge of the filter paper. Neatly fold the filter paper once to fit into the 50mL conical tube labeled for the appropriate sample ID.

- (7) Repeat steps 1–4 at least two more times or until the entire sample has been filtered. After all the sample has been filtered, DI water from a wash bottle may be used to rinse any particulates attached to the sides of the magnetic filter funnel onto the filter paper. NOTE: since this water is touching the DNA sample DI water is better than tap water.
- (8) Place the tube with field sample filter papers into cold storage. If work is at a laboratory, use a –20°C non-frost-free freezer, if work is in a mobile trailer, place tubes into a cooler filled with ice during the work day. Use a sealable plastic bag designated for field samples only, to keep the sample tubes organized and separated from equipment control samples. Seal the plastic bag after each new sample is added. At the end of the day, transfer all of the tubes to a cooler lined with dry ice (replaced as needed to keep samples frozen). The freezer or cooler should be secured (i.e., locked) if samples are left for any period of time unattended.
The number of filters used to process the sample is up to the discretion of personnel processing the sample, however in the DNA lab, filters must be extracted one at a time. Therefore, if the water sample exhibits an excessively slow filtration rate, multiple filters should be used. Also up to the discretion of the personnel processing the sample is the amount of sample water to run through a single filter. A general rule is to run one-third of a 2L sample through a single filter; however, if the sample water is extremely turbid, for example, less water should be put through a filter. At the other end of the spectrum, if the sample water is extremely clear, more than one-third of a 2L sample may be run through a single filter. Do not place more than 10 filters into a single 50-mL tube. If more than 10 filters are generated, use additional 50-mL tubes, making sure they are clearly labeled with the sample ID and make a note on the data sheet.
- (9) On the field datasheet (Exhibit 2) next to the appropriate sample ID, mark the time (use AM PM or military time for clarity) of filter completion and the initials of the person that processed the sample.
- (10) Change gloves and sterilize the workstation between samples. Repeat steps 1–8 until all samples have been processed.
- (11) When filtering, if the water collection carboy becomes full, disconnect the carboy from the vacuum and manifold and dispense water in a sink separate from the one used to clean equipment. Once emptied, reconnect the carboy to the vacuum and manifold and proceed with the filtering process.
CAUTION: Be sure to open manifold valve and turn off the vacuum air supply when disconnecting and connecting the carboy so as to prevent explosion of the glass.
- (12) If sample is accidentally spoiled during the filtering process (e.g., bleach was used to rinse filter funnel instead of DI water, forceps from previous sample used, etc.), immediately throw away ruined samples. If portions of the sample are still viable, place in 50mL conical tube. On the outside of the sample tube, label with the amount of the viable sample (e.g., 2/3 sample). On datasheet, label with the same information (e.g., 2/3 sample) next to appropriate sample ID. Note the reason for the ruined or diminished sample.

3.2.5 Equipment and Work Area Cleaning After Filtering Each Sample

- (1) Fill a 500mL glass beaker with 10% bleach solution. Forceps designated for used filter paper must be switched out for each sample. Used forceps will be placed in beaker with 10% bleach solution for a minimum of 10 min for sterilization. Once sterilized, remove forceps from bleach solution and rinse thoroughly before use.

- (2) Fill at least a 10-qt plastic tub (e.g., Rubbermaid® plastic storage bin) with 10% bleach solution. Once a sample has been processed, the filtering apparatus must be dismantled (i.e., the magnetic filter funnel should be separated into the upper and lower parts), rinsed to remove any particles and/or film, and placed in the plastic tub with the 10% bleach solution for a minimum of 10 min for sterilization. Ensure there are no air bubbles preventing the bleach solution from fully contacting the entire filter cup interior. Once sterilized, remove the two parts of the magnetic filter funnel and thoroughly rinse before use. Rinsing should continue until all residues and scent of bleach can no longer be detected.
- (3) In between each sample, dispose of bench paper. Wipe down surface with 10% bleach solution using wash bottle and paper towels. CHANGE GLOVES! Cover work station with new bench paper.

If any deviations from this QAPP occurred during water sample collection in the field or during processing of samples, clearly describe the deviations on Exhibit 16. Even if there were no deviations from the QAPP, Exhibit 16 forms should be sent to the eDNA Project Coordinator following a sampling event to satisfy reporting requirements in section 1.6. Be sure to note any changes in personnel from the pre-trip plan on Exhibit 16 when the report is filed.

Old 4.2 Shipping Filters

- (1) If filters: Corrugated boxes (minimum outer dimensions 12" X 12" X 12") with styrofoam cooler inserts will be prepared for shipment. The number of boxes to prepare depends upon the number of samples collected (e.g., a 120-sample collection will require more boxes for shipping than a 50-sample collection). Filtering equipment controls should be placed into separate plastic bags during shipping, but centrifuge equipment controls can be mixed in with samples.

If centrifuge tubes: Any shipping containers that will hold the tubes and prevent damage to the tubes will work.

- (2) For filters or non-preserved centrifuge samples: The bottom of the coolers will be lined with solid blocks of dry ice (approximately 1–2 inch thickness). Oven-mitt type gloves must be worn by personnel that are handling dry ice to protect hands. If block dry ice is not available, pellets may be used, but avoid powder or flake.
- (3) For filtered samples: Remove the 15mL conical tubes with control filter paper from secure (i.e., locked) –20°C freezer and place in clean 1-gal resealable bag (e.g., Ziploc®). Multiple bags may be used if the entire sample does not fit in one bag. Seal over the opening of all bags used with tamper-evident tape (e.g., Evidence Tape – NC9709516). The individual packing the samples should sign the tape. Be sure to remove as much air as possible from all resealable bags used before sealing.

Be sure bags are secured so that they are tamper-evident. There are several ways to do this, here are two: 1) Close and seal bags, removing as much air as possible. Wrap tamper-evident tape or clear tape around the bag in two perpendicular directions so that the bag cannot slide out of the tape. If you don't use tamper evident tape, be sure to sign across where the tape meets itself with a permanent marker. 2) Close and seal bags, removing as much air as possible. Place tamper evident tape parallel to the bag seal, securing with three (3) staples. This option does not allow for clear tape with a signature.

When ambient temperature is above 60⁰F, more dry ice is needed for shipping than when it is cooler. If possible use both block and pellet dry ice to ensure sample integrity when shipping during warm weather. Place a ~10-lb block of dry ice on the bottom of cooler. Place a bag of samples on the block, layer approximately 1 in. of dry ice pellets on top of bag before placing another bag in the cooler. Repeat until only 2 inches of space is left at the top of cooler and fill the space with dry ice pellets. If pellets are not available, use a minimum of 20 pounds of block dry ice. Leave the bottom block whole, but break up the other block and distribute among the bags of samples. Before closing the styrofoam cooler, record the inside temperature on the datasheet (Exhibit 2). Place the styrofoam lid on top of the sample contents and seal with tamper-evident tape, ensuring the tape crosses the lid and body of the cooler. If tamper-evident tape is not available, use packing tape and sign across where the tape overlaps as well as across where the lid meets the body of the cooler.

Old 5.5 Qiagen DNeasy Kit (or equivalent kit) Procedure for *filters*

- (1) Remove samples that have been designated to be extracted from freezer.
- (2) Obtain one lyse and spin kit per filter to be extracted, open packages and organize tubes in rack. Label both caps of each tube per filter (one tube per filter). You will have time to label the rest (3 more 1.5mL lab supplied MCT, one spin filter tube, 3 Qiagen collection tubes) during the 1-hour incubation. Be sure you have added positive and negative extraction controls to each eDNA extraction procedure batch.

- (3) Add 350 μ L ATL to the top of each basket tube.
- (4) Add 25 μ L protease K to the ATL in each tube.
- (5) Remove the appropriate filter sample, carefully tear off the edge of the filter so that it fits into the top of the basket tube. Only one filter can be extracted per MCT. If more than two extractions are required for one sample, combine products into a single tube once extractions have been completed (during step 17). Be sure to push the filter down into the ATL/proteinase K mixture (use a clean pipet tip), do not tap the lyse baskets on the counter or else the buffer will leak through.
- (6) Place the basket tube into the collection tube and incubate at 55°C for 1 hour. During incubation, label two more MCTs, and a spin-column assembly for each sample, and set up three additional collection tubes per sample. Print labels for archived extracts.
- (7) Remove from incubator and centrifuge at $\geq 16,000 \times g$ for 1 minute. Remove the assembly, archiving the filter only until the case is closed. Archive tube and filter at -80°C, until results are finalized, then dispose.
- (8) Add 375 μ L Buffer AL.
- (9) Add 375 μ L ethanol (96 – 100% molecular grade). Mix thoroughly by vortexing. If liquid gathers around the lid, briefly spin to reduce contamination.
- (10) Transfer about half of the mixture by pipet into a DNeasy Mini spin column placed in a 2 mL collection tube. Centrifuge at $\geq 6000 \times g$ for 1 minute. Discard flow-through and collection tube.
- (11) Transfer the remaining mixture by pipet onto the same spin column and place in a new 2 mL collection tube. Centrifuge again at $\geq 6000 \times g$ for 1 minute. Discard flow-through and collection tube.
- (12) Place spin column in a new 2 mL collection tube. Add 500 μ L Buffer AW1. Centrifuge at $\geq 6000 \times g$ for 1 minute. Discard flow-through and collection tube.
- (13) Place spin column in a new 2 mL collection tube. Add 500 μ L Buffer AW2. Centrifuge at 18,000 $\times g$ for 3 minutes. Discard flow-through and collection tube. Be careful to avoid sloshing the ethanol in the collection tube up onto the filter column. It is important to prevent ethanol from touching the filter because ethanol is a PCR inhibitor.
- (14) Transfer the spin column to a new 1.5 mL or 2 mL MCT.
- (15) If there are 8 or fewer filters per sample, elute the DNA by adding 200 μ L Buffer AE to the center of the spin column membrane. Incubate for 1 minute at room temperature (15 - 25°C). Centrifuge at $\geq 6000 \times g$ for 1 minute. If there are more than 8 filters, elute with only 100 μ L Buffer AE so that all of the replicates can be pooled into one extraction tube.
- (16) Discard the spin column, combine multiple extractions for a single sample if necessary. Store the eluted DNA samples at -20°C. If DNA is to be immediately used for PCR, keep on ice.

Old 5.6 Original PCR Procedure (used 2009-2013)

- (1) If DNA samples (extraction elutes) are removed from freezer, note on freezer/ambient log (see Exhibits 7-9). Also note on sample log (Exhibit 6).
- (2) Use preprinted 96-well plate map (Exhibits 12-13) or build plate map in LIMS to determine which samples will be pipetted into which wells. Clearly mark plate identification on bottom edge skirt of plate. Write plate identification information (e.g. FY_case#_sample

numbers_species_initials_date) in lab notes Legible labels for use while working must be complete to allow for easy down-stream processing in the sequencing lab.

- (3) Make sure sample map for each plate is entered into the LIMS or attached to lab notes and a signature is written across the map and lab book page.
- (4) Follow DNA amplification protocol detailed below.

Primers specific to either *Hypophthalmichthys molitrix* (Silver Carp) or *H. nobilis* (Bighead Carp) are used to screen eDNA samples and amplify unique DNA sequences in each species potentially present in the eDNA samples by PCR. The PCR programs used to amplify the extracted DNA are specific to the primer set used. The PCR protocol has been optimized to utilize Platinum® *Taq* DNA polymerase (Invitrogen Corporation, Carlsbad, CA) in the eDNA screening. If other brands of *Taq* are used, optimization of the recipe and thermal profiles must be executed. Eight reactions are set up for each sample, in addition to negative (DNA blank) and positive (DNA extracted from tissue²) controls for each master mix. The PCR reactions are prepared as follows:

- (1) Wipe lab bench area with 10% bleach, 75% Ethanol, or commercial DNA sterilization wipes. Also wipe down work area with PCR hood. Use built-in UV lamps to radiate clean room for 30 min prior to PCR set-up.
- (2) Electronic pipettors should be wiped down with one of the solutions or wipes listed in Step 1.
 - In the clean reagent room, obtain all PCR master mix reagents (using only those that have not expired and that have been tested and found viable).
 - 10X PCR buffer (comes in *Taq* kit)
 - 10mM equally mixed dNTP solution (2.5 mM per nucleotide)
 - 50 mM Mg²⁺ solution (concentration in Platinum *Taq* kit; use what comes with your brand)
 - Species-appropriate forward primer
 - Species-appropriate reverse primer
 - *Taq* DNA polymerase (we use Platinum, but any hot-start *Taq* can be used)
 - Sterile molecular grade water (commercially sterile or Millipore filtered, autoclaved)

Allow reagents to thaw. Do not vortex primers or *Taq* too violently.

- (3) Record in lab notebook the lot number of all reagents used.
- (4) Prepare PCR master mixes in clean reagent room. The master mix volume can be adjusted according to the number of samples to be processed. In order to make sure that master mix does not run out prior to supplying all the desired reactions (this may occur as a result of minor errors or variations in pipetting volumes), it is generally helpful to make more than enough master mix than is needed for the desired number of reactions. For example, make enough master mix for 100 reactions when actually preparing for 96 reactions. NOTE: If positive extraction controls consist of a different species of DNA, be sure to make a small separate master mix for those samples and use primers specific to the content of the control sample. Negative extraction controls should be amplified with the Silver or Bighead Carp master mix.

² Extract from tissue using commercial DNA extraction kit (e.g., Qiagen DNeasy Blood & Tissue Kit), and manufacturer protocol. Run test PCR before relying on any DNA extract for eDNA assay positive controls.

(a) Each Initial PCR 1X reaction should contain:

- 2.5 μ L 10X PCR buffer
- 0.5 μ L dNTP (10 mM mixed dNTP)
- 0.75 μ L Mg²⁺ solution (50mM)
- 0.5 μ L forward primer (10 μ M working dilution)
- 0.5 μ L reverse primer (10 μ M working dilution)
- 0.25 μ L Platinum® *Taq* polymerase (= 1.25 U)
- 19.0 μ L sterile water.

Move prepared mix from reagent room into PCR room.

- (5) Remove DNA extracts from freezer or fridge (fill out logs as needed), vortex (quick touch) and quick-spin down the extract tubes. Take them into the PCR room. Place the 96-well PCR plate onto a clean surface, positioned from left to right.
- (6) Fill the plate wells with 24 μ L PCR mix. Carefully pipette 1 μ L of each sample to be screened into each well of a column, changing the pipette tip between each sample. Each column of eight wells should be filled with the same sample (i.e., eight replicates per sample to be tested). The first 11 columns of the PCR plate can test 11 different samples for one target species. Into the 12th column, pipette 1 μ L of sterile water into the bottom three wells (F, G, H) and pipette 1 μ L of each of the target species positive control DNA into each of the top four wells (A, B, C, D). Leave the intervening well (E) empty.
- (7) Place the positive control DNA back in to the appropriate -20°C freezer and change gloves immediately in order to reduce risk of contamination.
- (8) Place PCR film over the PCR plate and press firmly (or use an automatic plate sealer) to ensure the edges of all wells are sealed. Gently tap a few times on the lab bench to ensure thorough mixing of each reaction. Spin down the plate in the plate spinner to ensure all DNA is down in the master mix.
- (9) Place the 96-well PCR plate in the thermal cycler, close and secure lid, and select the appropriate PCR thermal program (thermal cycle programs for Silver Carp and Bighead Carp utilize different annealing temperatures). The thermal programs for the current eDNA markers (Jerde et al. 2011) both consist of:
 - Initial denaturation at 94°C for 10 minFollowed by 45 cycles of:
 - 94°C for 1 min,
 - 50°C for Silver Carp program or 52°C for Bighead Carp for 1 min
 - 72°C for 1.5 min.Followed by:
 - final extension at 72°C for 7 min
 - 4°C hold temperature until plate removed from thermal cycler.
- (10) Record the plate ID, thermal cycler unit or head, plate orientation, and run times for the PCR plate in the PCR log (Exhibit 10).
- (11) Place cycled PCR plates and product in designated -20°C freezer for long-term (more than overnight) storage, in the designated 4°C refrigerator for short- or mid-term storage (1–12 hours). If you leave for the night, the thermal cyclers are set to hold at 4°C forever. Remove plates promptly in the morning.

(12) Under no circumstances should you open or uncover PCR plates that have been cycled in the PCR room. Only open cycled plates in the post-PCR rooms.

5.7 Gel Electrophoresis of eDNA PCR Assays (original method used 2009-2013)

5.7.1 Purpose

Once amplified, the DNA samples should then be subjected to gel electrophoresis in order to visualize the amplified DNA. This method is useful in determining the presence of DNA from the target species in different aquatic environments.

5.7.2 Source

PCR product following amplification can be taken either from cold storage (see #11 above) or directly from the thermal cycler.

5.7.3 Gel Electrophoresis Assurance and Chain-of-custody

This stage of DNA processing is particularly susceptible to pipetting error. It is also highly susceptible to mislabeling and, consequently, confounding of sample results.

Draw or otherwise produce a map of which sample will be electrophoresed on which gel and in which lane of the select gel.

Carefully pipette samples so as to avoid:

Injecting samples to incorrect wells.

Piercing the bottom of sample wells and losing PCR product.

Spill over from adjacent wells.

Record all solution batch numbers or name/date identification for stock solutions. Record precast gel batch identification number if appropriate.

Centrifuge plates, strip tubes, etc. before removing film or caps in order to prevent aerosol cross-contamination.

Any revisions to the DNA amplification protocol must be approved by the eDNA Project Leader (and documented) and incorporated into a revised QAPP.

5.7.4 Option A Procedure

Prepare 2% agarose gels with SB (sodium hydroxide and boric acid) buffer and allow the gel to polymerize for a minimum of 25–30 min prior to loading samples. Gels can be prepared at any time prior to PCR or immediately after PCR. However, once you begin loading a gel finish loading and run the gel immediately.

To prepare PCR samples for gel electrophoresis, transfer 10µl from each well of the 96-well plate to new wells in an identically labeled 96-well plate. Add 2µl of loading dye (see recipe below) to each well with PCR product (loading dye = 500µl 6X loading dye, 500 µl DMSO, 1µl SYBR Green I)

Place the 2% agarose gel in the electrophoresis chamber that contains SB Buffer and remove the gel combs. In the first well of each row on the agarose gel, load 100bp DNA ladder/loading dye mix. Next, load 10µL of each sample mixture (i.e., each PCR reaction and loading dye), and negative controls into the remaining wells. Be sure 10 µl of a positive control PCR product is in the last lane of each row. Run electrophoresis at ~250V for ~45 min depending on migration times through the gel. Times and voltages required to run each gel are approximate (different buffers and higher content agarose gels will require different run times and voltages, use what works in your lab).

Be sure to annotate the gel loading map in the notebook as you observe the gel in the geldoc. Interpret positive samples and note successful positive and negative controls on each gel. After documentation (5.8), dispose of gel in the garbage.

5.7.5 Option B Procedure

Pre-cast 2% E-Gel® 48 gels (Invitrogen) are used with the E-Base™ system (Invitrogen).

Open E-gels and load into the bases.

Remove gel from the pouch. Remove comb from the gel.

Slide gel into the two electrode connections on the Mother E-Base™ or Daughter E-Base™. If gel is properly inserted, a fan in the base begins to run, a red light illuminates, and digital display shows 20 min.

Load each gel within 30 min of removing gel from the pouch and run within 15 min of loading.

Selecting Program on E-Base™

Connect the Daughter E-Base™ to a Mother E-Base™ or another Daughter E-Base™ if running multiple gels.

Select program EG by pressing and releasing the pwr/prg (power/program) button on the base.

Loading E-Gel® 48 Gels

Load 15µL PCR product into each well of an E-Gel® 48 gel. Keep all sample volumes uniform. Load with a multichannel pipettor.

Load appropriate DNA ladder (distinct bands between 0-500 bp) into far left well (labeled M) and positive control PCR product into the far right marker well. Ensure the marker salt concentration is similar to that of adjacent samples (2% gel uses 100 bp DNA Ladder).

Load 15µL of sample buffer containing the same salt concentration as the sample, or sterile water, into any empty wells.

Run Conditions

To begin electrophoresis, press and release the pwr/prg button on the Mother E-Base™ and Daughter E-Base™. The red light changes to green.

At the end of the run (signaled with a flashing red light and rapid beeping), press and release the pwr/prg button on the base to stop the beeping and flashing red light.

Remove gel cassette from the base and analyze results.

Note: if a gel is removed before a run is complete, a gel must be replaced and the unit allowed to run out until the timer counts down to zero. There is no option to reset the base.

5.8 eDNA Gel Documentation and Storage (original method used 2009-2013)

5.8.1 Purpose

Once eDNA gels have been visualized, the results must be documented, interpreted (i.e., scored), and recorded. In some cases, very light bands may be visible, making scoring difficult. Documentation, labeling and saving for sequence confirmation, and storage are critical for later quality control review.

5.8.2 Source

Following electrophoresis, agarose gels should be immediately documented. Following documentation, PCR products requiring sequencing must be labeled and organized for sequencing.

5.8.3 Gel Documentation and Storage Assurance and Chain-of-custody

Because of the difficult nature of scoring some results, careful records must be kept of all gels and results. These results must be maintained so as to minimize the risk of tampering or data loss.

Gel image quality must be assessed at the time images are obtained. Images should exhibit all bands on gels as clearly as possible, if this is not possible, it must be noted on the gel data sheet (Exhibit 14). All gel digital image files should be saved and should be archived at the end of each working day. All gel image data are referenced to the samples case number to make sure the consistency of the sample custody.

Gel score data should be entered and stored in the appropriate database in an Excel file and on the data sheet in the laboratory notebook, or in LIMS.

All reports should reviewed by the eDNA Processing Leader before being reported.

A paper copy of the report should be held in the files for 5 years.

Electronic copies of all reports should be held for 5 years or longer, as space permits.

Any substantive revisions to the DNA amplification protocol must be approved by the eDNA Processing Leader and approved by the eDNA Coordinator. Any such changes must be incorporated into a revised QAPP.

5.8.4 Procedure

After electrophoresis is complete, remove casting tray with gel from the electrophoresis chamber and place the gel onto the gel scanner (BioRad Molecular imager FX), select DNA ethidium bromide stain gel, set up scanning area, and then select 100 micrometer to start scanning the gel.

Alternatively, place the gel on a UV transilluminator equipped with a digital camera, such as the Alpha red Imager (Cell Biosciences, Inc.), and capture a digital photograph of the gel.

After the gel scanning is done, properly label file name and save the file on the hard drive immediately.

If not using LIMS, print out a picture of the gel image and insert into lab book. A copy should be kept with the Project Lab Book. Be sure to sign across the print out and the lab book page.

5.9 Gel Interpretation (original method used 2009-2013)

5.9.1 Purpose

Once a gel is visualized, the quality of the results and presence of potential positive bands must be assessed in order to determine which samples need to be further assayed.

5.9.2 Source

Immediately following the cessation of electrophoresis, the agarose gel containing the eDNA PCR products should have been visualized on either the UV-based imager or the laser-based imager. In both cases, the gel image should be captured (saved to hard disk) immediately and then printed.

5.9.3 Gel Interpretation Quality Assurance and Chain-of-custody

The positive controls should have bright bands at the appropriate migration distance (number of base pairs), indicating a positive reaction.

No bands at the targeted sizes (~200bp silver, ~300bp bighead) should be observed in the negative controls.

If any of the initial PCR reactions are positive (i.e., a visible band at the appropriate migration distance), the initial sample is designated a “presumptive positive”.

Record the number of presumptive positive reactions for each sample both in the gel electrophoresis lab notebook and in the excel file on the lab computer.

Presumptive positive results will initiate a series of results confirmation mechanisms (see below). These mechanisms include screening the transport and equipment controls, and DNA sequencing.

Once presumptive positives are documented:

Fill in the quality control results in the eDNA sample log (Exhibit 6).

Notify the eDNA Processing leader.

Color in the plate seal above the wells containing presumptive positive samples on the PCR product plate. Move all plates requiring sequence confirmation into the freezer in the sequencing room. Plates without positives can be discarded.

5.10 Confirmation of Positive Results (original method used 2009-2013)

5.10.1 Purpose

These confirmation mechanisms are initiated if a sample returns as a positive for the PCR test (any number of the eight reactions, e.g., one of eight up to eight of the eight PCR reactions).

5.10.2 Source

Positive results for Asian carp eDNA require that those positive samples be further assayed. The original DNA elutes from samples should be located in designated -20°C freezer.

5.10.3 Gel Interpretation Assurance and Chain-of-custody

Presumptive positive assays (PCR reactions) are validated through DNA sequencing and testing of additional control samples.

Any revisions to the DNA QA/QC amplification protocol must be approved by the eDNA Processing Leader and approved by the assigned USFWS senior executive. Any such changes should be incorporated into a revised QAPP.

5.10.4 Procedure

Conduct PCR assays of the paired equipment control for each presumptive positive. DNA extraction, amplification, documentation, and interpretation following protocols detailed above (Sections 5.6–5.9).

Ensure that the transport blanks (see 2.2.2 (6) and 2.3.2 (10)) have been tested for that sample group (i.e., from the same cooler in which the presumptive positive sample was transported).

For all presumptive positive samples, bidirectional sequencing confirmation is performed. This is done by using a commercially available gel extraction kit (e.g., Qiagen Qiaquick Gel Extraction kit) per the manufacturer's recommendations on the positive PCR reactions, or E-Gel® CloneWell Agarose Gels (Invitrogen) per manufacturer's recommendation.

If the equipment control and transport blanks test negative, the sample is designated a "confirmed positive."

The following sequencing reaction can be done either by cloning (TA TOPO cloning kit used for sequencing per manufacturer's recommendation) then sequencing, or by a direct Sanger sequencing method (ABI BigDye® Terminator v3.1 or v1.1 Cycle Sequencing Kit) modified by WGL. BigDye Terminator Reaction Master Mix for 1X reaction:

- 1 µL BigDye terminator mix,
- 4 µL 5X reaction buffer,
- 0.8 µL either SC/BH forward primer, and
- 10.2 µL of water.

Add 16 µL of master mix to the 4 µL of purified DNA. Total reaction size is 20 µL.

The positive control reaction of sequencing was done per manufacturer's recommendation.

For each pGEM control PCR master mix:

- 1 µL BigDye terminator mix,
- 4 µL 5X reaction buffer,
- 2 µL m13 primer,
- 8 µL water, and
- 2 µL pGEM.

Add 20 µL to each control well.

Place the PCR plate on the thermal cycler and begin temperature cycling protocol. Program the thermal cycler as follows: 25 cycles of [96°C for 10 sec, 50°C for 10 sec, 60°C for 4 min], then ramp to 4°C.

Option 1: To clean the BigDye reaction with EDTA precipitation:

Spin plate after removing from thermal cycler (just to make sure that everything is at the bottom of the well).

Add 5 µL of 125mM EDTA to each well.

Add 60 µL of 100% EtOH.

Seal the plate and mix by inverting four times.

Incubate at room temperature (RT) for 15 min.

Spin plate at 3000xg for 30 min (at 4°C) or at 2000 x g for 45 min. Proceed to next step immediately.

Invert the plate and spin at 185 x g for 1 min (time from when rotor starts).

Add 60 µL of 60% EtOH.

Spin at 1650 x g for 15 min at 4°C.

Invert plate and spin at 185 x g for 1 min.

Resuspend samples in 20 µL Hi-Dye.

Option 2: To clean the BigDye reaction with Sephadex in Centri-SEP spin columns or Millipore plates, use columns for 1-16 samples and plates for 17 or more.

Centri-SEP column procedure

Materials list:

Spin columns (preloaded with dry sephadex, caps, and bottom caps), one per sample

Pipets and tips

Centrifuge with MCT rotor

Reagent grade water

Labeled 1.5-mL MCT and tube rack

Vortexer

Column Hydration

Tap column on counter to settle sephadex gel into the bottom.

Remove cap and add 800 µl sterile ddH₂O. Replace cap, invert, and mix well on vortexer, ensuring all gel is hydrated. Invert again, vortex and place in rack.

Let sit 30 minutes at room temp in a tube rack.

While columns sit, label 1.5ml MCT with sample names for collecting cleaned product.

Remove excess water

Check each tube for bubbles, if there are bubbles in the gel, invert the tubes and vortex so all the slurry moves toward the cap.

Invert and gently place in tube rack, allowing gel to settle.

Remove caps, then bottom, and place column in collection tube to drain.

Allow to drain until about 200-250 μ l water has drained. If needed, gently apply pressure with a gloved finger to get the water draining.

Discard fluid, replace column in collection tube.

Place columns into centrifuge, making sure the indicator tabs are up.

Spin at 750xg(rcf) for 2 min

Discard the collection tube, blot any water off the bottom of columns and place column into labeled sample collection tube.

Sample processing

Hold the column up to eye level, and carefully place all of the cycle sequencing product onto the center of the packed column, being careful to not disturb the column. Don't touch the side of the column with the product or the pipet tip.

Place collection tube into centrifuge with caps open and facing inward and the indicator tab of the column facing up.

Spin at 750xg(rcf) for 2 min. Discard spin column.

If you have more than 32 samples, you must dry filtrates in the spin vac at $\sim 60^*$ for ~ 45 minutes. Once dry, you may freeze for up to two weeks or go directly to analyzing on the sequencer. If you have 32 samples or less, you may run those directly on the sequencer in the elution water.

Millipore plate sephadex procedure

Materials list:

Millipore filter plate with centrifuge alignment frame

Plain 96-well plate to catch waste water (can reuse the same one)

Sequencing plate (with bar code)

Sephadex G50-fine

Millipore column loader and tray

Centrifuge with plate rotor

Reagent grade water

Prepare sephadex plate:

Pour dry sephadex into the black metal loading plate which is in the plastic catchment tray.

Use the clear squeegee to level each well you need for cleanup (tape off unused wells).

Scrape excess powder into the catchment tray so you don't waste too much sephadex.

Invert a multiscreen plate over the metal tray and hold them together while you invert the tray to fill the wells with sephadex. Make sure you are filling the wells you wish to use! Tap gently to make sure all of the sephadex moves into the filter plate.

Pour excess sephadex from the tray back into the sephadex container and cap tightly.

Add 300 μ l of water to each well of the plate and let sit *3 hours at room temp.* (these plates can be prepared ahead of time, wrapped tightly in plastic wrap, placed in a Tupperware with a moist towel and refrigerated for two weeks.)

Remove excess water and pack columns prior to use:

Place the filter plate over a plain 96-well plastic plate, and load into the plate rotor. Don't use the interior lid because it does not fit over stacked plates.

Centrifuge at 910xg(rcf) for 5 min.

Dump the waste water into the sink and rinse catchment plate (set aside for another use).

Clean sequencing reactions with the columns.

Use the multichannel pipet to carefully add reactions to the *center* of each column.

Place the filter plate over a 96-well sequencer plate making sure wells A1 are aligned.

Centrifuge at 910xg(rcf) for 5 minutes.

Dry filtrates in the spin vac at $\sim 60^{\circ}\text{C}$ for ~ 20 minutes. You may seal plate and freeze for up to two weeks or go directly to analyzing on the sequencer. If you have 32 samples or less, you may run those directly on the sequencer in the elution water.

Once samples are dry, add 15 μ l HiDi to each sample. Samples in Hi-Dye can be stored at 4°C overnight, but may not be left any longer than 12 hours.

To sequence:

Denature samples with HiDi for 5 min at 95°C in thermocycler (do not denature samples run wet)

Place immediately on ice

Load into sequencer plate and onto sequencer.

Resulting sequencing reactions that are successful are screened in GenBank (<http://www.ncbi.nlm.nih.gov/blast>) using the BLAST (Basic Local Alignment Search Tool) algorithm. If

the resulting sequence is a positive match to the targeted species of Asian carp, the sample is designated a “confirmed positive – sequenced”.

References: User Manual, “BigDye® Terminator v3.1 Cycle Sequencing Kit”
http://www.ibt.lt/sc/files/BDTv3.1_Protocol_04337035.pdf

“TOPO TA Cloning® Kit for Sequencing” http://tools.invitrogen.com/content/sfs/manuals/topotaseq_man.pdf

“QIAquick Gel Purification Kit”

http://molecool.wustl.edu/krolllab/Kroll_Lab_Protocols/Molecular%20Biology%20protocols/Cloning%20protocols%20folder/Gel%20extraction-Qiagen.pdf

Old 5.5.4 PowerWater Procedure for *filters*

- (9) Remove samples from freezer if filters, note on freezer and sample logs (see Exhibits 7-9).
- (10) Be sure you have added positive and negative extraction controls to each eDNA extraction procedure batch.
 - (b) Before proceeding with extraction, a positive control filter is prepared by pipetting 300 µl of a mixed slurry of homogenized Silver and Bighead carp tissue or cells directly onto a sterile filter paper. Alternative species (e.g. – sturgeon) may be used as the positive control to reduce risk of sample contamination from carp tissue. Alternative species must have PCR primers that (1) do not cross-react with carp DNA and (2) can be run on the same thermocycler settings as carp samples .
 - (c) Additionally, an extraction negative control sample should be prepared by placing a new filter paper in a new sterile 1.5mL microcentrifuge tube (MCT) and pipetting 300 µl of sterile lab DI water directly onto the filter. A batch of extraction blanks can be prepared in advance and kept frozen at –20°C.
 - (d) For every extraction batch of filter samples processed, conduct DNA extraction (below) on one frozen, sterile extraction negative control filter and one prepared positive control filter.
- (11) For all samples and cooler, equipment, and extraction controls, follow the DNA extraction protocol detailed below. For each filter, you will need one spin column and 4 1.5/1.7 ml lab supplied MCT and 5 Powerwater collection tubes.

This DNA extraction utilizes the PowerWater DNA Isolation Kit (MoBio Laboratories, MoBio Inc.) and the protocol is adapted from the manufacturer's protocol (<http://www.mobio.com/images/custom/file/14900.pdf>).

- (a) Place Solution PW1 in a 55°C water bath for 5–10 min to dissolve any precipitates that have formed at room temperature. Remove Solution PW1 from the water bath immediately prior to use.
- (b) Remove the appropriate filter sample from –20°C freezer and transfer the filter(s) to a labeled 5mL PowerWater Bead Tube. If DNA will be extracted from multiple filter samples, continue to remove each filter sample from –20°C freezer immediately prior to filter transfer. Each PowerWater Bead Tube will hold up to two filters per sample. If any filtered water samples required more than two pieces of filter paper, split the filters into two per PowerWater Bead Tube.
Note: Change gloves between the transfers of each sample to avoid cross-contamination of samples.
- (c) Add 1mL of Solution PW1 to the PowerWater Bead Tube and secure the cap tightly. Mount the tube on a vortex adaptor (MoBio Inc.) and vortex on high for 5–10 min, or until the contents of the bead tube appear liquefied. Times can vary depending on the number of filter papers being extracted. A bead beater can be used on a large batch of bead tubes if available.
- (d) Centrifuge the tubes at 4,000 x *g* for 8 min at room temperature. Ensure centrifuge is balanced before centrifuging. Transfer 650-800 µl supernatant using a 1mL pipette to a labeled 1.7mL lab supplied MCT.

- (e) Centrifuge tubes at 13,000 x *g* for 1 min and carefully transfer 650 µl of the supernatant with a pipette into a new labeled 1.7 mL lab supplied MCT. Be sure to avoid any beads or filter debris.
- (f) Add 200µL of Solution PW2, vortex briefly, and incubate at 4°C for 5 min. It should appear cloudy.
- (g) Centrifuge the tubes at 13,000 x *g* for 1 min and carefully transfer 650 µl of the supernatant with a pipette into a new labeled lab-supplied 1.7 mL MCT.
- (h) Add 650µL of Solution PW3 and vortex briefly. Load 650µL of supernatant onto a spin filter, place spin filter into a MoBio 2mL tube and centrifuge at 13,000 x *g* for 1 min. Discard the flow through and collection tube. Place spin filter into a new MoBio 2mL tube and load another 650 µl , centrifuge and repeat until all the supernatant has been pass through the spin filter.
- (i) Place the spin filter basket into a new labeled MoBio 2mL collection tube and add 600µL of Solution PW4.
- (j) Centrifuge the tubes at 13,000 x *g* for 1 min and discard flow through. Place spin filter in a new, labeled MoBio 2mL tube.
- (k) Add 550µL of Solution PW5 and centrifuge at 13,000 x *g* for 1 min. Discard flow through, place spin filter into a new MoBio 2mL labeled tube and centrifuge again at 13,000 for **2 min**. Be sure all traces of EtOH are gone.
- (l) Place the spin filter into a new labeled 1.7mL lab supplied MCT labeled with the sample identification number.
- (m) Add 100µL of sterile water (autoclaved, de-ionized) to the center of the white filter membrane, let it sit for 1-2 minutes, then centrifuge at 13,000 x *g* for 1 min.
- (n) Discard the spin filter and store the eluted DNA samples at -20°C. If more than one extraction tube was required for a single sample, combine all replicates into one final extraction tube.

DNA extraction elutes should be placed into a designated freezer for overnight or longer storage, or, if used for PCR within 1-4 hours, stored in the refrigerator. Make note of sample addition to freezer log if necessary (see Exhibit 7). Note completion of extraction on sample log.

OLD Appendix D: Sample Bottle Management Plan

The WGL study testing used sampling demonstrated that sample bottles can be reused for eDNA sampling, but recommendations were for implementation of a decontamination specialist to oversee and confirm that decontamination was conducted according to the QAPP. The Regional Office has decided that WGL will serve as the single decontamination facility for the Asian carp eDNA monitoring program.

WGL will clean and prepare bottles according to the QAPP and store them in the lab in a clean room. WGL will package bottles according to the following procedure, and send them as needed to the field offices.

Empty bottles for field samples:

- (1) New card board boxes and plastic liners will be purchased by WGL. Boxes will be assembled as needed and lined with the plastic bags.
- (2) Cleaned and autoclaved bottles will be securely closed and placed in the bag.
- (3) Bags will be sealed with tamper evident tape, boxes sealed and shipped to field stations. Water-filled field blanks may need to be sent separately, but all efforts will be made to get field blanks distributed at the annual training meeting each spring (if it is held in La Crosse).
- (4) Field stations will receive boxes, store sealed until they are ready for labeling.
- (5) Field stations will prepare coolers according to the QAPP, in as clean of an area as possible at the station.
 - a. Anytime boxes are opened, staff should be in clean clothes and use a new pair of clean gloves for actually handling the bottles. For example, you may open the box with un-gloved hands. Then, put on gloves to open the bag and touch the bottles.
- (6) Once clean coolers are ready, boxes may be opened, bottles labeled, and placed into clean coolers.
- (7) After use, field staff can use the same bag and box to return the bottles to WGL.

Cooler (field) blanks:

- (9) Plastic bags fit to hold one container will be purchased by WGL
- (10) Cleaned bottles will be filled with reverse osmosis tap water at WGL and autoclaved.
- (11) After cooling, bottles will be securely closed, and placed in the bag.
- (12) Bags will be twisted closed with wire closures.
- (13) Filled bottles will be distributed at the annual field training meeting held at WGL so that each field station will start out the season with the total estimated number of field blanks needed for the sampling season.
- (14) Field stations can store these prepared field blanks as long as needed, because as each bottle is wrapped individually.
- (15) Field stations will prepare coolers according to the QAPP, in as clean of an area as possible at the station.
 - a. Anytime boxes are opened, staff should be in clean clothes and use a new pair of clean gloves for actually handling the bottles. For example, you may open the box with un-gloved hands. Then, put on gloves to open the bag and touch the bottles.
- (16) Once clean coolers are ready, boxes may be opened, bottles labeled, and placed into clean coolers.
- (17) After use, field staff can use the same bag and box to return the bottles to WGL.

WGL will have designated shelves in the garage for boxes of dirty bottles.

A note on labels: We've found some great labels that withstand all sorts of abuse and are available on GSA. Avery laser white weatherproof address labels #5520.

Appendix I. Internal Report by Whitney Genetics Lab

Validation of IBI Scientific and Qiagen DNA extraction kits for use in the early detection and monitoring of invasive carp using environmental DNA

Kyle M. Von Ruden, Nicholas M. Berndt, Emy M. Monroe: US Fish and Wildlife Service, Whitney Genetics Laboratory

Introduction

Environmental DNA (eDNA) has become increasingly used as a surveillance tool to monitor for the genetic presence of aquatic invasive species or threatened and endangered species (Jerde 2011). Environmental samples generally have low levels of the target species DNA (Dejean et al. 2011), thus it is critical to have minimal loss of DNA during processing in the lab.

Once an eDNA water sample is collected, the organic matter is typically concentrated by filtering or centrifugation. Extraction of total DNA from filters or pellet is the first step in workflow. Detection of target DNA in the sample depends on the quantity and quality of DNA which is extracted from the field sample. Commercially available extraction kits may vary in the quantity and quality of target DNA copies available at the end of extraction, so it is critical to be able to maximize both aspects of extraction.

Extraction is a time-consuming step in the lab, especially when there are thousands of eDNA samples to be processed, and this step is often the “bottleneck” in processing. In addition to labor time, other considerations in choice of extraction kits are cost and the ability to purchase individual reagents or pieces of each kit as needed to avoid waste of kit components. Current protocols used in the Whitney Genetics Lab for the processing of eDNA samples in the early detection and surveillance of bigheaded carps is outlined in great detail in the Quality Assurance Project Plan (QAPP). Originally, the QAPP called for use of MoBio PowerWater kits for extraction, but in 2013 after a rigorous comparison study conducted with two other labs, Qiagen DNeasy Blood and Tissue kits were approved for extraction (Amberg et al. in press). The patent on Qiagen kits recently expired, and IBI Scientific created a “copycat” kit called the gMAx mini kit, which uses the same chemical buffers and DNA-binding membranes in a spin kit as the Qiagen version. The IBI kit is less costly at 2.1 cents per sample compared to 2.7 cents per sample, and IBI will sell the spin columns separately unlike Qiagen. This is helpful to reduce reagent waste because there are often left-over reagents that can't be used because the spin columns are used up first.

The objective of this study was to determine whether the IBI kit is as good as or better than the Qiagen kit by comparing copies of target DNA found in three different types of samples. In order to avoid unnecessary contamination of the eDNA lab with Asian carp DNA, bluegill DNA was assayed with real-time quantitative markers (qPCR) (Takahara et al. 2003) after extraction.

Methods

Three sets of 25 samples (24 for the Mississippi River set) were collected or created, filtered according to the QAPP, and then half of the total number of filters were extracted with each kit. To homogenize samples between filters, each 2L sample was inverted multiple times and split into 500ml per filter two times creating a total of one filter per kit per sample. Three different sample types consisted field-collected water, aquarium water, and tap water spiked with bluegill cells collected from the virology lab at the center. Field water was taken from a backwater of the Mississippi River, the aquarium water came from a holding tank of bluegills and largemouth bass, and tap water was spiked with 1ml of cultured

bluegill cell line. Bluegill was chosen as a surrogate to invasive carp because they are active in winter, don't carry contamination concerns, are locally available, and can be detected with a high-quality qPCR assay (Takahara et al 2003).

Once samples were filtered, each set of 25 was extracted following the manufacturer's protocol for their respective kit. Extracts were then analyzed in eight replicate qPCR reactions following methods in the QAPP. Plates were loaded on an Eppendorf epMotion 5075 and cycled on Bio-Rad CFX384 Touch™ Real-Time PCR Detection Systems. Results were based off average starting quantities (SQ) of DNA copy numbers and extraction kits were compared to each other by sample using a Paired T-test.

Results

The average amount of DNA measured in eight replicate qPCRS from each extract is presented in (Figure 1; field samples top panel, aquarium samples lower panel). Extractions using both kits for the cell line samples were overwhelmed with DNA and are not shown. Paired t-tests comparing the total copies of bluegill DNA in each sample type indicate that there was a significant difference between the two kits ($p=0.0003$ field, and $p=0.0004$ aquarium) and in 22 of the 24 comparisons, the IBI kit extracted more target DNA copies than the Qiagen kit.

Discussion

The IBI gMAX kit extracted significantly more target DNA than the Qiagen kit. The field samples had lower overall copies for both kits, but this was expected because diluted environmental samples typically yield less target DNA. The aquarium samples yielded high amounts of naturally sloughed DNA, and IBI performed better than Qiagen here as well.

Results for our cell spiked samples appeared to overload each kit with Qiagen being maxed at 5×10^6 cells and IBI at 1×10^7 cells (www.ibisci.com, www.qiagen.com). Yield and quality of DNA can be affected when overloading an extraction column with cells. Thus, these results were not considered in our analysis.

Extraction time using the IBI kit was approximately one hour less and each filter cost approximately \$0.60 less to extract. This time savings adds up to hours during the week that can now be used by WGL staff to move monitoring cases along more quickly, significantly reducing turn around time for reporting results. Further efficiency can be realized by completely using all kit reagents because IBI will sell the spin columns separately, but Qiagen will not. Because the IBI kit is advertised as a replica of the Qiagen kit, switching from one kit to the other does not require a large change in protocol in the lab, thus it can be seamlessly integrated into our normal workflow and added as an extraction option in the QAPP. Since the IBI kit performed at least as well as the Qiagen kit, data generated by the lab will remain of the highest quality.

Our results show that IBI Scientific gMAX Mini Kit extracts more copies of the target DNA compared to Qiagen's DNeasy® Blood & Tissue Kit. When considering other aspects of extracting DNA samples in a high through-put facility, the IBI kit also appears to be more efficient and cost friendly. Based on this study, we recommend using IBI Scientific gMAX Mini Kit for extraction of eDNA samples in WGL.

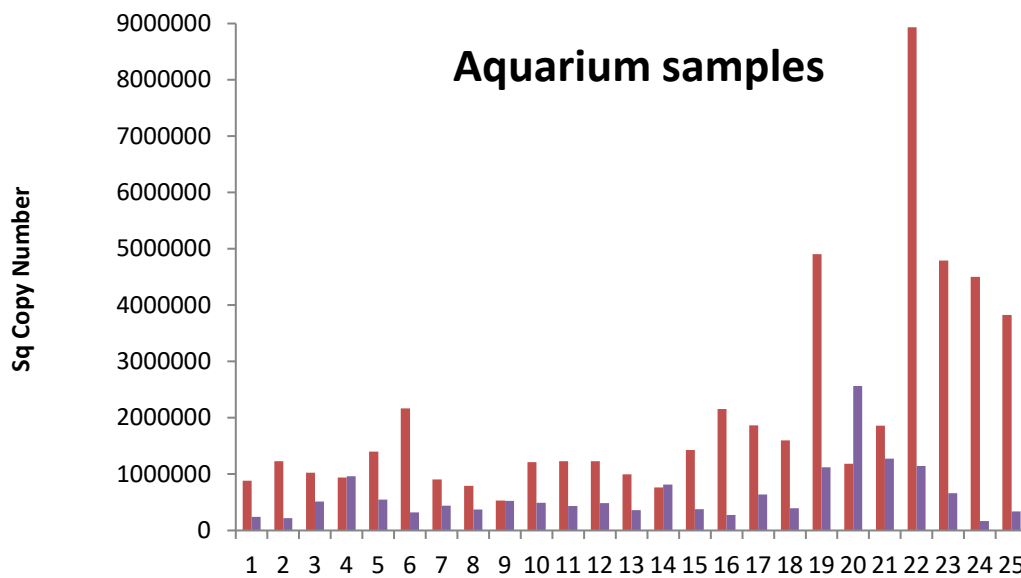
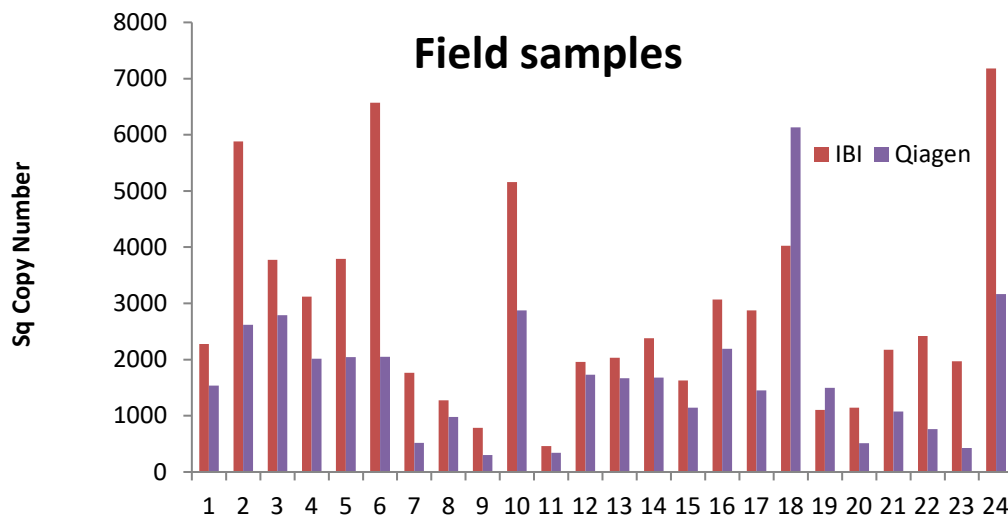


Figure 1. Average copies of bluegill DNA per octet for each sample using IBI and Qiagen extraction kits. Sample number is on the x-axis, and Sq copy number is on the y axis. IBI extraction kit is labeled in red, and Qiagen is purple.

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Takahara T, Minamoto T, and Doi H. 2003. Using environmental DNA to estimate the distribution of an invasive fish species in ponds. PLoS ONE 8: e56584. doi:10.1371/journal.pone.0056584

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<http://www.fws.gov/midwest/fisheries/eDNA/QAPP-2014.pdf>

Appendix J. Internal Report Whitney Genetics Lab

HemT internal positive control for determining inhibition in eDNA monitoring samples

Kyle M. Von Ruden, Maren T. Tuttle-Lau, Nicholas M. Berndt, Nikolas S. Grueneis and Emy M. Monroe
US Fish and Wildlife Service, Whitney Genetics Laboratory

Introduction

Quantitative PCR (qPCR) is used to detect and quantify very small amounts of genetic material in a water sample. Genetic material in an environmental sample is called environmental DNA or eDNA, and the ability to detect the presence of the genetic material is of interest to resource managers. However, surface waters are likely to contain several known inhibitors such as humic and tannic acids and algal cells which can prevent the amplification of target DNA in a sample by blocking the action of DNA *taq* polymerase, and thus create false negative results. In order to overcome this potential problem of PCR inhibitors, WGL tested and will adopt an Internal Positive Control (IPC) for the 2015 monitoring season. One procedure used to account for the presence of inhibition is to amplify synthetic DNA or a reference gene at the same time as the target gene and compare the copy number (Nolan et al. 2006, Randall et al. 2010). This procedure is the most commonly used method to detect inhibition in laboratories spanning from clinical diagnostic settings, forensic settings to environmental research (Hoorfar et al. 2004, Kontanis and Reed 2006).

The US Geological Survey Columbia Environmental Research Center (USGS-CERC) developed an IPC (Table 1) made up of a novel mouse gene, HemT, which encodes for a hematopoietic cell-specific transcript (Xue et al. 1999). Known numbers of the HemT will be spiked into each well of the plate containing field samples, which will then be quantified using standard curves for that target. If fewer copies of the spike are measured in a sample, inhibition is assumed, and the extract will be cleaned up with a PCR clean-up kit (OneStep Inhibitor Removal kit by Zymo Research, Irvine, CA), and re-amplified (Turner et al. 2015). Samples will then continue through the eDNA workflow. This method will not determine what particular inhibitor may be present, and will only test for inhibition due to blockage of *taq* activity. The objective of our study was to re-analyze three cases from the 2014 sampling season to develop the methodology of the IPC and determine how to precisely define inhibition, how to overcome inhibition, and develop data processing pipelines for the upcoming 2015 eDNA season.

Table 1. Sequences for the HemT primers, probe, and ultramer used to access inhibition.

Product	Sequence 5'-3'
HemT Forward Primer	TCTGAGTGTCCCTCGAATCT
HemT Reverse Primer	GCAGTCCTTGAGAACATAGAGC
HemT Probe	TGA CAG TCT CCT TTC GTG TGA ACA TTC G
HemT Ultramer	CTA CAT AAG TAA CAC CTT CTC ATG TCC AAA GCT CTC TGA GTG TCC CTC GAA TCT CAG ACG CTG TAT GAC AGT CTC CTT TCG TGT GAA CAT TCG GCT GCT CTA TGT TCT CAA GGA CTG CAC

Methods

Preliminary tests - An IPC protocol was obtained from CERC for further method development at WGL. First, we had to determine if the addition of the IPC target and primers and probes reduced the efficiency of the ACTM 1 and 3 carp markers. This was done by adding the IPC components to four replicate standard curves and comparing qPCR performance to several standard curve results from the 2014 eDNA monitoring season (Table 2). The ACTM 1 and 3 markers performed equal to results in the 2014

monitoring season (Table 3). After this initial test, 12 replicate standard curves with the IPC and ACTM 1 and 3 were also tested to confirm repeatability and accuracy of the IPC when competing with ACTM 1 and 3 standards (Table 3).

2014 monitoring season re-runs - Three cases (10089, 10103, and 10104) from the 2014 monitoring season were tested to compare detection results with the IPC. Because standard curve wells have varied amounts of the HemT target, and the rest of the plate has 100 copies of the HemT target, each plate is made with two master mixes. The master mix for all unknown field samples plus the 4 negative control samples had 10^2 (100) copies of the HemT target in each reaction, whereas the mix for standard samples did not have any target HemT included, so that the proper dilution could be used to create the standard curve. Samples were run in replicates of eight with 2 replicate standard curves per plate according the QAPP. All reactions were set up for qPCR on an Eppendorf epMotion 5075 and analyzed using Bio-Rad CFX384 Touch™ Real-Time PCR Detection Systems.

Each 20µl qPCR reaction for the standards consisted of 10.0µl of Taqman® Environmental Master Mix, 1.0µl of HemT forward and reverse primer mix at 5.0µM, and 0.75µl of HemT probe at 2.5µM, 1.0µl of ACTM1/3 forward and reverse primer mix at 10µM, 1.0µl of ACTM1/3 Probe at 2.5µM, 4.25µl of water along with 1.0µl of the appropriate gBlock standard dilution and 1.0µl of the appropriate HemT standard dilution. Cycling conditions were as follows: 95°C for 10min, followed by 40 cycles of (95°C for 15 sec, 60°C for 1 min, followed by a plate read).

Table 2. Paired HemT IPC and gBlock standards run in duplicate on every plate.

Standard dilution copy number of HemT IPC	Standard dilution copy number of ACTM 1 and ACTM 3 gBlock
10 ⁵	6250
10 ⁴	1250
10 ³	250
10 ²	50
10 ¹	10

Results

Preliminary tests - Both the paired standard tests of four and twelve replicate standard curves resulted in R² and Efficiencies that performed within the WGL reporting range without any standard points being removed (Table 3 and Figure 1), indicating that the reactions had enough reagents to amplify all three targets without negatively affecting efficiency of the reactions. One target failed to amplify in the lowest ACTM 1 standard (10 copies), but the rest of the standards allowed for generation of standard curves with R² and efficiency values within WGL limits. The Limit of Detection (LOD) for ACTM 1 and 3 remained at 10 copies, which is important when detecting low copy numbers in eDNA samples.

Table 3. Comparisons of mean efficiencies, R² and slopes from the 2014 monitoring season and preliminary tests of the HemT IPC spike.

	FAM			HEX		
	Efficiency	R ²	Slope	Efficiency	R ²	Slope
2014* season	93.9 (7.62)	0.99 (0.01)	-3.49 (0.21)	96.4 (9.08)	0.98 (0.01)	-3.43 (0.24)
Four replicate standard curves	91.9 (14.4)	0.98 (0.01)	-3.53 (0.36)	100.6 (12.5)	0.98 (0.01)	-3.31 (0.28)
Twelve replicate standard curves	100.6 (11.06)	0.97 (0.01)	-3.31 (0.26)	103.4 (19.9)	0.95 (0.01)	-3.24 (0.43)

*mean values from 6 standard curves off of 3 plates from 6 cases analyzed in July 2014 to January 2015.

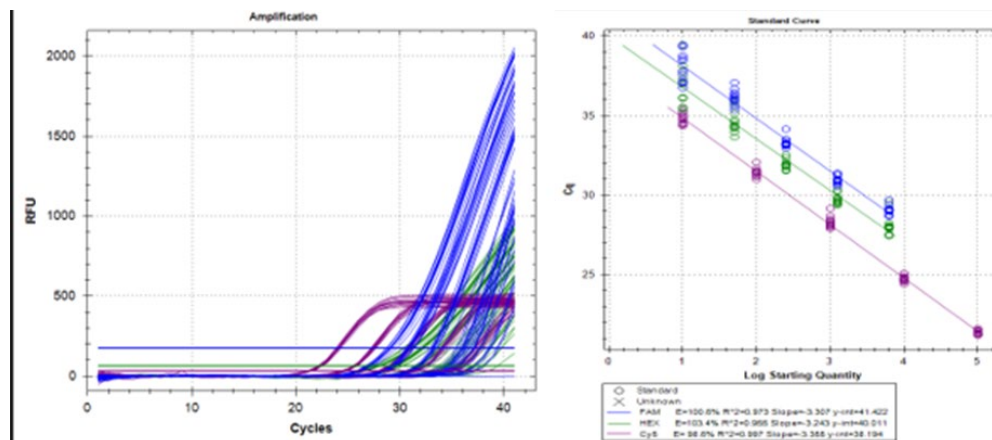


Figure 1. CFX Manager Software screen capture of the twelve replicate standard curve preliminary test (Left panel). ACTM 1 is represented by the blue lines (FAM), ACTM 3 represented by the green lines (HEX) and the IPC spike is represented by the purple line (Cy5). Right panel shows standard curves with data on each curve in the lower box.

2014 monitoring season re-runs - Case 10089 was chosen for reanalysis because it had the highest average number of filters (10) per sample from the 2014 monitoring season. An uninhibited average C_q, or the reference C_q, was calculated for each plate using the mean C_q for the duplicate 10² copy standard wells and the four Negative/NTC wells with the 10² copies of the IPC. This reference C_q was used to determine the threshold for inhibition in all other unknown samples. Initially, inhibition was defined as any sample with a C_q 2 cycles or more above the reference C_q. This resulted in zero samples being inhibited for case 10089. After further review of literature (Hartman et al. 2005, Turner et al. 2015) we changed how potential inhibition would be determined. Inhibition is now defined as any single replicate of the eight replicate PCRs run per field sample which has a C_q greater than the reference C_q by more than the range of C_qs used in the reference calculation, or at least 1 cycle if the range is less than one. Any sample well that had no C_q for the IPC is considered completely inhibited. Using these guidelines, 10 samples were determined as inhibited, and were re-analyzed after using a OneStep™ PCR Inhibitor Removal Kit by Zymo Research (Turner et al. 2015). After clean-up, nine of the samples were no longer inhibited, while the other sample had only one replicate of its eight that still showed signs of inhibition. There were no further presumptive positives for Asian Carp once the samples were purified.

Case 10103 consisted of 37 samples and was found to have four samples positive for either bighead or silver carp, as well as nine inhibited samples (Figure 2). Of those nine inhibited samples, eight were re-amplified using a 1:1 dilution. Four of these samples were cleared of inhibition after the dilution and one of the samples was then also confirmed positive for silver carp. Further dilutions of 2:1 and 3:1 finally alleviated inhibition in all but one of the remaining samples, and no further carp DNA was detected. One

sample remained mildly inhibited, but no further steps were taken to try and eliminate inhibition in that particular sample, because in the future, all inhibited samples will be cleaned with OneStep Inhibitor Removal kits to expedite processing and allow for rapid confirmation and case completion.

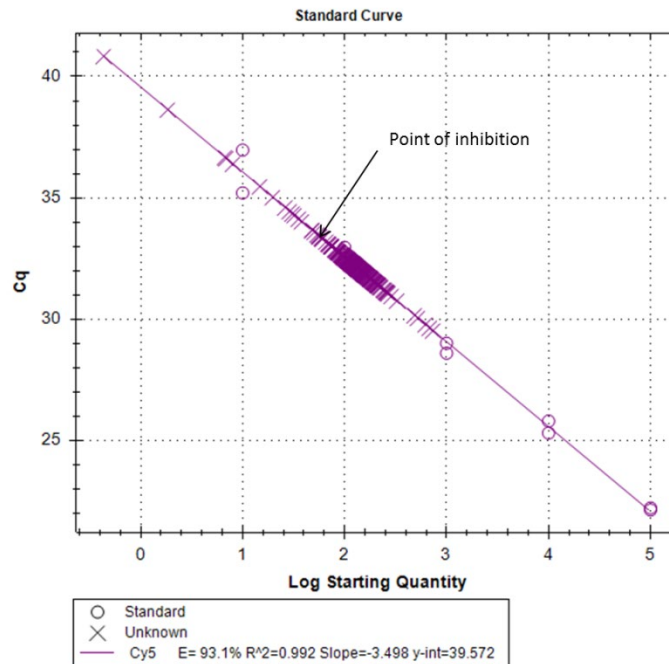


Figure 2. IPC standard curve showing the point of inhibition based on our guidelines for reference Cq in case 10103. Samples with Cq greater than this point are considered inhibited and will be re-amplified after clean-up with a PCR clean up spin kit.

Case 10104 consisted of 31 samples and was also re-analyzed with the IPC. None of these samples were inhibited, thus all samples remained negative for silver and bighead carp (data not shown).

Conclusion

Our results show the addition of the HemT IPC primers, probe, and template have no negative effects on the performance of our previously validated Asian Carp Markers and also the HemT IPC can be used to indicate inhibition in the activity of *taq* polymerase. Based on these results we recommend amending the QAPP for the 2015 eDNA monitoring of Asian Carp at WGL to include the HemT Internal Positive Control in all cases in an effort to quantify the rate of inhibition, and then remove inhibitors with a simple clean up kit, which will eliminate this source of false negative results.

To this end, WGL has incorporated the HemT IPC in the initial assay screening all samples for the ACTM 1 & 3 markers. Samples shown to be inhibited will be cleaned with the PCR inhibitor clean up kit (see above), and then re-assayed with the ACTM 1 & 3 markers. Presumptive positive samples will be moved through the confirmation assays, using the now inhibitor-free extract. The total number of inhibited samples will be tracked by case so that trends at particular sites or at particular times of year can be monitored.

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Appendix K. Internal Report Whitney Genetics Lab

Validation of centrifugation for eDNA sample collection and processing

Emy Monroe, Whitney Genetics Laboratory, U.S. Fish & Wildlife Service

Richard Lance, Environmental Laboratory, U.S. Army Corps of Engineers Research & Development Center

Chris Rees, Upper Midwest Environmental Science Center, U.S. Geological Survey

Tim Strakosh, Green Bay Fish and Wildlife Conservation Office, U.S. Fish & Wildlife Service

Introduction

Environmental DNA (eDNA) has been applied as an early detection and surveillance tool for Asian carps in tributaries of the Great Lakes and the Upper Mississippi and Ohio Rivers by resource agencies. The current protocol in use, the Quality Assurance Project Plan (QAPP), was initially developed by the U.S. Army Corps of Engineers, based on the methods of Jerde et al. (2011). The QAPP requires 2-L water samples be collected and then filtered within 16 hours, which is problematic for some surface waters that contain large amounts of filter-clogging particulate matter (e.g., tributaries of Lake Erie). Various methods of sample collection for eDNA analysis are found in the literature including smaller volume grab samples (i.e., 15 and 50 mL) that are concentrated by centrifugation (Ficetola et al. 2008, Dejean et al. 2011, Minamoto et al. 2012, Foote et al. 2012, and Thomsen et al. 2012) and larger volumes that are filtered, such as those outlined in the QAPP. Both centrifugation and filtration methods have been field validated and were successful at identifying organismal DNA at low levels in their respective studies. It may be more time and cost-effective for the QAPP to allow the use of smaller water volumes that concentrate DNA by centrifugation. Prior to implementation of centrifugation methodology for early detection and monitoring programs, a study must be conducted to determine if the techniques yield comparable detection rates of eDNA samples collected in the same location at the same time.

Project Overview

The current QAPP requires collection of a 2-L water sample which must be filtered within 16 hours to avoid DNA degradation. While this technique may be useful to concentrate DNA from the water sample, it also concentrates suspended materials, resulting in the need for several filters for a single sample. For example, in the Chicago Area Waterways (CAWS), on average one 2-L sample requires 4 filters (Whitney Genetics Lab (WGL) case log 2013 and 2014); however in the Maumee and Sandusky Bays of Lake Erie, one 2-L sample required upwards of 20-45 filters (C. Olds, pers. comm.), and the maximum for 2014 for a single 2L water sample was 65 filters (WGL case log 2014). Additionally, one case of 200 samples in 2014 averaged 10 filters per sample. The total number of filters processed in 2014 at WGL was over 23000, but total samples reported was only 6330 (WGL case log 2014). This large number of filters per sample pushed sample processing up against the 16-hr time limit for field staff, cost \$2.70 per filter to extract in the lab, and increased the time necessary for laboratory personnel to extract a single case of samples. According to the QAPP, the extraction kits (Qiagen DNeasy) can only handle one filter per extraction resulting in a large number of extractions in the laboratory. Filtering water also creates multiple opportunities for contamination among samples to occur. The 2-L sample containers are challenging for field staff to store, move, and rapidly cool due to size and weight. Large coolers are required to move and store samples with sufficient ice to prevent DNA degradation. Boat size and number of sample coolers limit the number of samples that can be taken per trip.

The ability to collect smaller volumes of water would increase field sampling efficiency, because all sampling containers needed for a collection event could be carried in a boat at one time. The smaller volumes would also require less ice to rapidly cool and prevent further DNA degradation. The use of

sterile centrifuge tubes and centrifugation reduces contamination risk since exposure is limited to water decanting after pellet centrifugation. Centrifuged samples also reduce potential DNA degradation or loss during shipping because they are preserved in 95% ethanol or 70% isopropyl, which will last indefinitely, unlike the filters which are shipped in dry ice. Laboratory time and cost savings are also a result because the entire pellet from one to five centrifuge tubes can be collected on a single sterile buccal swab and processed in a single extraction.

Preliminary studies and results

Preliminary studies comparing centrifugation and filtration have been conducted by federal labs as part of the environmental DNA calibration study (ECALS (<http://www.asiancarp.us/ecals.htm>) labs), but contamination in the trials precluded any interpretation of the data (ACRCC 2014). WGL conducted two preliminary studies to examine the feasibility of using the centrifugation method to concentrate eDNA in water samples. The first study conducted by ECALS laboratories occurred simultaneously with validation of an alternate extraction method in 2013. For this study, samples were collected from the Black River (La Crosse County, WI) and spiked with a slurry of silver carp slime and feces with a known amount of DNA (Amberg et al. in press). Two-liter water samples were collected and spiked with 0, 200, 750, 1000, and 2000 ng of DNA (5 treatment classes) and immediately extracted. At the same time, 10 replicates of these same treatments were being filtered for use in the Upper Midwest Environmental Sciences Center (UMESC) bridging study (Amberg et al. in press) testing the two extraction kits. Each 2-L sample from the five treatments was mixed by inversion, and twenty 50-ml sterile centrifuge tubes were filled. The samples were then centrifuged at ~4500 rcf (max speed on Sorvall Legend STR) at 4°C for 30 minutes. Water was carefully decanted; making sure the pellet remained intact in the bottom of the tube, and the pellet was covered with 5-15 ml of isopropanol, and spun again at ~4500 rcf for 5 minutes at 4°C. Excess isopropanol was decanted carefully to remove as much liquid as possible without disturbing the pellet. Samples were stored at room temperature on open shelves until processing. The day before extracting, samples were prepared by evaporating all residual isopropanol in a laminar flow hood. Samples were placed in centrifuge tube racks, moved into a sterile hood area, had caps removed, and were left to dry. Each batch of tubes included a hood negative control to test for contamination during the drying process. Samples were then moved into the extraction room where they were extracted with the Qiagen DNeasy Blood and Tissue Kit per the QAPP. Each sample was processed according to Amberg et al. (in press) for both conventional (cPCR) markers (Jerde et al. 2011) and quantitative PCR markers (qPCR; Merkes et al. 2014). Results from the centrifuged samples were compared to 10 replicate filtered samples run in WGL in the Amberg et al (in press) study. Overall, the centrifuged samples had comparable results to the filtered samples in both assays (Tables 1 and 2). Although these results seemed promising, it is important to note the 20 centrifuged samples are pseudo replicates from one 2-L spiked sample. Thus, further confirmation was required.

The second preliminary study was executed in fall of 2013, when 120 paired samples (N = 240) were collected in four sites (60 samples per site) in the Chicago Area Waterway System (CAWS). Filtered samples (N = 120) were collected as part of the formal early detection and monitoring program (MWRG Plan 2013, <http://www.asiancarp.us/documents/MRP2014.pdf>), but an additional five 50-ml samples (centrifuged) were collected side-by-side (N = 120) with each 2-L sample (filtered). These were extracted with the Qiagen DNeasy kit according to the QAPP. Since eDNA of Asian carp is not consistently detected in the CAWS, markers for detecting eDNA of bluegill (Takahara et al. 2003) and common carp (Barnes et al. 2014) were used to compare detection of DNA between the two processing methods within each site. It should be noted that Takahara's bluegill marker will also detect other *Lepomis* species, but it should do so equally in both sample types. Results from this second preliminary study based on field

samples indicated that the processes do not differ (Paired Chi-square test by sample site, $p=0.435$ bluegill and $p=0.947$ common carp) (Figure 1).

Both preliminary studies indicated equal rates of DNA detection between the two methods to process field samples, but neither study used early detection markers for Asian carp in field samples. Thus the goal of this study was to compare results of bigheaded carp eDNA amplification from 2-L water samples that were filtered and 50-ml samples that were centrifuged from surface waters containing known abundances of bigheaded carps. This study used samples from the Illinois River in areas that have low, medium, or high levels of Asian carp (details below). Field work for the study was carried out by the Green Bay Fish and Wildlife Conservation Office (FWCO) with assistance from the Carterville, Columbia, Alpena, and La Crosse FWCOs. Laboratory analyses were carried out at the U.S. Army Corps of Engineers Engineering Research and Development Center (ERDC), the U.S. Fish and Wildlife Whitney Genetics Lab (WGL), and the U.S. Geological Survey Upper Midwest Environmental Sciences Center (UMESC).

Methods

Paired water samples were collected and processed by centrifuging and filtering from three reaches with low, medium, and high carp densities (Figure 2, Table 3). Each reach was sampled in a 2.5-km long section encompassing the area of interest. Water samples within each selected section were taken at 23 sites following a probabilistic sampling design targeting areas where eDNA had the highest probability of accumulation (QAPP). At the selected site, surface water (< 4 cm) was collected in a sterilized container approximately 10 L in volume. The surface water was homogenized and distributed into three 2-L bottles and fifteen 50-ml tubes designated for that site. Each 2-L bottle and set of five 50-ml tubes is a replicate ($n=3$) for that site. A new 10-L container was used for each eDNA accumulation site and not reused during this study. Two of the 23 sampling sites were randomly selected for cooler blanks filled with DI water (i.e., three 2-L bottles and fifteen 50-ml centrifuge tubes per site). The negative controls did not replace the collection of water samples at the site, but served as negative controls. All samples were filtered or centrifuged according to the QAPP in mobile eDNA trailers and sent to the laboratories. One set was shipped directly to ERDC, and the other two were hand-delivered to WGL personnel who then distributed the final set to UMESC for analysis. Three study reaches in the Illinois River (Figure 2) were identified based on Asian carp densities (Table 3): Brandon Road Pool (low), Marseilles Pool (medium), and La Grange Pool (high; Figure 2; see also Baerwaldt et al. 2014). Samples were collected within a 2.5 km stretch immediately below the upstream barrier (lock and dam structure) within each reach (Figure 3).

All preparation activities followed those specified in the QAPP and other guiding documents/protocols (e.g., eDNA Trailer SOP). Water samples within each randomly selected section were taken at 23 sites following a probabilistic sampling approach described above. Targeted areas included backwaters, island side channels, pooled areas, below and around structures, confluences of tributaries, and any areas where floating debris accumulates. Actual sample collection locations were determined by the Collection Crew Leader from *in situ* observations of wind direction, accumulation areas, and water levels. No eDNA sampling occurred within 5 days after a significant rainfall event (more than 1.5 inches in a 24-hr period) or on the rising limb of a hydrograph of the river as it exceeded flood stage.

Samples were collected according to the QAPP, and a total of 225 2-L samples and 1125 50-ml samples were collected. All samples were processed according to the QAPP, including centrifuge samples (QAPP already contains method for centrifugation which is allowed for research purposes), and DNA was extracted using the Qiagen DNeasy kits. At the time this study was planned, the QAPP used conventional PCR markers from Jerde et al. (2011); however, after samples had been collected in Spring of 2014 but

before they were analyzed (June at ERDC and winter at UMESC and WGL), new qPCR markers had been validated and thus adapted in the QAPP (Farrington et al. 2015), and these new markers were used to analyze samples. The validation study provided limits of detection (3-9 copies) and limits of quantification (10 copies) for these new markers, therefore a sample is detected as positive for a marker if starting copies of template DNA are between 3-9, and a sample can be detected as positive, and starting copies of template DNA can be reported as a numerical value for 10 copies or greater.

Data from each lab was reported in two ways: samples confirmed positive for Bighead, Silver, or both species, and copy number. The overall probability of detection for positive samples was calculated for each reach by each processing method to assess detection rate. The detection rate for both filtration and centrifugation was then used to calculate the number of samples needed to achieve a specified detection probability using equations modified for binomial variables (McArdle 1990, Reed 1996, and Kery 2002). All eDNA samples were assumed to be comparable and independent, therefore the probability of not detecting Asian carps in N eDNA samples is

$$\text{Probability } (N \text{ unsuccessful samples}) = \alpha(1 - p)^N$$

where α is the probability of making a Type I error under the hypothesis that the eDNA is actually present (i.e., concluding the eDNA is absent when it is actually present), p is probability of detection, and N is the total number of eDNA samples. Solving for N gives the number of samples required at a desired Type I error rate.

$$N = \log(\alpha) / \log(1 - p)$$

As more samples are collected, the probability of detecting presence of Asian carp eDNA (p^*) increases and can be calculated as

$$p^* = 1 - (1 - p)^N$$

Samples that had detections with any of the 6 markers were used to test for differences in copy number between the two processing methods using a permutational multivariate analysis of variance (PERMANOVA) based on Euclidean distance matrix in Primer V6 (Anderson et al. 2008). The PERMANOVA is a non-parametric multivariate approach which does not make any assumption of distribution, is insensitive to correlation among response variables and zeros, and allows the use of copy numbers from all the markers in one test (Anderson 2001). Specific contrasts were used to test for the difference between centrifuging and filtration within each of the reaches using Type III sum of squares and 9999 permutations.

Results

Samples were successfully collected and two sets shipped to WGL and the third to ERDC. Samples were checked in, and held until processing (WGL held both UMESC and WGL samples until processing). Filters were stored at -80°C and centrifuged samples preserved with isopropyl were held at ambient lab temperature. At WGL this ambient storage was in open shelves. Samples were processed at ERDC in June. Samples were processed at WGL in December and at UMESC, in January. All WGL samples passed quality control checks, and thus are included in analysis. However, there were some control samples (centrifuge control 13, hood control 7, and extraction negative 7) that at first appeared to be contaminated in the set analyzed at ERDC. Upon closer inspection, only the centrifuge control was presumptive positive with one of 8 reactions amplifying both ACTM markers, but it was overall negative since the confirmation markers for both species failed to detect. The other two control samples had just

one of the ACTM markers detected, so they were not presumptively positive, thus all of ERDCs data were used in the final analysis. Unfortunately, UMESC data had to be discarded from analysis for two reasons. 1) Centrifuged samples 1-25 completely failed amplification compared to WGL and ERDC. To further investigate potential reasons for this failure, 10 μ l of each extract was electrophoresed in 2% agarose gels with 5 WGL samples from the same sample set for comparison. The UMESC extracts did not have as much DNA (much fainter streaks) or as wide a range of DNA lengths (all less than 100 base pairs) compared to WGL extracts (data not shown). The lack of large strands indicates samples may have degraded during storage at room temperature exposed to lab lights, or that the extraction kit reagents failed. Kit failure is possible, since it was noted by the technician that some of the buffers had crystallized and were used without re-dissolving the buffer. 2) Filtered samples 51-75 from the high-abundance carp reach of the river also completely failed amplification. Again, extracts were electrophoresed and compared to 5 extracts from WGL samples from the same set of samples. The gel revealed orders of magnitude less DNA than those extracted by WGL and DNA all less than 100 base pairs (data not shown), which indicates failure of extraction kits since the filters were stored in the dark in ultra-cold freezers until they were processed. Thus, results will only be based on two replicates (WGL & ERDC) instead of three.

Overall, results between ERDC and WGL had similar rates of detection for both species in all three reaches (Table 4). Mean copy numbers (8 replicate reactions x 25 samples) varied between labs, but were similar among reaches for each processing method. Mean copy numbers also reflected the Asian carp density from their respective reaches (i.e., high density reach had higher copy number), and for the most part, centrifuged samples had higher copies than filtered samples (Table 5). Detection probability was calculated by reach for each method using the results from both labs for each individual site. For example if WGL (+) and ERDC (-) then the site was considered (+). Detection probabilities were similar for the medium and high reaches, but centrifuging had a 26% detection rate compared to 0% for filtration in the low density reach (Table 6). The total length of the study reach was 2.50 km with an average width of 0.12 km and a total area of 0.30 km². Therefore, using centrifugation a 95% detection probability would require 10 samples (i.e., 10 sets of five 50 ml tubes) to be collected per 2.5 km reach or 4 samples per river km. To achieve a 99% detection probability at total of 15 samples per 2.5 km or 6 samples per river km would be collected.

For the statistical analyses, the copy numbers were averaged for the replicate samples between the two labs. Therefore, every site had an average copy number for each of the six markers. The average copy numbers were then log₁₀ transformed, and a dissimilarity matrix was then generated based on Euclidean distance for the PERMANOVA. Results from the PERMANOVA showed significant differences between centrifuging and filtration for all three reaches ($P < 0.001$; Table 7). Centrifuging had significantly higher copy numbers than filtration for high and low density reaches, but filtration had significantly higher numbers in the medium density reach (Tables 5 and 7). Reasons for higher numbers in the filtered samples from the medium reach could be related to differences in inhibitors between reaches, or other confounding environmental variables, but that is beyond the scope of this study. However, a statistical difference in the medium reach where filtering produced higher copy numbers is not as relevant in a detection program, since the overall detection rate is a difference of 96% versus 100%, and both methods would provide positive results for this particular reach. Since early detection programs focus on detection in low-density reaches, it is important that the centrifugation method was able to detect DNA when the filtering method was not.

Conclusions and Recommendations

This study strongly supports the use of centrifuging as a method to process eDNA field-collected samples in early detection and monitoring programs, most notably due to its performance in the low-abundance carp reaches of the Illinois River where centrifuged samples were able to detect carp DNA, but *filtered* samples were *not*. One potential explanation for why centrifuging outperformed filtering is that smaller volumes of water will have smaller amounts of inhibitors (Gibson et al. 2012), which would improve detection over heavily inhibited filtered samples. This study also confirms centrifugation as a method for processing eDNA samples in other applications, such as confirmation of spawning events or detection of over-wintering habitats. There are several benefits to centrifuging over filtering, but the most important is preventing contamination in the field. The reduced handling in the field creates far fewer chances for cross-sample contamination, and single-use, sterile tubes eliminate contamination between sampling events. In other agencies, field staff could fill both field blanks and centrifuge control samples in the lab or processing trailer, but WGL will fill all field blanks and distribute as needed. In addition, there are large improvements in efficiency in the field and lab which will allow for the collection and processing of many more samples within the sampling season. Thus, based on the same outcome in three different studies comparing centrifugation to filtration as a water processing method, we recommend that centrifugation be approved for use in the early detection and surveillance of bigheaded carps, specifically in the Quality Assurance Project Plan.

Tables and Figures

Table 1. Qiagen extraction kit conventional PCR results of twenty 50-mL samples processed by centrifugation from one 2-L sample container, compared to ten 2-L replicates processed by filtration.

Quantity of DNA (ng)	*Centrifuged Number positive bands counted (80)	Centrifuged Number samples positive (20)	*Filtered Number positive bands counted (20)	Filtered Number samples positive (10)
(0)	0	0	0	0
(200)	32	14	16	9
(750)	67	20	20	10
(2000)	77	20	20	10
(4000)	77	20	20	10
Extraction Negative	Na	0	0	0
Extraction Positive	Na	All +	All +	All +
PCR Negative	Na	0	0	0
PCR Positive	Na	All +	All +	All +

* For centrifuged samples, one swab represents one sample for a total of 20 samples per treatment. Four replicate reactions for cPCR for centrifuged samples, two replicate PCRs for filtered samples.

Table 2. Qiagen extraction kit quantitative PCR results of twenty 50-mL samples processed by centrifugation taken from one 2-L sample container, compared to ten 2-L replicates processed by filtration.

Quantity of DNA (ng)	*Centrifuged Number positive curves counted (40)	Centrifuged Number samples positive (20)	Centrifuged Ave Cq value ¹ (SE)	*Filtered Number positive curves counted (20)	Filtered Number samples positive (10)	Filtered Ave Cq value ¹ (SE)
(0)	0	0	0 (0)	0	0	0 (0)
(200)	25	15	36.83 (0.21)	19	10	23.50 (0.20)
(750)	40	20	35.58 (0.18)	19	10	29.44 (0.23)
(2000)	38	20	34.03 (0.22)	20	10	27.71 (0.11)
(4000)	36	20	31.84 (0.20)	20	10	27.28 (0.13)
Ext Negative	Na	0	0	0	0	0
Ext Positive	na	All +	33.18 (0.31)	All+	All+	36.29 (0.15)

* For centrifuged samples, one swab represents one sample for a total of 20 samples per treatment. Two replicate reactions for filtered samples and 4 replicate reactions for centrifuged samples.

¹Cq value calculated on positive samples, zero readings were not included in summary numbers.

Table 3. Catch per unit effort of bighead and silver carp in selected pools of the Illinois Waterway in 2013. Data were acquired from the IDNR, SIU, and INHS from projects outlined in the Monitoring and Response Plan for Asian Carp in the Upper Illinois River and Chicago Area Waterway System (2013). All of the sites used within each project were fixed and chosen as a likely area of inhabitation by Asian carp within that pool.

Pool	Electrofishing (fish/hr)		Gill Netting (fish/100 yds)		Hoop Netting (fish/set)	
	Bighead	Silver	Bighead	Silver	Bighead	Silver
Brandon Road	0	0	0	0	0	0
Marseilles	0	1.73, 5.88	0.38	0.87	0.07, 0.04	0.96
La Grange	0	16.78, 46.53	1.07*	3.47*	0.71	na

*2012 data.

Table 4. Confirmed detections for Bighead and Silver carp DNA in water samples collected from river reaches with varying Asian carp densities and processed in the field with filtering and centrifuging.

Asian Carp Density	Processing Lab	Filtered Water (2-L Bottles)			Centrifuged Water (50-mL tubes)		
		Silver Positive	Bighead Positive	Both Positive	Silver Positive	Bighead Positive	Both Positive
High	ERDC	23	23	23	23	23	23
	WGL	19	19	19	23	23	23
Medium	ERDC	23	21	21	18	9	8
	WGL	23	21	21	19	14	12
Low	ERDC	0	0	0	2	1	1
	WGL	0	0	0	1	3	0

*total sample number less cooler blanks, 69 for each lab.

Table 5. Mean copy number for 25 samples (from 8 replicate reactions) for each of six Asian carp qPCR markers amplified in water samples collected from river reaches with varying Asian carp densities and processed in the field with filtering and centrifuging. Limit of detection is 3-9 copies, limit of quantification (LOQ) is 10 copies. Samples with copy numbers above the LOQ are reported, but those that detected but were below the LOQ are designated (+).

Fish Density	Lab	ACTM1		ACTM3		BHTM1		BHTM2		SCTM4		SCTM5	
		Filter	Cent.	Filter	Cent.	Filter	Cent.	Filter	Cent.	Filter	Cent.	Filter	Cent.
High	ERDC	128	272	58	165	64	17	168	24	70	163	243	156
	WGL	234	654	93	510	12	22	46	32	54	357	295	644
Medium	ERDC	33	16	17	10	+	+	+	+	43	17	39	+
	WGL	54	27	43	22	23	+	16	+	21	21	32	33
Low	ERDC	0	20	+	21	0	50	0	107	0	11	0	+
	WGL	+	23	+	25	0	27	0	55	0	17	0	24

Table 6. Detection probabilities for centrifuging and filtration processing methods were calculated for each of the reaches. A site was considered (+) for Asian carp eDNA if either or both WGL or EDRC had a confirmed (+) for that site.

Asian Carp Density	Filtered water (2-L bottles)	Centrifuged water (50-ml tubes)
High	100%	100%
Medium	100%	96%
Low	0%	26%

Table 7. PERMANOVA results table contrasting the differences of centrifuging and filtration in different reaches of density of Asian carp based on average copy number from WGL and EDRC for six markers at each site. Table reports degrees of freedom (df), Sum-of-squares (SS), Mean square (MS), the F-statistic (Pseudo-F), and the p-value (*P*).

PERMANOVA					
Source	df	SS	MS	Pseudo-F	<i>P</i> (perm)
Overall	5	2486.3	497.25	122.44	0.0001
Low	1	26.359	26.359	7.7438	0.0001
Medium	1	85.825	85.825	24.404	0.0001
High	1	118.9	118.9	22.593	0.0001
Res	132	536.07	4.0612		
Total	137	3022.3			

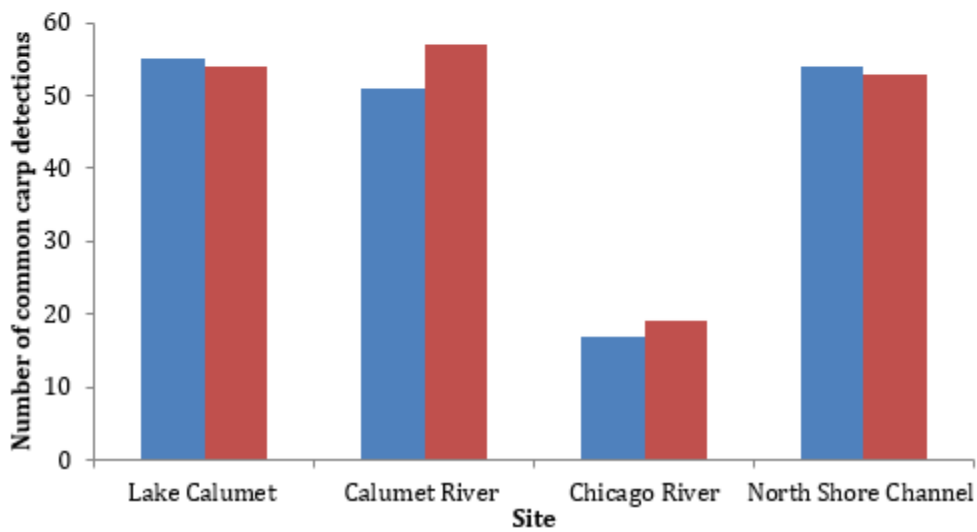
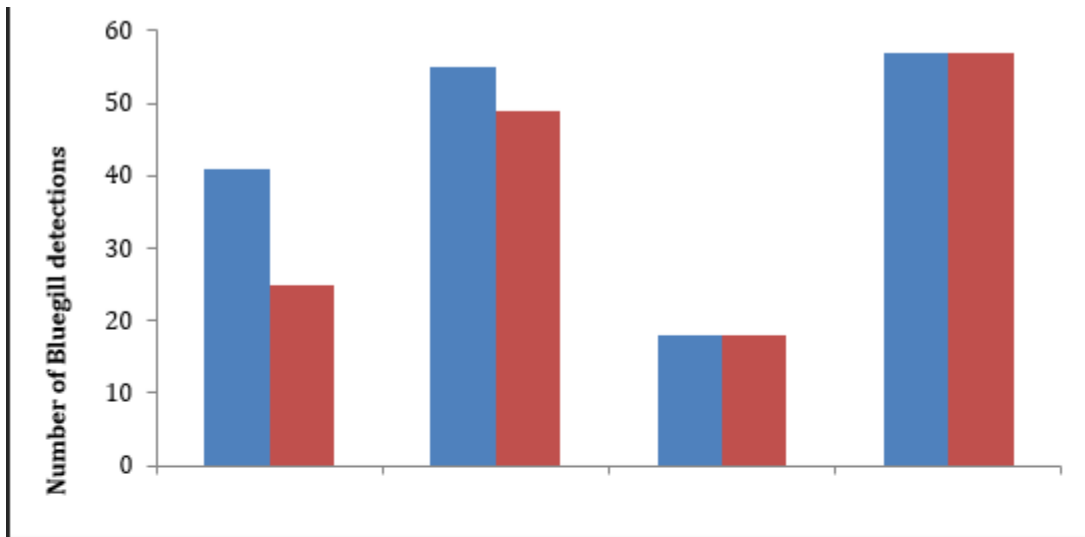


Figure 1. Detection of bluegill (top) and common carp (bottom) eDNA in four sites in the Chicago Area Waterway System. Detection of eDNA in centrifuged samples in blue, filtered samples in red. Due to a combined sewage overflow (CSO), there were only 20 samples collected in the Chicago River instead of 60.

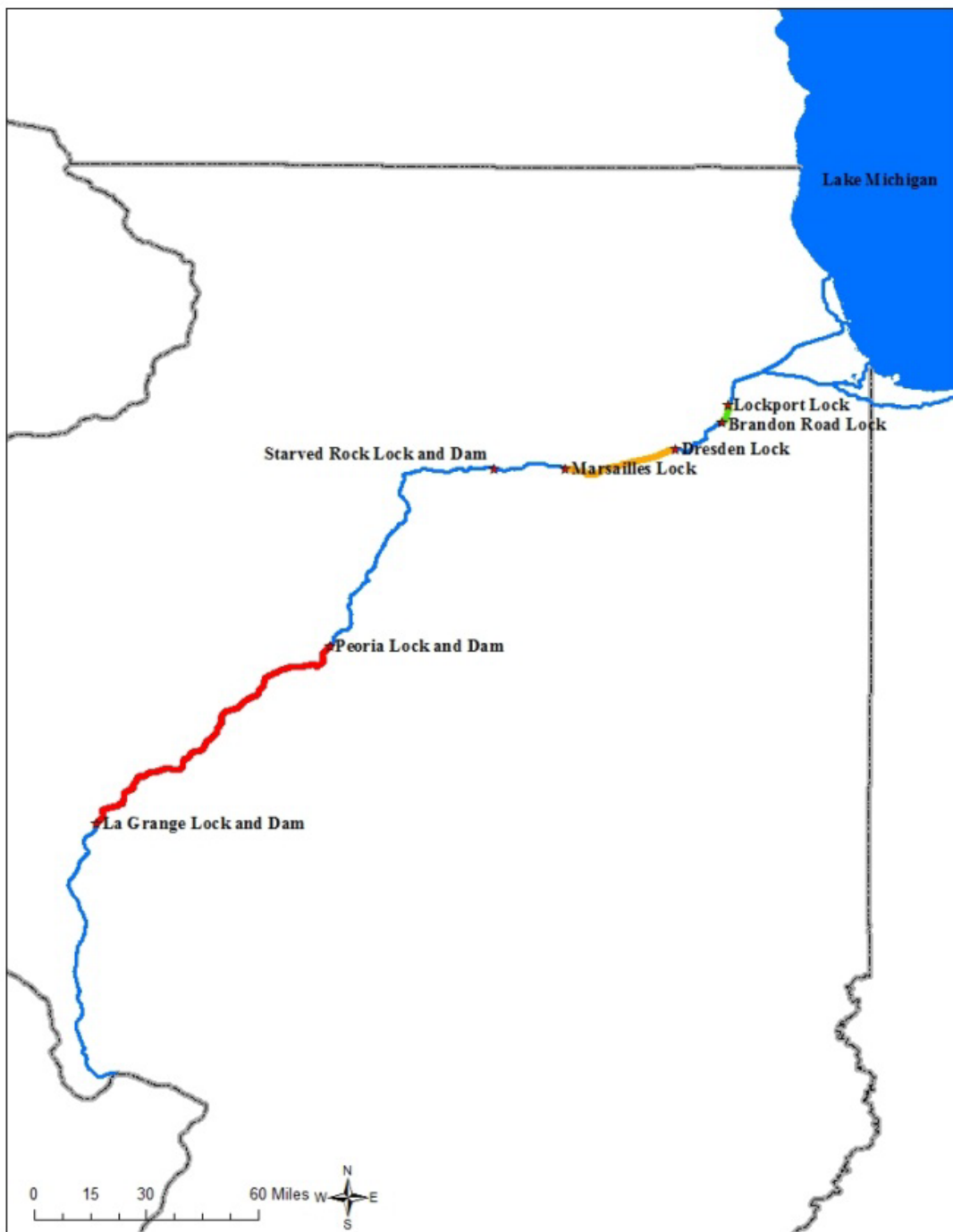


Figure 2. Map of the Illinois Waterway. Highlighted pools indicate sites selected as high (red), medium (yellow), or low (green) concentrations of Asian carp. Brandon Road pool (green), Marseilles pool (yellow), and La Grange pool (red) were selected based on sampling data from the Monitoring and Response Workgroup Fish Surveys. Note: figure misspells 'Marsailles'.

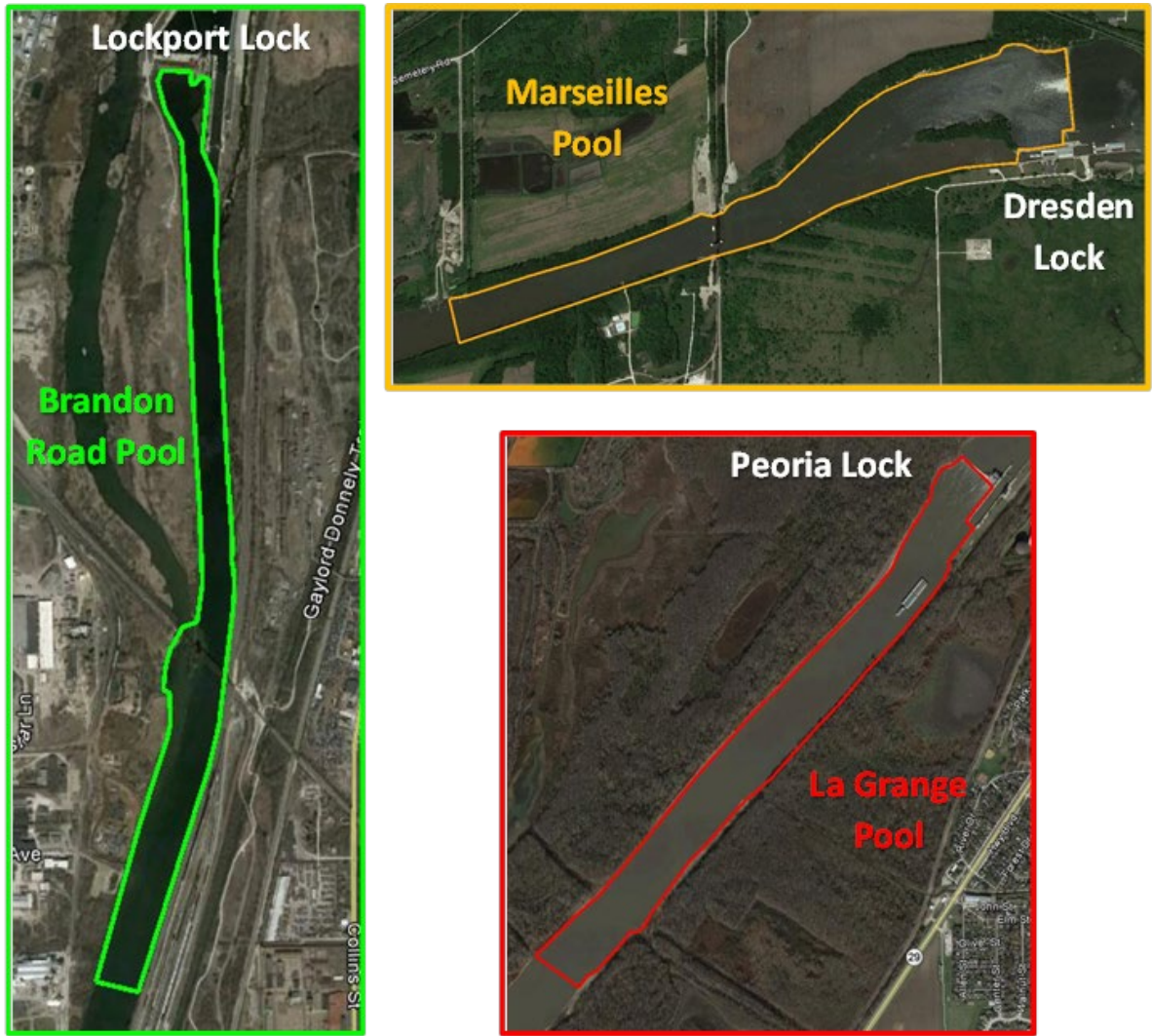


Figure 3. Study reaches in the Illinois River. Each polygon encompasses a study reach 2.5 river km below the upstream lock in the high (red), medium (orange), and low (green) bigheaded carp density pools.

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