Maryland Biological Stream Survey

Laboratory Methods for Benthic Macroinvertebrate Processing and Taxonomy

Maryland Department of Natural Resources
Monitoring and Non-tidal
Assessment Division
Ecological Assessment Program
580 Taylor Avenue, C-2
Annapolis, Maryland 21401

November 2000
(revised January 2019)

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Governor

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Prepared by Dan Boward and Ellen Friedman

Maryland Department of Natural Resources
Monitoring and Non-tidal Assessment Division
580 Taylor Avenue, C-2
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Contents

1 Introduction

This manual describes the methods used for benthic macroinvertebrate processing, identification, and data management for Maryland Department of Natural Resources Maryland Biological Stream Survey (MBSS) and Maryland Stream Waders (MSW) Programs. It is intended to serve as the Standard Operating Procedure for DNR staff involved in benthic processing and identification as well as a guide for other agencies, organizations, and businesses wishing to use comparable methods. Field methods for MBSS and Stream Waders benthic sampling may be found in the MBSS and Stream Waders Sampling Manuals.

2 Sample Check-In and Inspection

Upon arrival at the DNR Field Office (see Contact Information, Appendix A) list each sample on the Benthic Macroinvertebrate Sample Chain of Custody Form (Appendix B).

Each sample bucket is given a unique "Log Number" by Field Office staff. The Log Number is sequential for each calendar year with the first two digits indicating the year of collection and the last four digits indicating the sequential number of each sample bucket in the order that it is received by the lab (e.g., 000487 is sample bucket number 487 in calendar year 2000). Log Numbers, which are kept in a separate written notebook for each calendar year, are especially useful in avoiding confusion related to duplicate samples taken at the same site and for tracking the status of sample buckets by indicating sample condition (e.g., rotten sample, dry sample).

Check each sample bucket for an adequate quantity of preservative (see Appendix C for a description of preservative). Ideally, there should be about twice as much preservative as there is sample material (by volume). If preservative is low due to spillage or evaporation, add more. Check sample buckets for cracks and poorly-fitting lids. Correct these problems as needed.

Store samples in an area with good ventilation (ambient air temperature should not exceed 100°F) until processed.

3 Laboratory

3.1 Preparation and Subsampling

Fill out all information on a small label to be placed inside the picked sample jar (a 60 ml snap cap vial works well). The label should include the site name, log number, collector, date collected, sub-sampler, number of grids picked, and pertinent remarks. Use cotton bond paper or a type of paper that will not degrade in ethanol over time. Under a fume hood, remove the sample bucket lid and inspect the sample contents. Verify that sample numbers on both outside and inside labels are the same and complete. Note any instances of sample

drying, dried organisms, mold, unusual color or odors, etc. in the comments section of the Bench Sheet.

Over a large and well-ventilated sink, pour the sample contents through a U.S. Standard #30 (600 micron mesh) sieve, catching the ethanol preservative in a clean bucket positioned beneath the sieve. Once most of the ethanol is poured through the sieve, remove it from the sink. Gently rinse the interior of the sample bucket with tap water (sides, bottom, and lid) into the sieve until the ethanol odor is undetectable. Check that all organisms are removed from the sample bucket. Save the ethanol in the original labeled sample bucket for sortate storage (only ethanol that is not degraded [i.e., without a pungent odor or without discoloration] is saved for reuse). Rinse the sample material on the sieve with tap water to remove fine sediments. Clean large objects such as stones, sticks, and large leaves with a scrub brush to remove organisms. Discard these large objects after inspection. If the sample from a site required multiple buckets, all the sample material should be placed in the sieve at one time (if possible) and gently combined to make sure the sample material is homogeneous before splitting sample into the subsample tray.

Position the subsampling tray (see Appendix C for a description of MBSS standard subsampling tray) on a flat and level surface in good light. Rinse the contents of the sieve into the subsampling tray. Ensure that all sample material is transferred to the tray. Spread the sample material evenly over the entire tray bottom. Add tap water to the tray until sample material is completely covered. Allow sample material to hydrate for about 10 minutes. If the quantity of sample material is more than one sample bucket (about 86 ounces), the material may be split into (approximate) halves (or split more if necessary). The subsampling steps are repeated for each half. When splitting a sample, half of the picked organisms should be picked from each tray (60 from first tray, 60 from second tray) always completely picking the last randomly chosen grid.

Using a random numbers table or a similar method of choosing numbers, randomly choose a number between 1 and 100 (there are 100 5cm^2 grids in the subsampling tray). After positioning a light over the grid to be picked, begin removing organisms from the randomly chosen grid with forceps and place them in a watch glass or container with 95% ethanol. Remove floating organisms first and disregard any organisms that float into the grid while the remainder of the grid is being picked.

Entry-level processors should place picked organisms into a watch glass to be viewed by the lab supervisor under a low magnification stereoscope to verify that no plant debris, etc. was picked and counted as an organism. This is done until the lab supervisor is confident that the processor can separate organisms from other sample material. This is not necessary with an experienced processor capable of separating organisms from sortate.

Keep a tally of the total number of organisms removed from the subsample tray and placed in a container (60 ml snap cap vial). Also keep a tally of the number of grids required to reach approximately 120 organisms. While subsampling, any organism that extends over a line separating multiple grids is considered to be in

the grid containing its head. If the processor is unsure which end is the head, then the organism is considered to be in the grid being picked if that grid contains greater than 50% of the organism.

If the total number of organisms removed from the first grid is equal to or greater than 120, subsampling is complete for the sample. If not, repeat the above process for another randomly-chosen grid. Continue this process until at least 120 organisms have been subsampled. The last grid chosen must be picked in its entirety. For some samples, the total number of organisms may be less than 120, even after picking all grids in the subsample tray. The 120 organism target is used to allow for organisms that are missing parts needed for identification or non-organism material counted in the subsample.

Once the target number of organisms is tallied, note the number of grids required for the subsample on the label. If the sample was split and subsampled twice, make a note of the number of grids needed to get the first and second group of (approximately) 60 organisms. The total number of grids is divided by the number of trays picked and rounded up, if necessary, to a whole number. This number is entered on the bench sheet when identifying the sample. For example, if two trays are picked for one sample and the first tray contained 60 organisms in 6 grids and the second tray contained 60 organisms in 10 grids, then the number of grids to be entered on the sample's bench sheet would be 8. Once the label is completely filled out it is placed in the 60ml snap cap jar with the picked sample.

After subsampling, pour the remaining sample material back into the laboratory sieve, draining off the water. Place the sample material back into the original sample bucket(s) and add the original ethanol. Store the sample as described in Section 6.0.

Ensure that the subsample tray and laboratory sieve are rinsed well and free from remaining organisms prior to beginning another sample.

3.2 Identification

A list of taxonomic keys used for the identification of MBSS benthic macroinvertebrates can be found in Appendix E. Note that this list may be updated more often than this manual is revised.

Fill out the information at the top of a blank MBSS Benthic Macroinvertebrate Laboratory Bench Sheet (Appendix D), include Site Name, Log Number, Collector, Collection Date, Subsampler, Number of Grids, Date IDed, and Taxonomist Name.

3.2.1 Core and Targeted MBSS

For core (randomly-selected) and targeted MBSS samples, most organisms are identified to genus, if possible, using stereo scopes.

Refer to Appendix G for decisions rules on exceptions. Those taxa not

identifiable to genus (due to small size or damage) may be left at family level or higher. These are noted on the bench sheet at the higher taxonomic level. Counts at levels higher than genus are not assumed to be different taxa from those identified to genus. Likewise, counts at levels higher than family are not assumed to be different taxa from those identified to family.

When entering taxa and respective counts into the Microsoft Access program, each entry is prompted with an 'Exclude?' checkbox option (Appendix F), This Exclude checkbox should be checked when an organism should not be included in any taxa richness metric counts for IBI calculations. This box should only be checked when an organism can only be identified to family level (or above) due to immaturity, size, or damage, and the sample includes the taxon from the same family (or above) that has been identified to genus level.

3.2.1.1 The process for identifying Chironomid larvae is as follows:

General: Divide all Chironomid larvae within the subsample into Subfamilies (i.e., Chironominae, Orthocladiinae, Tanypodinae, Diamesinae) or Tribes (i.e., Tanytarsini, Chronomini) and count the total number in each group. If either the total number of Chironomids or the total number of individuals within a Subfamily or Tribe is ten or less, all larvae are identified (using slide mounts...see below). If there are more than 10 total Chironomids or more than 10 individual Chironomids within a Subfamily or Tribe than approximately 20% of the individual larvae within each Subfamily or Tribe are slide mounted and identified and then all genera are multiplied by five and record the total extrapolated number of genera for the entire Chironomid group. For example, if you have a total of 60 Chironomid larvae in a subsample which are separated into 20 Orthocladiinae, 15 Chironomini, 15 Tanytarsini, 5 Tanypodinae and 5 Diamesinae, you would slide mount 4 Orthocladinae, 3 Chironomini, 3 Tanytarsini, all 5 Tanypodinae and all 5 Diamesinae.

Clearing and mounting larvae

Remove Chironomid larvae from the ethanol and place in water for about 10 minutes. Ensure that the larvae are totally immersed in the water and not floating. Place the larvae in 10% KOH in a small heat-resistant crucible. Heat them on low heat using a hotplate until the internal tissues are clear. If unable to use a hotplate, the larvae can be placed in room temperature KOH overnight or until internal tissues are cleared. Place the larvae in water again for about 5 minutes. Return the larvae to ethanol.

With a drop or two of ethanol on a microscope slide, place several cleared larvae in a row with all heads toward one edge of the slide and dorsum down (mouthparts upward). Do not allow the

larvae to dry, as air bubbles within the integument may block essential structures from view. Add one or two drops of mounting media (CMCP 10/CMCP 9AF) next to the larvae. Carefully lower a cover slip (one edge down first) over the larvae. Try to prevent movement of the larvae and air bubbles from being trapped beneath the coverslip. Gently press on the coverslip with a pencileraser to spread mouthparts and extrude air. Identify the larvae using a compound microscope. After identification, place a bead of clear nail polish around the edge of the cover slip to render the mount permanent. Detailed procedures for the mounting and identification of Chironomid larvae may be found in EPA (1990) or Epler (2001). Store all slide mounted Chironomid larvae in a slide storage box with the corresponding box of subsamples from the same sampling year.

Chironomid pupae are identified to genus (if possible) without subsampling or mounting.

3.2.1.2 Mounting Oligochaeta

Place Oligochaetes in a drop of ethanol on a microscope slide. Place several drops of mounting medium (CMCP 10/CMCP 9AF) over the organisms. Carefully place a cover slip over the worms and gently press with a pencil eraser to remove bubbles. Place the slide in a drying oven on low heat for 5 to 10 minutes or until tissues clear.

Place counts of all organisms in the subsample on the Bench Sheet. Include comments on sample condition, etc. in the Comments section of the Bench Sheet. All identified non-Chironomid and non-Oligochaete organisms are placed into a glass snap cap vial and stored in numerical (Log Number) order.

3.2.2 Volunteer Collected Samples (Stream Waders Program)

Identify organisms to family (if possible). Use the Bench Sheet as described above at the family (or higher) level.

4.0 Quality Assurance/Quality Control

4.1 Repeated Subsampling

Using sequential Log Numbers, every 20th sample (if two buckets were required at a site, they should be treated as a single unit) is randomly chosen for re-subsampling and identification according to the following procedure:

A. subsample and identify the sample as usual EXCEPT - identify Chrionomids to Subfamily or Tribe (do not slide mount the larvae) and

Oligochaetes to Class.

B. return the once-identified organisms to the original sample bucket containing the sortate and preservative, and re-subsample.

C. identify the second subsample according to standard procedures (i.e., slide mount Chironomid larvae and Oligochaetes and identify them to genus and family, respectively, if possible).

D. QC comparisons are made on the two taxa lists and benthic Index of Biotic Integrity (BIBI; see Southerland et al. 2005) values generated from the two subsamples (of the same sample). Note that the BIBI generated from the second subsample (the one with genus-identified chironomids) should be calculated with subfamily or tribe level chironomid counts. Differences of less than 1 BIBI value are generally considered acceptable.

4.2 Taxonomy

Questionable identifications are verified by consulting other DNR benthic taxonomists, regional experts, and regional keys for certain taxonomic groups. Maryland DNR requires that MBSS and Stream Waders benthic taxonomists pass both the EPT East, Other Arthropods East, and North America Chironomidae tests administered by the Society for Freshwater Science.

5.0 Sample Storage and Disposal.

All subsamples are archived indefinitely in 60ml snap top vials containing 95% ethanol. Pencil-written labels include Site name, sample date, and log number. Vials are stored in cardboard boxes separated and labeled according to sampling year. Sample sortate is kept in the original 86 ounce plastic bucket for 5 years (e.g., sortate from samples collected during spring 2010 are kept until spring 2015). Sortate is discarded by pouring the material in the 86 ounce bucket through a #500 micron sieve over a sink, flushing the ethanol down the drain, and discarding the sample material in an appropriate trash receptacle. Once sortate is discarded, sample buckets are washed and old labels are removed to prepare them for reuse, if possible.

6.0 Literature Cited

Boward, D. M. 2000. Maryland Stream Waders. Volunteer Stream Sampling Manual. Maryland Department of Natural Resources. Monitoring and Non-tidal Assessment Division. Annapolis, Maryland.

EPA 1990. Macroinvertebrate field and laboratory methods for evaluating the biological integrity of surface waters. U.S. Environmental Protection Agency. EPA/600/4-90/030. Cincinnati, Ohio.

Epler, John H. 2001. Identification Manual for the Larval Chironomidae (Diptera) of North and South Carolina. A guide to the taxonomy of the midges of the southeastern United States, including Florida. Raleigh, NC.

Southerland, M., Rogers, G., Kline, M., Morgan, R., Boward, D., Kazyak, P., Klauda, R., and Stranko, S., 2005. New Biological Indicators to Better Assess the Condition of Maryland Streams. Versar, Inc. Columbia, Maryland.

Southerland, M.T. 2005. New Biological Indicators to Better Assess the Condition of Maryland Streams. Maryland Department of Natural Resources. Monitoring and Non-tidal Assessment

Stranko, S. 2009. Maryland Biological Stream Survey Sampling Manual. Maryland Department of Natural Resources. Monitoring and Non-tidal Assessment Division. Annapolis, Maryland.

White, J. 1999. Ecological Application Data System (EDAS): A User's Manual. Tetra Tech, Inc. Owings Mills, Maryland.

Appendix A

Contact Information

Benthic sorting and taxonomy

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Benthic macroinvertebrate data management and use in stream assessments

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Appendix B

Maryland Department of Natural Resources
Monitoring and Non-Tidal Assessment Division
580 Taylor Avenue
Annapolis, MD 21401

MBSS Benthic Macroinvertebrate Sample Chain-of-Custody Sheet

Site ID	Collector (print)	Collection Date (DD/MM/YY)	Date Delivered to Field Office (DD/MM/YY)	Relinquished By (print)	Received by (print)	Field Office Log Number

Comments

Appendix B (continued)

Guidance for 1997 MBSS Benthic Macroinvertebrate Sample Chain-of-Custody Sheet

General

This sheet provides a means of tracking the transfer of benthic macroinvertebrate samples between field collecting crews and DNR field office personnel responsible for processing the samples. If multiple sample buckets are delivered for a single site, enter each bucket on a separate row. If entries are repeated down a row, it is not necessary to enter the information in each cell. Simply use an arrow or quote marks to indicate the information is repeated down the row. Please write as legibly as possible following the guidelines below. The entry of a printed name indicates responsibility of the individual for relinquishing or receiving each sample.

1. **Site ID**	Enter the site ID just as it appears on the field data form.
2. **Collector (print)**	Print the name of the person who collected the benthic sample.
3. **Collection Date**	Enter the date the sample was collected (using DD/MM/YY format) just as it appears on the field data form.
4. **Date Delivered to Field Office**	Enter the date the sample was delivered to the field office using DD/MM/YY format.
5. **Relinquished By (print)**	Enter the printed name of the person relinquishing the sample to the appropriate field office staff member.
7. **Received By (print)**	Enter the printed name of the person receiving the sample at the field office.
8. **Field Office Log-In Number**	(Done by field office personnel) Enter the Benthic Sample Log-in number.
9. **Comments**	Place any pertinent comments regarding the delivered samples, including unusual circumstances, here. Examples include “label for sample from site X fell off - see label in bucket” or “some of sample for site Y spilled while in transport”.

Appendix C Supplies and Equipment (all vendor information – late 2018)

Sample bucket

Basix 86 oz. Freezable Deli Food Storage Containers w/ Lids - Package of 20 - Food Storage White (2018 pricing - pack of 20 for $26.95).

Vendor:

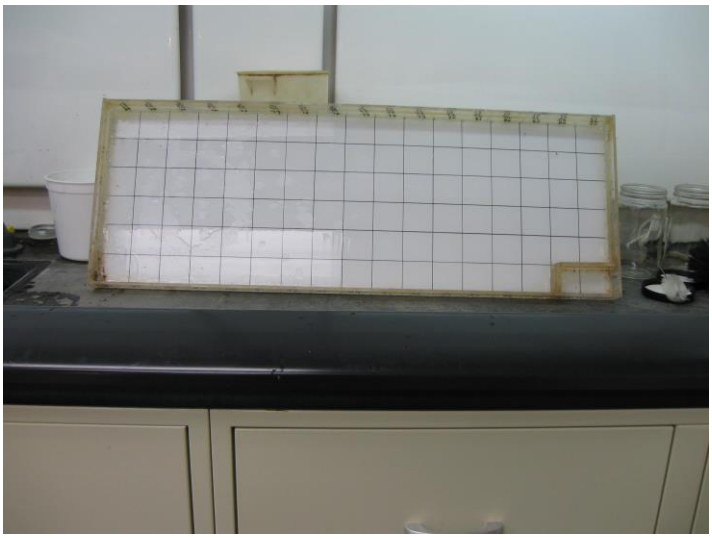
AMAZON (see https://www.amazon.com/gp/product/B01H42J8B8/ref=oh_aui_detailpage_o00_s00?ie=UTF8&psc=1

95% denatured ethanol

54 gallon drum; 2011 price = $484.60

Vendor:

ChemStation Chesapeake
3310 Childs St.
Baltimore, MD 21226
(410) 752-2084
(410) 752-0001



Subsampling Tray

100cm X 25cm plastic tray with 4" high walls; 100 5cm X 5cm black square grids drawn on the tray bottom. Trays used by DNR were constructed by DNR staff. For detailed information on the DNR subsampling tray, contact Ellen Friedman, Neal Dziepak or Dan Boward.

Laboratory Sieve

12” diameter brass sieve; U. S. #30 (600 µm mesh); Catalog Number 04-884P. Vendor:

Fisher Scientific
2000 Park Lane Dr
Pittsburgh, PA 15275
800-766-7000
www.fishersci.com

Subsample Storage Vial

60 ml snap cap vial; catalog number 03-335-10B; Case price is $193.59. per case of 72

Fisher Scientific
3970 Johns Creek Court
Suwanee, GA 30024
800-766-7000
www.fishersci./us/en/home.html

Mounting Medium for Chironomidae and Oligochaeta

The two products used are CMCP-9AF and CMCP-10. The mixture used by DNR staff for mounting Chironomidae and Oligochaeta is 2/3 CMCP-9AF and 1/3 CMCP-10.

Masters Chemical Co.
890 Lively Boulevard
Wood Dale, Il 60191
Phone 630-238-9292

Appendix D

Portion of the MBSS Benthic Laboratory Bench Sheet

MBSS Benthic Macroinvertebrate Laboratory Bench Sheet

Site: _____-_____-_____-_____ Collection Date _____ Date IDed _____
Log No. _____ Subsampler _____ Taxonomist _____
Collector _____ No. of Grids _____

GORDIIDAE		**GAMMARIDAE**		**SIPHLONURIDAE**		**PERLODIDAE**	
		Gammarus sp.		*Siphlonurus sp.*		*Clioperla sp.*	
DUGESIIDAE						*Cultus sp.*	
Cura sp.		**TALITRIDAE**		**ODONATA**		*Diploperla sp.*	
Girardia sp.		Hyalella sp.		**AESHNIDAE**		*Isoperla sp.*	
				Boyeria sp.			
PLANARIIDAE		**PALAEMONIDAE**				**PTERONARCYIDAE**	
Phagocata sp.		*Palaemonetes sp.*		**CALOPTERYGIDAE**		*Pteronarcys sp.*	
				Calopteryx sp.			
OLIGOCHAETA		**ISOPODA**				**TAENIOPTERYGIDAE**	
ENCHYTRAEIDAE		**ASELLIDAE**		**COENAGRIONIDAE**		*Oemopteryx sp.*	
LUMBRICULIDAE		*Caecidotea sp.*		*Argia sp.*		*Strophopteryx sp.*	
NAIDIDAE		*Lirceus sp.*		*Enallagma sp.*		*Taeniopteryx sp.*	
TUBIFICIDAE				*Ischnura sp.*		*Taenionema sp.*	
Limnodrilus sp.		**CAMBARIDAE**				**HEMIPTERA**	
Spirosperma sp.		*Cambarus sp.*		**CORDULEGASTRIDAE**		**BELOSTOMATIDAE**	
		Orconectes sp.		*Cordulegaster sp.*		*Belostoma sp.*	
HIRUDINEA		*Procambarus sp.*					
BACTRACOBDELLA				**CORDULIIDAE**		**CORIXIDAE**	
ERPOBDELLIDAE		**INSECTA**		*Somatochlora sp.*		*Palmacorixa sp.*	
		COLLEMBOLA				*Trichocorixa sp.*	
GLOSSIPHONIIDAE		**ISOTOMIDAE**		**GOMPHIDAE**			
Placobdella sp.		*Isotomurus sp.*		*Arigomphus sp.*		**GERRIDAE**	
				Dromogomphus sp.		*Gerris sp.*	
PISCICOLIDAE		**EPHEMEROPTERA**		*Gomphus sp.*		*Trepobates sp.*	
Piscicola sp.		**AMELETIDAE**		*Hagenius sp.*		*Limnoporus sp.*	
		Ameletus sp.		*Lanthus sp.*		*Metrobates sp.*	
GASTROPODA				*Progomphus sp.*			
ANCYLIDAE		**LEPTOPHLEBIIDAE**		*Stylogomphus sp.*		**NOTONECTIDAE**	
Ferrissia sp.		*Habrophlebia sp.*				*Buenoa sp.*	
		Leptophlebia sp.		**LESTIDAE** *Lestes sp.*		*Notonecta sp.*	

Appendix E

List of Commonly-Used Taxonomic Keys

Merritt, Cummins, and Berg. 2008. An Introduction to the Aquatic Insects of North America. 4th Edition.

Morse, John C., W. Patrick McCaferty, Bill P. Stark and Luke M. Jacobus (Editors), 2017: Larvae of the Southeastern USA Mayfly, Stonefly and Caddisfly Species (Ephemeroptera, Plecoptera and Trichoptera) Clemson University.

Peckarsky, B. L., P. R. Fraissinet, M. A. Penton, and D. J. Conklin, Jr. 1990. Freshwater Macroinvertebrates of Northeastern North America. Comstock Publishing Association. Ithaca, New York.

Pennak, R. W. 1989. Freshwater Invertebrates of the United States. Third Edition. John Wiley and Sons, Inc. New York, New York.

Wiggins, G. B. 1996. Larvae of the North American Caddisfly Genera (Trichoptera). Second Edition. University of Toronto Press. Toronto, Canada.

Appendix F

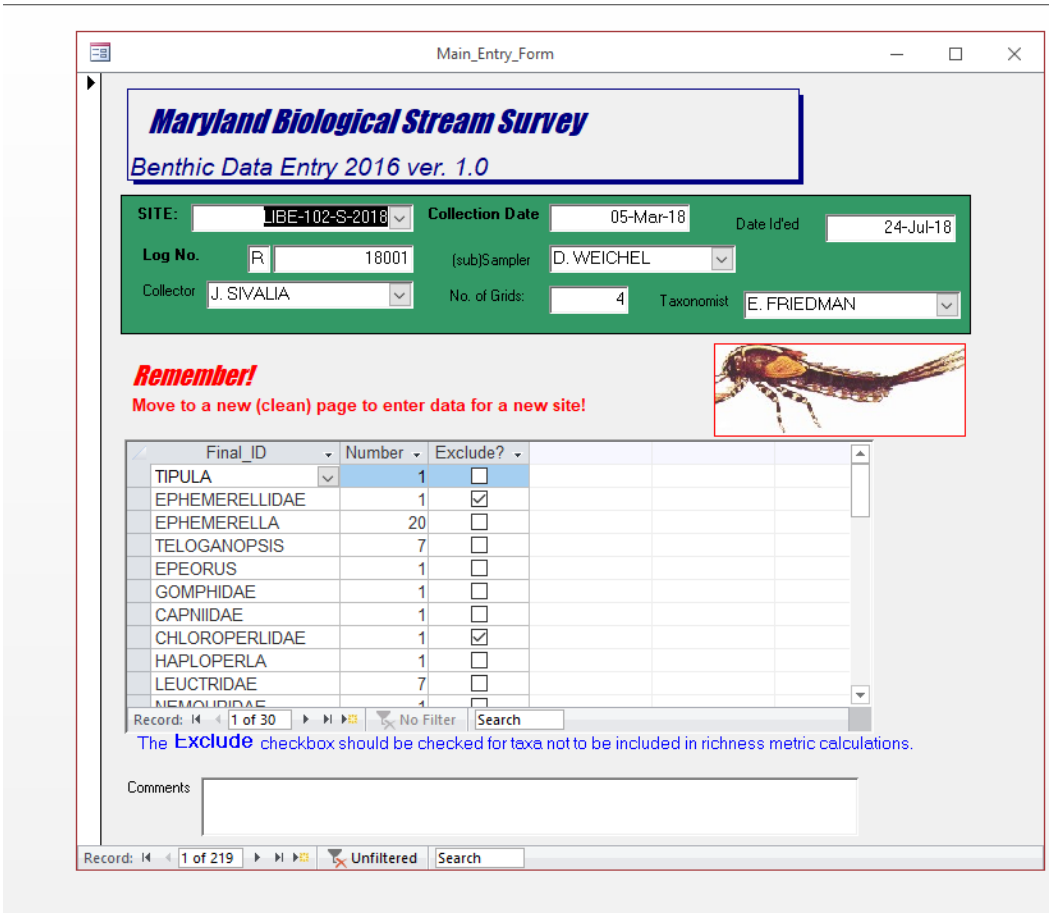
Overview of Data Entry, Management, and Analysis

Use Microsoft Access (Office 2016 Version) to enter data from the Bench Sheet. Look-up Tables for sites and taxonomic names are provided in the program and these are updated at least annually by DNR staff as needed. The data entry screen is shown below. All benthic data (including taxon, counts, and site information) are double entered by two individuals with results compared visually following the second entry

Once taxonomic counts are entered into Access, total organisms per subsample counts are evaluated, along with supplemental environmental (e.g., habitat, water chemistry, land use) data. Those samples with fewer than 60 organisms are evaluated carefully. For these sites, Best Professional Judgement is used to determine if low counts are likely due to sampling error or impairment at the site.

For details on MBSS data management and storage, contact a staff person listed in Appendix A.

Data Entry Screen from Access Program



APPENDIX G

MBSS Decision Rules for Benthic Macroinvertebrate Taxonomy

Taxon	Phylum	Class	Order	Family
IGNORED/NOT PICKED				
ACARI	Arthropoda	Arachnida		
CARABIDAE	Arthropoda	Insecta	Coleoptera	Carabidae
LAMPYRIDAE	Arthropoda	Insecta	Coleoptera	Lampyridae
TALITRIDAE	Arthropoda	Malacostraca	Amphipoda	Talitridae
COPEPODA	Arthropoda	Crustacea	Copepoda	
OSTRACODA	Arthropoda	Crustacea	Ostracoda	
CLADOCERA	Arthropoda	Crustacea	Cladocera	
NOT ID'ED LOWER THAN PHYLUM				
NEMATODA	Nematoda			
NOT ID'ED LOWER THAN ORDER				
BRANCHIOBDELLIDA	Annelida	Oligochaeta	Branchiobdellida	
NOT ID'ED LOWER THAN FAMILY				
BRACONIDAE	Arthropoda	Insecta	Hymenoptera	Braconidae
CHRYSOMELIDAE	Arthropoda	Insecta	Coleoptera	Chrysomelidae
DOLICHOPODIDAE	Arthropoda	Insecta	Diptera	Dolichopodidae
ENCHYTRAEIDAE	Annelida	Oligochaeta	Haplotaxida	Enchytraeidae
EPHYDRIDAE	Arthropoda	Insecta	Diptera	Ephydridae
GORDIIDAE	Nematomorpha	Nematomorpha	Gordioidea	Gordiidae
HAPLOTAXIDAE	Annelida	Oligochaeta	Tubificida	Haplotaxidae
LUMBRICULIDAE	Annelida	Oligochaeta	Lumbriculida	Lumbriculidae
NOCTUIDAE	Arthropoda	Insecta	Lepidoptera	Noctuidae
PELECORHYNCHIDAE	Arthropoda	Insecta	Diptera	Pelechorhynchidae
PODONOMINAE	Arthropoda	Insecta	Diptera	Chironomidae
SALDIDAE	Arthropoda	Insecta	Hemiptera	Saldidae
SARCOPHAGIDAE	Arthropoda	Insecta	Diptera	Sarcophagidae
SCIOMYZIDAE	Arthropoda	Insecta	Diptera	Sciomyzidae
SMINTHURIDAE	Arthropoda	Insecta	Collembola	Sminthuridae
TORTRICIDAE	Arthropoda	Insecta	Lepidoptera	Tortricidae
ID'ED TO FAMILY BUT SHOULD NOT BE SAMPLED				
UNIONIDAE	Mollusca	Bivalvia	Unionoida	Unionidae

APPENDIX H

Glossary of Terms

Bench sheet – Paper document for handwritten (pencil) entry of benthic macroinvertebrate taxon, counts, site and sampling information, and lab processing and identification information.

Grid – A 5 cm X 5 cm square drawn on the bottom (outside) of the MBSS/Stream Waders subsampling tray. The tray includes 100 such squares.

Processing – The entire series of steps from checking in an MBSS/Stream Waders sample, washing the sample, placing the sample material in the subsampling tray and subsampling.

Picking – The process of removing individual specimens from the MBSS/Stream Waders subsampling tray and placing them in the appropriate container during the subsampling process.

Sample – Benthic material (living and non-living) removed from a stream, placed in one or more sample buckets, field preserved and delivered to the lab for processing and identification.

Sortate – Sample material remaining after the subsampling process is complete.

Subsample – Benthic macroinvertebrates removed (picked) from the subsampling tray for subsequent identification. The target number of individual specimens is 120.