

RECLAMATION

Managing Water in the West

Open Access Web-Based Database of Invasive Mussel Research

Research and Development Office
Science and Technology Program
(Final Report) ST-2019-7105-01

The screenshot displays the 'Mussels Database Management' web application. At the top, a navigation bar includes links for 'Home', 'Reports', and 'Visualization'. The main heading is 'Mussels Database Management'. On the left, a sidebar contains five 'Quick Add' buttons: 'Sample', 'PCR And Sequencing', 'Microscopy', 'Sample Prep', and 'Purge'. The right side of the interface features two primary sections. The 'Batch Upload' section includes a 'Submission Type' dropdown menu set to 'Sharepoint', a 'File to Submit' field with a 'Choose File' button and the text 'No file chosen', and a 'Submit Sample' button. Below these are two bulleted instructions: 'CSV should be formatted in the following order' and 'The first line should be a header that contains the following fields', followed by a list of required fields: 'Sample Code', 'Released (true/false)', and 'Release Date (mm/dd/yyyy)'. The 'Edit Sample' section below it contains a search bar with a 'Go' button, and two dropdown menus labeled 'By Location:' and 'By Water Body:'.



Mission Statements

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The Department of the Interior (DOI) conserves and manages the Nation's natural resources and cultural heritage for the benefit and enjoyment of the American people, provides scientific and other information about natural resources and natural hazards to address societal challenges and create opportunities for the American people, and honors the Nation's trust responsibilities or special commitments to American Indians, Alaska Natives, and affiliated island communities to help them prosper.

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Open access web-based database of invasive aquatic research and water quality

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Acronyms and Abbreviations

AIS: Aquatic Invasive Species

CPLM: Cross-polarized light microscopy

EcoLab: Reclamation Ecological Research Laboratory

GPS: Geospatial Positioning System

IRO: Information Resources Office

PCR: Polymerase chain reaction

RISE: Reclamation Information Sharing Environment

SEM: Scanning electron microscopy

TCS: Technical Services Center

Executive Summary

In the 12 years since quagga mussels were first identified in Lake Mead, the Bureau of Reclamation's Ecological Research Laboratory (formerly known as the Reclamation Detection Laboratory for Exotic Species / RDLES) has analyzed over 17,000 water samples for early detection of mussels. A broad array of data are associated with these samples, including field collection measurements, water quality and sample parameters, and laboratory results from microscopic and molecular biological analyses. Prior to the current projects these data were recorded in multiple spreadsheets, which lacked standardization, and presented significant challenges for querying data to produce reports and facilitate data analysis.

The primary focus of this project was to develop a database to house and manage the large amount of data already generated by the Ecological Research Laboratory's invasive mussel early detection program, and to provide a system for deposition of new data. TSC researchers collaborated with IRO staff to design and develop the database, and a web-based portal for accessing it. This project has developed a centralized system for organizing and accessing mussel early detection data. The database will provide a basis for integrating these data into RISE, to allow open access to the data and to integrate mapping and other visualization tools to facilitate data analysis.

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Background

Zebra and quagga mussels are freshwater dreissenid bivalve mollusks that are native to Eastern Europe and Central Asia. They were first discovered in North America in the late 1980s in the Great Lakes, likely having been accidentally introduced through discharge of ballast waters from commercial shipping vessels. They proliferated and spread quickly through connected watersheds and nearby waters. Due to their abundance and attachment to hard substrates they can have significant impacts on human water usage, including water distribution and hydroelectric power generation. They can also impact native organisms and alter ecosystems functions due to the high rates of particulate clearance from the water column associated with their filter feeding.

Given that water is a precious resource in the Western United States, both for human consumption and agriculture, as well as for hydroelectric power generation, the potential westward expansion of dreissenid mussels was, and remains, a subject of significant concern. The first discovery of these invasive mussels in the Western United States came with the identification of quagga mussels in Lake Mead in 2007, where it was apparent that a large and well-established population was already present.

In response to this discovery a large-scale effort was undertaken to survey western reservoirs, lakes, and rivers for the presence of dreissenid mussels. Scientists at the Bureau of Reclamation's Technical Services Center (TSC) have taken a leading role in these efforts, coordinating water sampling and conducting analysis for early detection of mussels using both microscopy and molecular biology techniques. These efforts at early detection of mussel introductions have continued in TSC's Ecological Research Laboratory (EcoLab; formerly named the Reclamation Detection Laboratory for Exotic Species [RDLES], and colloquially referred to as "the mussel lab"). To date over 17,000 samples have been collected and analyzed, and the laboratory continues to analyze approximately 1,500 samples per year. The majority of these samples are collected in the summer months of May through September, when mussel spawning is most likely to occur.

Due to the rapidity with which the mussel detection program was initiated in response to initial discoveries, data recording procedures were established in a relatively ad hoc fashion, with data pertaining to sample collection, preparation, and analysis being tabulated across multiple spreadsheets. Although record keeping for samples was thorough, the fragmentation of the data, as well as a lack of standardization for key items such as the name of the sampled waterbody and a referenced geographic location for sample collection made it difficult to query the data in the aggregate and to extract data of interest for reporting and detailed analysis.

The current project endeavored to create a database that would house all archival data on mussel detection in a unified and geographically referenced format, as well as to provide a streamlined system for the entry and storage of new data as they are generated.

Methods and Previous Work

Previous funding from the Bureau of Reclamation's Science and Technology Program supported initial work to develop a relational database of mussel early detection data from the Ecological

Research Laboratory. Previous work established that all data entries would be georeferenced based on the sampling location, facilitating future work on data analysis and visualization. During the previous portion of the project and organizational schema for the relational database was developed in Microsoft Access, and reported GPS location data for some samples was aggregated.

The current project operated as a collaboration between EcoLab researchers and Information Resources Office (IRO) staff. Early in the project it was decided that the database would be transitioned from Access to MySQL to facilitate web-based access to the database.

A first step in organizing data for the database was georeferencing sampling locations for all samples. Each sample was assigned to a water body and sampling location, and water body names and sampling location names were conformed so that naming was consistent across samples. Previous recordkeeping had relied on transcription of names provided with samples, and in many cases both water bodies and sample locations had been assigned more than one name. All sampling locations were also assigned to reference geographic coordinates in decimal degrees. Where possible, GPS coordinates provided with the sample were used to assign the sample location. For most of these samples the coordinates were provided in another coordinate system such Universal Transverse Mercator (UTM) or degrees, minutes, seconds (DMS) and had to be converted to decimal degrees. All GPS coordinates were also checked on a map to confirm that they were in the correct waterbody and matched the recorded sampling location. For samples where GPS coordinates were not available, a reference location was chosen on the map, based on the sample location name. When a sample location was not provided or could not be identified, a midpoint in the water body was chosen and the sample location was denoted as “unknown”. To avoid a proliferation of separate sample locations, each sample location was considered to encompass all samples collected within a 200-meter radius of the selected reference location.

Each waterbody in the database has a table of associated data, which include not only the waterbody name, but also the state(s) where it is located, the relevant Reclamation area office, whether it is connected to Reclamation waters, and facility, water, and land owners at the waterbody, as these data are available. Location tables include the sample location name, the state where the sample location is, latitude and longitude in for the reference geographic location in decimal degrees, and information on whether these coordinates were derived from a GPS record or selected on a map (recorded as “Google Earth”, although another source could be recorded as appropriate). Both Waterbody and Location records each are assigned a unique identification number that is used as a key for linkage to other tables.

TSC scientists worked with IRO staff to establish waterbodies and sample locations in the MySQL database, and to incorporate sample data. Working from EcoLab datasets an updated database schema was developed to encompass all data collected and generated by the EcoLab for mussel detection, and to characterize data types (Figure 1).

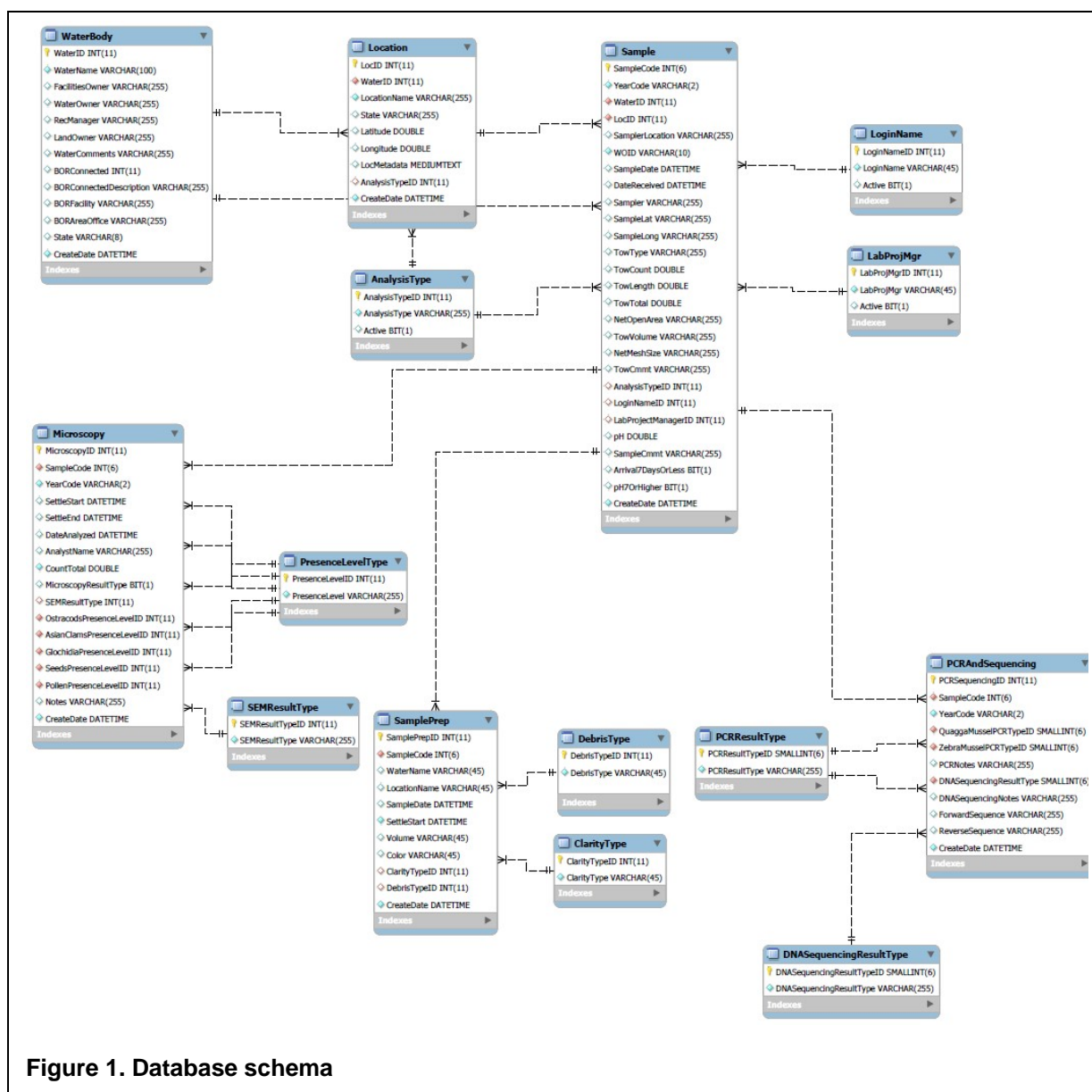


Figure 1. Database schema

A web-based interface for the database was developed to allow data entry, access, and generation of reports, as described below. Initial development of the web interface for the database was deployed on the IRO “Development” server where functionality was evaluated. A stable operating version of the web interface and database was then deployed in the IRO “Test” server, and is regularly backed up, allowing for redeployed after any service interruption. The “Development” version of the web interface and database remain in place, allowing development and testing of any new features or bug fixes before deployment to the operational version.

Results

Sample and data submission

A website for the database was developed by IRO staff and the site is password protected, so that only approved EcoLab staff can access and edit the database. Web-access to the database is built around a homepage that allows addition of data from various stages of sample management, preparation, and analysis in the Ecological Research Laboratory (Figure 2). These include:

- Sample
- Sample Prep
- Microscopy
- PCR and Sequencing
- Purge

For each of these data types there are two methods of data entry, either through a Quick Add dialog box that allows direct entry of data for a single sample, or through a Batch Upload dialog box that allows submission of comma separated value (csv) files containing data for multiple samples. Specifics on each of the sample types are described below.

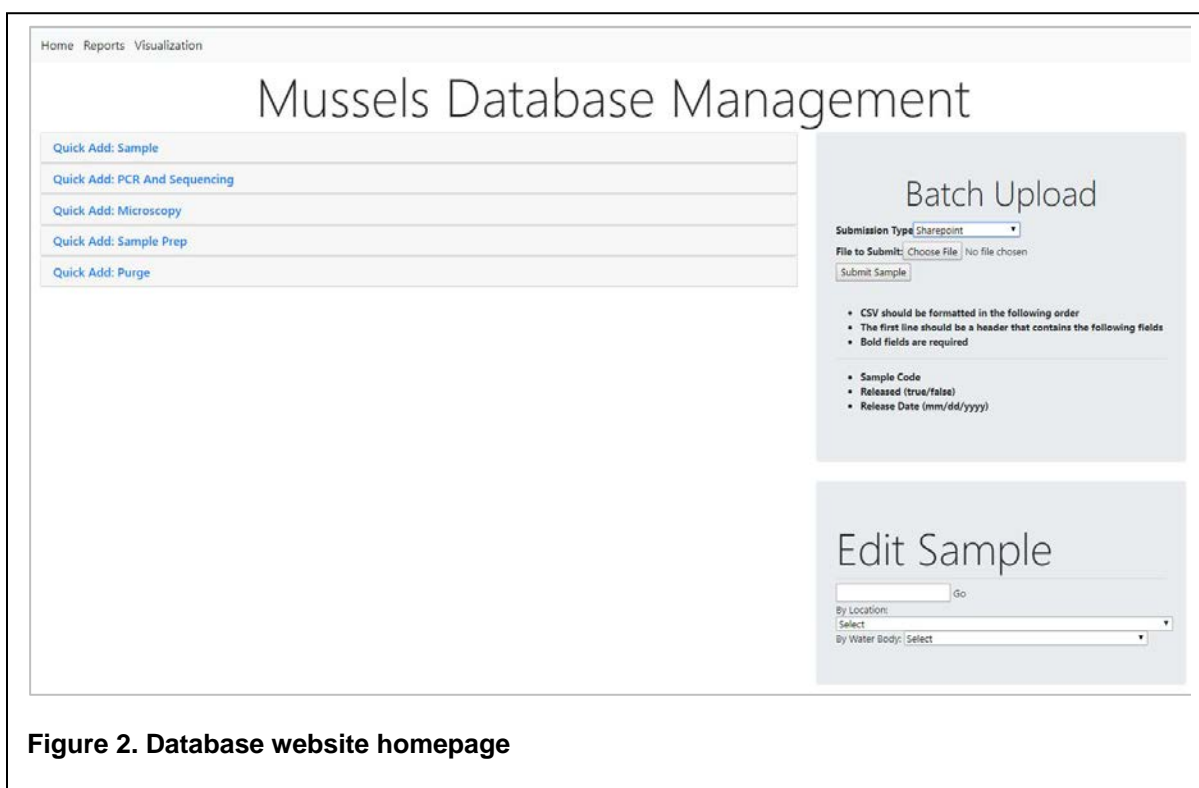


Figure 2. Database website homepage

Sample

The “Sample” heading encompasses data associated with sample collection in the field and receipt in the Ecological Research Laboratory. Fields included in the Sample data are:

- **WaterBodyID**
- **LocationID**
- **WOID**
- Sampler Location (from bottle)
- **Sample Date (mm/dd/yyyy)**
- **Date Received (mm/dd/yyyy)**
- Sampler / Client
- Latitude
- Longitude
- Tow Type (V or H)
- Num. of Tows
- Tow Length (meters)
- Tow Total (Num. X Length)
- Net OpenArea (sq.m)
- Tow Volume (cu.m) (Total x Area)
- Net MeshSize (um)
- Tow Cmmt
- **Analysis Type**
- LogIn Name/Initials
- Lab Project Manager
- pH
- Sample Comment

Fields listed above in bold type are mandatory and a value must be included for these.

In the Quick Add dialog box several of these fields are selected from drop-down menus (Figure 3). The “Water Body” drop-down includes a list of all waterbodies entered in the database. Once “Water Body” is selected the “Location” drop-down is updated to contain only a list of sample locations associated with the selected waterbody. Once “Location” is selected the default analysis type appears in that drop-down menu.

If the waterbody and/or location of a sample is not already present in the database, hyperlinks at the bottom of the Quick Add dialog box labeled “Create Waterbody” and “Create Location” take the user to a new page where information can be entered to generate a new feature. Once the “Submit” button is hit the user can return to the homepage and the new Waterbody or Location will be available in the relevant dropdown menu.

Once all relevant information is entered in the Quick Add: Sample dialog box, the “Submit” button can be hit and the sample will be entered in the database. A unique “Sample Code” number will be generated, and a green banner will appear at the top of the webpage reporting that the sample has been successfully entered.

Batch Upload is generally not used for Sample data entry, but the functionality is available. For Batch Upload a csv will should be generated with headers matching the field names listed in the Batch Upload dialog box (Figure 4). The csv file can then be uploaded using the “Choose File” button and entered using the “Submit Sample” button. As with the Quick Add, successful submission will be reported on a green banner at the top of the page.

The image shows a web-based form titled "Quick Add: Sample". The form is organized into several sections with labels and input fields. At the top, there is a dropdown menu for "Water Body" with "ABIQUIU RESERVOIR" selected. Below this is a "Location" dropdown menu with "DAM INLET" selected. The form then lists various fields: "WOID", "Sampler Location", "Sample Date", "Date Received", "Sampler", "Sample Latitude", "Sample Longitude", "Tow Type", "Tow Count", "Tow Length", "Tow Total", "Net Open Area", "Tow Volume", "Net Mesh Size", "Tow Comment", "Analysis Type" (with "FlowCAM & PCR" selected), "Login Name", "Lab Project Manager", "pH", and "Sample Comment". At the bottom of the form, there are two buttons: a blue "Submit" button and a grey "Clear Fields" button. Below the buttons, there are two links: "Create Waterbody" and "Create Location".

Quick Add: Sample

Water Body

Location

WOID

Sampler Location

Sample Date

Date Received

Sampler

Sample Latitude

Sample Longitude

Tow Type

Tow Count

Tow Length

Tow Total

Net Open Area

Tow Volume

Net Mesh Size

Tow Comment

Analysis Type

Login Name

Lab Project Manager

pH

Sample Comment

[Create Waterbody](#) | [Create Location](#)

Batch Upload

Submission Type

File to Submit: No file chosen

- CSV should be formatted in the following order
- The first line should be a header that contains the following fields
- Bold fields are required

Waterbody and Location must use the ID. [Click here to look them up.](#)

- **WaterBodyID**
- **LocationID**
- **WOID**
- **Sampler Location (from bottle)**
- Sample Date (mm/dd/yyyy)
- Date Received (mm/dd/yyyy)
- Sampler / Client
- Latitude
- Longitude
- Tow Type (V or H)
- Num. of Tows
- Tow Length (meters)
- Tow Total (Num. X Length)
- Net OpenArea (sq.m)
- Tow Volume (cu.m) (Total x Area)
- Net MeshSize (um)
- Tow Cmmt
- Analysis Type
- **LogIn Name/Initials**
- **Lab Project Manager**
- **pH**
- Sample Cmmt (LogIn Condition)

Figure 4. Batch Upload Sample

Sample Prep

The Sample Prep dialog is used to enter data collected when water samples are placed in Imhoff settling cone in the laboratory. Fields included in the Sample Prep data are:

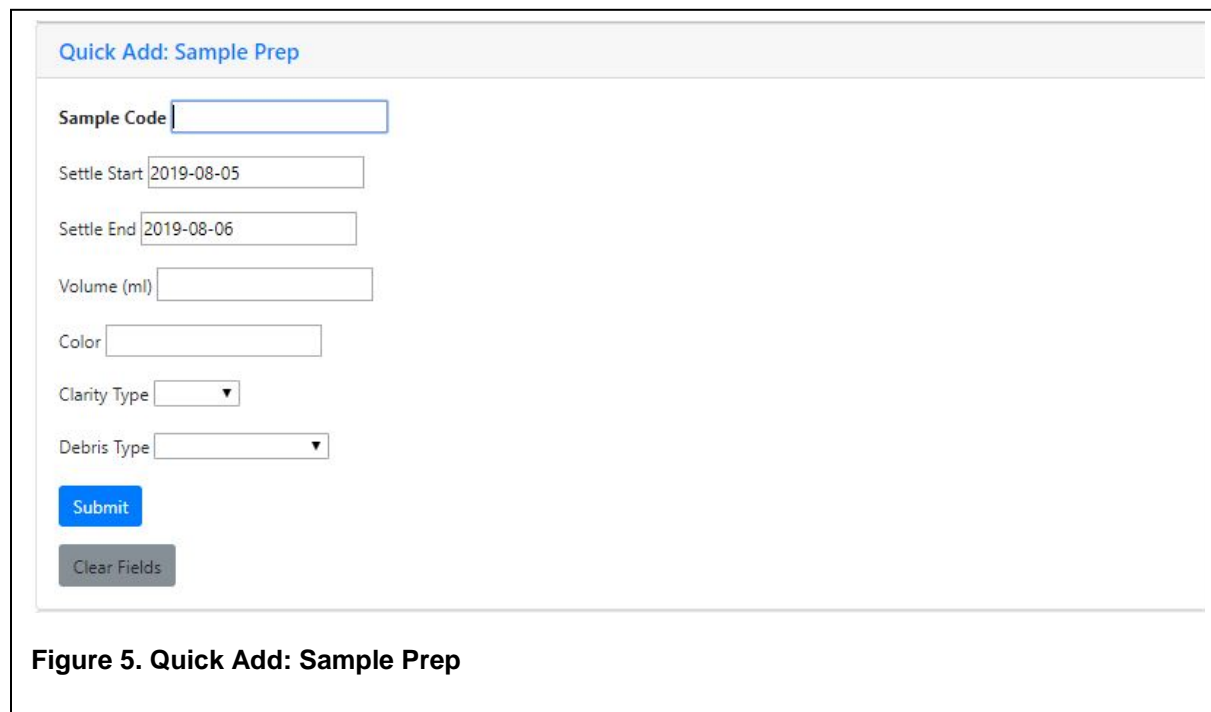
- **Sample Code**
- Settle Start
- Settle End
- Volume (ml)
- Color
- Clarity Type
- Debris Type

Fields listed above in bold type are mandatory and a value must be included for these.

The “Settle Start” and “Settle End” fields refer to that dates that the sample is placed in, and removed from, the Imhoff cone, respectively. By default, in the Quick Add dialog box the “Settle Start” field autofills with the current date, and “Settle End” field autofills with the next day’s date (Figure 5). When the Batch Upload dialog is used to upload Sample Prep data the appropriate date values should be entered in the csv file, as these values will not autofill (Figure 6).

The required “Sample Code” field refers to the unique numerical ID assigned when Sample data are submitted to the database, as described above.

Sample Prep data submission is finalized as described above for Sample data, with a green banner appearing to report successful data submission.



Quick Add: Sample Prep

Sample Code

Settle Start

Settle End

Volume (ml)

Color

Clarity Type

Debris Type

Figure 5. Quick Add: Sample Prep

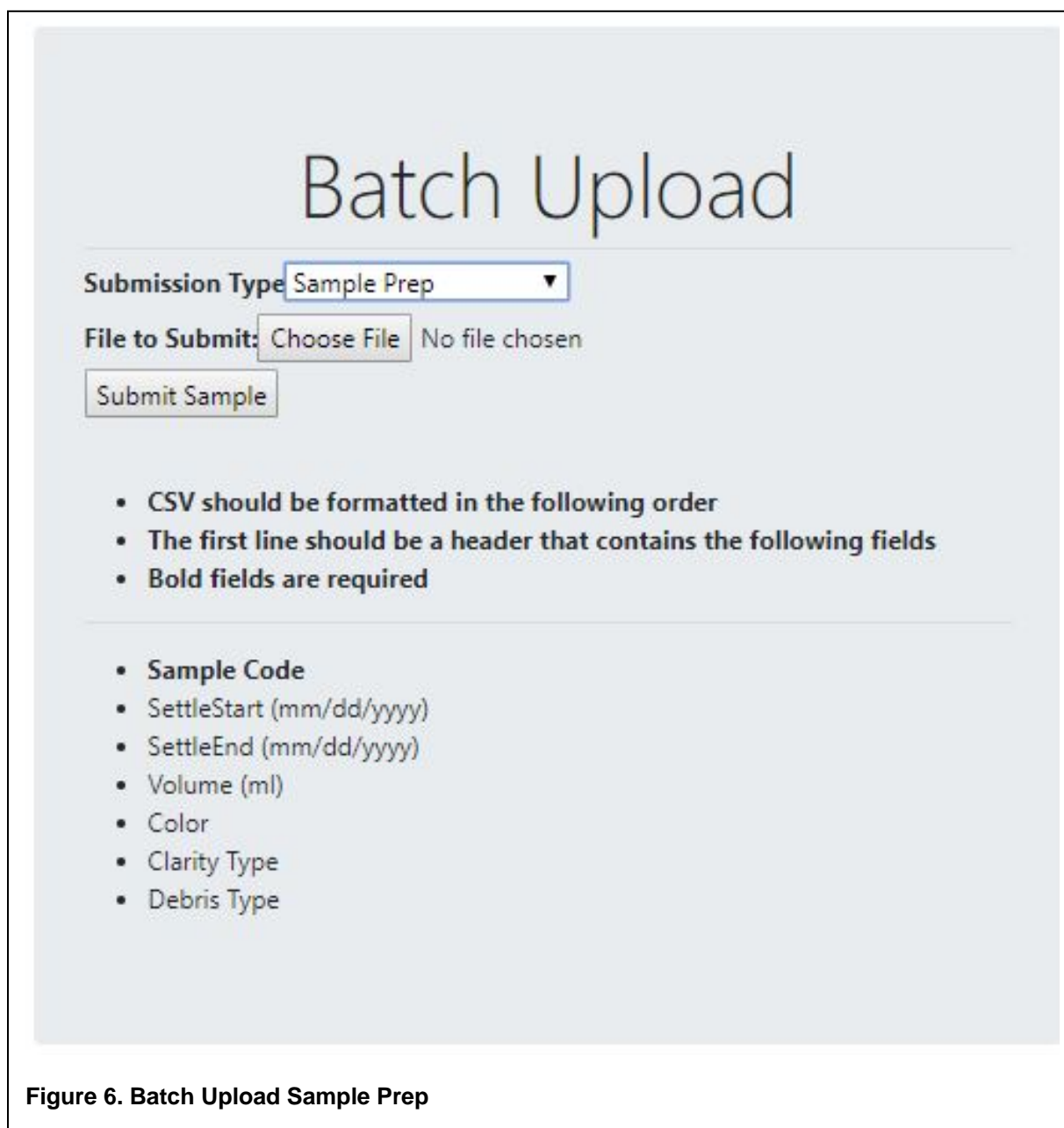


Figure 6. Batch Upload Sample Prep

Microscopy

The Microscopy dialog is used to enter laboratory data from cross-polarized light microscopy (CPLM) and scanning electron microscopy (SEM) analyses. Fields included in the Sample Prep data are:

- **Sample Code**
- Date Analyzed
- Analyst Name
- **Count Total**

- **Asian Clam Presence Level**
- **Glochidia Presence Level**
- **Ostracods Presence Level**
- **Pollen Presence Level**
- **Seeds Presence Level**
- **SEM Result Type**
- Notes

Fields listed above in bold type are mandatory and a value must be included for these.

“Count total” refers to the number of dreissenid mussel veligers observed in the sample. The default value for this field is “0”. “Asian Clam Presence Level”, “Glochidia Presence Level”, “Ostracods Presence Level”, “Pollen Presence Level”, and “Seeds Presence Level” fields have five possible conditions, “None”, “Low”, “Medium”, “High”, and “Present – Not Quantified”. “Low” refers to between one and nine observations in a sample. “Medium” refers to between 10 and 30 observations in a sample. “High” refers to more than 30 observations in a sample. “Present – Not Quantified” is recorded when the organism is noted to be present in the sample, but not quantified. This condition is primarily used for entry of incomplete archival data. By default, the value for all of these fields is “None” in the Quick Add dialog box (Figure 7). When the Batch Upload dialog is used to upload Microscopy data the appropriate values for these fields should be entered in the csv file, as these values will not autofill (Figure 8).

Quick Add: Microscopy

Sample Code

Date Analyzed

Analyst Name

Count Total

Asian Clam Presence Level

Glochidia Presence Level

Ostracods Presence Level

Pollen Presence Level

Seeds Presence Level

Sem Result Type

Notes

Figure 7. Quick Add: Microscopy

Batch Upload

Submission Type

File to Submit: No file chosen

- CSV should be formatted in the following order
- The first line should be a header that contains the following fields
- Bold fields are required

- **SampleCode**
- DateAnalyzed (mm/dd/yyyy)
- Analyst Name Initials
- **Count Total (15mL)**
- SEM Result
- Ostracods
- Asian clams
- Glochidia
- Seeds
- Pollen
- Notes

Figure 8. Batch Upload Microscopy

Accepted conditions for “SEM Result Type” are “Not Tested”, “Positive”, “Negative”, or “Pending”. By default, the value for this field is “Not Tested” in the Quick Add dialog box. When the Batch Upload dialog is used to upload Microscopy data, the appropriate value for this field should be entered in the csv file, as the value will not autofill.

The required “Sample Code” field refers to the unique numerical ID assigned when Sample data are submitted to the database, as described above.

Microscopy data submission is finalized as described above for Sample data, with a green banner appearing to report successful data submission.

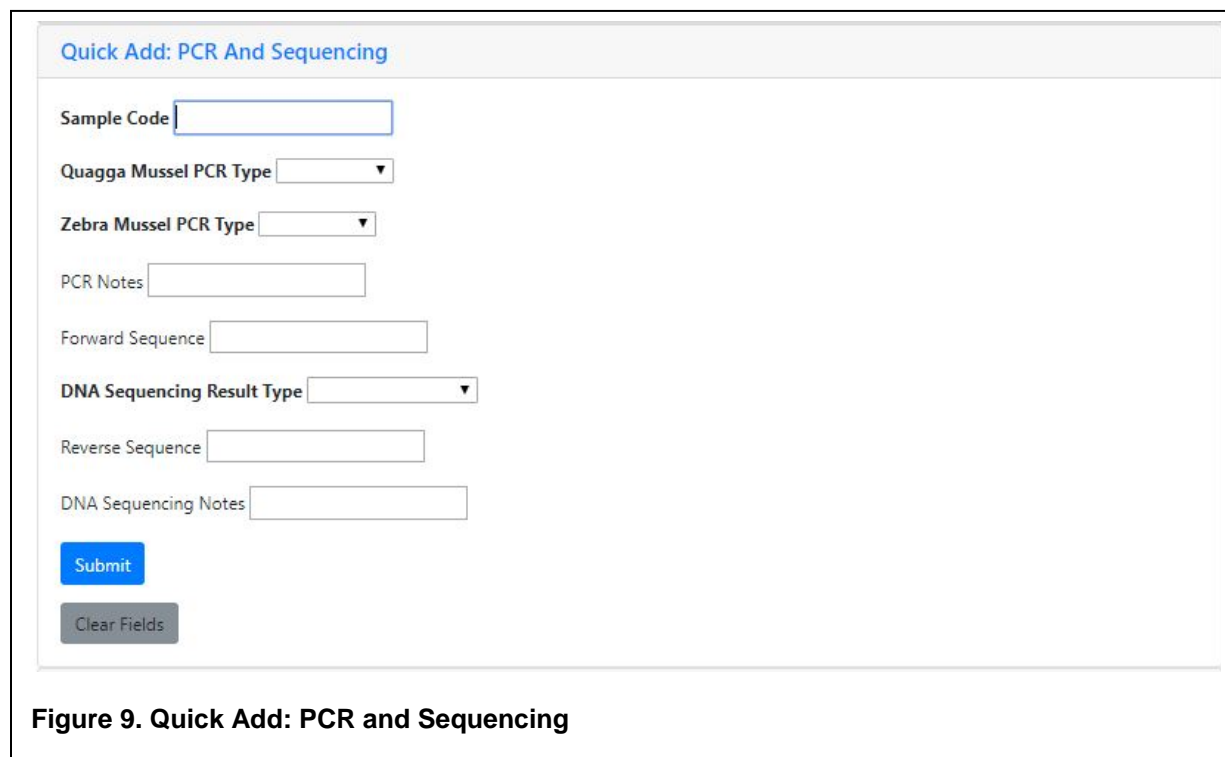
PCR and Sequencing

The PCR and Sequencing dialog is used to enter laboratory data from molecular biology analyses (Figures 9 and 10). Fields included in the PCR and Sequencing data are:

- **Sample Code**
- **Quagga Mussel PCR Type**
- **Zebra Mussel PCR Type**
- PCR Notes
- **DNA Sequencing Result Type**
- Forward Sequence
- Reverse Sequence
- DNA Sequencing Notes

Fields listed above in bold type are mandatory and a value must be included for these.

“Quagga Mussel PCR Type” and “Zebra Mussel PCR Type” refer to results from species-specific conventional polymerase chain reaction (PCR) analyses. Accepted conditions for these fields are “Not Tested”, “Positive”, “Negative”, or “Pending”.



Quick Add: PCR And Sequencing

Sample Code

Quagga Mussel PCR Type

Zebra Mussel PCR Type

PCR Notes

Forward Sequence

DNA Sequencing Result Type

Reverse Sequence

DNA Sequencing Notes

Figure 9. Quick Add: PCR and Sequencing

Batch Upload

Submission Type **PCR And Sequencing** ▼

File to Submit: **Choose File** No file chosen

Submit Sample

- CSV should be formatted in the following order
- The first line should be a header that contains the following fields
- Bold fields are required

- Sample Code
- Quagga Mussel PCR
- Zebra Mussel PCR
- PCR Notes
- **DNA Sequencing Result**
- DNA Sequencing Notes
- Forward Sequence
- Reverse Sequence

Figure 10. Batch Upload PCR and Sequencing

“DNA Sequencing Results” refer to the results of Sanger sequencing analysis performed on positive PCR reaction products. Accepted conditions for these fields are “Not Tested”, “Positive”, “Negative”, “Non-Sequencable”, or “Pending”.

The required “Sample Code” field refers to the unique numerical ID assigned when Sample data are submitted to the database, as described above.

PCR and Sequencing data submission is finalized as described above for Sample data, with a green banner appearing to report successful data submission.

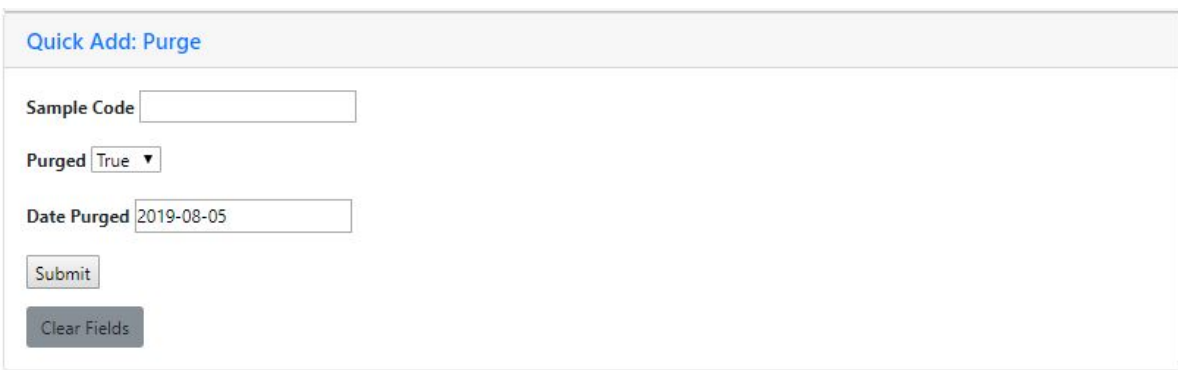
Purge

The “Purge” dialog is used to record when water samples are discarded following a holding period after analysis. Fields included in the Purge data are:

- **Sample Code**
- **Purged**
- **Date Purged**

All samples fields are required. “Sample Code” field refers to the unique numerical ID assigned when Sample data are submitted to the database, as described above. “Purge” refers to whether the physical sample has been discarded and can be “True” or “False”. By default, it is set to “True” in the Quick Add dialog box (Figure 11) but must be explicitly recorded in a csv file for Batch Upload (Figure 12). “Date Purged” refers to the date the physical sample was discarded. By default, it is set to the current day’s date in the Quick Add dialog box but must be explicitly recorded in a csv file for Batch Upload.

Purge data submission is finalized as described above for Sample data, with a green banner appearing to report successful data submission.



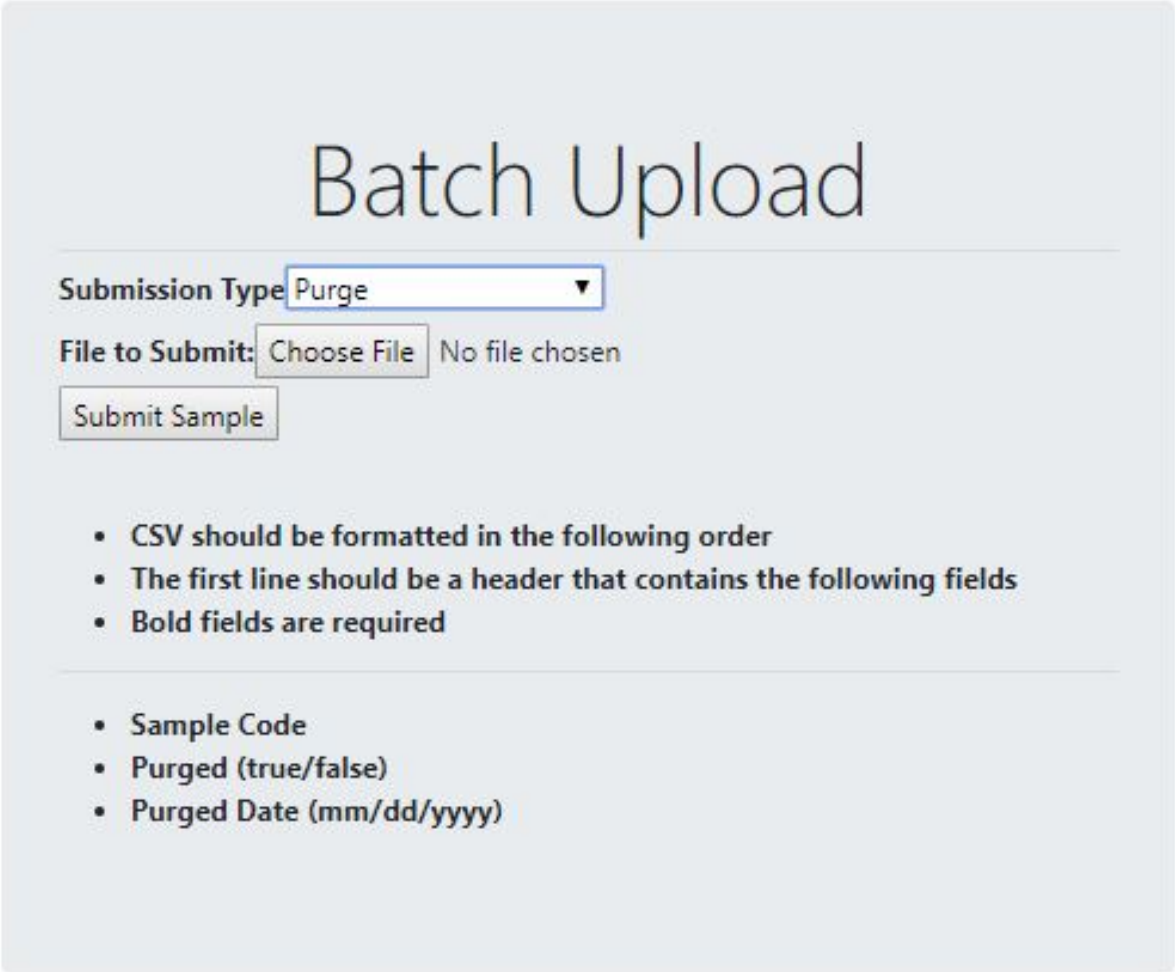
Quick Add: Purge

Sample Code

Purged

Date Purged

Figure 11. Quick Add: Purge



Batch Upload

Submission Type: **Purge**

File to Submit: **Choose File** No file chosen

Submit Sample

- CSV should be formatted in the following order
- The first line should be a header that contains the following fields
- Bold fields are required

- **Sample Code**
- **Purged (true/false)**
- **Purged Date (mm/dd/yyyy)**

Figure 12. Batch Upload Purge

SharePoint

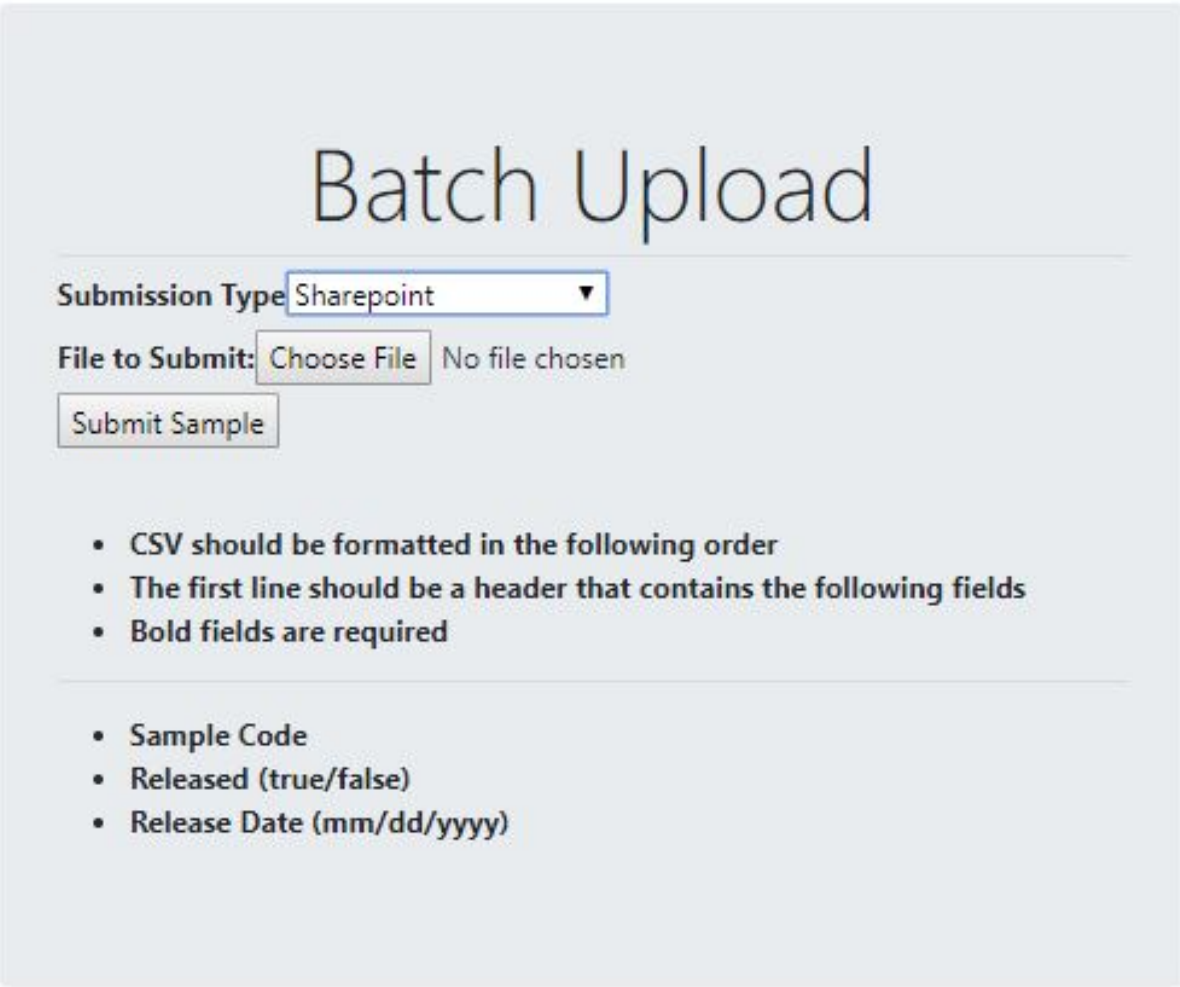
Distribution of mussel early detection and monitoring results from the EcoLab to clients, partners, and stakeholders is performed through release on a secure custom SharePoint database and associated website. The “SharePoint” dialog is used to record when analysis results are released to clients on the mussel detection SharePoint website. Fields included in the Purge data are:

- **Sample Code**
- **Released**
- **Date Released**

All samples fields are required. “Sample Code” field refers to the unique numerical ID assigned when Sample data are submitted to the database, as described above. “Released” refers to whether the sample data has been uploaded and released on the SharePoint site, and can be “True” or “False”. “Date Released” refers to the date the sample data were uploaded to the SharePoint site and clients were notified.

Because SharePoint data are always handled in csv files, “SharePoint” data can only be entered through the Batch Upload dialog (Figure 13).

SharePoint data submission is finalized as described above for Batch Upload of Sample data, with a green banner appearing to report successful data submission.



The screenshot shows a web-based interface titled "Batch Upload". Below the title, there is a "Submission Type" dropdown menu with "Sharepoint" selected. To the right of the dropdown is a "File to Submit:" label, followed by a "Choose File" button and the text "No file chosen". Below these elements is a "Submit Sample" button. Further down, there are two bulleted lists. The first list contains three items: "CSV should be formatted in the following order", "The first line should be a header that contains the following fields", and "Bold fields are required". The second list contains three items: "Sample Code", "Released (true/false)", and "Release Date (mm/dd/yyyy)".

Batch Upload

Submission Type: **Sharepoint**

File to Submit: **Choose File** No file chosen

Submit Sample

- CSV should be formatted in the following order
- The first line should be a header that contains the following fields
- Bold fields are required

- **Sample Code**
- **Released (true/false)**
- **Release Date (mm/dd/yyyy)**

Figure 13. Batch Upload SharePoint

Sample Code and Barcode tracking

As part of sample processing in the EcoLab, a barcode label is affixed to each sample after it is logged in. When samples are set up in settling cones second barcode label is affixed to a beaker containing a collection test-tube for the bottom 15ml of the settled sample. The 1D barcode on these labels encodes the “Sample Code” and can be scanned with a wired or Bluetooth-enabled barcode scanner compatible with the computer or mobile device used to access the database. Scanning this code when the cursor is in the “Sample Code” text box of the Quick Add dialogs for “Sample Prep”, “Microscopy”, “PCR and Sequencing”, or “Purge” simplifies entry of the Sample Code and minimizes the potential for errors associated with manual input. Generation of barcodes from a “Sample Report” is described below.

Data viewing

Waterbodies and Locations

Selection of the appropriate waterbody and location corresponding to a sample during Sample login is key to the integrity of the database, reporting of results to clients, and future data analysis. Selection of the appropriate waterbody and location can be challenging. Some waterbodies are referred to by multiple name variations or even more than one name. Likewise, sampling locations may have more than one name, no formal name, or samples may only be given an alphanumeric code for the sampling location.

Waterbody and location name can be checked against a master list available by following a hyperlink labeled “Click here to look them up.”, which is in the Batch Upload dialog box when “Sample” is selected from the dropdown menu. The linked “Locations list” displays all waterbodies and locations, along with geographic coordinates (Figure 14). Each Waterbody and Location name is also a hyperlink.

Locations list								
Waterbody Name	Waterbody ID	Location Name	Location ID	State	Latitude	Longitude	Locmetadata	Createdate Actions
ABIQUIU RESERVOIR	389	DAM INLET	1	NM	36.238	-106.429	GOOGLE EARTH	2017-08-09 show edit
ABIQUIU RESERVOIR	389	DAM OUTLET	2	NM	36.24	-106.422	GOOGLE EARTH	2017-08-09 show edit
ABIQUIU RESERVOIR	389	UNKNOWN	3	NM	36.253	-106.445	GOOGLE EARTH	2017-08-09 show edit
ADAMS-MCGILL RESERVOIR	404	UNKNOWN	4	NV	38.377	-115.108	GOOGLE EARTH	2017-08-09 show edit
ADOBE CREEK RESERVOIR	58	BOAT RAMP	5	CO	38.208	-105.452	GPS	2017-08-09 show edit

Figure 14. Locations list

For Waterbody names the search function in the browser can be a useful method for identifying the appropriate name in the waterbody. Some waterbodies are referred to as both “Lake” and “Reservoir”, or “Lake” may be placed before or after the unique proper name. For example, “Lake Granby” may sometimes be referred to as “Granby Lake” or “Granby Reservoir”. Searching for “Granby” will identify the appropriate Waterbody name used in the database. Checking the state where the Waterbody is located and the sample was collected is also important, because in some cases two different Waterbodies share elements of the same proper name. For example, there are two Waterbodies names “Clear Lake” in the database, one in Oregon and one in Utah. For disambiguation in the database these have been assigned the Waterbody names “Clear lake (OR)” and “Clear Lake (UT)”. For Waterbodies where two different names are in common usage, both have been included in the Waterbody name, with the Reclamation reference name followed by the alternate name in parentheses. For example, the waterbody formed by Tiber Dam in Montana is officially called “Lake Elwell” by Reclamation, but is locally referred to as “Tiber Reservoir”. The Waterbody name in the database is therefore labelled “Lake Elwell (Tiber Reservoir)” to aid in identification and minimize confusion.

The Waterbody link leads to a list of information for the Waterbody, as well as all Locations associated with that waterbody (Figure 15). The sampling location provided by the sample

collector can be compared to Location names already in the database. If geographic coordinates are provided by the collector these can also be compared to geographic coordinates for Locations in the database. If a geographic location for sample collection is provided and does not match any of the Locations currently in the database, and new Location entry can be generated. If the sample name does not match a Location in the database, and no geographic coordinate data are provided, or the provided coordinate data appear to be incorrect, the sample Location can be selected as “Unknown”. If an “Unknown” Location is not available for the chosen Waterbody, one can be generated, with the geographic coordinates set to a location near the midpoint of the Waterbody, as selected in a mapping program such as Google Earth.

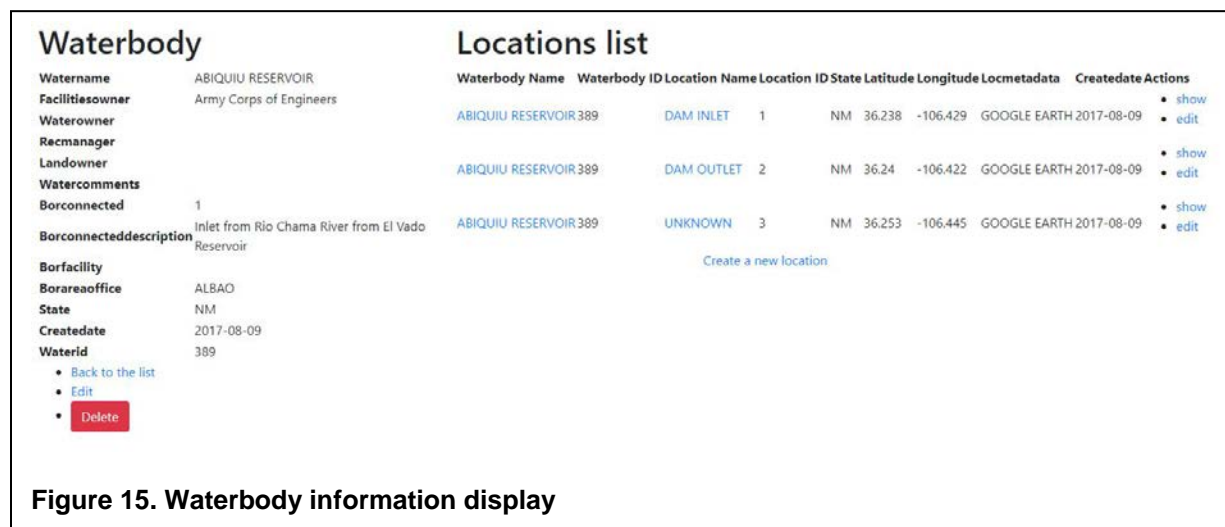


Figure 15. Waterbody information display

Sample data

Data for any individual sample can be accessed using the “Edit Sample” dialog box in the lower right corner of the homepage. Entering the unique numerical “Sample Code” and hitting “Go” will take the user to a page with tabular presentation of “Sample”, “Sample Prep”, “Microscopy”, and “PCR and Microscopy” for the sample (Figure 16). Each of these samples can be edited or deleted using buttons at the bottom of the page.

The “Edit Sample” dialog box also contains dropdown menus labeled “By Location” and “By Waterbody”. Selecting a Waterbody and Location from the “By Location” menu takes the user to a page containing data on the Location and a list of all samples in the database corresponding to that Location. Selecting the Sample Code for any of these samples takes the user to the sample data page, as described above. Selecting a Waterbody from the “By Waterbody” menu takes the user to a page containing data on the Waterbody, and a list of all Locations corresponding to the Waterbody. Selecting any of the listed Locations takes the user to that specific Location page, as described above.

Reports and data export

Three interactive dialogs have been developed to query the database with specific parameters and to produce a downloadable report in a csv file. A dialog to generate these reports is accessed by selecting the “Reports” link at the top of the homepage.

Home
Reports
Visualization

Mussels Database Management

Sample

Sample Code	J190033
Location	BOAT RAMP
Woid	SRP 2019
Water Body	SAGUARO LAKE
Create Date	2019-04-26
Year Code	J
Sampler Location	BOAT LAUNCH
Sample Date	2019-04-17
Date Received	2019-04-19
Arrival 7 Days Or Less	False
Sampler	USBR JIMMY HASTINGS
Sample Latitude	
Sample Longitude	
Tow Type	
Tow Count	5
Tow Length	9
Tow Total	45
Net Open Area	
Tow Volume	
Net Mesh Size	
Tow Cmnt	
Login Name	Annie Quattlebaum
Lab Project Manager	Diane Minch
Sample Cmnt	
Ph	7.5
Ph 7 Or Higher	True
Analysis Type	Veliger Count
Purged	True
Purged Date	2019-08-09

ListEditDelete

Microscopy

Microscopy Id	5566
Sample Code	J190033
Create Date	2019-06-10
Date Analyzed	2019-05-23
Analyst Name	Molly Maier
Count Total	0
Analysis Volume	15
Microscopy Result Type	Negative
Notes	
Asian Clams Presence Level	None
Glochidia Presence Level	None
Ostracods Presence Level	Medium
Pollen Presence Level	None
Sem Result Type	Not Tested
Seeds Presence Level	None

ListEditDelete

PCR and Sequencing

Pcr Sequencing Id	5619
Samplecode	J190033
Create Date	2019-06-20
Pcr Notes	
Dna Sequencingnotes	
Forward Sequence	
Reverse Sequence	
Dna Sequencing Result Type	Not Tested
Quagga Mussel Pcr Type	Not Tested
Zebra Mussel Pcr Type	Not Tested

ListEditDelete

Sample Prep

Sample Prep Id	35
Sample Code	J190033
Settle Start	2019-04-30
Settle End	2019-05-01
Volume	300
Color	None
Debris Type	None
Clarity Type	Clear
Create Date	2019-04-30

ListEditDelete

Figure 16. Sample data page

Sample report

A “Sample report” is designed to be created after a batch of samples are logged into the database using the “Sample” dialog. It creates a csv file containing information including the sample Waterbody, Location, and sampling date, and this csv file can be accessed in the Dymo Label standalone application to print barcode labels for sample tracking. Sample reports can be generated by date, with options being:

- Sample Date Year
- Date Code
- Today

“Today” returns only samples entered into the database on the same day the report is generated. This option is used most frequently, as labels are printed as soon as samples have been entered.

SharePoint report

Distribution of mussel early detection and monitoring results from the EcoLab to clients, partners, and stakeholders is performed through release on a secure custom SharePoint database. The “SharePoint report” dialog is used to generate a csv file formatted for direct upload to the SharePoint site. These SharePoint reports include samples for the selected year, where “Microscopy” data has been entered in the database, and “SharePoint: Released” has not been set to “True”.

Custom report

The “Custom report” dialog is designed for retrieval of data, particularly “Microscopy” and “PCR and Sequencing” results, matching a selected set of temporal and/or geographic parameters.

Conclusions and Recommendations for Next Steps

Conclusions

During this project a relational database and secure web portal have been developed, which allow for centralization storage of EcoLab data on invasive mussel detection and monitoring, as well as efficient entry of new data. Data in the database are linked to georeferenced Waterbodies and locations, and these geographic locations have standardized names. The system is designed for easy and efficient generation of report files, which support sample tracking, reporting to clients, and other data analyses.

Recommendations for Next Steps

RISE integration

The proposed scope of this project initially included the goal of providing open-access to data collected in the developed database. During the project, the Reclamation Information Sharing Environment (RISE) platform was identified as the best option for such data release. The RISE system has the potential for development of visualization tools, such as mapping and charting, that would increase the utility. It would also allow integration of EcoLab mussel data with mussel detection data collected independently by Reclamation’s Pacific Northwest Regional Laboratory, as well as comparison to other Reclamation datasets, such as water quality and hydrology. Finally, because the RISE platform has already been granted Authority to Operate, data release would be greatly streamlined as compared with development of a standalone open-access system, which would have to undergo an independent ATO review.

Because the RISE platform remains in development, transfer of data from the EcoLab mussel database to RISE was not feasible during the current project. Funding for a follow-on project dedicated to mussel data integration in RISE has been submitted to Reclamation’s Science and Technology office and is currently undergoing review.

Data sensitivity

Mussel detection data have significant ramifications for waterbodies. A positive finding may trigger increased expenditures for mitigation and watercraft inspection and could form the basis for restrictions on recreational access. For all these reasons mussel detection data generated by the EcoLab are considered sensitive, and results are distributed through a secure SharePoint site, as discussed above. When a positive finding is made, the Aquatic Invasive Species (AIS) coordinator for the state with the effected waterbody has discretion to decide whether or not the public is notified of the finding, based on their criteria for what constitutes a “positive” finding. This generally requires a positive finding by both microscopy and PCR. For this reason, there may be cases where the EcoLab has reported a sample as positive but the state AIS coordinator has not made the result public and has not labeled the waterbody as “suspect” or “positive”.

With regards to integration of EcoLab mussel detection data in RISE, the potential sensitivity of these data must be a primary consideration. Discussions between EcoLab staff and state AIS coordinators regarding these issues have already begun and will continue throughout the project if funding from Reclamation’s Science and Technology Program is approved.

