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 DEP Statewide Biological Database (SBIO), an updated version of which is now in use and hereafter will be referred to as SBIO2. Use of this SOP indicates that the user has been trained in the use of the DEP LIMS and/or SBIO2, 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 SBIO2.

2. SUMMARY OF METHOD

The taxonomic result of a macroinvertebrate or algal sample (the number of taxa) is entered into LIMS. The class of the dominant taxon is entered as the result for ALGAL-ID or BLOOM-ID test codes. Taxonomic data are entered, verified and marked complete in the Statewide Biological Database (SBIO2). A report is generated. The sample result in LIMS is then compared to the SBIO2 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, and a final LIMS Report is automatically generated, and a notification emailed 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, and it isn’t likely that an entire job will be finished at the same time. For an algal sample, both the wet and diatom components should be completed before data is entered in SBIO2. Traditionally, all algal bench sheets for a single job folder are completed before data are entered into SBIO2.

3.2 DEP Laboratories Laboratory Information Management System (LIMS)

In order to enter results (i.e. number of taxa) 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 (SBIO2)

In order to enter data into SBIO2, 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 SBIO2 Database Administrator or place a message in the DEP Laboratories HelpDesk. LIMS→General→Help Desk.4. Procedure

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Entry, verification, and authorization of taxonomic data in LIMS and SBIO2 is performed by individuals designated by the Taxonomy Supervisor.

4.1 LIMS Sample Result Entry – Changing status from "V" to "C":

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

4.1.2 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.

4.1.3 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 4.1.5. 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 4.1.3.1) and/or complete (see 4.1.3.2) the Preparation Worksheet for the sample.

Note: Multiple test codes and Sample ID's can be selected by using the [Shift] or [Ctrl] key on the computer keyboard and selecting multiple rows.

4.1.3.1 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 4.1.3.2. Exit the Prep Worksheet Manager module.

4.1.3.2 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.

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

Note: 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.

Note: For Stream Condition Index (SCI) samples with 2 replicates, the result, analyst, and analysis date to be entered are those from replicate 2.

Analyst: For invertebrate data, enter the taxonomist who identified the wet portion of the sample as the analyst.

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Analysis date: The date a sample was completed is the last date that all identifications were completed.

Result: Enter the total number of taxa, as calculated in SBIO2 for the sample type. Enter the taxonomic class of the dominant alga for ALGAL and BLOOM tests.

For "No Result":

- 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).
- 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.
- 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.

  For example, if the target number of individuals couldn't be reached, add the comment "not enough material to reach target number of individuals" in the comment field. More explanation as to why or what was done will be added in SBIO2.
- 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.
- A result of "No dominant taxon" is used when there is no dominant taxon identified for ALGAL and BLOOM test codes.

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 or a qualifier.

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

Note: Sometimes an NCR requires that a qualifier be attached to a result and/or a comment be entered to explain the NCR. Be sure to check each sample for an NCR.

4.1.6 Repeat Steps 4.1.4 to 4.1.5 until information for each sample ID has been entered.

4.1.7 Save the 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.

Note: The results can also be saved by entering [Ctrl+S] on the computer keyboard or choosing Result/Save from the Result Editor menu.

Note: 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

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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.

4.1.8 An SBIO2 report is needed to verify invertebrate analytical results and perform authorization in LIMS. See section 4.3.

4.2 LIMS Sample Result Authorization – Changing status from "C" to "A":

4.2.1 In LIMS, open Laboratory/Technical/Results Editor. Check the "C" test status box. As in step 4.1.4, choose the Analysis Group and select the appropriate test codes and sample ID's.

4.2.2 Per SOP BG-01, verify LIMS results with the SBIO2 report for the sample(s).

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

4.2.4 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.

4.2.5 Once LIMS entry and tracking entry are completed, bench sheets are routed to their appropriate location per sample type for filing:

- Invertebrate bench sheets are kept in the filing cabinet located in B205 or are filed by project in A216K.
- Folders that contain algal data will be filed by year and project in the appropriately marked 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.

4.2.6 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.

4.3 SBIO2 Data Entry

4.3.1 Before taxonomic data can be entered in SBIO2, the station (site) must exist or be set up in SBIO2. 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 SBIO2.

4.3.1.1 For all ALGAL-ID samples, except those collected by water management districts, the samplers set up the Visit ID. For BLOOM-ID and quantitative algal samples, the taxonomy staff sets up the Visit IDs.

4.3.2 Establish a SBIO2 sample for each station/date (Visit ID).

4.3.2.1 Open SBIO2 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

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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, sample types to collect, 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 WIN/STORET # and SBIO2 Visit ID at the top of the bench sheet in the appropriate space provided.

Note: 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.

4.3.2.2 During sample set-up, the sample must be assigned to a survey. If no appropriate survey exists, contact the SBIO2 Database Administrator to create a new survey. The SBIO2 sample cannot be set up until the survey exists.

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

Note: 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.

Note: Diatoms were incorporated and both counts (unit and cell) were performed in the Everglades and SFWMD projects. If either of these parameters changes during the course of a project, they should be changed for the survey description in SBIO2; older samples will not be affected, and samples from that date forward will carry new designations.

4.3.3 For each analytical sample type (macrobenthos, periphyton or phytoplankton), establish a new gear ID (BenthID, PeriID, or PhytoID) in SBIO2. 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 are Hester-Dendy replicates, which are separate replicates, but have the same Visit ID and Benth ID. During data entry, each replicate is entered as its own replicate, but they're contained in 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 SBIO2 that the sample is a duplicate or replicate. Differentiate between a field and lab duplicate. This information is important for those using the data.

Note: If the sample is a qualitative BLOOM-ID, the sample is set up under the Algal Complaint Survey. The box "Bloom Response?" is automatically checked. A comment should be added to state the dominant taxon or co-dominant taxa found in the sample. If there was not a dominant taxon in the sample, then that should be stated.

Note: For an Algal ID or Bloom ID sample, a comment should be entered stating the dominant taxa found in the sample.

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4.3.3.1 Double-click one of the blank lines under the appropriate gear (i.e. analytical sample type; macrobenthos, periphyton or phytoplankton). Enter the metric, sample type, and gear used. The sample is now set up and ready for taxonomic entry.

Note: The test code on the bench sheet will indicate analytical sample type. Test codes beginning with MI are macroinvertebrates, PRN or DTM are periphyton, and PKD or DTY are phytoplankton. It also is labeled at the top of the bench sheet in most cases.

4.3.4 For macroinvertebrate data select the appropriate visit ID-gear ID that corresponds to the sample needing taxonomic data entered. To find the appropriate SBIO2 Visit ID:

4.3.4.1 Login to SBIO2. Choose menu item “Lab Activities” and select Benthos.

4.3.4.2 For samples that have been completed and need data entry, the benchsheet is given to the appropriate staff to add the appropriate gear and set up the replicate information. This process changes the Visit ID from “New” to “Existing”. The benchsheet is then handed back to the person that will enter the data. Under “Lab Activities”, choose Benthos. To find the Visit ID for the sample which you are entering data, type it into the Search box. Make sure the “Visit ID” radio button is selected.

4.3.4.3 Make sure you fill in the Rep 1 and 2 identifiers. To enter taxa, press the + sign at the bottom of the screen as many times as there are taxa to be entered.

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

4.3.4.4 Enter all of the taxa on the benchsheet. Once that is complete, make sure the individuals entered match the numbers calculated on the benchsheet. If not, any errors should be caught during the verification process. Press save.

Note: Occasionally, SBIO2 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 SBIO2, or more lines have been added than there are taxa. Simply delete the extra lines or combine the taxa numbers that were entered twice. SBIO2 will not allow you to save your entry until the corrections have been made.

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

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.

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

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4.3.5 For algal data select the appropriate visit ID-gear ID that corresponds to the sample needing taxonomic data entered. To find the appropriate SBIO2 Visit ID:

4.3.5.1 Login to SBIO2. Choose menu item “Lab Activities” and select Algal Data Entry and QC.

4.3.5.2 For samples that have been completed and need data entry, the benchsheet is given to the appropriate staff to add the appropriate gear. The benchsheet is then handed back to the person that will enter the data. Under “Lab Activities”, choose Algal Data Entry and QC. To find the Visit ID for the sample which you are entering data, type it into the Search box. Make sure the “Visit ID” radio button is selected.

Note: If no taxa (or other data) have been entered search under “New”. If some taxa have been entered on either the Diatom side or the Phytoplankton side search under “Existing”. For Bloom IDs that will also have quantitative data under the same Visit ID you will search under “New” when it is time to enter the quantitative data (The Bloom ID data should already have been authorized and there will be no existing data under the Visit ID). This creates a new Algal ID number under the same Visit ID.

4.3.5.3 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 taxa you are entering, and use the arrow keys to scroll down. Select the correct taxon and then press enter.

4.3.5.4 Enter all of the taxa on the benchsheet. Once that is complete, make sure the individuals entered match the numbers calculated on the benchsheet. If not, any errors should be caught during the verification process. Press save.

Note: Algal count types (unit or both unit/cell) are set according to the survey. If a sample has unit and cell counts, a “B” for both should appear in the count type box in the upper right of the screen and these counts are entered in the appropriate field on the data entry screen. For samples having only unit counts, a “U” for unit will appear in the upper right part of the screen.

Note: The person designated to mark samples complete in SBIO2 will incorporate the diatoms before marking the sample complete.

Note: For Bacillariophyta the number is added to the wet taxa list from the benchsheet with the number of frustules being the value for unit and cell count. The number of Bacillariophyta is also added to the appropriate box above the taxa list.

Note: Occasionally, SBIO2 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 SBIO2, or more lines have been added than there are taxa. Simply delete the extra lines or combine the taxa numbers that were entered twice. SBIO2 will not allow you to save your entry until the corrections have been made.

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

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For periphyton or phytoplankton, this comment may be that the algae in the sample was sparse and after certain amount of time, counting was discontinued.

4.3.6 When finished entering all taxonomic data for a Visit ID-gear ID, click Save. Record the name and date for SBIO2 entry on the bench sheet.

4.3.7 Continue entering data following steps 4.3.4 and 4.3.5 until all bench sheets (separate or in folders) have been entered into the SBIO2 database.

4.3.8 Verify data entry per SOP BG-01. Record the names and date of SBIO2 verification on the bench sheet. Give the bench sheets or folder to the person designated to mark samples complete in SBIO2.

4.3.9 Mark the sample(s) complete in SBIO2. Initial and date the bench sheet for SBIO2 completion.

- 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.
- If the thirty-day period has passed, the SBIO2 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.

Note: For algal samples, diatoms should be reincorporated before sample is marked complete again. Verify that resulting data are accurate, especially for taxa common to the Wet ID and Diatom ID.

4.3.10 Retrieve data for entry and/or verification in LIMS or reporting to clients using the Reports button.

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

- For macroinvertebrate samples that require SCI score component to be entered in LIMS, enter the SCI score generated by SBIO2 and the date it was generated into LIMS per section 4.1.

Note: For SCI samples, 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.

Important: The SCI comment will overwrite the Taxa entry comment in LIMS, if there is one. Therefore, combine the comments and use the same comment for both the Taxa and SCI components.

5. REFERENCES

5.1 SOP BG-01, *Data Entry Verification*

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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.

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