Analyses of Algal Bloom and Algal Identification Samples

(Modified from *Standard Methods 10200F* and *10900C*)

1. SCOPE AND APPLICATION

1.1 This method details the rules and procedures for identifying the dominant taxon (or co-dominant taxa) for non-diatom algae in phytoplankton and periphyton bloom samples.

1.2 This method is used for qualitative phytoplankton samples collected by the methods established in SOP FS 7000, *General Biological Community Sampling* (FS 7110, *Phytoplankton Bloom Sampling* and FS 7240, *Algal Mat Sampling for Taxonomic Identification or Toxin Analysis*).

1.3 This method is to be used for samples with Laboratory Information Management System (LIMS) test codes “BLOOM-ID” and “ALGAL-ID”.

1.4 This test was developed for identification only; no attempt should be made to determine whether a sample looks like it represents an algal bloom. If the customer determines more information is needed, a full wet ID (PKD-QN-C/DTY-QN-C analyses) should be scheduled.

2. SUMMARY OF METHOD

2.1 The BLOOM-ID or ALGAL-ID sample is checked out from Receiving and taken to the Algal Lab.

2.2 Phytoplankton samples are inverted gently to mix well. Mats and filamentous algae do not require mixing.

2.3 The phytoplankton method uses a modified version of SM 10200F.2. An Utermöhl counting chamber is used for algal identification, not for counting. Phytoplankton identifications in the wet material are performed at 400X to 450X magnifications. Dilutions are not required. Periphyton identifications are performed at 5X-40X magnifications.

2.4 The dominant taxon (or co-dominant taxa) is identified and reported.

3. APPARATUS AND EQUIPMENT

3.1 Inverted microscope (calibrated and maintained per SOP AB-01)
3.2 Disposable transfer pipettes
3.3 Glass slides
3.4 Utermöhl counting chamber
3.5 Cover slips, 24 x 60 mm
3.6 Petri dishes, 100 x 15 mm
3.7 Forceps
3.8 Filter paper to fit Petri dish
3.9 Laboratory counter
3.10 Labeling tape and marker
3.11 Safety equipment (see section 10)

4. REAGENTS AND CHEMICALS

4.1 Lugol’s Solution (prepared per SOP AB-07)

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5. SAMPLE COLLECTION AND PRESERVATION

5.1 Samples are collected, preserved, and delivered to the lab according to SOP FS 7000 (Section 7110, *Periphyton Bloom Sampling* and Section 7240, *Algal Mat Sampling for Taxonomic Identification or Toxin Analysis*).

6. SAMPLE RECEIPT AND HANDLING

6.1 BLOOM-ID and ALGAL-ID samples may arrive in any of a variety of container types. They can be collected when a bloom is observed during routine sampling events and for which sampling was not necessarily planned (i.e. scheduled in LIMS). They may also be collected when a quick response is needed due to a reported event and there is not time to schedule and receive a kit from the DEP Lab in Tallahassee.

6.2 Custody – Check Out

6.2.1 Periphyton: Follow SOP AB-10.1, Steps 6.1.1-6.1.3, for sample check-out procedures.

Phytoplankton: Follow SOP AB-11, Steps 6.1.1-6.1.3, for sample check-out procedures.

6.2.2 Open X:\Labs\BizhubScans\Receiving. Using the event ID on the job label, open the file with the submittal sheets for that event. Print the submittal sheets and place them in the labeled purple folder created in the previous step.

6.2.3 In LIMS\Custody\Print Prep Labels, select the **Algal Logbook Label** button and print one label (using the small SATO printer). Place the label in the *Algal Logbook*.

6.3 Custody – Check In

6.3.1 Follow SOP AB-10.1, Step 6.1.2 (periphyton) or SOP AB-11, Step 6.1.2 (phytoplankton), replacing **CheckOut button** with **CheckIn button**.

6.4 Preservation and Hold Times

6.4.1 Do not chemically preserve BLOOM-ID or ALGAL-ID samples.

6.4.1.1 If the sample needs to be kept after analysis, the sample can be preserved with buffered formalin (periphyton, prepared per SOP IZ-38) or Lugol's (phytoplankton) after the sample has been viewed by an analyst to determine the dominant species.

6.4.2 Per DEP SOP FS 7000, bloom samples should be kept in the dark and on ice. They have up to 36 hours from time of collection to be analyzed; however, SM 10200 allows for samples to be stored in a dark refrigerator if they are not going to be shipped immediately after collection or analyzed immediately upon receipt.

6.4.2.1 If the algae have not been kept cool or in the dark prior to receipt and they are degraded and unidentifiable, the customer will be contacted and informed that the sample cannot be analyzed. It will be reported as "No Result" with an "O" qualifier. A non-conformance report (NCR) will be created in LIMS.

7. SAMPLE ANALYSIS PROCEDURE

7.1 Periphyton and algal mat samples:

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7.1.1 Using forceps or gloved hands, place periphyton in a petri dish.

7.1.2 Take a small portion of the periphyton from the dish and place it on a slide. Place a coverslip on the slide.

7.1.3 Place the slide on the stage of the inverted microscope.

7.1.4 Use appropriate objectives to identify the periphyton to the lowest possible taxonomic level.

7.1.5 Repeat step 7.1.2 and analyze another portion of the sample. Repeat 2 -3 times to ensure the dominant taxon or co-dominant taxa have been represented. Other taxa may also be identified.

7.1.5.1 For other taxa present, scan the sample and identify the taxa to the lowest possible taxonomic level. If there is an abundance of taxa, record the most common taxa.

7.1.6 Record the dominant taxon or co-dominant taxa and the other taxa on the BLOOM-ID/ALGAL-ID benchsheet. If the sample was not periphyton, note that on the benchsheet. Complete the benchsheet with sample analysis information, including sample/sample container observations, microscope ID, magnification (power) used for identification, grid length, other taxa present, and total wet taxa.

7.1.6.1 Note any distinctive or unusual characteristics about the sample, such as color or smell.

7.1.6.2 Although grid length is not needed for analysis of qualitative samples, it is good practice to record it on the benchsheet.

7.2 Phytoplankton samples:

7.2.1 Mix the contents of the sample by gently inverting the centrifuge tube 3 or 4 times. If the gentle inverting of the tube does not dislodge all settled material from the bottom of the tube, invert a little more vigorously. Be careful of shaking the sample too vigorously, however, as this tends to break up some blue-green colonies.

7.2.2 Using a transfer pipette, fill the cell of the Utermöhl counting chamber with the well-mixed sample so that the liquid is barely higher than the sides of the Utermöhl counting chamber. Using a designated transfer pipette, add 1 drop of Lugol's solution to the counting chamber. Slide a cover slip sideways to cover the cell opening to ensure that no air bubbles are introduced.

7.2.3 Place filter paper (2 pieces) into a Petri dish and moisten with DI water. Carefully place the filled Utermöhl counting chamber onto the filter paper, and then cover the dish. Let the sample settle just long enough to allow proper identification, typically 1 hour.

Note: The Petri dish creates a moist environment while the sample is settling, thus avoiding the formation of an air bubble due to evaporation. Be sure that the filter paper is smooth and that the Petri dish is placed on a level surface during settling. Otherwise, the algal cells will tend to settle out on one side of the Utermöhl counting chamber and will not be evenly distributed.

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Note: In order to give quick turnaround on results, the sample may be identified before the sample has settled for 1 hour if the analyst determines accurate identification of the dominant taxon or co-dominant taxa is possible.

If the dominant taxon or co-dominant taxa have been identified after the sample has settled for less than 1 hour, the sample may need to settle for more time in order to identify other taxa. Use professional judgement.

7.2.4 Remove the counting chamber from the Petri dish and carefully wipe away any excess moisture, particularly on the underside. Place counting chamber on the stage of the inverted microscope.

Note: Be careful not to tip the counting chamber or bump it as this will cause the algal cells to dislodge from the bottom and float, making accurate identification difficult.

7.2.5 Position the stage so that the left edge of the counting chamber is in view. Move a short distance to the right and observe all algae within the Whipple grid. Always move from left to right across the cell during the progression to a new field. This eliminates the possibility of accidentally changing directions and viewing fields more than once.

7.2.6 At 400X magnification, identify non-diatom algae to the lowest possible taxonomic level. Only algae that appear to have been alive at the time of collection should be counted. Algal cells/colonies/filaments without chloroplasts should NOT be identified.

7.2.7 For BLOOM-ID and ALGAL-ID samples, there is no count performed. Simply scan the sample to determine the dominant taxon (or co-dominant taxa). Other taxa are also identified.

7.2.7.1 The sample should be well homogenized before analysis; however, some large colonies of taxa, such as *Microcystis* sp., do not homogenize easily. Also, samples with low taxa density or diversity, even if they have been well mixed, may not be fully represented in the chamber slide. Professional judgement is used to determine the dominant taxon or co-dominant taxa.

7.2.7.2 Some *Microcystis* sp. colonies are visible in the sample to the naked eye as floating algal specks. If *Microcystis* sp. specks are observed in the sample, and there are no other taxa present in high levels in the Utermöhl chamber, then *Microcystis* sp. is recorded as dominant. If specks are observed and another taxa is dominant in the Utermöhl chamber, then the taxa are recorded as co-dominant. In all cases, specks must be removed and mounted on a slide to determine identity.

7.2.7.3 If the sample appears to contain no dominant species or is cluttered with many taxa, counts may be performed as a method to help determine co-dominance. Three to five fields of view are counted. The number of algal units are recorded on the benchsheet for each of the most prevalent species for each field of view. An average is then calculated for each species identified in the fields. Comparing averages, professional judgement is used to determine which species are co-dominant, if any. There can only be two co-dominant taxa. If three or more taxa occur at nearly the same quantity, then “no clear dominance” is recorded on the benchsheet.

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7.2.7.4 For other taxa present, scan the sample and identify the taxa to the lowest possible taxonomic level. If there is an abundance of taxa, record the most common taxa.

7.2.8 Record the dominant taxon or co-dominant taxa and the other taxa on the BLOOM-ID/ALGAL-ID benchsheet. If there is no dominant taxon or if the sample is not algae, note that on the benchsheet. Complete the benchsheet with sample analysis information, including sample/sample container observations, settling time, microscope ID, magnification (power) used for identification, grid length, cell depth, other taxa present, and total wet taxa.

7.2.8.1 Note any scum, specks, discoloration, smell, or any other distinctive or unusual characteristics about the sample.

7.2.8.2 Although the cell depth and grid length are not needed for analysis of qualitative samples, it is good practice to record it on the benchsheet.

7.2.8.3 Do not count Bacillariophyta as a taxon.

7.2.8.4 Occasionally, a BLOOM-ID sample will require a dilution. Dilution information should be calculated and recorded. The information gives the analyst an overall idea of the density of the algae in the sample. Refer to SOP AB-05 for dilution calculation formulas.

Samples not requiring a dilution have a dilution factor of 1 (1x). It is recorded this way because of the way it is used in the density calculation cited in Standard Methods. This is also the density calculation used in the Statewide Biological Database.

7.2.9 Diatom identification is not normally performed for BLOOM-ID and ALGAL-ID samples. If diatoms are highly dominant and, after viewing the sample, it is suspected that the bloom taxon is a diatom, then the dominant diatom(s) are analyzed and identified after the non-diatom identification is completed.

7.3 In *Algal Sample* logbook, record the necessary information for the completed sample.

7.4 Entry, verification, and authorization of taxonomic data in SBIO and LIMS is performed per SOPs BG-01 and BG-03 and an SBIO report is generated.

7.5 The Taxonomy Manager verifies the information on the SBIO report and sends it to the appropriate customers as a .pdf file. The BLOOM-ID sample results are posted to the DEP Florida Algal Bloom website.

8. QUALITY CONTROL

8.1 QC of Taxonomic Identification is performed per SOP AB-14.

8.2 Refer to the Laboratory Quality Manual for all QC procedures and documentation.

9. DOCUMENTATION AND DATA ARCHIVAL

9.1 Use a pen with black ink for all logbook and benchsheet entries.

9.2 DEP Laboratory Information Management System (LIMS) and Statewide Biological Database (SBIO).

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9.3 Algal Logbook Labels printed from LIMS.

9.4 FDEP Algal Taxonomy Bloom-ID/Algal-ID benchsheet printed from LIMS.

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

9.6 If a problem occurs during sample processing, submit a nonconformance report (NCR) describing the problem and the corrective action. To create an 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.

10. SAFETY

10.1 Wear lab coat, latex or vinyl gloves, and eye protection as appropriate.

10.2 Use proper safety equipment, a lab hood or chemical ventilation system, and keep face away from open containers of chemicals. Work in a well-ventilated area.

10.3 Refer to the Material Safety Data Sheet (MSDS) for information about reagents and chemicals in this SOP.

10.4 Refer to the Laboratory Health and Safety Plan.

11. POLLUTION PREVENTION AND WASTE MANAGEMENT

11.1 Refer to the Laboratory Health and Safety Plan.

12. REFERENCES

12.1 DEP Laboratory Quality Manual, https://floridadep.gov/dear/florida-dep-laboratory/content/dep-laboratory-quality-assurance-manual-and-sops

12.2 DEP Laboratory Health and Safety Plan, https://www.fldepnet.org/content/dear/bureau-laboratories-safety-documents

12.3 *Standard Methods* 10200: *Plankton*; 10200F: *Phytoplankton Counting Techniques* (2017)

12.4 *Standard Methods* 10900: *Identification of Aquatic Organisms*; 10900C: *Key for Identification of Common Freshwater Algae (Plates 1A, 1B, 4A, 4B and 28-40)* (2017)

12.5 SOP AB-01, *Compound and Inverted Microscope Calibration*

12.6 SOP AB-07, *Preparation of Lugol's Solution*

12.7 SOP AB-10.1, *Periphyton Sample Receipt & Sample Handling for Taxonomic Analysis*

12.8 SOP AB-11, *Phytoplankton Sample Receipt & Sample Handling for Taxonomic Analysis*

12.9 SOP AB-14, *Algal Identification Quality Control (QC) Procedures: Initial Demonstration of Proficiency, Ongoing QC, Monthly QC, and Quarterly QC*

12.10 SOP BG-01, *Data-Entry Verification*

12.11 SOP BG-03, *Taxonomic Results and Data Entry*

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12.12 SOP LB-002, *Non-conformance Reporting System*

12.13 SOP IZ-38, *Formalin Assay, Recycling and Buffering*

12.14 SOP FS 7000, *General Biological Community Sampling* (FS 7110, *Phytoplankton Bloom Sampling* and FS 7240, *Algal Mat Sampling for Taxonomic Identification or Toxin Analysis*).

Appendix of Changes

12/16/2019 Removed BLOOM-ID/ALGAL-ID references from other algal SOPs upon the creation of this SOP.

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