LT 7200. Stream Condition Index (SCI) Determination

1. DEFINITION: The SCI is a community-based biological assessment of stream health using benthic macroinvertebrates sampled via 20 sweeps of a D-frame dipnet, with organisms identified to the lowest practical taxonomic level.

2. SAMPLING

2.1. Perform physical/chemical characterization and habitat mapping according to FT 3001.

2.2. Perform a habitat assessment according to FT 3100.

2.3. Conduct SCI D-frame dipnet sampling according to FS 7420.

3. LABORATORY ANALYSES

3.1. Sample Preparation

3.1.1. Equipment and Supplies

Waterproof paper

Permanent marker

U.S. No. 30 mesh sieve

Ethanol-filled squeeze bottle (80%)

Pan marked with a grid of 24 5-cm squares (gridded pan)

Random number table

250-mL glass jar

Dissecting microscope

Compound microscope

100 x 15 mm petri dish or other appropriate container

Forceps

Vials for picked organisms (1 or 2 dram)

Laboratory counter

Macroinvertebrate Bench Sheet (may vary from lab to lab)

Discard bucket

Lighted magnifier

Ruler

Lab coat

Latex gloves

Properly fitted respirator

Safety glasses

3.1.2. Methods

3.1.2.1. Make two labels to go into each of the vials of picked bugs that clearly identify the sample. This could include information such as the sample identification number, station identification, date sampled, and replicate number.

3.1.2.2. Include the entire sample in this reduction and homogenization process.

3.1.2.3. Place sample material into a U.S. No. 30 mesh sieve over a discard bucket. Empty the contents of the sample into the sieve slowly, making sure not to lose any of the sample material. The formalin should go through the sieve and collect in the bucket. Once the sample is finished draining, pour the waste formalin into the proper container. Follow proper safety protocols (personal protective equipment, ventilation and handling) when handling samples preserved with formalin.

3.1.2.4. Gently rinse the sample material with tap water. Pull out large twigs, leaves, plants, etc., and place into a gridded pan. Wash fine debris (silt, mud) through the (U.S. No. 30 mesh) sieve. Repeat steps 3.1.2.3 and 3.1.2.4 until the entire sample from all the jugs has been processed. Visually inspect large debris (leaves, plants, twigs) held in the pan for animals before discarding. This inspection is best accomplished by observing it with a lighted magnifier. Randomly place found organisms into the gridded pan with the rest of the unpicked sample.

3.1.2.5. Thoroughly mix the sample so that a homogeneous distribution of organisms is achieved in the detrital matrix. Place the sieved sample in a labeled, gridded pan. Each 5-cm square should have a pre-assigned number (1-24). Liquid present in the sample should be sufficiently reduced to prevent material from shifting among squares during the sorting process. There are 24 total 5-cm squares in a standard pan. If the sample is small and does not cover all 24 squares, spread it out across a number of squares that is divisible by three (e.g., 18,12, 21). Use a straightedge to delineate the edges of a grid while removing the sample.

3.1.2.6. Randomly select eight separate squares (or 1/3 of the total grids). A random number table is recommended. Remove the contents of these squares, in their entirety, and place in another labeled, gridded tray. Thoroughly mix the sample in the second tray so that a homogeneous distribution of organisms is achieved in the detrital matrix. Use a straightedge to delineate the edges of a grid while removing the sample.

3.1.2.7. Randomly select one square from the second tray, remove the contents of this square in its entirety, and place it into a third container (such as a gridded tray or Petri dish). After selecting your square, you may need to add some ethanol or water (in addition to a cover) to the trays to prevent them from drying out.

3.1.2.8. The intent of this step is to achieve a final target count of 150 (with an acceptable range of 140-160) organisms**. Note that if the correct counting range can not be achieved, the calculation of a reliable final score is diminished.** Randomly select an aliquot (any fraction of the square; for example, ¼, 1/8, etc.), remove its contents, and place it in a separate, labeled container. You may divide this aliquot further, if necessary, to achieve the target number of organisms.

3.1.2.9. Place the container under a dissecting scope set at low power (approximately 7x or 10x). In a deliberate, systematic manner, pick every organism from the final aliquot and place it into an alcohol-filled vial (clearly identified as per

section 3.1.2.1). Keep a running total of the number of organisms picked. When started, finish sorting this aliquot in its entirety.

3.1.2.10. Save the container (petri dish) until you have ten (10), and have a co-worker recheck them as described in LQ 7000. After a container has been checked, you may discard the material in the remaining containers.

3.1.2.11. If you have not reached the minimum count of 140 organisms, repeat steps 3.1.2.7-3.1.2.10. You may use whatever size aliquot is necessary in order to reach the target count of organisms.

3.1.2.12. If you have exceeded the maximum count of 160 organisms, randomly sub sample 150 organisms. This may be accomplished by placing the organisms into a Petri dish that has been subdivided evenly into 16 squares. With the aid of a dissecting microscope, remove and discard any terrestrial organisms, pieces of worms and other organisms without heads. If still not within the target range, randomly select a square in the Petri dish and remove **all** the organisms in that square. Repeat this process until you have the target number of individuals.

3.1.2.13. If you have not reached the minimum target count of 150 (with an acceptable range of 140-160) after completely sorting the previous square from 3.1.2.7, go back to the second tray, randomly select a new square, and continue steps 3.1.2.8-3.1.2.12 until the target count has been obtained. If an obvious organism is observed but its grid number was not selected and no examples of that organism were present in the grids that were selected, you may note that organism as qualitatively observed. Do not include the organism in the analysis.

3.1.2.14. Record the number of squares, grids and aliquots selected (e.g., 8/24, 2/12, 1/4) to enable conversion to total abundance present in the original sample. Failure to record the number of squares and grids selected (out of the total possible) compromises the usefulness of the data. Save any remaining material in the third container and the remaining squares from the second tray in separate air-tight containers until both portions have been completely processed. This material may be necessary if the target counts fall below the acceptable range during the identification process.

3.1.2.15. Return to the tray in step 3.1.2.6 and without re-homogenizing repeat the entire process from steps 3.1.2.7-3.1.2.14 to obtain a second 150 (with acceptable range of 140-160) count. Place the organisms in a second vial.

3.1.2.16. If the entire sample is processed, and there are insufficient individuals for both (or one) of the aliquots to achieve the minimum of 140 organisms, this indicates an extremely unusual condition, either an environmental stressor (e.g., toxicity, lack of habitat, desiccation, etc.) or sampling error (e.g., sampling during flood conditions). **If this occurs, a final Stream Condition Index score should not be calculated, and the "X" qualifier should be used during reporting. "X" means there were insufficient individuals present in the sample, suggesting an extreme environmental stressor or sampling error.**

3.1.2.17. Record the date the sorting of the sample is completed.

3.2. Slide Preparation (Based on Beckett, D.C. and Lewis, P.A. 1982. An efficient procedure for slide mounting of larval Chironomidae. Trans. Amer. Microsc. Soc. 101: 96-99; Epler, J. 1992, Identification manual for the larval Chironomidae (Diptera) of Florida; and Pluchino, E. 1984, Guide to the common water mite genera of Florida.)

3.2.1. Equipment and Supplies

Dissecting microscope

25 x 75 mm glass microscope slides

12-mm and 18-mm diameter round #0 or #1 cover slips

Transparent tape and razor blade

Pencil

Forceps or needle

1 N KOH

Mounting medium (CMC-10)

3.2.2. Methods

3.2.2.1. Prepare the slides for labeling. This task is most easily accomplished by lining up several slides with long ends together and applying a row of transparent tape to the right side of each slide. Usually, three slides are left taped together until organisms are mounted. Use a razor blade to separate the slides during the identification process.

3.2.2.2. Label each slide so it can be uniquely identified. For example, write the sample number, sample date, and abbreviated site information on each slide label with a soft pencil. Other station identifiers along with the total number of slides, the initials of the mounter, and the date mounted can be written on a small piece of paper and attached to the tray on which the slides are placed to dry. This is often helpful when identifying the organisms.

3.2.2.3. Place a drop of CMC on the slide for each organism you are mounting. An excess of CMC may be used, which will help to form a seal around the cover slip when it is pressed down. Mount three midges/worms per slide, under separate 12-mm cover slips. In the case of very large specimens, mount two per slide under separate 18-mm cover slips.

3.2.2.4. Using a needle or forceps, place the specimen in the CMC, ventral side up if it is a midge or mite.

3.2.2.5. Using forceps, place the cover slip over the specimen.

3.2.2.6. Using forceps or the eraser of a pencil, press the cover slip onto the specimen. Apply sufficient pressure to spread the mandibles and labrum. At this point, you may also orient the specimen by pushing or pressing the cover slip in various ways. Be careful not to break the cover slip, as the pressure required to flatten the specimen may be great. Mounting of aquatic mites requires more CMC along with a greater amount of pressure. Make sure you use enough of both. Otherwise, air will accumulate under the cover slip and the necessary structures will not be visible. Mites can be soaked in 1N KOH for softening before mounting.

3.2.2.7. Set the slides aside to dry; it may take 1 to 2 days for the slides to dry completely. Recheck the labels on the slides to make sure that each one has the correct sample number.

3.3. Organism Identification (Modified from *Standard Methods 10500C*)

3.3.1. Equipment and Supplies

Dissecting microscope

Compound microscope

Identification references

Forceps

Vials (1- or 2-dram)

Petri dishes (100 x 15 mm or 60 x 15 mm) or Syracuse watch glasses

Laboratory counter (optional)

Microscope slides

12-mm diameter cover slips

Macroinvertebrate Bench Sheet (may vary from lab to lab)

Pen

Pencil

3.3.2 Methods

3.3.1.1. Sort and process samples according to section 3.1. Make permanent slide mounts of worms and midges according to section 3.2 when needed.

3.3.1.2. Identify organisms other than worms, midges, and aquatic mites with a dissecting microscope, unless higher magnification is needed. Make permanent slide mounts of worms, midges, and water mites as necessary from the 100-organism sample.

3.3.1.3. You may choose to separate the organisms into like groups. To do this, place the groups into smaller (60-mm diameter) individual petri dishes or Syracuse watch glasses, or group the animals within the larger dish.

3.3.1.4. Identify the organisms to the lowest practical taxonomic level, using the most appropriate identification reference for each group. See LT 7900 for guidance concerning “lowest practical taxonomic level”. Enumerate organisms concurrently, and then place them back into the labeled vial with the forceps. Remove the animals as you count them in order to avoid counting any of them twice. It will take some time until sufficient experience with identification procedures and references is gained. In addition to the identification manuals, maintain a reference collection that can be used to compare specimens and facilitate identification. After using a dichotomous key to arrive at the name of an unknown organism, check the organism’s geographic range, habitat preferences, and morphological diagnosis to confirm that the identification is correct. Do not identify an organism by simply flipping through some pictures and assigning a name based on a superficial resemblance. Another taxonomist will recheck sample identifications according to LQ 7000.

3.3.1.5. If a large number of one or a few taxa are present, use a laboratory counter to keep a running total to facilitate the enumeration process. Temporarily label counters to avoid mistakes. If you do not use a counter, tally the number of each taxon on your bench sheet.

3.3.1.6. If an organism is encountered in your laboratory for the first time, remove it and place it in an individual vial for inclusion in the reference collection. Make a note of this on the bench sheet, so that it can be located in the future, if necessary.

3.3.1.7. A compound microscope is required to identify worms, midges, and aquatic mites. Sometimes, parts of other organisms (*e.g.*, mayfly labrums, etc.) must be mounted for proper identification. Most midges and mites can be recognized at 400x (40x objective and 10x eyepiece). Prepare specimens from these groups according to section 3.2.

3.3.1.8. If the structures that must be observed cannot be seen, you may need to use a 100x oil immersion objective. This procedure will give a magnification of 1000x.

3.3.1.9. Identify the specimens to the lowest practical taxonomic level. See LT 7900 for guidance concerning "lowest practical taxonomic level". Write the organism name or code directly on the slide label. If the specimen has no head or belongs to a group not classified as a benthic macroinvertebrate (e.g., nematode), draw a horizontal line through the slide label to indicate that it will not be counted. Specimens that are missing their heads are not counted. This situation will most often be encountered with the worms, as the heads are difficult to discern under the dissecting microscope when the pieces are mounted.

3.3.1.10. Record the individual taxon names and enumerate the organisms for each taxon on your bench sheet. Use of the laboratory counter will facilitate this operation, especially where large numbers of individuals are present.

3.3.1.11. Tally the number of organisms identified.

3.3.1.12. Follow proper Taxonomic Quality Assurance procedures (see LQ 1000).

4. DATA REDUCTION

4.1. For FDEP staff, enter all data into SBIO (the Florida Statewide Biological Database).

5. INDEX CALCULATION

Perform the following calculations based on collapsed data as outlined in LT 7100, Section 4.2.

5.1. Calculate and record the biological metrics for long-lived and sensitive taxa according to LT 7100, Sections 5.1 and 5.2, respectively.

5.2. Calculate and record the % very tolerant taxa according to the taxa list below (Fore, 2004). These taxa are identified as very tolerant to human disturbance.

Order	Family	Genus	Taxon (very tolerant)	Synonyms
Basommatophora	Ancylidae	*Hebetancylus*	*Hebetancylus excentricus*	
		Laevapex	All species	
	Physidae	*Physella*	All species	
	Planorbidae		All genera and species	
Coleoptera	Haliplidae	*Peltodytes*	All species	
Diptera	Chironomidae	*Larsia*	All species	

Order	Family	Genus	Taxon (very tolerant)	Synonyms
		Chironomus	*All species*	*Tendipes, Chaetolabis*
		Cladopelma	*Cladopelma*	
		Cricotopus	All species	
		Cryptochironomus	All species	
		Dicrotendipes	*Dicrotendipes modestus*	
			Dicrotendipes neomodestus	
		Glyptotendipes	All species	
		Goeldichironomus	All species	
		Kiefferulus	*Kiefferulus*	
		Polypedilum	*Polypedilum beckae*	*Asheum beckae Pedionomus beckae*
			Polypedilum illinoiense grp.	*Polypedilum illnoense*
Diptera	Chironomidae	*Polypedilum*	*Polypedilum tritum*	*Chironomus tritum*
		Tanypus	All species	*Pelopia*
		Tanytarsus	*Tanytarsus sp. f epler*	
	Stratiomyidae	*Odontomyia*	*Odontomyia*	*Eulalia*
	Tipulidae	*Tipula*	*Tipula*	*Nippotipula Playttipula Yamatotipula*
Haplotaxida	Naididae	*Bratislavia*	*Bratislavia unidentata*	
		Dero	All species	
		Nais	*Nais communis* complex	*Nais communis*
				Nais elinguis
				Nais pardalis
				Nais variabilis
Haplotaxida	Naididae	*Pristina*	*Pristina synclites*	
	Tubificidae	*Haber*	*Haber speciosus*	
		Limnodrilus	All species	*Camptodrilus*
Heteroptera	Mesoveliidae		All genera and species	
Hoplonemertea	Tetrastemmatidae	*Prostoma*	*Prostoma rubrum*	

Order	Family	Genus	Taxon (very tolerant)	Synonyms
Lepidoptera	Pyralidae		All genera and species	
Lumbriculida	Lumbriculidae	*Lumbriculus*	All species	
Odonata	Libellulidae	*Pachydiplax*	*Pachydiplax longipennis*	
	Coenagrionidae	*Argia*	*Argia sedula*	
		Enallagma	*Enallagma cardenium*	*Enallagma coecum*
		Ischnura	All species	*Anomalagrion*
Mesogastropoda	Hydrobiidae	*Pyrgophorus*	*Pyrgophorus platyrachis*	*Pyrogophorus platyrachis*
	Thiaridae	*Melanoides*	All species	
Rhynchobdellida	Glossiphoniidae		All genera and species	

5.3. Tally the numbers for taxa richness (total taxa), Ephemeroptera taxa, Trichoptera taxa, % Dominance, and % Tanytarsini.

5.4. Refer to Merritt and Cummins, An Introduction to the Aquatic Insects of North America to determine the number of clinger taxa and % filter feeders. For clinger taxa, include only those taxa whose sole habit is listed as “clinger”.

5.5. Evaluate and record the biological metrics according to the scoring system in Tables LT 7200-1, 7200-2 and 7200-3.

LT 7210. REFERENCES

1. Beckett, D.C. and Lewis, P.A., An Efficient Procedure for Slide Mounting of Larval Chironomidae, Trans. Amer. Microsc. Soc. V. 101, pp. 96-99, 1982.

2. Epler, J., Identification Manual for the Larval Chironomidae (Diptera) of Florida,1992.

3. Pluchino, E., Guide to the Common Water Mite Genera of Florida,1984.

1. Merritt, R.W., and Cummins, K.W., An Introduction to the Aquatic Insects of North America, Third Edition, 1996.

2. Fore, L., R.B. Frydenborg, D. Miller, D. Whiting, J. Espy, and L. Wolfe. Development and Testing of Biomonitoring Tools for Macroinvertebrates in Florida Streams. Florida Department of Environmental Protection, 2007.

Appendix LT 7200
Tables, Figures and Forms

LT 7200-1

SCI metric scoring formulae for converting metric values to a metric score ranging from 0 to 10. In each equation, 'X' stands for the raw metric value; "ln" stands for the natural log.

SCI metric	Northeast	Panhandle	Peninsula
Total taxa	10 * (X–16)/26	10 * (X–16)/33	10 * (X–16)/25
Ephem. taxa	10 * X /3.5	10 * X /6	10 * X /5
Trichoptera taxa	10 * X /6.5	10 * X /7	10 * X /7
% Filterer	10 * (X–1)/41	10 * (X–1)/44	10 * (X–1)/39
Long-lived taxa	10 * X /3	10 * X /5	10 * X /4
Clinger taxa	10 * X /9	10 * X /15.5	10 * X /8
% Dominance	10 – (10 * [(X–10)/44])	10 – (10 * [(X–10)/33])	10 – (10 * [(X–10)/44])
% Tanytarsini	10 * [ln(X + 1) /3.3]	10 * [ln(X + 1) /3.3]	10 * [ln(X + 1) /3.3]
Sensitive taxa	10 * X /11	10 * X /19	10 * X /9
% Very tolerant	10 – (10 * [ln(X + 1)/4.4])	10 – (10 * [ln(X + 1)/3.6])	10 – (10 * [ln(X + 1)/4.1])

1 Follow Steps 2-5 for each of the two 150 aliquots . If there are less than two aliquots, stop at Step 1 and report a null result with a qualifier of "X" ("too few to calculate").

2. Determine the bioregion for the sample and calculate each of the 10 SCI metrics using the appropriate equation in the table above.

3. Change any of the resulting individual SCI metrics score that are >10 to 10 and any that are <0 to 0.

4. Sum the 10 SCI metric scores; check that the sum is between 0 and 90. If it is not, verify that the correct equations were used.

5. Divide the sum of scores by 0.9. Do not round the result to get the aliquot score.

6. Average the two aliquot scores from step 5 and round to the nearest integer (decimal portions <.50 round down; >=.50 round up). This value will be reported as the final score with an "A" qualifier (for "averaged value").

7. Use Table 7200-2 to assign a category to the result calculated in Step 6.

Table LT 7200-2

Category names, ranges of values for SCI, and example descriptions of biological conditions typically found for that category. Narrative metric descriptions are not used to score metrics, rather they describe values associated with a range of index values.

SCI category	SCI range	Example Description
Category 1 ("exceptional")	71–100	Higher diversity of taxa than for Category 2, particularly for Ephemeroptera and Trichoptera; several more clinger and sensitive taxa than found in Category 2; high proportion for Tanytarsini; few individuals in the dominant taxon; very tolerant individuals make up a very small percentage of the assemblage
Category 2 ("healthy")	35–70	Diverse assemblage with 30 different species found on average; several different taxa each of Ephemeroptera, Trichoptera, and long-lived and, on average, 5 unique clinger and 6 sensitive taxa routinely found; small increase in dominance by a single taxon relative to Category 1; very tolerant taxa represent a small percentage of individuals, but noticeably increased from Category 1
Category 3 ("impaired")	0–34	Notable loss of taxonomic diversity; Ephemeroptera, Trichoptera, long-lived, clinger, and sensitive taxa uncommon or rare; half the number of filterers than expected; assemblage dominated by a tolerant taxon; very tolerant individuals represent a large proportion of the individuals collected