

Marion County Public Health Department Benthic Macroinvertebrate Sampling Fact Sheet

Aquatic benthic macroinvertebrates, or "macros", are found in streams across the world and contribute greatly to the aquatic ecosystem. These larval insects and mollusks may be small, but they make up a large part of the aquatic community. They perform many important functions including breaking down organic matter and providing food for other species. Over one hundred difference species of macros can be found in streams here in Marion County including larval caddisflies, mayflies, and dragonflies.

WHY SAMPLE FOR MACROINVERTEBRATES?

Many studies have shown that macros can be a good indicator of water quality in streams. This is because many species are very intolerant to pollution, while some can survive higher amounts. They are also largely immobile with each individual encompassing a very small area, unable to move away from sources of pollution. Due to this, an accurate reading of the water quality can be measured by identifying what species are found during sampling. This is especially important in urban areas such as Marion County, as pollution levels trend higher in these areas than those that are more rural.

Another reason why macroinvertebrates are used as an indicator of water quality is that they can be collected and identified with equipment such as dip-nets and identification keys that are much easier to obtain than very expensive laboratory equipment.

SAMPLING METHOD

MCPHD uses the sampling procedure developed by the Muncie Bureau of Water Quality, which involves timed-interval sampling of various parts of the stream. Simple D-nets are used to sample in and around the most shallow and fast-moving sections of stream, known as riffles. Sampling is focused in and around riffles because that is the preferred habitat for most aquatic macroinvertebrates. By incorporating "bank sweeps" macros that primarily live in riparian vegetation and root masses can also be collected.

Three samplers are assigned to each site. Sampling begins with a 1-minute "kick-shuffle" in which all samplers sample the width of the riffle itself. The second and third phases are 2-minute "bank sweeps", in which samples are collected along the bank vegetation. Each sampler is assigned to a separate area of the stream – one upstream of the riffle, one downstream, and one in the riffle. Sampling upstream and downstream of the riffle allows us to compare the number of species and individuals between varying sections of stream. Collected samples are then picked through by the samplers for 15 minutes, with specimens stored in alcohol until they can be identified in a lab. The physical characteristics of each site are also recorded because they can have a large impact on the macroinvertebrate communities present in each stream.

WHAT ARE METRICS?

Metrics or indices are the number values used to interpret the site data. The data analysis used by MCPHD integrates several community, population and functional parameters into the interpretation. Each parameter, or metric, measures a different component of community structure and has a different range of sensitivity to pollution stress. This approach provides a more valid assessment due to the variety of parameters evaluated.

METRICS USED FOR MCHD MACROINVERTEBRATE PROJECT

Hilsenhoff Biotic Index (HBI)

The modified HBI classifies individual taxa based on their tolerance or intolerance to various levels of domestic wastes. The HBI is calculated by multiplying the number of organisms in each Insecta and/or Crustacea taxon by the pollution tolerance value assigned to each taxon, adding these for all individuals represented in the sample, and dividing by the total number of individuals in the sample. High index numbers indicate poor water quality.

HBI index = S (Xi*t)/n

S = the summation of Xi*t
Xi = the number of individuals in each taxon
t = tolerance value for each taxon in the sample
n = number of individuals in the sample

Explanation 0.00-3.75 Excellent 3.76-4.25 Very Good 4.25-500 Good 5.01-5.75 Fair 5.76-6.50 Fairly Poor 6.51-7.25 Poor 7.26-10.00 Very Poor

Shannon-Weaver Mean Diversity

A mean diversity measurement of species composition. The calculation is affected by richness of species and by the distribution of individuals among the species (species composition) and may range from zero to 3.321928 log N. Mean diversity (d) is calculated using the formula.

d = C (N log10 N - Sni log10 ni)/N

C = 3.321928 (converts base 10 log to base 2)

- N = total number of individuals
- ni = total number of individuals in the i-th species

Number of Taxa: Count of the number of taxa (families) found in the sample. A high variety is good.

Number of Individuals: Total count of individuals collected in sample.

% Dominant Taxon: Measure of the percent composition of the most abundant family from the sample. A high percent dominance is not good.

EPT Count: Count of the number of individuals in the three generally pollution sensitive orders – Ephemeroptera (mayflies), Plecoptera (stoneflies), and Trichoptera (caddisflies). A high variety is good.

EPT Index: Count of the number of taxa (families) in each of the 3 generally pollution-sensitive orders – Ephemeroptera (mayflies), Plecoptera (stoneflies), and Trichoptera (caddisflies). A high variety is good.

EPT/Total Count: EPT count divided by the total number of individuals in the sample. A higher number is good.

Chironomid Count: Total of individual chironomids (midge larvae) collected in sample.

EPT abundance/Chironomid abundance: EPT count divided by Chironomid count. A lower chironomid abundance is good.

% abundance of Chironomid larvae: Compares the number of chironomids to the total number of organisms in the sample. (The number of organisms in the chironomidae family is divided by the total number of organisms in the sample to calculate a percent composition.) A low percentage is good.

