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). 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

The taxonomic result of a macroinvertebrate or algal sample (the number of taxa) is entered into LIMS. The order of the dominant taxon is entered as the result for ALGAL or BLOOM test codes. Taxonomic data are entered, verified and marked complete in the Statewide Biological Database (SBIO). A report is generated. 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 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 complete before data is entered in SBIO. Traditionally, all algal bench sheets for a single job folder are completed before data are entered into SBIO.

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 (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.

4. PROCEDURE

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

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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 4.1.5.1) and/or complete (see 4.1.5.2) 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. 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.

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

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Result: Enter the total number of taxa, as calculated in SBIO for the sample type. Enter the taxonomic order 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 a 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 SBIO.
- A "No Result" entry indicates there was no dominant taxon in the sample for ALGAL and BLOOM test codes.

Remark (qualifier code): LIMS qualifier codes are one-letter codes such as 'A' denoting that the result is an average of more than one value. An "O" qualifier denotes that the analysis was not performed so the customer should not be charged (i.e. the sample was received by the lab and assigned a LIMS number, but was not prepped). A complete list of LIMS qualifier 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 a 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 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.

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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 SBIO 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 SBIO 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 filed by project in B205, A216K or A216Q.
- Algal folders that have companion macroinvertebrate data will be given to the Invertebrate group for filing. Folders that have only algal data will be filed in A216F by year and project.
- Algal folders are placed in the LIMS Event folder holding area located at the front of the Biology Section office. The contents of the folder will then be filed in the Event folder where it will remain until the LIMS report is certified.

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, designated Biology staff retrieve the Event folder from the holding area located at the front of the Biology Section office and a Biology Manager certifies the Event. A LIMS report is automatically generated and the top sheet is printed and filed in Biology. An electronic notification is sent to the customer.

4.3 SBIO/SBIO 2 Data Entry

4.3.1 Before taxonomic data can be entered in SBIO, the station (site) must exist or be set up in SBIO 2. If the station does not exist, notify the person responsible for station set-up. This person gathers the necessary information to establish a STORET # and set up the station correctly in SBIO.

4.3.2 Establish a SBIO sample for each station/date (Sample ID).

4.3.2.1 Open SBIO2 with your user name and password (it's the same for SBIO and SBIO2). Under the "Field Activities" tab, click "Station Visits". A new window will open. Click the "new visit" button, and type in either the 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, sample types to collect, and collector. You must enter data into all of these fields in order to generate a sample ID. Once all of this

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information is completed, hit save and the Sample ID will be generated Record the STORET # and SBIO Sample ID at the top of the bench sheet.

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 sample 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 SBIO 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. 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 SBIO; 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 SBIO. 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. 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.

Note: If the sample is a qualitative BLOOM-ID, the sample is set up under the Algal Complaint Survey. The box “Bloom Response?” should be checked. If a Caspio case number is available, enter the number into the Caspio field. 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 sample, a comment should be entered stating the dominant taxa found in the sample.

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 Select the appropriate Sample ID-gear ID that corresponds to the sample needing taxonomic data entered. To find the appropriate SBIO Sample ID:

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4.3.4.1 Login to SBIO. Choose menu item Samples/Samples (Ctrl + S).

4.3.4.2 Click [Find]. On the "Find Sample Data for:" screen, enter the appropriate information to retrieve desired sample(s). Alternately, if you have the SBIO Sample ID, click [Find by ID], and enter the SBIO Sample ID. You can also click [Find by LIMS ID] if the sample gear(s) had a LIMS number entered when the SBIO sample was created. When the list of sample(s) appears, double click the sample desired for data entry.

4.3.4.3 Under the appropriate gear type (macrobenthos, periphyton, or phytoplankton) for data entry, double-click on the row of the gear ID for which you are about to enter.

For periphyton samples, enter replicate data from the bench sheet by first clicking [No changes to main info] then clicking the [Add Rep Info] button. For phytoplankton samples, just click on the [Add Rep Info] button. Enter the data from the Wet ID Algal bench sheet.

Note: If a folder contains more than one replicate for a given sample ID, the number of replicates will have to be changed before data for the additional replicates can be entered.

Note: Regardless of whether the sample is quantitative or qualitative, all available replicate information should be entered as recorded on the bench sheet, including the number of diatoms in the Wet ID.

4.3.6 Enter the scientific name, the count, and the identifier for each taxon on the bench sheet.

- For macroinvertebrate data entry, Click [Add more taxa…]. Remember to change the identifier as appropriate for different replicates or for the mounted identifications if different from the person who identified the wet material.
- For algal data entry, Click [Add more taxa…] or [Add more diatoms…], whichever is appropriate. In general, the "Wet taxa" section is for the Wet ID data and the "Diatom" section is for the Diatom ID data; the count for Bacillariophyta will be included on the "Wet" side. For exceptions and specific Everglades algal sample instructions, see Steps 4.3.6.1 and 4.3.6.2.

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.

Refer to the survey information on the data entry screen to determine if diatoms should be incorporated. In general, diatoms are not to be incorporated for non-Everglades samples. "Incorporating" means that the relative proportions of the valves identified on the diatom slide are applied to the total diatom frustule count in the wet ID.

4.3.6.1 For qualitative Everglades samples [periphyton (QLEV)]: both wet and diatom taxa should be entered on the "Wet" side; the "Bacillariophyta" count from the wet ID bench sheet should not be entered as a wet taxon. Each diatom taxa count should be divided by two and that number (rounded up if

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necessary) should be entered into SBIO. If the number of diatoms for a particular taxon has a count of one, just enter one as the count. Note: Counts are divided by two in order to represent a diatom frustule since the count recorded on the bench sheet is a count of valves (2 values per frustule). Since this is a qualitative analysis, counts do not have to be exact. Relative proportions of taxa present are more important than absolute counts.

4.3.6.2 For quantitative Everglades samples [periphyton (QNEV) or phytoplankton]: wet taxa should be entered on the Wet side, and diatom taxa on the Diatom side; the "Bacillariophyta" count from the wet ID bench sheet should not be entered as a wet taxon; diatoms should be incorporated. Diatom counts (valves) should be entered as they appear on the bench sheet (i.e., do not divide by two).

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

4.3.7 When finished entering all taxonomic data for a Sample ID-gear ID, click [Save & Done]. Record the name and date for SBIO entry on the bench sheet.

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/PeriID/PhytoID 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 periphyton or phytoplankton, this comment may be that the algae in the sample was sparse and after certain amount of time, counting was discontinued.
- For macroinvertebrates, this comment may be that the entire sample gear was picked and not enough organisms were found to meet the target.

4.3.8 Continue entering data following steps 4.3.6 and 4.3.7 until all bench sheets (separate or in folders) have been entered into the SBIO database.

4.3.9 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.

4.3.10 Mark the sample(s) complete in SBIO. Initial and date the bench sheet for SBIO 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 SBIO Database Administrator must be contacted. The change will be evaluated for potential impacts to calculated and/or reported metrics. In some

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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.

4.3.11 Retrieve data for entry and/or verification in LIMS or reporting to clients using the Reports button on the Sample Information screen.

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 SBIO 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.

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*

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.

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