

## ***LQ 1000. LABORATORY QUALITY CONTROL***

1. INTRODUCTION: Use these procedures to support the sampling efforts described in the respective FS-series DEP SOPs as well as for related laboratory procedures described in the LT-series DEP SOPs indicated below.
2. SCOPE AND APPLICABILITY: Use these SOPs only for the indicated sampling efforts and supporting laboratory component operations. These SOPs apply to quality control procedures *not* specified in the NELAC Quality Systems document.

### ***LQ 2000. (RESERVED)***

### ***LQ 3000. (RESERVED)***

### ***LQ 4000. (RESERVED)***

### ***LQ 5000. (RESERVED)***

### ***LQ 6000. (RESERVED)***

## ***LQ 7000. QUALITY CONTROL FOR BIOLOGICAL COMMUNITY ANALYSIS***

The following DEP SOP sections specifically apply to activities performed using FS 7000 – FS 7400 and LT 7100 – LT 7500 as indicated, but may also be used for variations of these procedures used to produce other macroinvertebrate taxonomic data submitted to DEP. In addition, see LD 7200, Documentation for Biological Laboratory Quality Control.

### **LQ 7100. Laboratory Quality Control for Algal Identification**

Perform these quality control procedures when analyzing samples collected per FS 7200.

1. GENERAL REQUIREMENTS: Perform the following quality control activities for all taxonomic identifications.
  - 1.1. Maintain copies of appropriate taxonomic identification keys
  - 1.2. Meet an initial demonstration of proficiency
  - 1.3. Perform QC procedures listed below

#### **LQ 7110. INITIAL DEMONSTRATION OF PROFICIENCY**

Perform these quality control procedures to insure a new analyst has achieved a minimum proficiency of Algal identification.

1. GENERAL REQUIREMENTS:

- 1.1. Achieve 60% correct at the genus level for soft algae or 60% correct at the species level for Diatoms in the Consistency Identifications procedure (LQ 7130). A recommended target level of 80% correct is suggested.
- 1.2. The new analyst should re-identify a minimum of 10 samples previously identified by a proficient analyst.
2. Perform the following criteria with re-identified samples.
  - 2.1. Sample selection and preparation
    - 2.1.1. Samples to be re-identified for wet identification should have less than 40% diatoms in the original ID.
    - 2.1.2. Samples to be re-identified for wet identification or diatom identification should not be samples with very low densities or taxa counts in the original ID or samples that were "problem" samples in the original ID such as very dirty samples. These samples are difficult to achieve agreement on due to factors other than analyst proficiency.
    - 2.1.3. If the sample is identified using a settling chamber (e.g., Utermohl, Sedgewick Rafter, or Palmer-Maloney) and the integrity of the sample cannot be preserved long enough for a second identification to occur, the second analyst will prepare and settle a new aliquot of sample. Be sure to use the same dilution or concentration as the first analyst. If possible, use a counting chamber with the same cell depth as the first analyst. Identify and enumerate to the same counting endpoint (i.e., number of units or number of fields) as the first analyst.
    - 2.1.4. If the sample is identified using a semi-permanent or permanent slide, use the same permanent slide mount for the re-identification.
  - 2.2. Sample analysis
    - 2.2.1. After the new analyst has re-analyzed a sample, insure at least the targeted similarity (e.g., Bray-Curtis Similarity Index) was achieved.
      - 2.2.1.1. If the similarity cutoff is not met, combine taxa in the sample to the generic level. The goal of combining taxa to the generic level is to determine if the new analyst requires further training to differentiate algal units to species as compared to genus.
      - 2.2.1.2. If the QC has passed at the generic but not the specific level, compare the taxa lists from the two analysts. If there are differences in level of identification of a given taxon, target additional training to bring the analysts to the same level of identification. An inexperienced analyst may identify a taxon to a higher level than an experienced analyst. Pinpointing those taxa makes targeting additional training more effective and less time consuming.
    - 2.2.2. Continue with re-identifications until 10 samples have been successfully re-identified.
    - 2.2.3. After 10 re-identifications have been successfully completed, the newly-proficient analyst should have 10% of samples re-identified by another analyst until an additional 10 samples have successfully passed the similarity cutoff. The analyst should then have 5% of samples re-identified as outlined in LQ 7120.

## **LQ 7120. ONGOING QUALITY CONTROL**

Perform these quality control procedures to insure analyst maintain a minimum proficiency of Algal identification.

### **1. Perform the following criteria with ongoing quality control samples.**

#### **1.1. Sample selection and preparation**

1.1.1. When 20 samples of a particular type of sample have been analyzed, ask another analyst who also performs that type of identification to randomly choose a sample from the list.

1.1.2. Divide samples into four categories: freshwater periphyton, freshwater phytoplankton, marine periphyton, and marine phytoplankton.

1.1.3. If the sample is identified using a settling chamber (e.g., Utermohl, Sedgewick Rafter, or Palmer-Maloney) and the integrity of the sample cannot be preserved long enough for a second identification to occur, the second analyst will prepare and settle a new aliquot of sample. Be sure to use the same dilution or concentration as the first analyst. If possible, use a counting chamber with the same cell depth as the first analyst. Identify and enumerate to the same counting endpoint (i.e. number of units or number of fields) as the first analyst.

1.1.4. If the sample is identified using a semi-permanent or permanent slide, use the same permanent slide mount for the re-identification

#### **1.2. Sample analysis**

1.2.1. The QC analyst will identify the selected sample and compare the taxonomic identifications and unit counts.

1.2.2. If the analyst does not obtain the target similarity value (e.g., Bray-Curtis Similarity Index), then corrective action is required.

#### **1.3. Corrective Action**

1.3.1. If the similarity cutoff is not met, combine taxa in the sample to the generic level. The goal of combining taxa to the generic level is to determine if the analyst requires further training to differentiate algal units to species as compared to genus.

1.3.1.1. If the similarity of the sample passes the cutoff the QC has been successfully passed at the generic level.

1.3.2. If the QC has passed at the generic but not the specific level, compare the taxa lists from the two analysts. If there are differences in level of identification of a given taxon, target additional training to bring the analysts to the same level of identification.

1.3.3. If the QC does not pass at any level of comparison (genus vs. species), the sample must be re-identified by both analysts. Perform the following steps along with LQ 7140 to pinpoint taxa and/or counts that are problematic.

1.3.3.1. Compare the differences between taxa list. Those taxa contributing the highest percentage of the dissimilarity between samples should be examined to determine the source of the discrepancy (count, level of identification, etc.). All taxa contributing 5% or more of the total inter-sample dissimilarity should be examined.

1.3.3.2. If the sample passed the QC at some level, this list can be used to pinpoint areas where additional training is needed. If the sample did not pass the

QC at any level, this list should be reviewed and identifications corrected, and the sample should be re-identified by both analysts.

1.3.4. Re-identifications of any QC sample should be put through the steps outlined in this SOP to determine if the re-identification passed QC standards and if problem areas have been corrected.

## **LQ 7130. CONSISTENCY IDENTIFICATIONS**

Perform these quality control procedures to insure that multiple analysts maintain a minimum comparability of algal identification. This procedure tests the ability of multiple analysts to correctly and consistently identify a single organism. Laboratories with only one analyst are not required to routinely perform this procedure, but are encouraged to do so with external analysts.

1. Perform the following criteria with consistency identifications.

### **1.1. Sample selection and preparation**

1.1.1. Once a quarter, all analysts doing a particular type of identification participate in an internal consistency exercise.

1.1.2. The sample chosen for this quarterly exercise should be one that has not been analyzed previously.

1.1.3. The sample can be scanned by the group to ensure that it has enough taxa to complete the exercise.

1.1.4. Rotate samples chosen for this procedure through samples from periphyton (qualitative and quantitative) and phytoplankton.

1.1.5. A minimum of 50 specimens per quarter must be identified.

### **1.2. Sample analysis**

1.2.1. Each analyst takes a turn choosing one specimen to identify.

1.2.2. Without discussion, each analyst writes down his or her identification of the chosen specimen, identifying the specimen to the lowest level of which they are capable.

1.2.3. After everyone has identified the specimen, the analysts compare identifications and discuss any differences before moving on to the next specimen.

1.2.4. Once a consensus is reached, the "correct" identification is noted on the bench sheet.

1.2.4.1. "Correct" is the best identification as agreed upon by the group.

1.2.4.2. In some cases, it may be agreed that the most correct answer is to back up to a higher taxonomic level such as genus or family.

1.2.5. If a consensus cannot be reached, the analysts will note the lowest level at which they agree as the "correct" identification. These taxa are tracked so that those occurring more than once may be submitted to outside experts for resolution.

1.2.6. All identifications are compared in order to calculate percentages of incorrect IDs, correct IDs, and IDs that differ only in the level of taxonomy. The results of this comparison are used to identify areas where additional training is needed, outside verification is needed, or better references are needed. For each exercise, the target minimum goal is 60%.

1.2.7. If 60% of taxa are not identified correctly by an analyst, results should be re-examined to identify the source of the problem. Adjustments, further training and/or outside consultation may be required.

1.2.7.1. Compare microscopes and adjustments to assure that all equipment is working properly.

1.2.7.2. Level of identification (genus or species) as a source of misidentification should be rectified with additional training, or with standardization of level of identification, as appropriate.

1.2.7.3. Consistency identifications are an opportunity for all analysts to share their expertise with each other.

1.2.7.4. Perform the procedures in LQ 7140 to pinpoint where differences between analysts are occurring.

1.2.8. A cumulative list of taxa identified in consistency exercises will be kept. A combination of new and previously-identified taxa should be included in each consistency exercise, if possible. The purpose of keeping track of taxa examined is to ensure that a wide range of taxa are used in QA consistency exercises over time.

#### **LQ 7140. CORRECTIVE QUALITY CONTROL EXERCISES**

Perform these quality control procedures if re-identifications are consistently falling below the minimum target for similarity. This exercise is designed to assess differences among analysts or sample aliquots due to sample processing that might introduce bias.

1. Perform the following criteria ongoing quality control samples.

1.1. Sample selection and preparation

1.1.1. A person not participating in the exercise should choose and code three samples for analysis.

1.1.2. Samples should be of the same general type (phytoplankton, periphyton, etc.), but different samples may be used for diatom and soft algae analysis if they are identified via separate analyses.

1.1.3. Diatom samples should be chosen from those with high diatom abundance; soft algae samples should be chosen from those with high soft algae abundance. This can be determined with a preliminary scan of some sample material using the inverted microscope.

1.1.4. Analysts will not be told the identity of any sample analyzed in this exercise until the exercise is completed. The analyst will be told the type of sample (periphyton, phytoplankton, etc.) as this will determine how the sample is prepped and analyzed.

1.1.5. This exercise is performed separately for diatom and soft algae taxonomists if different analysts perform the two types of identification.

1.1.6. For each sample, prepare one slide or counting chamber and label it in such a way that the identity of the sample is undisclosed.

1.1.7. The person setting up the exercise should retain a list of the identity of the samples.

1.2. Sample analysis

1.2.1. Each analyst identifies each of the three samples twice for a total of six analyses per analyst. Record each analysis (identifications and counts) on a separate QC data sheet labeled by sample code and analysis number.

1.2.1.1. Perform analyses on each of the three samples before performing the second analysis of the three samples.

1.2.1.2. Do not refer to the first analysis of the same sample when performing the second analysis. Each analysis is designed to be independent.

1.2.2. After analysis of the duplicate samples, insure the similarity is at least the targeted minimum similarity.

1.2.2.1. There are 15 pair-wise similarity comparisons for each sample identified twice by three analysts.

1.2.2.2. If all intra-sample similarities are greater than the targeted minimum similarity, the intra-sample similarity portion of this procedure has been passed.

1.2.3. If the similarity cutoff is not met, combine taxa in the sample to the generic level. The goal of combining taxa to the generic level is to determine if the analyst requires further training to differentiate algal units to species as compared to genus.

1.2.4. If the intra-sample similarities are greater than the targeted minimum similarity, the QC has been successfully passed at the generic level.

1.2.5. If the intra-sample similarities do not pass the similarity cutoff at any level, stop the exercise and determine what taxa contribute most to the differences between counts.

1.2.6. Those taxa contributing the highest percentage of the dissimilarity between samples should be examined to determine the source of the discrepancy (count, level of identification, etc.). All taxa contributing 5% or more of the total inter-sample dissimilarity should be examined.

## **LQ 7200. (Reserved)**

## **LQ 7300. Laboratory Quality Control for Macrophyte Taxonomic Identification**

1. GENERAL REQUIREMENTS: Perform the following quality control activities for all taxonomic identifications.

- 1.1. Maintain copies of appropriate taxonomic identification keys
- 1.2. Establish and maintain a current reference specimen collection.
- 1.3. Retain extramural experts to verify identifications.

## **LQ 7310. LAKE VEGETATION INDEX (OPTIONAL)**

Perform these quality assurance procedures to insure taxonomist maintain a minimum proficiency for macrophyte identification. This procedure is optional and can be used as additional quality control in conjunction with the annual Lake Vegetation Index (LVI) consistency test described in FA 4330

1. QUALITY CONTROL FREQUENCY:

- 1.1. Perform the following quality control procedure for 5% of all original field samples with a minimum of 1 per year.
- 1.2. Calculate and retain cumulative performance data for each taxonomist.
2. QUALITY CONTROL ACCEPTANCE CRITERIA
  - 2.1. The target single-analyst cumulative correct identification rate is 90% of the total number of individual taxa (10% cumulative error rate).
  - 2.2. Verify a minimum of 30 distinct taxa per analyst per year.
  - 2.3. Verifying taxonomists must have a 90% cumulative correct identification rate.
3. QUALITY CONTROL PROCEDURE
  - 3.1. Randomly identify a sample for QC check before performing the actual sampling. Then, complete section 3.2, Field Verification below. Complete the laboratory verification (section 3.3) only if it is impractical to perform a field exercise (for example, if only 1 taxonomist is available). *The selected sample is defined as a QC sample.*
  - 3.2. Field Verification
    - 3.2.1. Two independent taxonomists perform the LVI as described in FS 7310 on the same 4 sections of the same lake. Return unknowns to laboratory for identification as described in the method. Be sure to keep each taxonomist's unknowns separate.
    - 3.2.2. Compare the Lake Vegetation Index Data Sheets of both taxonomists. If there is a disagreement with an identification, consult with the original taxonomist until a consensus is reached, utilizing additional experts as warranted.
    - 3.2.3. Record the identification of the field sample, the date of the QC check and the name of the taxonomist performing the QC check.
  - 3.3. Laboratory Verification
    - 3.3.1. Perform FS 7310 Lake Vegetation Index. NOTE: Collect and return to the laboratory all taxa that were identified in the field on the Lake Vegetation Index Data Sheet, Form FD 9000-7 (*i.e.*, recorded as being present) along with all unknowns.
    - 3.3.2. Have a second taxonomist identify all the taxa in the QC sample to the lowest practical taxonomic level.
    - 3.3.3. Record the presence of each taxon on the Lake Vegetation Index Data Sheet (Form FD 9000-7).
    - 3.3.4. Record the identification of the original field sample, the date of the QC check and the name of the taxonomist performing the QC check.
    - 3.3.5. Obtain the original Lake Vegetation Index Data Sheet (Form FD 9000-7) and compare with the data obtained from the QC check above. If there is a disagreement with an identification, consult with the original taxonomist until a consensus is reached, utilizing additional experts as warranted.
  - 3.4. Record all taxonomic discrepancies and comments associated with the QC check for the original field sample.
  - 3.5. Calculate and retain cumulative performance data for each taxonomist, per the criteria in section 2 above.

## **LQ 7400. Laboratory Quality Control for Macroinvertebrate Taxonomic Identification**

Perform these quality control procedures, as applicable, when using LT 7100 – LT 7300.

1. GENERAL REQUIREMENTS: Perform the following quality control activities for all taxonomic identifications.

- 1.1. Establish and maintain a current type specimen collection.
- 1.2. Retain extramural experts to verify identifications.
- 1.3. Participate in the DEP Taxonomic Quality Control Round Robin program. Participation is required for all taxonomists generating data to be entered into the DEP Statewide Biological Database (SBIO).

## **LQ 7410. LABORATORY QUALITY CONTROL FOR MACROINVERTEBRATE SORTING**

1. Perform the following quality control check on all samples sorted in the laboratory for LT 7200 (Stream Condition Index) and LT 7300 (Lake Condition Index).

- 1.1. After sorting all organisms from aliquots of an original field sample or subsample, separately retain the material remaining from each of the sorted aliquots for quality control (QC) checking.
- 1.2. Have a second taxonomist randomly select one of the sorted aliquots and perform a QC check for sorting efficiency by examining the aliquot and retrieving and counting any organisms found.
- 1.3. After all organisms sorted from the original field sample or subsample have been counted and identified, record the total number of organisms found in the sample or subsample and the total number found in all QC checks. Determine the sorting efficiency according to the formula in section 1.4 below.
- 1.4. Calculate the sorting efficiency for the sample or subsample using the following formula:

$$\text{Sorting efficiency (\%)} = [Total\ organism - QC\ organisms] \div Total\ organisms \times 100$$

Where:

Total organisms  $\equiv$  Total number of organisms counted (sorted) in the sample or subsample plus QC organisms

QC organisms  $\equiv$  Total number of organisms counted (sorted) in the QC check(s) for the aliquot(s)

- 1.5. Perform the sorting efficiency QC check (sections 1.1 – 1.3 above) for 10% of all aliquots processed for each original field sample or subsample.
2. Record the sorting efficiency for each analyst.
- 2.1. The target control limit for *cumulative* sorting efficiency is 95% as calculated in section 1.4 above. Take precautionary measures when single-analyst cumulative sorting efficiency falls below 95%.
  - 2.2. Take corrective action when single-analyst *cumulative* sorting efficiency falls below 90% as calculated in section 1.4 above.



## **LQ 7420.      LABORATORY QUALITY CONTROL FOR MACROINVERTEBRATE TAXONOMIC IDENTIFICATION**

Use the QC procedures in this section for all wet identifications and for all slide-mounted identifications of midges, worms and mites.

1. QUALITY CONTROL FREQUENCY: Perform the following quality control procedure for 5% of all original field samples or subsamples processed and enumerated.
2. QUALITY CONTROL ACCEPTANCE CRITERIA
  - 2.1. The target single-analyst cumulative correct identification rate is 95% of the total number of individual organisms and 95% of taxa identified in all samples or subsamples enumerated by the analyst (5% cumulative error rate).
  - 2.2. Similarly, control performance for analysts enumerating organisms for subgroups of taxonomic specialty according to the same criteria above.
3. QUALITY CONTROL PROCEDURE
  - 3.1. Randomly select 5% of the processed and enumerated original field samples or subsamples for QC checking. *The selected samples or subsamples are defined as QC samples.*
  - 3.2. Have a second taxonomist identify the organisms in the QC samples to the lowest practical taxonomic level using the most appropriate taxonomic key for each taxonomic group.
  - 3.3. Record the name and number of individual organisms identified for each taxon enumerated in the QC sample.
    - 3.3.1. Record the identification of the original field sample or subsample checked, the date of the QC check and the name of the taxonomist performing the QC check.
  - 3.4. Obtain the original field sample or subsample enumeration data and compare with the data obtained from the QC check above. If there is a disagreement with an identification, consult with the original taxonomist until a consensus is reached, utilizing additional experts as warranted.
  - 3.5. Record all taxonomic discrepancies and comments associated with the QC check for the original field sample or subsample.
  - 3.6. Calculate and retain cumulative performance data for each taxonomist according to each area of taxonomic proficiency, per the criteria in section 2 above.

## **LQ 8000.    REFERENCES (RESERVED)**