# Algal Identification Quality Control (QC) Procedures: Initial Demonstration of Proficiency, Ongoing/Individual QC, Group QC, and Annual QC

## 1. SCOPE AND APPLICATION

1.1 This SOP outlines procedures for quality control for diatom and wet algal identifications in four parts: Initial Demonstration of Proficiency (IDOP); Ongoing/Individual QC; Group QC; and Annual QC. Daily discussions are encouraged, particularly about samples that have new or different taxa, or ones that prompt questions. This SOP is to be used for samples with LIMS test codes BLOOM-ID, ALGAL-ID, and those that begin with DTM, DTY, PKD, and PRN.

## 2. SUMMARY OF METHOD

2.1 For the phytoplankton (PKD/DTY) and periphyton (PRN/DTM) analyses, new analysts first successfully re-identify 10 samples and pass QC (>70% similarity of taxa lists). Another analyst then conducts ongoing QC on 10% of the new analyst's samples until they have successfully passed (>70% similarity of taxa lists) 10 ongoing QC samples. The new analyst does not need to pass 10 re-identifications or 10 QCs in a row. After a total of 20 passing samples, IDOP is achieved and ongoing QC is conducted on 5% of samples.

2.2 For the BLOOM-ID and ALGAL-ID IDOP, new analysts successfully re-identify 20 consecutive samples with 100% accuracy for the dominant taxon or co-dominant taxa or the lack of dominance of any taxon. Similarity of taxa is also determined for other taxa in the sample. A combination of passing dominance QC and similarity QC is used to demonstrate proficiency. Ongoing QC for BLOOM-ID and ALGAL-ID is performed during each week that at least one sample of either type is received.

2.3 Analysts participate in Group QC exercises throughout the year as a means of ensuring that analysts are making comparable identifications and that they are continuing to educate themselves on common and uncommon taxa in Florida waters.

2.4 When there are two or more full-time analysts employed, they participate in an annual QC, for which they each analyze 3 samples twice and taxa lists are compared to determine intra-sample and inter-analyst variability (goal is >70% similarity between lists).

2.5 If any QC measure fails to pass, the source of the error(s) is determined and corrected. Further training may be conducted, or samples may be re-analyzed.

## 3. SOFTWARE, DATABASES, AND TECHNICAL DOCUMENTS

3.1 Primer-E software and documentation. Refer to SOP AB-15 for Primer-E software accessibility and instructions.

3.2 Microsoft Excel software

3.3 Statewide Biological Database (SBIO)

3.4 DEP Laboratory Information Management System (LIMS)

3.5 Blank algal identification bench sheet, printed from LIMS

3.6 Phytoplankton and Periphyton Algal Identification QC Log (Analyst-specific, stored in B227A)


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3.7 Algal sample(s)

3.8 Original algal identification bench sheet

3.8.1 The original bench sheet may be in one of several places depending on the stage of analysis or data entry in which the sample resides. Check with supervisor.

3.9 QC Spreadsheets, located in \\fldep1\DEAR\Labs\Lab5\Biology\AlgalCommon\QCSpreadsheets

3.9.1 Initial Demonstration of Proficiency (IDOP): QC-Training (diatom/wet) folder→analyst-specific folder; create sample-specific Excel file

3.9.2 Ongoing Quality Control: Working QC summary workbook (Wet or Diatom)

3.9.3 Group Quality Control: Group QC workbook

3.9.4 Annual QC Procedures: Annual QC Bench Sheets

## 4. QUALITY CONTROL METHODS

4.1 Phytoplankton and Periphyton Initial Demonstration of Proficiency

4.1.1 The new analyst must read and sign off on all Algal Biology SOP's.

4.1.2 The new employee re-identifies a minimum of 10 samples previously identified by a proficient analyst. Wet identification should be performed using SOP AB-03 for periphyton and SOP AB-05 for phytoplankton. Diatom identification should be performed using SOP AB-03.1 or AB-05.1. It is customary, but not required, for new analysts to be trained on periphyton before phytoplankton.

4.1.2.1 The new analyst's supervisor or designated trainer will choose samples to be re-identified. Samples to be re-identified for wet identification should have less than about 40% diatoms in the original ID.

4.1.2.1.1 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 70% agreement on due to factors other than analyst proficiency, so using them as proficiency samples "stacks the deck" against the new analyst.

4.1.2.2 If the sample is a phytoplankton or periphyton wet ID, the second analyst will prepare and settle a new aliquot of the sample, using the same dilution as the first analyst. If possible, a counting chamber with the same cell depth as that of the first analyst is used.

4.1.2.3 If the sample is a diatom sample, use the permanent slide mount.

4.1.2.4 New analysts do not need to successfully re-identify 10 samples in a row; however, the new analyst should not fail three re-identifications in a row, and the number of passing samples should be greater than the non-passing samples.

4.1.2.5 The person(s) training the new employee determines if the new analyst has spent adequate time examining previously identified samples in conjunction with the associated bench sheets and has shown a willingness to ask for help with identifications.


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4.1.3 For each sample, create an Excel spreadsheet with the taxonomic identifications and unit counts, either by typing the names and units or by an SBIO retrieval (see note).

Note: To assist data entry, the taxonomic data for each sample can be retrieved from SBIO (taxa as entered, by sample, matrix, with phylogeny for the particular algal type), saved using the LIMS# as the file name, and opened in Excel. This provides most of the taxa and counts along with the phylogeny that can be used to create an aggregation file (step 4.1.4). Some taxa names, unit counts, and phylogeny may need to be added to the SBIO list. Save the phylogeny as a separate file "_Agg" before the .xls extension or as worksheet within the file.

4.1.3.1 Open a previous training Excel file. Go to File→Save as… and rename it with new analyst, sample, and date information. Use the naming format of Trainee Analyst's Initials_Original Analyst's Initials_Quantitative/Qualitative_ Phytoplankton/Periphyton/Diatom_LIMS#_analysis date.

Example: A file for an initial proficiency re-identification performed by Jane A. Doe on a sample originally identified by John B. Deer on sample #123456, a qualitative phytoplankton sample, on March 17, 2008 would be named JAD_JBD_QL_PKD_123456_031708.xls.

4.1.3.1 Re-type the file name into the first cell of row one (A1).

4.1.3.3 Enter the taxa names into the first column ("Taxa").

4.1.3.2 Enter the original unit counts of the person being QC'ed into the second column ("Count A").

4.1.3.2.1 If a wet identification sample has cell counts, enter those into a separate spreadsheet. These counts will be used to assess if cells are being counted correctly but will not be used for purposes of assessing identification proficiency.

4.1.3.3 Enter the second set of QC unit counts (trainer's identifications) into the third column ("Count B").

4.1.3.4 Enter zeros where there is no count.

4.1.3.5 Save the spreadsheet.

4.1.4 Analyze each QC sample separately using PRIMER-E (per SOP AB-15). Conduct Bray-Curtis similarity analyses on these data, first with species level, non-transformed data.

4.1.4.1 If the Bray-Curtis similarity is >70%, the QC analysis has been completed satisfactorily (passed).

4.1.4.2 If the similarity value is <70%, repeat the analysis with a square root transformation.

4.1.4.2.1 Square root transformation lessens the effect of differences in counts (large numbers of Alga #1 in sample A vs. B) when there are large differences in the number of units among the taxa present.

4.1.4.2.2 If the similarity is still < 70%, repeat the analysis at genus-level using a taxa aggregation file.


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4.1.4.2.3 If the similarity is still < 70%, conduct the genus-level analysis with square root transformed data.

4.1.4.3 Record all similarity values, whether the QC passed at species or genus level, and the file name (.xls or _Agg.xls) on the QC bench sheet (paper), in the Excel taxa/unit file, and in the Excel QC Summary file.

4.1.5 If the QC has passed at the genus level but not at the species level, compare the taxa lists from the two analysts. If differences exist between taxa lists, give additional training to bring the analyst up to the same level of proficiency.

4.1.6 If the QC does not pass at any level of comparison (genus vs. species) or at any level of transformation, perform the SIMPER analysis in PRIMER (per SOP AB-15) to determine which taxa contributed the most to the differences in counts.

4.1.6.1 The SIMPER output lists the taxa in order of the greatest differences between the two counts. The Bray-Curtis dissimilarity between counts is one minus the Bray-Curtis similarity between counts. Each taxon that is not identical in the two samples contributes a portion of the inter-count dissimilarity.

4.1.6.2 Using the taxa list and Average Dissimilarity values generated from the SIMPER analysis, compare the differences between the taxa lists.

4.1.6.2.1 Those taxa contributing the highest percentage of the dissimilarity between samples (from the column labeled “Contrib%” on the Results Log) should be examined to determine the source of the discrepancy (count, level of identification, etc.).

4.1.6.2.2 All taxa contributing 5% or more of the total inter-sample dissimilarity should be examined.

4.1.6.2.3 The SIMPER results should be shown to the new analyst. The trainer and the new analyst should discuss any questionable identifications or counts while examining an aliquot of the sample in question.

4.1.6.2.3.1 Sometimes what appears to be a counting error may simply be due to the patchiness of the sample distribution (i.e. clumps of algae that are not broken up during sample processing). This can usually be determined by looking at more of the sample.

4.1.7 If the QC does not pass at any level of comparison or transformation, the sample cannot be counted towards the ten successful re-identifications needed to establish proficiency.

4.1.8 Continue with re-identifications and analysis (steps 4.1.2 through 4.1.7) until 10 samples have been successfully re-identified.

4.1.9 After 10 samples have been successfully re-identified, the analyst in training should have 10% of samples QC’d by another analyst until 10 additional samples have passed the 70% QC threshold.

4.1.9.1 After the second 10 samples have passed QC, the standard 5% of samples will be QC’d (see section 4.2 Ongoing Quality Control below).


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4.1.9.2 While new analysts do not need to successfully pass 10 QCs in a row, the new analyst should not fail three re-identifications in a row, and the number of passing samples should be greater than the non-passing samples.

4.1.10 Record the date of IDOP for the assigned Method in the LIMS training module.

4.2 BLOOM-ID and ALGAL-ID Initial Demonstration of Proficiency

4.2.1 After a new analyst has read and signed off on all Algal Biology SOPs and the person(s) training the new employee feels that the new analyst has spent adequate time re-examining samples, reviewing the literature, reference materials and microscope photos of common bloom forming and algal mat forming/periphytic species, the new employee should begin independent identification of samples previously identified by a proficient analyst.

4.2.2 Twenty consecutive samples should be re-identified for dominance with 100% accuracy. For each sample, the new analyst must correctly identify the dominant taxon, co-dominant taxa or the lack of dominance. If a sample is incorrectly identified or partially identified, the sequence should be restarted until 20 consecutive samples are identified. Prepare and perform ALGAL-ID and BLOOM-IDs per SOPs AB03 and SOP AB05.

4.2.2.1 BLOOM-IDs and ALGAL-IDs are not preserved. New analysts must re-identify samples as they arrive at the lab at the same time the official analysis is taking place. Analysts must take care not to share information about the dominance identification until the testing analyst can record their identification.

4.2.3 An Excel spreadsheet should be created in the following folder to document all passed and attempted re-identifications in X:\Labs\Lab5\Biology\AlgalCommon\QCSpreadsheets\QC-wet training.

4.2.3.1 The file should contain the LIMS sample number, the sample collection date, the new analyst's identification, the reported identification, and any relevant comments.

4.2.4 Other taxa present should also be identified by the new analyst. The other taxa should be entered into PRIMER-E along with the original identifier's other taxa and a similarities test run. A passing score is ≥70% similarity. Refer to Steps 4.1.4-4.1.9 for detailed passing criteria.

4.2.4.1 Samples to be re-identified for other taxa identification should not be samples with very low densities or low taxa counts in the original ID. These samples are difficult to achieve 70% agreement on due to factors other than analyst proficiency, so using them as proficiency samples "stacks the deck" against the new analyst. Around 7 or more other taxa should be acceptable for re-identifications.

4.2.4.2 New analysts do not need to successfully pass 20 other taxa present QCs in a row; however, the new analyst should not fail three re-identifications in a row, and the number of passing samples should be greater than the non-passing samples.

4.2.4.3 Document all passed and attempted other taxa re-identifications in the Excel spreadsheet located in X:\Labs\Lab5\Biology\AlgalCommon\QCSpreadsheets\QC-wet training.

4.2.4.4 The file should contain the LIMS sample number, the sample collection date, the new analyst's identification, the reported identification, any relevant comments, the similarity percentage, and pass/fail.


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4.2.5 When 20 samples in a row have been passed for dominance identifications, and 20 samples have passed for other taxa present, then a demonstration of proficiency has been shown for BLOOM-ID/ALGAL-ID analyses. Record the date of IDOP for the assigned Method in the LIMS training module.

4.3 Phytoplankton and Periphyton Ongoing Quality Control

4.3.1 Each taxonomist records in his/her assigned Phytoplankton and Periphyton Algal Identification QC Log (Wet or Diatom) all the samples he/she has analyzed.

4.3.2 When 20 samples of a particular analysis type have been processed, another analyst, who also performs that type of identification, is asked to randomly choose a sample from the list.

Example: If identifying diatoms, ask another analyst who does diatom identifications to perform the QC on that sample. If only one person performs that type of identification, he/she must QC his/her own sample.

4.3.3 The second analyst then identifies the selected sample following the appropriate SOP from step 4.1.2 and enters the data into an Excel spreadsheet following step 4.1.3.

4.3.3.1 Save diatom ID QC spreadsheets to \\fldep1\DEAR\Labs\Lab5\Biology\AlgalCommon\QCSpreadsheets\QC-diatom working.

4.3.3.2 Save wet ID QC spreadsheets to \\fldep1\DEAR\Labs\Lab5\Biology\AlgalCommon\QCSpreadsheets\QC-wet working.

4.3.3.3 Save the spreadsheet to the appropriate folder using the naming format of First Analyst's Initials_Second Analyst's Initials_Quantitative or Qualitative_ Phytoplankton or Periphyton_LIMS#_analysis date.

Example: A file for a QC performed by Jane A. Doe and John B. Deer on sample #123456, a qualitative phytoplankton sample, on March 17, 2008 would be named JAD_JBD_QL_PKD_123456_031708.xls.

4.3.4 PRIMER-E will be used to conduct QC analysis and record similarity values per steps 4.1.4 through 4.1.9.

4.3.4.1 Identifications determined to be incorrect are corrected on the bench sheet and in SBIO. If the supervisor determines that the sample should be re-identified by both analysts, the 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. If a sample is re-analyzed and the second set of analyses passes the QC, the second result should be reported in SBIO.

4.3.4.2 Within a sample, low algal density or high taxa evenness are two examples of why similarity may not meet the 70% threshold.

4.3.4.3 If the supervisor and analysts determine that the differences in the taxa lists are due to variability within the sample or level of experience rather than identifications, the sample does not need to be re-identified.

4.4 BLOOM-ID and ALGAL-ID Ongoing Quality Control


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4.4.1 Every week that at least one BLOOM-ID/ALGAL-ID sample is received, all analysts will QC a sample to identify the dominant taxon, co-dominant taxa, or lack of a dominant taxon. If only one sample is received, then only that sample will be QC'd. If more than one sample is received, then any sample may be QCed. Results are saved in the QC-BLOOM-ALGAL ID spreadsheet located in X:\Labs\Lab5\Biology\AlgalCommon\QCSpreadsheets\Bloom QC.

4.4.2 The same day or the next day, analysts will also identify other taxa in the sample BLOOM-ID/ALGAL-ID sample selected in 4.4.1. Primer-E is used to determine similarity. Results are saved in the QC-BLOOM-ALGAL ID-Full Taxa list [year] spreadsheet located in X:\Labs\Lab5\Biology\AlgalCommon\QCSpreadsheets\Bloom QC.

4.4.2.1 Because BLOOM-ID/ALGAL-ID samples are not preserved, it is preferable that all QCs should be performed the same day as the original analysis; however, during peak bloom season, there may not be enough time for the everything to be identified. In these situations, the QC may be performed the next morning.

4.5 Group Quality Control Exercises

4.5.1 Each month that at least one appropriate sample is analyzed (i.e., a sample that contains a variety of taxa, a sample that contains new or different taxa, or a sample that prompts questions), analysts participate in a practical internal exercise.

Note: Some projects, such as SFCANALS and BLOOM-RESP, contain very few taxa or contain a high quantity of the same taxa. While these may be used for the QC exercise, other projects, such as LAKESREF, may be more appropriate. Professional judgement will determine which samples are appropriate. Refer to Section 4.1.2 for more guidance.

4.5.2 Sitting around a single microscope, the analysts take turns choosing a specimen to identify. Without discussion, each analyst writes down his or her identification of the chosen specimen in the first column on the Algal Identification Group QC Bench Sheet, identifying the specimen to the lowest level of which s/he is capable.

4.5.2.1 Using a single microscope, instead of each analyst using their own, removes variability associated with differences in scopes and gives all analysts the same view of each taxon.

4.5.3 After everyone has identified the algae in the sample, the analysts compare identifications and discuss any differences.

4.5.3.1 Group QC sessions are an opportunity for all analysts to share their expertise with each other. There is no pass or fail.

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

4.5.3.2.1 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, for which this occurs frequently, can be submitted to outside experts for resolution.


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4.5.3.3 In some cases, the identifications and discussion take considerable time, especially with three or more analysts. It is not desirable to take more than one 8-hour period per month to complete this exercise. If possible, 25 different taxa should be identified.

4.5.4 Any incorrect identifications should be re-examined to identify the source of the problem. Adjustments, further training and/or outside consultation may be required.

4.5.4.1 Compare microscopes and adjustments to assure that all equipment is working properly. If analysts' microscopes differ, then their identifications may also.

4.5.4.2 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.

4.5.4.3 Keeping track of taxa examined ensures that a wide range of taxa are used in Group QC sessions over time. This list is in AlgalCommon /QCSpreadsheets/Group QC.

4.6 Annual QC Procedures

4.6.1 The Annual Exercise is designed to assess all variability (intra-analyst, inter-analyst, intra-sample, and inter-sample). The analysis of this exercise may help identify potential areas of bias within taxonomic data generated by the Algal Taxonomy Workgroup.

4.6.2 Detailed instructions are designed to apply to QC exercises with three analysts for either diatoms or soft algae. The design of this exercise gives the desired 16-18 data sets for statistical comparison, for which number of analysts is unimportant.

4.6.2.1 If only two analysts participate, four samples must be analyzed as described.

4.6.2.2 If four analysts participate, only two samples need to be analyzed.

4.6.3 The Taxonomy Supervisor should choose and code three samples from the backlog for analysis.

4.6.3.1 Samples for diatom and soft algae analysis should be of the same general type (phytoplankton, periphyton, Everglades, etc.), but different samples may be used.

4.6.3.2 The supervisor setting up the exercise should retain a list with the identity of the samples. Analysts will not be told the identity of any sample analyzed in this exercise until the exercise is completed. They will be told the type of sample (periphyton, phytoplankton, etc.) as this determines how the sample is prepped and analyzed.

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

4.6.2 For each sample, prepare one aliquot or permanent slide mount for analysis following SOP AB-03 for periphyton prep, SOP AB-02.01 for diatom prep, or SOP AB-05 for phytoplankton prep. Code aliquots or slides A-C so that the analyst cannot determine the identity of the individual sample. Aliquots and/or slides will be referred to as samples in the remainder of this SOP.

4.6.3 Every analyst identifies each of the three samples twice for a total of six analyses following SOP AB-03 for periphyton, SOP AB-05 for phytoplankton, and SOP AB-03.01 or AB-05.1 for diatoms. Record each analysis (identifications and counts) on a separate QC data sheet labeled by sample code and analysis number.


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4.6.3.1 Perform analyses on each of the three samples before performing the second analysis of the three samples. Do not refer to the first analysis of the same sample when performing the second analysis. Each analysis is designed to be independent.

4.6.4 In Excel enter the data from the analyses by entering a cumulative list of taxa found in the first column and entering the unit counts from each analysis into a separate column.

4.6.4.1 Code each column at the top by sample, analyst and replicate, using a single cell. Each data row should contain a unique taxon.

4.6.4.1.1 Examples of a unique analysis code for column headings would be A-MH-1 or C-MC-2.

4.6.4.2 Enter zero (0) for each sample where a taxon present in one analysis is absent in another.

4.6.4.3 Insert a row at the top of the spreadsheet and enter a title detailing the date and the exercise in the top left cell (A1).

4.6.4.3.1 Choose a title and file name that clearly identifies the QC exercise. An example of a title cell might be: Annual QC: samples EVGSLOU1234, WakSprg123 and RIVOAKTST, Analysts Hua, Chen and Dasher, May 23, 2003.

4.6.4.4 Using the title created, save the spreadsheet to: \\fldep1\DEAR\Labs\Lab5\Biology\AlgalCommon\QCSpreadsheets\Annual_QC.

4.6.4.5 Add additional information as needed.

4.6.5 Conduct Bray-Curtis similarity analyses in PRIMER-E (per SOP AB-15) with species- and genus-level taxa lists with and without square root transformation to determine the optimum percent similarity between counts.

4.6.5.1 Similarity between replicate counts of a single sample by a single analyst (intra-sample variability) and similarity between counts of the same sample by each pair of analysts (inter-analyst variability) will be examined.

4.6.5.2 If similarities are >70%, the QC exercise has passed.

4.6.5.3 If the intra-sample or inter-analyst similarities do not pass the 70% cutoff at species or genus level with square root transformation, conduct SIMPER analyses (per SOP AB-15) to determine which taxa contributed the most to the differences between counts.

4.6.5.4 After examining the similarity matrices, assign analyst and sample factors to the data in PRIMER-E and conduct ANOSIM analyses (per SOP AB-15) on the similarity matrices with the most passing tests.

4.6.5.5 If the criteria of the ANOSIM analyses are not met as specified in SOP AB-15, taxa lists and results of the SIMPER analysis should be examined to determine the causes of the differences, and further training and discussions should be targeted in those areas.

## 5. QUALITY CONTROL AND DOCUMENTATION

5.1 Use a pen with black ink for all logbook and bench sheet entries.


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5.2 DEP Laboratory Information Management System (LIMS)

5.3 Phytoplankton and Periphyton Algal Identification QC Log

5.4 QC bench sheets

5.5 To correct raw data entries, place a single line through the incorrect entry, write the corrected entry near the error, initial and date the correction. If the correction requires an explanation, write a comment and reference the error.

5.6 If a problem occurs during sample processing, submit a nonconformance report (NCR) describing the problem and the corrective action. To create a NCR, open LIMS and go to Laboratory/Administrative/Non-Conformance Report. For a decision tree regarding issuance of NCR's, refer to SOP LB-002.

5.7 See the DEP Laboratory Quality Manual Bureau Quality Manual

## 6. REFERENCES

6.1 DEP Laboratory Quality Manual, http://www.floridadep.org/labs/library/progplan.htm

6.2 SOP AB-03, *Periphyton Non-Diatom Taxonomic Analysis*

6.3 SOP AB-03.1, *Periphyton Diatom Species Proportional Counts*

6.4 SOP AB-05, *Phytoplankton Non-Diatom Taxonomic Analysis*

6.5 SOP AB-05.1, *Phytoplankton Diatom Identification and Species Proportional Counts*

6.6 SOP AB15, *Biological Community Comparisons using PRIMER_E Software*

6.7 LB-002, *Non-conformance Reporting System*

## Appendix of Changes:

03/17/2008 Combined the analysts' portions of AB09, AB09_01, AB09_02, and AB09_03 to create AB-14-1.0. Updated file names and location references for bench sheets and ongoing taxa lists. Added requirement for documenting ongoing proficiency. Added requirement to include date as part of filename for QC data files. Removed the requirement to keep a spreadsheet of results from the Monthly QC (formerly called Monthly Round Robin). Added Scope and Application, Summary, and Appendix of Significant Changes.

01/25/2011 Re-organized layout to reduce redundancy.

03/25/2015 Formatted for 508 compliance. Updated links.

09/20/2017 Added the initial demonstration of proficiency requirements for BLOOM-ID and ALGAL-ID samples; Added referenced SOPs to the References section and standardized SOP naming format.

10/23/2019 Changed "Quarterly QC" to "Annual QC" throughout the document. Changed "Monthly QC" to "Group QC" throughout and modified the language in that section to allow flexibility during times of high sample load, too few analysts, and lack of appropriate samples to QC. Added a new section for BLOOM-ID/ALGAL-ID QC. Reformatted


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