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Taxonomic Results and Data Entry

1. SCOPE AND APPLICATION

1.1. This method details the process by which taxonomic results are entered into the DEP Laboratory Information Management System (LIMS) and the updated DEP Statewide Biological Database (SBIO). Use of this SOP indicates that the user has been trained in the use of the DEP LIMS and/or SBIO, whichever is needed for the type of entry being performed.

1.2. This method is to be used for all quantitative or qualitative macroinvertebrate, periphyton or phytoplankton samples with LIMS test codes beginning with “MI”, “PRN”, PKD”, “DTM”, “DTY”, "ALGAL" or "BLOOM".

1.3. This SOP is not meant to be an in-depth SOP on the functionality and use of either LIMS or SBIO.

2. SUMMARY OF METHOD

2.1. Taxonomic data are entered, verified and marked complete in the Statewide Biological Database (SBIO). An SBIO report is generated for ALGAL-ID and BLOOM-ID test codes. The taxonomic result of a macroinvertebrate (the number of taxa and SCI score, if applicable) or algal sample (the number of taxa) is entered into LIMS. For ALGAL-ID and BLOOM-ID test codes, the class of the dominant taxon is entered as the LIMS result with a comment stating the dominant taxon/taxa. The sample result in LIMS is then compared to the SBIO report to verify that the sample results match. The LIMS verified sample result is then authorized. When all samples in a LIMS Job are authorized, the Job is authorized. When all Jobs in a LIMS Event have been authorized, the Event is certified. Upon event certification, a final LIMS Report is automatically generated and a notification email sent to the customer. Raw taxonomic data sheets are filed for storage.

3. APPARATUS AND EQUIPMENT

3.1. Completed algal or macroinvertebrate bench sheets: Because of the way algal and macroinvertebrate samples are analyzed, there will usually be bench sheets from several different jobs to enter into LIMS. It is not likely that an entire job will be finished at the same time. Data can be entered into SBIO upon completion of test analysis.

3.2. DEP Laboratories Laboratory Information Management System (LIMS): In order to enter results into LIMS, the User must have a username and password for LIMS and access to the module Laboratory/Technical/Results Editor. To receive this username and password, the User’s supervisor should request it using the Network/LIMS account module found on the DEP Laboratories Intranet site.

3.3. DEP Statewide Biological Database (SBIO): In order to enter data into SBIO, the User must have a username and password with at least “Data Entry” level access. To receive a username and password with that access, contact the DEP Laboratories SBIO

Database Administrator or place a message in the DEP Laboratories HelpDesk. LIMS→General→Help Desk.

4. SBIO DATA ENTRY PROCEDURE: Entry, verification, and authorization of taxonomic data in LIMS and SBIO is performed by individuals designated by the Taxonomy Supervisor.

4.1. Establish an SBIO sample for each station/date (Visit ID). Before taxonomic data can be entered in SBIO, the station (site) must exist or be set up in SBIO. If the station does not exist, notify the person responsible for station set-up. This person gathers the necessary information to establish a WIN/STORET # and sets up the station correctly in SBIO.

4.1.1. For all MI, DTM/DTY, PKD/PRN, and ALGAL-ID samples, except those collected by water management districts, the samplers set up the Visit ID. For BLOOM-RESP qualitative and quantitative algal samples, the taxonomy staff set up the Visit IDs.

4.2. Open SBIO with your username and password. Under the “Field Activities” tab, click “Station Visits”. A new window will open. Click the “new visit” button, and type in either the WIN/STORET number or Station Nickname in the “enter search criteria” box. Once it is located, highlight the correct station and then enter the sample date using the “visit date” box. Then select the following: survey, salinity type, and collector. You must enter data into all of these fields in order to generate a visit ID. Once all of this information is completed, hit save and the Visit ID will be generated. Record the SBIO Visit ID at the top of the bench sheet in the appropriate space provided.

4.2.1. When setting up a sample, if a message appears stating that there is already a sample with that same station and date, then that existing sample should be used. The sample being set up when this message was received should be cancelled out of, which will prevent a new visit ID from being established.

4.2.2. During sample set-up, the sample must be assigned to a survey. If no appropriate survey exists, contact the SBIO Database Administrator to create a new survey. The SBIO sample cannot be set up until the survey exists.

4.2.2.1. When a new survey is set up, make the selection whether or not there is periphyton or phytoplankton data and if so, that diatoms will not be incorporated and that wet taxa counts include unit counts, unless otherwise required for that specific project. If either of these parameters changes during the course of a project, they should be changed for the survey description in SBIO; older samples will not be affected, and samples from that date forward will carry new designations.

4.2.2.2. The survey is normally equivalent to the program or project for which a sample was collected.

4.2.2.3. If the sample is a BLOOM-RESP, the sample is set up under the Algal Complaint Survey. The box “Bloom Response?” is automatically checked.

4.3. To establish a new gear (BenthID, PeriID, or PhytoID) and enter data, go to "Lab Activities" and select either Algae or Invert Data Entry and QC. Use the Visit ID to establish a new gear ID for each analytical sample type (macrobenthos, periphyton, or phytoplankton). Click the "New" radio button. Duplicates or replicates taken at the same station/date that are to be considered separately are set up as individual gears with their own BenthID, PeriID or PhytoID. The exception to this is Hester-Dendy replicates, which are separate replicates, but have the same Visit ID and BenthID. For all other analyses, each replicate is entered as a replicate within the same gear and analyzed as one sample. For duplicates or replicates, record the BenthID, PeriID or PhytoID on the bench sheet that corresponds to that sample and enter a note in the comment section of SBIO that the sample is a duplicate or replicate. Differentiate between a field and lab duplicate. This information is important for those using the data.

4.3.1. Gears and data entry are often created and entered at the same time; however, a gear can be created and saved so data entry can occur at a later time.

4.3.2. The test code on the bench sheet will indicate which gear to select. In most cases, it is also labeled at the top of the bench sheet. Test codes beginning with MI are macroinvertebrates, PRN or DTM are periphyton, and PKD or DTY are phytoplankton.

4.3.3. Enter all applicable benchsheet information (metric, sample ID, sample type, analysis date, rep prep information, etc.).

4.4. Enter taxa. Navigate to appropriate Data Entry and QC form, select appropriate community type (algal only), "Existing," and Search by "Visit ID." To enter taxa, click the first box under the "scientific name" heading. The drop-down menu will be displayed. Type in the first few letters of the taxon you are entering and use the arrow keys to scroll down. Select the correct taxon and then press enter. Enter the number of individuals (invert), cells and units (algal) counted for each taxon identified.

4.4.1. If the Visit ID has been created but no data, such as prep information, have been entered, then a gear ID will not show up. Choose "new" and fill in the prep information, etc. (Step 4.3).

4.4.2. Occasionally, SBIO will give you an error "String does not allow duplicates". This can be one of two reasons: There has been a taxon added twice in SBIO, or more lines have been added than there are taxa. Simply delete the extra lines or combine the taxa numbers that were entered twice. SBIO will not allow you to save your entry until the corrections have been made.

4.4.3. For macroinvertebrate data, fill in the Rep 1 and 2 identifiers. Click the + sign at the bottom of the screen as many times as there are taxa to be entered.

4.4.4. If the target number of individuals for the sample gear was not met, add a comment to the BenthID/PeriID/PhytoID comment field explaining why the target was not reached. This comment should include what work was done on the sample gear and the outcome.

4.4.4.1. For invert, the comment may be that the entire sample gear was picked and not enough organisms were found to meet the target.

If it is determined that the sample gear was collected appropriately under the appropriate conditions, add the comment, “Was confirmed site sampled appropriately.” Add any possible explanations provided by the sampler.

4.4.4.2. For algal, the comment may be that the algae in the sample were sparse and after a certain amount of time, counting was discontinued.

4.4.5. For SCI samples, both replicates are entered at once by pressing the tab button once the taxon is found from the drop-down menu.

4.4.6. For algal data, wet algae and diatoms will be entered in two separate taxa lists. The Bacillariophyta count should be entered in the wet taxa list (number of frustules is used for unit and cell count) and in the “Total Counts” box.

4.4.6.1. If diatoms are to be incorporated, that should be done before marking the sample complete.

4.4.7. For BLOOM-RESP and HAB-ROUTNE samples, quantitative and qualitative algal data will be entered under the same Visit ID, but with different gears.

4.4.7.1. There will be no counts entered for these qualitative samples. A comment should be entered in the “Comments” box stating the dominant taxon found in the sample.

4.4.7.2. For marine/brackish Lyngbya and Lyngbya-like filamentous algae, the comment will be either “Dominant taxon was Lyngbya-like filamentous cyanobacteria (cf. Lyngbya wollei)” or “Dominant taxon was Lyngbya-like filamentous cyanobacteria (cf. Lyngbya majuscula).”

4.4.7.2.1. Include the species name in the presence/absence list so if the name changes in the future, a taxa list retrieval would provide the entered and the current name.

4.4.8. For quantitative periphyton samples, verify the calculated total area of the slides scraped recorded on the benchsheet BEFORE entering the value into the “Area Scraped” box. Verify that the area scraped was entered into SBIO correctly during data entry verification (Step 4.6.).

Note: The area of one slide is 3,750 mm2 front and back, excluding sides.
Total Area Scraped = (# slides) x 3,750 mm2

4.5. Once all taxa have been entered, make sure the individuals entered match the numbers calculated on the benchsheet. If not, any errors should be caught and corrected during the verification process. Click save. On the benchsheet, record the name of the person who entered the data and the date of data entry.

4.5.1. For Algal samples, match number of individuals and number of taxa to the Total Counts box.

4.5.2. For Macroinvertebrates, click on Rep Prep Times to see the total counts and total time. Make sure they all match what is written on the benchsheet.

4.5.2.1. To see the total number of individuals entered in SBIO, go to the first taxon entered and press tab until the number entered is visible for both replicates. This number should reflect both the total organisms on the benchsheet, and the total of wet and mounted individuals entered into the prep information

4.6. Verify data entry per SOP BG-01. Record the names and date of SBIO verification on the bench sheet. Give the bench sheets or folder to the person designated to mark samples complete in SBIO.

4.7. Mark the sample(s) complete in SBIO. Initial and date the bench sheet for SBIO completion.

4.7.1. If an error is detected within thirty days after a sample is marked complete, the sample gear can be marked incomplete, necessary changes made and verified, and re-marked complete. Add a comment to the gear denoting what changes were made so that if any calculated metrics or scores changed, anyone comparing the new metrics/scores to old metrics/scores will know the reason for the change.

4.7.2. If the thirty-day period has passed, the SBIO Database Administrator must be contacted. The change will be evaluated for potential impacts to calculated and/or reported metrics. In some cases, the change cannot be allowed, but a comment can be added to the sample. These changes will be evaluated on a case by case basis.

4.7.3. For algal samples, if diatoms should be incorporated, then reincorporate them before sample is marked complete again. Verify that resulting data are accurate, especially for taxa common to the Wet ID and Diatom ID.

4.8. To retrieve data for entry and/or verification in LIMS or for reporting to clients, use the Reports button.

4.8.1. How data is to be retrieved, formatted, and delivered to the client depends on the client's needs and will differ for different projects.

5. LIMS DATA ENTRY PROCEDURE: Changing status from "V" to "C"

5.1. In LIMS, open Laboratory/Technical/Results Editor.

5.2. Based on the samples to be entered, a single analyst and analysis date can be chosen from the drop-down boxes and the autofill box checked OR the autofill box can be unchecked.

5.3. From "Sort by", choose how the samples will be sorted. Make sure only the "V" "Test Status" is checked. From "Analysis Group", select the Bio-Peri/Phyto for algal samples or select the Bio-Invertebrate for invertebrate samples. Select the appropriate test code from "Select test". Select the appropriate LIMS ID(s) from "Select sample ID". If the LIMS ID(s) appear in the list, go to Step 5.4. If a particular LIMS ID does not appear in the list, use LIMS Browser to check the status of the sample. If a sample is status "W", create (see 5.3.1) and/or complete (see 5.3.2) the Preparation Worksheet for the sample.

5.3.1. If the test status in LIMS Browser is “W” (waiting for prep), use Laboratory/Technical/Prep Worksheet Manager to select “Create a prep worksheet” (the first icon in the tool bar or Worksheet/Create). Locate the sample by choosing the appropriate SOP from “Preparation ID”. Highlight the sample and assign the sample to the person who performed the prep. Click the black check mark at the top of the screen to create the worksheet and assign the prep step. Do this for each sample needing a result entry but which does not appear in Results Editor. If the LIMS ID does not show up in the list of worksheets to be created, it’s possible that it was already created, but not completed. If this is the case, close Prep Worksheet Manager and proceed to Step 5.3.2. Exit the Prep Worksheet Manager module.

5.3.2. After the sample prep is completed, go back into the Prep Worksheet Manager module and select “Open a prep worksheet logbook” (the fifth icon in the tool bar or Worksheet/Open Prep Worksheet). Highlight the appropriate worksheet ID, open the logbook for that worksheet (double click or use first icon), highlight the samples in the list, set the correct prep person and prep start date and completion dates/times, and then click Complete. Do this for all samples prepped. The sample should now appear in Results Editor when status “V” is chosen.

5.4. For each LIMS ID, click on the row to highlight it. Once the row is highlighted, click on a column header to enter information into that particular data field. Enter the data and click “OK”. Enter the analyst, analysis date, result, and any remarks (qualifier codes) or comments needed.

5.4.1. Data fields can be changed for multiple samples at a time by using the [Shift] or [Ctl] key on the computer keyboard and selecting multiple rows.

5.4.2. Analyst: enter the taxonomist who identified the wet portion of the sample (invert), diatoms (algal), and soft algae (algal).

Analysis Date: enter the date that all identifications were completed for that analysis.

Result: MI, DTM/DTY, PKD/PRM – Enter the total number of taxa as calculated in SBIO for the sample type. ALGAL-ID/BLOOM-ID – Enter the taxonomic class of the dominant taxon/taxa. If there are co-dominant classes, enter “Other.”

Remark (qualifier code): A complete list of LIMS qualifiers can be found in Chapter 62-160 F.A.C.

Comments: Enter a comment to explain a “No Result” entry, qualifier, or non-conformance report (NCR). ALGAL-ID/BLOOM-ID – Add one of the following comments:

The dominant taxon was [result].

The co-dominant taxa were [result] and [result].

There was no clear dominant taxon in the sample.

If there are co-dominant algal taxa in different classes, add the comment:

The co-dominant taxa were [result] ([class]) and [result] ([class]).

For marine/brackish Lyngbya and Lyngbya-like filamentous algae, the comment will be "The dominant taxon was a filamentous cyanobacteria (Lyngbya-like)."

Important: If an SCI comment is added to a LIMS result, it will overwrite any Taxa entry comments; therefore, combine the comments and use the same comment for both the Taxa and SCI components.

5.4.2.1. For Stream Condition Index (SCI) samples with 2 replicates, the result, analyst, and analysis date to be entered are those from replicate 2. Enter the SCI score generated by SBIO.

5.4.2.2. Samples with "No Result":

5.4.2.2.1. If the target number of individuals was not met in both replicates and the SCI cannot be generated, enter "No Result" and the "X" qualifier code in LIMS. Add the comment "too few individuals to calculate SCI" in the comment field. If all of the material in the sample was sorted, state that in the comment as well.

5.4.2.2.2. If a sample was received but not prepped enter "No Result" and add qualifier code "O" (the customer is not charged). Initiate a Non-conformance Report (NCR).

5.4.2.2.3. If a sample was prepped but not identified, enter "No Result" with no qualifier code (the customer is charged). Add a comment in the comment field stating the problem and that the customer was notified. Initiate an NCR if needed.

5.4.2.2.4. If the sample was prepped and identified but the result cannot be obtained for the scheduled test code, enter "No Result" with no qualifier code (the customer is charged). Add a comment in the comment field stating the problem and that the customer was notified. Example: "not enough material to reach target number of individuals."

5.4.2.2.5. For ALGAL and BLOOM test codes, "No Result" with an "O" qualifier is used if sample was unable to be analyzed due to analyst error, was improperly preserved, or the algae was degraded. The customer is notified, and an NCR is initiated, if needed.

5.4.2.2.6. A result of "No dominant taxon" is used when there is no dominant taxon identified for ALGAL and BLOOM test codes.

5.4.2.3. Check for any Non-conformance Reports (NCR) by clicking "NC" at the top of the screen. Read the NCR, if present, and click "Close". Modify remarks (qualifiers) and comments as needed.

5.4.2.3.1. If an NCR is directly connected to a sample, add a comment stating "See Non-conformance Report #[enter number here]" and add any appropriate qualifiers to the Remarks column.

5.4.2.4. Save results by highlighting all rows for samples entered and clicking the red check mark at the top of the screen. Initial and date each bench sheet for LIMS entry. The results can also be saved by entering [Ctrl+S] on the computer keyboard or choosing Result/Save from the Result Editor menu.

5.4.2.4.1. For algal, if all analyses are complete for the sample (both wet and diatom ID are complete or diatom ID is not being performed), the bench sheet is placed in the job folder so that staff know to discard the working aliquot of the sample. Only the working aliquot of the sample is discarded. For every sample, there is an archive prepared that will not be discarded.

If diatom analysis has not been performed but is planned, the bench sheet is placed in the job folder and given to the diatom taxonomists.

5.4.2.5. An SBIO report is needed to verify invertebrate analytical results and perform authorization in LIMS. See Step 4.8.

5.5. LIMS Sample Result Authorization: Changing status from "C" to "A"

5.5.1. In LIMS, open Laboratory/Technical/Results Editor. Check the "C" test status box. As in Step 5.3, choose the Analysis Group and select the appropriate test codes and sample IDs.

5.5.2. Per SOP BG-01, verify LIMS results with the SBIO report for the sample(s).

5.5.3. If any errors are found during verification, correct the information in LIMS Results Editor. Save corrections by clicking the red check mark at the top of the screen. Initial and date each bench sheet for LIMS verification.

5.5.4. Authorize the verified results by highlighting the samples and clicking the red "A" at the top of the screen. Authorization is performed by those designated by the Taxonomy Supervisor.

5.5.5. Once SBIO data entry and LIMS result entry for all samples in a job are completed, verified, and authorized, bench sheets are routed to their appropriate location per sample type for filing:

5.5.5.1. Invertebrate bench sheets are kept in the filing cabinet located in B205 or are filed by project in A216K.

5.5.5.2. Folders that contain algal data will be filed by year and project in the appropriately marked filing cabinets in the hallway next to A216K. Some of the older algae folders (sampled approximately before 2008) that have companion invertebrates are filed in A216K.

5.5.6. Once all the samples have been entered, verified, and authorized for a LIMS Job, the Taxonomy Supervisor will review and authorize the Job. When all Jobs have

been authorized in a LIMS Event, a LIMS report is automatically generated. A Biology Manager certifies the Event report and the top sheet is printed and filed in Biology. An electronic notification is sent to the customer.

6. REFERENCES

6.1. SOP BG-01, *Data Entry Verification*

Appendix of Changes

10/02/2009	Reformatted the layout following SOP LB-001. Added “Summary of Method” section.
09/27/2011	Minor wording changes to notes of steps 4.1.5, 4.1.6 and 4.3.7.
09/26/2014	Updated instructions for Prep Worksheet Manager, 4.1.6. Minor wording changes to indicate workflow without naming specific positions.
09/28/2015	Edited and renumbered steps to reflect updates and clarify procedure. Formatted for 508 compliance.
12/19/2016	Updated link to Invert Workload Tracker, added procedures for ALGAL and BLOOM test codes, and added procedure for SBIO2 sample set-up.
12/22/2017	Removed references to workload tracking spreadsheets. SBIO2 was designed to track analysis times and other data that Legacy SBIO did not track.
02/05/2019	Deleted Section 4.3.6.1 and 4.3.6.2 regarding Everglades data entry and diatom incorporation; Section 4.3.4 just for macroinvertebrate data entry and 4.3.5 just for algal data entry; removed references to original SBIO and referred only to SBIO2; some formatting changes.
06/20/2019	Edited Remark (qualifier code) in Section 4.1.4 to reflect changes made in 62-160.700 F.A.C.
06/17/2020	Changed “order” to “class” in algal section 4.1.4. Clarified instructions in section 4.1.3.1. Added specifics regarding replicate info in section 4.3.3. Changed “taxa” to “taxon” in section 4.3.4.3. Added additional comment language in section 4.3.10. Added link to HelpDesk in section 3.3.3. Updated benchsheet file locations for both Invert and Algal. Removed 4.3.5.5—replicate algal data entry.
03/23/2021	Added Step 4.3.5.3: Enter benchsheet information; verify calculation of area scraped and entry into SBIO; included the surface area of 1 slide and calculation for total area; replaced “SBIO2” with “SBIO.”
06/21/2021	Re-formatted SOP; changed the order of operations (previously, LIMS data entry described before SBIO; now, SBIO data entry described before LIMS)
07/08/2021	Some clarification added to sections 4.4 and 4.5.2