

NOAA Technical Memorandum NOS ORCA 136 Appendices



**Baseline Clam Monitoring Study
Cannelton Industries Site
Sault Ste. Marie, Michigan
Summer 1997**

Seattle, Washington
September 1998

noaa

NATIONAL OCEANIC AND ATMOSPHERIC ADMINISTRATION

National Ocean Service

Office of Ocean Resources Conservation and Assessment
National Ocean Service
National Oceanic and Atmospheric Administration
U.S. Department of Commerce

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**Baseline Clam Monitoring Study
Cannelton Industries Site
Sault Ste. Marie, Michigan
Summer 1997: Final Report**

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Figure 7a. Total chromium concentration in tissues of clams deployed in Tannery Bay and at reference stations.

Figure 7b. Total chromium content in clams deployed in Tannery Bay and at reference stations.

Figure 8a. Lead concentration in tissues of clams deployed in Tannery Bay and at reference stations.

Figure 8b. Lead content in clams deployed in Tannery Bay and at reference stations.

Figure 9a. Total mercury concentration in tissues of clams deployed in Tannery Bay and at reference stations.

Figure 9b. Total mercury content in clams deployed in Tannery Bay and at reference stations.

Figure 10a. Methylmercury concentration in tissues of clams deployed in Tannery Bay and at reference stations.

Figure 10b. Methylmercury content in clams deployed in Tannery Bay and at reference stations.

Figure 11. End-of-test whole-animal wet weight for clams deployed in Tannery Bay and at reference stations.

Figure 12. Whole-animal wet-weight growth rates for clams deployed in Tannery Bay and at reference stations.

Figure 13. End-of-test tissue weights for clams deployed in Tannery Bay and at reference stations.

Figure 14. Percent lipids for clams deployed in Tannery Bay and at reference stations.

Figure 15. Percent solids for clams deployed in Tannery Bay and at reference stations.

Figure 16. Water temperatures in Tannery Bay and at reference stations.

Figure 17. Average daily temperatures in Tannery Bay and at reference stations.

9.0 APPENDICES

Appendix A	Draft standard guide for conducting field bioassays with marine, estuarine and freshwater bivalves.
Appendix B	Tissue chemistry laboratory reports.
Appendix C	Brooks Rand, Ltd., Standard Operating Procedures.
Appendix D	Statistical analyses and results for chemistry and growth.
Appendix E	Clam measurement data.
Appendix F	Photographs of sampling events and activities.

9.0 APPENDICES

APPENDIX A
DRAFT STANDARD GUIDE FOR CONDUCTING FIELD BIOASSAYS
WITH MARINE, ESTUARINE AND FRESHWATER BIVALVES

DRAFT Standard Guide for Conducting Field Bioassays with Marine, Estuarine and Freshwater Bivalves

1.0 Scope

1.1 This guide describes procedures for obtaining field data concerning: a) Bioaccumulation of chemicals in bivalve tissues; and b) Short- and long-term adverse effects on bivalves associated with exposure to contaminated or uncontaminated water or sediment under natural conditions in the field. These procedures are useful for testing most bivalves although modifications may be necessary for a particular species. They could also be applied to testing other animal groups. The simultaneous, synoptic measurement of bioaccumulation and bioeffects in the same organism permits the calculation of dose-response relationships where the dose can be defined as either the concentration of chemicals in water or sediment, and response is some biological effect like survival or growth or a biochemical estimate of animal health such as percent lipids or percent carbohydrates in bivalve tissues.

1.2 Other modifications of these procedures might be justified by special needs or circumstances. Although using appropriate procedures is more important than following prescribed procedures, results of tests conducted using unusual procedures are not likely to be comparable to results of many other tests. Comparisons of results obtained using modified and unmodified versions of these procedures might provide useful information concerning new concepts and procedures for conducting field bioassays with bivalves.

1.3 These procedures are applicable to water and sediment in marine, estuarine, and freshwater environments with almost any combination of contaminants. The procedures could be regarded as a guide to an exposure system to assess bioconcentration and toxicity of chemicals and the effects of natural factors. Materials either adhering to sediment particles or dissolved in water can be tested.

1.4 Bioconcentration results of these short- and long-term exposures can be reported in terms of absolute concentrations of chemicals in bivalve tissues (e.g., $\mu\text{g/g}$), mass of chemical per animal (e.g., $\mu\text{g/animal}$), rate of bioaccumulation, or bioaccumulation factors (if water or sediment concentrations are measured as well). Toxicity results can be reported in terms of survival or growth rate after exposure for some defined period. Most biochemical indicators can probably be used only as indicators of exposure although some may be used as indicators of effects (e.g., % lipids, carbohydrates, water). Field surveys can be designed to provide either a *qualitative* reconnaissance of the distribution of bioconcentration or toxicity in water or sediment or a *quantitative* statistical comparison of toxicity and bioconcentration among stations or relative to a reference or control site.

1.5 This guide is arranged as follows:

- 2.0 Referenced documents
- 3.0 Terminology
- 4.0 Summary of Guide
- 5.0 Significance and Use
- 6.0 Interferences
- 7.0 Hazards
- 8.0 Experimental Design
- 9.0 Apparatus
 - 9.1 Facilities
 - 9.2 Construction Materials
 - 9.3 Deployment Cages
- 10.0 Test Organisms
 - 10.1 Species
 - 10.2 Size and Age of Test Organisms
 - 10.3 Source
- 11.0 Field Procedures
 - 11.1 Collection
 - 11.2 Handling
 - 11.3 Holding
 - 11.4 Animal Quality
 - 11.5 Presort
 - 11.6 Distribution
 - 11.7 Attachment to PVC Frame
 - 11.8 Deployment
 - 11.9 Retrieval and End-of-Test Measurements
 - 11.10 Analysis of Tissues for Background Contamination
 - 11.11 Collection and Preparation of Tissues for Analysis
 - 11.12 Quality Assurance/Quality Control Procedures
 - 11.13 Sample Containers, Handling, and Preservation
 - 11.14 Logistics
- 12.0 Ancillary Methodology
 - 12.1 Temperature
 - 12.2 Food
- 13.0 Acceptability of Test
- 14.0 Interpretation of Results
- 15.0 Report
- 16.0 Keywords
- 17.0 Annexes

1.6 The values stated in the International System of Units (SI) (the Modernized Metric System) units are to be regarded as standard.

1.7 This standard may involve hazardous materials, operations, and equipment - particularly during field operations in turbulent waters. This standard does not purport to address all of the safety problems associated with its use. It is the responsibility of the user of this standard to establish appropriate safety and health practices and determine the applicability of regulatory limitations prior to use. Specific hazard statements are given in Section 7.

2.0 Referenced Documents

2.1 ASTM Standards:

D 1129 Terminology Relating to Water

D 3976 Practice for Preparation of Sediment Samples for Chemical Analysis

D 4447 Guide for Disposal of Laboratory Chemicals and Samples

E 380 Practice for Use of the International System of Units (SI) (the Modernized Metric System)

E 724 Guide for Conducting Static Acute Toxicity Tests Starting with Embryos of Four Species of Saltwater Bivalve Molluscs

E 729 Guide for conducting Acute Toxicity Tests with Fishes, Macroinvertebrates and Amphibians

E 943 Terminology Relating to Biological Effects and Environmental Fate

E 1023 Guide for Assessing the Hazard of a Material to Aquatic Organisms and Their Uses

E 1192 Guide for Conducting Acute Toxicity Tests on Aqueous Effluents with Fishes, Macroinvertebrates, and Amphibians

3.0 Descriptions of Terms Specific to This Standard

3.1 *bioaccumulation* - the net accumulation of a substance by an organism as a result of uptake from all environmental sources

3.2 *bioconcentration* - the net accumulation of a substance by an aquatic organism as a result of uptake directly from aqueous solution

3.3 *apparent steady-state bioconcentration factor* - a BCF that does not change significantly over a period of days or weeks between sampling intervals, that is, the BCF that exists when uptake and depuration are equal and bioconcentration (net accumulation) is zero over the measurement interval

3.4 *bioconcentration factor (BCF)* - the quotient, at any time during the uptake phase of a bioconcentration test, of the concentration of a material in one or more tissues of an aquatic organism at that time, divided by the effective average exposure concentration at that time of the same material in the solution which contains the organism, units of volume of solution per mass of organism. (BCFs are usually calculated so that the volume of solution, for example 1 L, is about comparable to mass of tissue, for

example, 1 kg, and the BCF is reported without units

3.5 *bioaccumulation factor* (BAF) - as above but including all environmental sources such as food and suspended sediment

3.6 *uptake* - acquisition of a substance from the environment by an organism as a result of any active or passive process

3.7 *depuration* - the loss of a material from an aquatic organism

3.8 *growth dilution* - process whereby the rate of accumulation is exceeded by the rate of tissue growth so that when the concentration is expressed on mass of chemical per mass of tissue over time, it appears as though depuration is occurring because the concentration ($\mu\text{g/g}$) is decreasing

3.9. *degrowth magnification* - process whereby the tissue mass is lost during the exposure period and the chemical mass remains constant over time, so that when the concentration is expressed on mass of chemical per mass of tissue over time, it appears as though bioaccumulation is occurring because the concentration ($\mu\text{g/g}$) is increasing

3.10. chemical concentration - mass of chemical per tissue mass (e.g., $\mu\text{g/g}$)

3.11. chemical content - mass of chemical per whole animal (e.g., $\mu\text{g/animal}$) can be used to normalize the expression of chemical uptake per unit time by eliminating the effects of growth on changing tissues masses

3.12. the words “must,” “should,” “may,” “can,” and “might,” have very specific meanings in this guide.

3.12.1 “Must” is used to express an absolute requirement, that is, to state that a test ought to be designed to satisfied the specified condition, unless the purpose of the test requires a different design. “Must” is only used in connection with factors that directly relate to the acceptability of the test.

3.12.2 “Should” is used to state that a specified condition is recommended and ought to be met if possible. Although violation of one “should” is rarely a serious matter, violation of several will often render the results questionable. Terms such as “is desirable” are used in connection with less important factors.

3.12.3 “May” is used to mean “is (are) allowed to,” “can” is used to mean “is (are) able to,” and “might” is used to mean “could possibly.” Thus the classic distinction between “may” and “can” is preserved and “might” is never used as a synonym for either “may” or “can.”

3.13 For definitions of other terms used in this guide, refer to Terminology D 1129, guide E 729, Terminology E 943, and Guide E 1023. For an explanation of units and symbols, refer to Practice E 380.

4.0 Summary of Guide

4.1 This guide describes procedures for exposing aquatic bivalves to contaminated and uncontaminated water and sediment under natural *in-situ* conditions in the field.

4.2 Although the approach can be used in a variety of aquatic applications to characterize exposure and effects over space and time, the primary assessment endpoints are intended to be bioaccumulation of chemicals in bivalve tissues to assess biological availability and the measurement of growth to assess sublethal effects. Growth is determined from changes in whole-animal wet-weight, shell length, tissue weight, and shell weight.

4.3 Bioaccumulation and growth are compared among test sites for ranking purposes, among reference and treatment sites, or among sites for temporal and spatial variability.

4.4 The toxicity of the water or sediment is indicated by the relative differences in growth among sites or over time. Bioavailability is assessed in the same way by comparing tissue concentrations. It is also possible to use the data to construct dose-response relationships and for source identification of point and non-point discharges by comparing bioaccumulation and bioeffects at various distances away from suspected sources of contamination.

4.5 It is highly recommended that the concentration of chemicals in water and sediment be made to support establishing the relationship between chemicals in various compartments in a preponderance-of-evidence approach.

5.0 Significance and Use

5.1 The test procedure in this guide is intended to simulate the exposure of bivalves under "natural," site-specific conditions. It is important to acknowledge that a number of "natural" factors can affect bivalve growth and the accumulation of chemicals in their tissues. For this reason, it is highly recommended that supplementary measurements be made on those factors most likely to affect bioaccumulation and growth such as temperature, food, suspended sediment, salinity, dissolved oxygen, pH, and the velocity of water currents. These field exposures can also be conducted in conjunction with laboratory bioassays to help answer questions raised in the field exposures. The field exposures can also be used to validate the results of laboratory bioassays.

5.2 Protection of a community of organisms requires averting detrimental contaminant-

related effects on the number and health of individuals and species within that population. These field exposures provide information on the toxicity and bioavailability of chemicals in water and sediment. Protection of the most sensitive species within a community will theoretically protect the community as a whole. Although bivalves generally are not the most sensitive species with respect to acute toxicity, sublethal endpoints such as growth are often more sensitive than mortality endpoints measured in most acute laboratory bioassays. Furthermore, their ability to concentrate chemicals in their tissues and survive collection, handling and deployment make them an excellent surrogate species. Other sensitive endpoints (e.g., reproduction and biochemical markers such as metallothioneins and DNA strand breaks) are currently being developed for a variety of bivalve species. In situ field bioassays with caged bivalves provide a convenient method for measuring bioaccumulation and growth in the same organism at the same time.

5.3 Bivalves are an abundant component of many soft bottom marine, estuarine, and freshwater environments. A number of freshwater species have become extinct over the past few decades and they may be an indicator of exposure to chemical contamination and associated biological effects. Intertidal marine bivalves make up a significant portion of many habitats and provide habitats for many additional species. They exhibit a variety of feeding modes such as filter-feeding and deposit feeding. As such, they are capable of integrating exposure to chemicals dissolved in water and sorbed on sediment particles on the bottom or in suspension. Freshwater bivalves are among the first taxa to disappear from benthic communities impacted by chemical pollution and have been shown to be more sensitive to than several other major taxa. The ecological importance of bivalves, their wide geographic distribution, ease of handling in the laboratory and the field and their ability to filter and ingest large volumes of water and sediment particles make them appropriate species for conducting field bioassays for bioaccumulation and bioeffects.

5.4 There is a very large database in the U.S. that already exists for field monitoring such as the NOAA Status and Trends Program, the California Mussel watch, California Toxics Monitoring Program (freshwater). Similar field monitoring programs exist in other countries. Numerous laboratory studies throughout the world have examined bioaccumulation and bioeffects in bivalves.

5.5 Field bioassays are conducted to obtain information concerning the bioavailability and bioeffects on bivalves after short- and long-term exposure to water and sediment under site-specific conditions. These bioassays do not necessarily provide information about whether delayed effects will occur, although a post-exposure observation period could provide such information if the bivalves were transplanted to a clean control or reference site after the exposure period. The test animals could also be brought into the laboratory under more controlled conditions to make other sublethal measurements such as gonad development, spawning, and an evaluation of the gametes and resulting embryos using other commonly accepted protocols such as the bivalve embryo tests.

This is one approach for establishing links between traditional laboratory bioassays and field monitoring.

5.6 Growth is one of the simplest sublethal endpoints to measure and should be done routinely as part of this test. It is more sensitive than mortality and reductions in growth have been related to adverse effects on bivalve populations. As many growth endpoints as are practical should be measured to provide a preponderance-of-evidence approach for assessing growth. For example, it has been shown that shell growth and tissue growth are decoupled and measuring only one of these endpoints could give a spurious interpretation to environmental effects on growth. Growth endpoints include but are not limited to: whole-animal wet weight, shell length, tissue weight, shell weight. Whole animal wet weights and lengths are non-destructive measurements and can be made multiple times over the course of the exposure period. At a minimum, whole-animal wet weights and lengths should be measured at the beginning and end of the test. Since tissue weights and shell weights provide a different perspective on animal health and may be related to different stressors they should also be measured at the beginning and end of the test. Since these measurements are destructive however, a surrogate sample should be used for the T_0 measurements. As many animals as are measured in chemical replicates at one site should be measured for tissue and shell weights at T_0 . In other words, if there are three chemical replicates of 100 animals each per station, three chemical replicates of 100 animals each should be measured at T_0 . Although tissue dry weights have less variability than wet weights, this approach is not recommended for the following reasons: 1) it is more time-consuming to dry all the tissues and make the weight measurements; 2) if it is a combined bioaccumulation and bioeffects test, the same tissues can be used for chemical analysis as in the wet weight measurements; and 3) this approach has been successful on numerous occasions and has never failed. Nevertheless, if additional testing clearly demonstrates an advantage to measuring dry weights, it would be relatively simple to alter the procedures accordingly.

5.7 Since bivalves are known for their ability to survive high concentrations of chemicals in water and sediment and accumulate high concentrations of those chemicals in their tissues, survival is not a very sensitive indicator of health. Nevertheless, since other factors such as mishandling can also affect survival, and caging the test animals in individual compartments facilitates those measurements, the total number alive and dead should be recorded at the beginning and end of the test. The sum of these numbers may be less than the number of bivalves at T_0 because of shell decomposition or predation. The total number of bivalves could also increase if larval stages have attached to the shells of test animals during the course of the test. Nevertheless, it should be relatively easy to identify the newly attached organisms and remove them from the shells before weighing. Bivalves that are not obviously dead or gaping should be probed to determine if they are still alive. Even then shells may stick together due to mucilaginous material or sediment clumps within the shells. Sometimes dead animals are not identified until the tissues are removed for chemical analysis.

This is another QA/QC check on the survival endpoint measurements.

5.8 Results of the bivalve bioassay can be used to predict bioaccumulation and bioeffects likely to occur on aquatic organisms under comparable field conditions in the assessment area or in other areas except that (a) motile organisms might avoid exposure when possible, and (b) bioaccumulation and bioeffects can be dependent on water or sediment characteristics, dynamics of equilibrium partitioning, and the route of exposure.

5.9 The bivalve field bioassay might be used to determine the temporal or spatial distribution of bioavailability and bioeffects in water and sediment. Test methods can be used to detect horizontal and vertical gradients in bioaccumulation in the water column and in sediments. Response criteria indicating possible toxicity include mortality and sublethal effects. Sublethal effects include, growth, scope for growth, filtration rate, and byssal thread production. **Although scope for growth is potentially more powerful than growth, it requires specialized equipment and training for measuring and is not as straightforward to interpret since the physiological measurements at the end of the exposure period are not necessarily related to the entire exposure period as are the growth measurements. Byssal thread production has also been shown to be a sensitive indicator of animal health but it is extremely time consuming to measure and has the same problem of interpretation and relating the measurement endpoint to the entire exposure period. Growth is the most easily measured endpoint in bivalves that is clearly related to the entire exposure period when measurements are made at the beginning and end of the test.**

5.10 Relative bioaccumulation and bioeffects using different species can be compared by exposing them in the field at the same time and to help explain the effects of various environmental factors on results of such tests.

5.11 Results of combined bioaccumulation and bioeffects are useful for studying biological availability of, and structure-activity relationships among sites.

5.12 Caged bivalve bioassay surveys are often part of more comprehensive analyses of biological, chemical, geological, and hydrographic conditions. A useful summary of field sampling design is presented by Green (28). Statistical correlation can be increased and costs reduced if additional samples are collected or additional *in-situ* monitors are deployed at the same time as the caged bivalves.

5.13 Results of bivalve field bioassays might be an important consideration when assessing the hazards of materials to aquatic organisms (see Guide E 1023) or when deriving water or sediment quality criteria for aquatic organisms (MacDonald et al; CANMET). They might also be useful for determining tissue residue criteria. Bivalve field bioassays might be useful in making decisions regarding the extent of remedial action needed for contaminated sites. They also provide a convenient method for

manipulative field experiments, hypothesis testing, and monitoring specific sites before, during, and after cleanup operations.

6.0 Interferences

6.1 This refined protocol has only been applied to field bioassays with caged bivalves for a few years; the methodology continues to develop and evolve over time as additional refinements are identified and with **emergence** of new research results. Because of the developmental nature of bivalve field bioassays, there are limitations to the methods described in this guide. Strictly speaking, the same can be said of any laboratory bioassay and this limitation should not be considered as a reason for not using the methods described in this guide.

6.2 Results of bivalve field bioassays will depend, in part, on the temperature, water and sediment quality, food supply, physical and chemical properties of the test environment, condition of the test organisms, exposure technique, handling and other unmeasured factors. Other factors potentially affecting results from bivalve field bioassays might include: _____.

6.3 Temperature of the test environment may be either outside the normal range of a particular species or may be near the limit of tolerance which could affect both bioaccumulation and bioeffects. This may be most important in intertidal transplants where air temperatures, particularly in the summer may be unsuitable. Extremely low temperatures could also be problematic.

6.4 Food supply is extremely important because it obviously affects both biological availability and associated biological effects.

6.5 Current speed is extremely important for filter-feeding bivalves because it delivers the food supply to the test organisms. It could also be important for benthic deposit feeders because flushing may reduce the potential effects of chemicals by dilution with clean water from outside the assessment area.

6.6 Salinity is particularly important in estuarine areas where a large river system extending from 0 ppt at the head of a river can have a gradient extending all the way to 33 ppt at the other end. In this particular case, it may be necessary to select several bivalve species for the assessment since no single species could tolerate such a range of salinities.

6.7 Testing at temperatures or salinities other than those at which they were collected might affect contaminant solubility, partitioning coefficients, and other physical and chemical properties.

6.8 Interactions between the sediment particles, overlying water, interstitial water, and

humic substances, and the sediment to overlying water ratio.

6.9 Interactions among chemicals that might be present in water and/or sediment.

6.10 Sediment grain size and organic content

6.11 Photolysis and other processes degrading chemicals during the course of the exposure.

6.12 Intermittent releases of chemicals at the test site based on plant operations

6.13 Maintaining acceptable quality of overlying water

6.14 Excess or inadequate food might change sediment partitioning and water quality parameters.

6.15 Resuspension or intermittent resuspension of sediment during the field bioassay

6.16 Changes in exposure to air during intertidal exposures or flushing with clean offsite water during tidal exchanges.

6.17 Limited opportunity for biological observations during the test because test organisms are in remote locations or because they are too deep or have buried in the sediment.

6.18 Natural chemical properties of the water or sediment that might not be within the tolerance limits of the test organisms

6.19 Recovery of test organisms from the field. Possible interferences include deployment arrays being washed away from storms, buried by underwater sediment shifts, theft, vandalism, or consumption by predators.

7.0 Hazards

7.1 Many materials can affect humans adversely if precautions are inadequate. Therefore, skin contact with all potentially toxic sediments and overlying water should be minimized by such means as wearing appropriate protective gloves (especially when washing equipment or placing hands into test water, effluents, sediment or cleaning solutions, laboratory coats, aprons, and glasses. Respirators may also be necessary in some hazardous waste sites or during oil spills.

7.2 Water and sediment, particularly in effluent areas, might contain organisms that can be pathogenic to humans. Special precautions when working in these areas might include immunization prior to deployments and the use of bactericidal soaps after

working in the water and the sediments.

7.3 Water and sediment might be contaminated with unknown concentrations of many potentially toxic materials. Any potentially contaminated water or sediment should be handled in a manner to minimize exposure of personnel to toxic compounds.

7.4 Use of ground fault systems is strongly recommended during measurements at the beginning and end of the tests where electronic equipment such as portable computers are used to record data electronically to help prevent electrical shocks because water is a good conductor of electricity.

7.5 *Unwanted Introductions*—With the current invasion of unwanted exotic species such as zebra mussels (*Dreissena polymorpha*) in freshwaters and clams (*Potamocorbula*) in marine waters it is important to verify that these species are already found in the area of concern before such transplants should be considered. Planning for regional and local permits sometimes takes considerable periods of time and the planning process should therefore begin early. Other unwanted introductions include parasites or diseases from infected bivalves such as oysters (*Vibrio marinus*). Similarly, unwanted pests could be introduced from microscopic attached forms on the shells of transplanted bivalves such as the freshwater weed *Hydrilla hydrilla*. The other potential problem that is unique to freshwater bivalves is the introduction of glochidia stages that are parasitic on fish for a portion of their life cycle. Although this is common in areas where the freshwater bivalves naturally reside, those interested in preserving fish stocks and their habitats may consider this an unnecessary threat.

8.0 Experimental Design

8.1 Decisions concerning such aspects of experimental design as number of test sites, number of cages per site, number of animals per cage should be based on the purpose of the test and the type of procedure used to calculate the results. The bivalve bioaccumulation/toxicity test can be used to test biological availability of chemicals in water and sediment as well as associated biological effects or to address the relative effects of different water and sediment quality parameters in the field at particular sites. The use of the term “reference” or “control” may be problematic in the field bioassay since true field controls may be impossible. The term reference site may be more acceptable. It should be acknowledged that bivalves transplanted in the overlying water above sediment or transplanted directly on or in sediment may not exclusively accumulate or be affected by contaminants in a particular medium. That is, bivalves in or on sediment may still filter and accumulate contaminants from overlying water. Conversely, bivalves transplanted in the water column may filter suspended sediment and accumulate contaminants from that sediment.

8.2 *Reference/Control Site*—Every field bioassay should have a reference or control site even if it does not fit the standard definition of the term. This site should be that

site in closest proximity without elevated concentrations of chemicals or physical chemical factors known to adversely affect bioaccumulation and growth of bivalves. A natural population of bivalves could also be used for comparative purposes, but these comparisons also should be treated with caution because there is evidence that caged bivalves have different growth rates and different rates of accumulation than natural populations. The reference/control site should represent an area with no contamination and physical conditions similar to the test sites. **Many investigators are now inclined to use multiple reference sites to allow for differences among sites that may be most similar to the treatment sites in other ways.**

8.3 Field Survey Design—Field bioassays can be designed to provide either a *qualitative* reconnaissance of the distribution of chemicals and their effects on bioaccumulation and growth in the caged bivalves or a *qualitative* statistical comparison of bioaccumulation and growth among stations. This is the primary advantage of the caged bivalve approach; the animals can be distributed along physical and chemical gradients to investigate any relevant factor that cannot be controlled. The experimental control is gained by placing the animals in these different environments and using that to develop the experimental design for specific factors. Station locations might be distributed along a known physical or chemical gradient in relation to the boundary of a disposal site, sewage outfall, or effluent pipe, or at sites identified as containing elevated concentrations of chemicals in water or sediment as identified in a reconnaissance survey. Comparisons can be made in both space and time. In pre-dredging studies, pre-effluent reduction, or pre-remedial action, a sampling design can be prepared to assess the bioaccumulation potential and associated effects of the area to be altered. This lends itself to a before-and-after type comparison. Such a design must include the appropriate number of stations the characterize the area.

The object of a *qualitative* reconnaissance survey is to identify sites with the potential for bioaccumulation and associated biological effects like growth. It is often conducted in areas where little is known about contamination patterns. To allow for maximum spatial coverage, the survey design might include only one cage of bivalves at each station. The lack of replication precludes statistical comparisons, but samples from sites where bioaccumulation of chemicals is elevated and growth rates are reduced can be identified for further study.

The object of a *quantitative* comparison is to test for statistically significant differences in effects among sites or between contaminated and uncontaminated sites.

8.4 Statistical Design—The exposure and effects data should be used to determine statistical differences among stations. The null hypotheses appropriate for this design are:

Null Hypothesis #1: There is no difference in growth (as estimated by changes in whole-animal wet-weight, shell length, or end-of-test tissue weight) between

sites and reference station,

Null Hypothesis #2: There is no difference in accumulation of chemicals of concern (as determined by tissue burdens) between sites and reference station, and

Null Hypothesis #3: There is no relationship between *other measurement endpoints* in bivalves and exposure to sediments containing COCs.

The number of cages per site, as well as the number of animals per cage is a function of 1) statistical requirements, and 2) chemical analysis requirements. To satisfy the exposure and effects assessments, the bivalves will be grouped by cages prior to deployment. For the effects endpoints, each individual bivalve represents a replicate. For the exposure endpoint (i.e., bioaccumulation), all individuals of a cage are composited and thus represent a chemical replicate. Therefore, the number of cages created for each station depends on the level of replication desired for the chemical analysis. A commonly used approach is to create three cages for each station, each consisting of 50 to 100 individuals. Three cages, each consisting of 100 individuals (5 bags of 20 bivalves each) will be tied to the PVC frames at each site. However, the final number of individuals is a function of the tissue requirements for the chemical analyses being performed and the tissue mass of the individual bivalves. For example, given three cages each consisting of 100 bivalves, the “n” for the effects assessment = 300, and the “n” for the exposure assessment = 3.

All test parameters measured at the end of the test (i.e., whole-animal wet-weight, shell length, tissue weight, shell weight and possibly, contaminant concentrations in tissues) will be statistically analyzed. Summary statistics (e.g., mean and standard deviation) will be calculated for each of these parameters on a station-by-station basis. The growth and tissue residue data should be assessed for normality and common variances before continuing with hypothesis testing. The null hypotheses should be assessed by conducting an ANOVA, or its non-parametric counterpart. If statistical differences are found, Dunnett's multiple range test, or its non-parametric counterpart, should be used to determine which stations are different from the reference(s).

The large “n” and detailed process used to ensure a very close, even size distribution of bivalves at the start of the test (see Section 11.6) results in a high degree of statistical power. It is possible to detect statistically significant differences between reference and test stations at the **0.2 g level what is this?**. An environmental significance, or likely adverse effect to the community, is expected when both a statistically significant difference is observed ($\alpha = 0.05$) **and** there is a 10 to 25 percent absolute difference between the test and reference station (**need citation here**).

The minimum desirable number of cages and organisms per cage should be calculated from (a) the expected variance within cages, (b) the expected variance between cages,

and (c) either the maximum acceptable width of the confidence interval on a point estimate or the minimum difference that is desired to be detectable using hypothesis testing (30). As the number of cages (that is, experimental units) per station increases, the number of degrees of freedom increases, and therefore, the width of the confidence interval on a point estimate decreases, and the power of a significance test increases.

At a minimum, each deployment cage should consist of one frame and five bags. The separate bags help to subdivide the test animals into similar groups without having one bag containing all the animals which may become too long and unwieldy. The number of animals per bag varies depending on the experimental design and the amount of tissue needed for chemical analyses. If replication for chemical analyses is required, tissues from all individuals of a cage will be composited to form one chemical replicate.

8.5 Test Duration—The caged bivalve bioassay begins when test organisms are placed in the water at a particular station. Bivalves should be exposed to site-specific conditions for a minimum of 30 days. An exposure period of less than 30 days is not generally recommended, particularly if metals are among the chemicals of concern. Chemical equilibrium for most chemicals is generally achieved in marine and freshwater bivalves within a period of approximately 60 - 90 days. However, if both exposure and effects endpoints are being measured, it may be advantageous to continue the test for 60-90 days to facilitate chemical equilibrium and allow adverse effects like growth an opportunity to manifest themselves.

9.0 Apparatus

9.1 Facilities—Sources of water and power and the ability to be protected from rain, snow, and wind can be of considerable help in sorting the animals at the beginning of the test and making the appropriate measurements and removing tissues for chemical analysis at the end of the test. Preparations can be made outdoors, but inclement weather can interfere with making accurate measurements. The portable analytical balance is particularly sensitive to winds although some protection can be provided by a wind barrier such as a lean-to. Making these measurements aboard boats or floating piers is not recommended.

9.2 Construction Materials—Equipment and facilities that contact the test water, sediment, and organisms should not contain substances that can be leached or dissolved by aqueous solutions in amounts that can adversely affect test organisms or add to the accumulation in their tissues. In addition, equipment and facilities that contact test water, sediment, and organisms should be chosen to minimize sorption of test materials from water. Glass, Type 316 stainless steel, nylon, high-density polyethylene, polycarbonate and fluorocarbon plastics should be used whenever possible to minimize dissolution, leaching, and sorption, except that stainless steel should not be used in saltwater. Concrete and rigid plastics may be used for weights,

and for cages, but they should be soaked, preferably in flowing seawater, for a week or more before use (9). Brass, copper, lead, cast iron pipe, galvanized metal, and natural rubber should not contact water, sediment, or test organisms before, or during the test.

9.3 Deployment Cages

9.3.1 The basic concept behind bivalve cages for field deployments is to maximize mesh size to maximize water flow to the test animals yet maintain a mesh size small enough to contain the test animals. Cages should be constructed of non-toxic materials as specified above and should be allowed to leach as described. Although many investigators have used non-compartmentalized cages with large numbers of animals in a clump, a number of studies have shown that such clumping can affect bioaccumulation and growth. The experimental control is enhanced with equal exposure to each bivalve and this can be accomplished with compartmentalized cages so that an accurate record can be maintained on individuals. This also increases the statistical power of the test, and permits multiple growth measurements on individuals which can be paired with individuals measurements of tissue residues although there is usually not sufficient tissue in one animal with standard chemical analysis.

9.3.2 Cages can be rigid with fixed compartments, as in plastic trays, or they can be flexible with compartments, as with mesh tubing attached to a rigid frame (Figure XX). The most versatile system combines a rigid framework constructed from Schedule 40 PVC pipe to which flexible mesh bags, created from mesh netting, are attached. The mesh netting used for these bags is similar to that used in bivalve aquaculture (i.e., oyster cultch net). The mesh bags are securely fastened to the PVC frame with knots and/or plastic cable ties (note: do not use cable ties with metal stop). Individual compartments in each bag are formed by securing a plastic cable tie around the mesh material in between individual bivalves. This method facilitates tracking individuals throughout the test and eliminates the need to mark or notch individuals. This design maximizes the experimental control of the test by allowing caged animals to be positioned at almost any point in the water column or on the sediments. Care should be taken so that the cable ties are not so tight that they constrict the mesh to the point that it does not allow the shell to open during respiration or to allow for bivalve respiration during the exposure period.

9.3.3 The final dimensions of the deployment cages depend on the size of the individual test organisms. Adequate space should be provided in each compartment to allow test animals to grow during the exposure period. For rigid cages, it is recommended that the individual compartments be at least twice the actual length, width, and height of the test animals. Because the flexible mesh is tubular in form (usually a 6" diameter material is used), it is not necessary to adjust the width/height dimensions. The length of each compartment in the mesh bag (i.e., the distance between constricting cable ties) should be approximately twice the length of the

individual within the compartment. The mesh bag should be long enough to accommodate the desired number of animals per bag (usually 10 to 20 depending on length of bivalve) plus sufficient material to allow secure attachment to the PVC frame. It is recommended that 12" of netting be available on either end of the bag for attachment. [Example: to accommodate 20 mussels 1" in length, the mesh tube should be 40" (2 x 20) + 24" (to attach to the PVC frame) = 64"] The PVC frame should be approximately 2" longer than the space occupied by the bivalves (in this example, a 42" long frame would be appropriate). The width of the frame should be about 2" greater than the distance occupied by all mesh bags to be attached to the frame when laid side-by-side (in this example, if 10 mesh bags are to be attached, each being 1" wide, then the PVC frame should be about 12" wide). (See Figure XX for example details)

9.3.4 Deployment cages should be constructed at least one week prior to initiation of the field study to allow sufficient time for soaking and leaching of volatile compounds associated with the PVC and the gluing compounds. Drill the PVC pipe approximately every 9 inches with a 1/4" hole to allow water to enter the pipe and maintain neutral buoyancy. Do NOT drill corners. The appropriate primer and glue should be used during construction of the deployment cages.

9.3.5 The final cage design should be appropriate for the environmental conditions, test duration, and test hypotheses. Table XX summarizes the more commonly used designs and provides application examples.

Insert Table XX:

Flat cage: suspend from floating piers, deploy directly on sediments

Table design: intertidal areas; legs used to stabilize unit and maintain position in high energy areas

Box design: mid-water deployments; deploy directly on sediments.

Use of predator/snow-shoe material

10.0 Test Organisms

10.1 *Species*—The environmental requirements and sensitivity of a prospective test species of bivalve should be established before it is widely used in field tests. The sensitivity and bioaccumulation potential of a prospective new test species should be compared with a reference species such as *Mytilus*, *Crassostrea*, *Corbicula*, *Dreissena*, *Elliptio*, or *Rangia* before the new species is used in routine field transplants. This is most commonly established in side-by-side transplants. The tolerance of a test species to variations in water quality parameters (temperature, salinity, dissolved oxygen, pH) and sediment characteristics (particle size, organic enrichment, sulfides) should be established before responses can be ascribed to contaminant effects. Choice of test species may have to be modified to accommodate conditions at different test sites and the question that is being asked in the experiment. Test species selection should be

based on conditions at the natural habitat of the species. The bivalve species to be used in the field bioassays should be selected on availability, sensitivity to chemicals of concern, tolerance to site-specific conditions (for example, temperature, salinity, food, water currents, grain size), and ease of handling in the field. Collectively, these criteria might dictate selection of a particular species. Ideally, species or genera with wide geographic distributions should be selected, so that test results can be compared among different sites and different test conditions. Depending on the particular question that is being asked, it may be most important to select species that are found, have been found, or could be found in the assessment area. Species used should be identified with an appropriate taxonomic key, and identifications should be verified by a taxonomic authority. It may be a good idea to conduct a small pilot study to ensure that the test animals can survive under the particular environmental conditions at a particular site. Tables XX and XY identify bivalve species previously used in transplant studies to assess the bioaccumulation and toxicity of contaminated water and sediment, respectively. The more commonly used species include:

10.1.2 *Mytilus sp.* is an intertidal bivalve that has been successfully used in transplant studies since the late 1970's (REF). The sensitivity of this species to salinities less than 10 g/kg limits its use to testing marine/estuarine areas, but the large data base that has been developed for the response of *Mytilus sp.* to a variety of habitats and chemicals establishes its usefulness as a test species as well as a reference species for comparing the sensitivity of other species. Species of the genus *Mytilus* are widely distributed on the West Coasts of North America (REF).

10.1.3 *Corbicula fluminea* is a freshwater bivalve (clam) that has been used extensively in field transplants and laboratory studies (REF). Their sediment burrowing ability, ease of handling, abundance in freshwater environments, and importance as probable prey (REF) make them good candidates for freshwater environments. Numerous laboratory studies have also been conducted on this species and several symposia have been conducted on its biology and ecology.

10.1.4 *Elliptio complanata* and *Anodonta grandis* are freshwater unionid mussels that have been used extensively for monitoring water column and sediment exposures in northern parts of the US and in Canada. Their burrowing ability, ease of handling, abundance in freshwater environments, and importance as probable prey (REF) make them good candidates for freshwater environments. They can be transplanted in the water column, into test sediments in containers or simply placed in bags on the bottom. Numerous laboratory studies have also been conducted on these species.

10.1.5 *Dreissena polymorpha* is a relative newcomer to bivalve field bioassays, but the rapid proliferation of this nuisance species has rapidly increased the number of laboratory and field studies that have been conducted on bioaccumulation and growth, among other things. In this species in particular, and with the others, it is important to limit unwanted introductions where the species are not already found.

10.1.6 *Macoma nasuta* is a marine clam that has been used extensively in laboratory and field studies to assess bioaccumulation and growth. It is a marine/estuarine species that is commonly found in many environments on several coasts. It has been successfully transplanted in many different areas, and there are a number of supporting laboratory studies.

10.1.7 *Rangia cuneata* is an estuarine species that is quite tolerant of freshwater conditions. It has been used in a number of field transplants as well as laboratory studies.

10.1.8 *Crassostrea sp.* has been used extensively in transplant studies in marine and estuarine studies. Oysters survive and grow better than marine mussels at lower salinities and accumulate many contaminants such as TBT and copper by about a factor of two above mussels. They are also more difficult to measure because of the irregular shell shape.

10.2 *Size and Age of Test Organisms*— All organisms should be as uniform as possible in age and size. The age or size class for a particular species should be chosen so that sensitivity to or bioaccumulation potential is not affected by state of maturity or reproduction. It is recommended that specimens in a sub-adult age class be used because this age class has the greatest potential for growth of somatic tissue, reproductive tissue, and shell. If adult specimens are used, the study should not be conducted during active spawning to prevent loss of accumulated lipophilic chemicals.

Shell length should be used to select bivalves. Shell length (for mussels = longest axis, generally from the anterior end near the beak to the leading posterior end; for **clams = _____**) should be determined with vernier calipers. The final size range used in the field study should be based on the maximum number of animals in the minimum size range. It is recommended that all test animals fall within a 5-mm range in shell length at the start of the test.

Bivalves can be counted and sorted according to size to determine whether sufficient numbers have been collected in the appropriate size range. To minimize variability in bioaccumulation and growth (or other bioeffects measurements), it is more important to minimize the size range rather than select a particular size. It should be remembered, however, that there is a tendency among many bivalves for the smallest animals to grow at the greatest rates and accumulate the highest concentrations of contaminants.

10.3 *Source*—All individuals used in a field study should be from the same population, because different populations of the same species might have different sensitivities to or bioaccumulation capacities of the same contaminant. Bivalves are usually collected from wild populations in an uncontaminated area although it may be easier to purchase species commonly used in aquaculture from field grow-out facilities or laboratory culture facilities. The advantages of using aquaculture animals is that the genetic and

environmental history of the test animals is well-documented and the assurances of being uncontaminated are greater. If animals are collected from the wild (or even collected from aquaculture) they should be measured for contamination in their tissues, particularly for the contaminants of concern. Collecting permits for field-collected bivalves might be required by some local and state agencies.

11.0 Field Procedures

11.1 *Collection*—Bivalves can be obtained from either natural populations or from culturing facilities. Natural populations should be sampled with methods appropriate to the tidal range. Intertidal populations can be sampled by hand; subtidal populations by SCUBA or with a small biological dredge or grab. Infaunal bivalves can be separated from sediment by gentle sieving. Sieves and containers used to collect and transport bivalves should be marked “live only” and should never be used for working with formalin or any other toxic materials. Water used for sieving should be at the same temperature and salinity as bottom water at the collection site. Particular care should be used when removing mussels from substrates to which they have attached to avoid damage to the byssal gland. Damage or removal of the byssal gland can lead to mortality. A knife or scissors should be used to sever the byssal mass and reduce the possibility of injury.

11.2 *Handling*—Bivalves should be handled as little as possible. When handling is necessary, it should be done carefully, gently, and quickly so that organisms are not unnecessarily stressed. Every effort should be made to maintain bivalves in well-aerated, flowing water for as long as possible between collection, sorting, and deployment procedures. When transporting bivalves over great distances that require extended periods of time, it is better to keep them moist and cold than to maintain them in water that could become stagnant and low in dissolved oxygen. This is best accomplished by keeping them in moist towels in an ice chest with cooling material.

The care of test organisms should be considered of paramount importance in conducting the field bioassay. If transport from the collection site to the measurement facility requires several hours, bivalves should be transported in moist paper, kelp, or other suitable non-toxic material. They should also be maintained at a temperature similar to that from which they were collected or slightly lower. Lower temperatures will reduce their metabolic rate and minimize energy requirements. During the rough sort, animals should also be kept out of water if sorting will take several hours but again they should be kept cool and moist. During the final sort when the most accurate weight and length measurements are taken animals should be completely submerged in water for at least 10 minutes to allow them to purge air from within their shells. Since the density of animals has been reduced by this time and the shells have been cleaned it is easier to maintain them in clean water. Nevertheless, water temperature should be checked regularly, it is usually a good idea to keep double-plastic bags filled with ice, particularly in temperate regions if the holding water starts to approach room

temperature. A rapid rise in temperature of adult organisms close to the spawning season could even induce spawning which would add another unwanted variable to the test.

11.3 *Holding*—Bivalves should be fully acclimated to the test temperature and salinity by holding them in the laboratory or in the field at conditions most similar to their deployment conditions. This also accomplishes another purpose in that in larger studies it is almost impossible to collect, sort, and deploy large numbers of animals in the same day. Bivalves should be collected the day before sorting to maximize the sorting time available during the next day and then the animals can be held overnight before transport to the deployment sites. Field-collected animals should be held for the minimum time period before deployment to avoid possible effects from holding either in field cages or laboratory tanks.

If test organisms are cultured or held for an extended period of time in the laboratory or at field control sites, the affect of this holding should be compared to that of animals freshly collected from the field to assure that holding stresses do not affect bioaccumulation or bioeffects.

During counting and sorting, the temperature of the water containing the bivalves should be held near or below the temperature at which they were collected, and should remain close to the holding temperature. The holding containers should be provided with flowing or aerated water at or near the collection/deployment temperature and salinity. If changes in temperature and salinity are necessary to bring bivalves from the collection site conditions to test site conditions, adjustments should be made gradually to allow the bivalves to acclimate. Infaunal bivalves will usually remain in the holding sediment until the sorting phase of the test and can be easily retrieved. Supplementary feeding should not be necessary since the holding period will be minimized in the laboratory and animals being held in the field will continue to feed.

11.4 *Animal Quality*—All bivalves used in a test must be of the same species and acceptable quality. A qualified bivalve taxonomist should be consulted to ensure that the animals in the test population are all of the same species. This is particularly important with some freshwater bivalves where species differences may be extremely difficult to determine based on shell morphology. Even in the genus *Mytilus* there are subtle differences that may not be obvious, particularly in areas where the two species could be found side-by-side.

Although it is extremely difficult to determine healthy animals when the shell is closed, gaping animals that close very slowly or do not close at all should not be used. Animals that smell putrefied should be pulled by the valves to determine if they are really alive. Enough bivalves should be collected to provide at least 20 percent more individuals than are required for the test.

Bivalves in holding containers should be checked repeatedly before the initiation of the test. Dead animals or animals that will not close easily should be discarded and replaced with some of the “extra animals” collected during the original “rough-sort” procedure. If greater than 5 percent of the bivalves appear unhealthy during the 48 hours preceding the test, the entire group should be discarded and not used in the test.

11.5 *Presort*—All bivalves collected will be presorted into 1 mm size groups to determine the narrowest size range with the maximum number of specimens. All bivalves in the predetermined sub-adult size class should be initially retained. After the pre-sort, the number of bivalves per each size category should be determined. The minimum range representing the greatest number of animals between X and Y mm will be used.

11.6 *Distribution*— A randomized distribution process (Salazar and Salazar, 1995) should be used to ensure an even distribution of bivalves across stations based on size. Once the final size range has been identified, the animals will be remeasured for length, weighed for the first time, and distributed to the mesh tubes as shown in **Figure X**. All animals in a 1-mm grouping are distributed among the mesh tubes before using animals from a larger size group. This process is repeated for the remaining size groups until the mesh tubes are filled; each station then has approximately the same number of individuals from the each size group.

Prepare the mesh bags that will be used to hold the bivalves during deployment. The mesh size should be just small enough to retain the bivalves within their “cage” yet large enough to permit adequate passage of water. The mesh bags (approximately 6 feet in length) should be knotted 1 foot from the end; an identification tag is attached to the mesh bag at the knot with a plastic cable tie. Identification tags should be made of durable plastic material. A water indelible, permanent marker should be used to label tags with cage number and bag number: **2—3**, indicates Cage 2, Bag #3. Color coded beads strung through a plastic cable tie and fastened to the mesh bag can also be used for purposes of identification.

Bivalves must be maintained in water during the measurement and distribution process, and the temperature must be maintained as close as possible to ambient. In most temperate latitudes this is accomplished by using plastic bags of ice and monitoring temperature with an aquarium thermometer that remains in the holding tray. It is essential that the bivalves be submerged prior to measurement. They must NOT contain any air between their valves. Do not use individuals that float, are buoyant at one end, or do not close upon stimulation. Bivalves that float contain air which must be released prior to use. Floating individuals can be transferred to a separate container, where, if left undisturbed, they will purge the trapped air.

The distribution process is based on bag number; all bags of a common number are filled at a given time. To initiate the distribution process, gather all bags that have a

“—1” on the label; there should be one for each cage number. Attach these bags to the PVC distribution frame in cage number sequence. Using the largest size class first, randomly take one specimen from the holding container, make sure it is alive and shells tightly closed, blot excess water from exterior of individual, and measure its length and weight. Record this data electronically to the Excel spreadsheet created for summarizing the data. Also record this information manually on the hard copy data sheets. Drop this individual into the first mesh bag on the distribution rack; affix a 4" cable tie around the mesh material above this individual; DO NOT OVER-TIGHTEN THE CABLE TIE, it should only be tight enough to prevent the animal from passing through. Randomly take another specimen from the holding container and measure its length and weight. Record data electronically and manually, drop individual into next mesh tube and affix cable tie. Repeat process until one individual has been placed into each mesh tube. Continue adding bivalves, one at a time to mesh tubes, completing one “row” before another is started. Use the averages generated on the Excel spreadsheet to compare cages and ensure a close, even distribution. There should be sufficient space between individuals to permit movement; total space between cable ties should be about 2X the length of the individual inside the “compartment.” The spreadsheet can be customized to keep a running tally of mean weights and lengths to help identify outliers that could actually be dead with shells stuck together, animals that have not been purged of air, or animals that do not fit the norm of the weight length relationship established for the majority.

Note: use the compartmentalized trays for the bivalves to be sacrificed for the T_0 , or initial, chemical measurements. Keep animals in order. At the end of the distribution process, remove the tissues for chemical analysis (see following section for procedures).

When all of the “Bags —1” have been filled, knot or cable tie the open end, leaving a tail length of approximately 1 foot. Place completed bags into cooler lined with ice and moist paper towels.

Repeat process, until all bags are filled. Sort bags by Cage Number, and using a cable tie, group these bags together. Transport bivalves to holding area (usually the reference site) and place in water overnight, or until ready to attach bags to the PVC cages.

To ensure statistical similarity among stations, an Analysis of Variance (ANOVA) is run on both length and whole-animal wet-weight data. Use the data in Excel spreadsheet, and the Excel statistical package to conduct an ANOVA. If the means are statistically different, redistribute test animals to bring eliminate this difference.

11.7 Attachment to PVC Frames—Attach the mesh bags to the PVC frame by knotting the tail ends of the mesh directly to the PVC. If there is insufficient material to make a secure knot, use 6" cable ties to firmly attach mesh to the PVC frame. Allow a little

slack in the mesh bag during attachment; the mesh should not be stretched so tightly that it restricts bivalve movement. If using a temperature recording devices, which is highly recommended since they are relatively inexpensive and help quantify one of the major factors affecting bivalve growth, attach to the frame at this time. If predators are of concern, wrap the PVC frame with a heavy duty plastic mesh (approximately 2.5 cm mesh size).

It may be necessary to adjust the length of the mesh bags so that they can be attached to the PVC frame without being too taught or too loose. During the attachment process, slide the cable ties as necessary to increase the over all length of the mesh bag without compromising the space available for each individual (i.e., do not decrease the space between animals so that there is insufficient space for them to open their valves during respiration).

11.8 *Deployment*—Deploy caged bivalves at sites. Use appropriate weights, anchors, and line to ensure the cage remains at the desired location.

11.9 *Retrieval and End-of-Test Measurements*—At each station, the PVC frames will be returned to the shore where they will be rinsed with site water to remove any foreign material. The exterior of the shells and the mesh bags will be wiped with paper towels if a sheen or other coating is present. A separate ice chest lined with ice and moist paper towels will be used to transport the bivalves to the processing site.

At the processing site, all bags constituting an cage will be processed together. Starting with Bag—1, remove the bivalves, starting at the end of the bag with the plastic label. Place bivalves into a compartmentalized plastic tray that has been drilled with holes to allow water circulation. **RETAIN ORDER OF Bivalves.** Place Bag—2 individuals in the same tray, starting with individual number 1 of Bag—2 following individual number 20 of Bag—1. Repeat with remaining bags until all bivalves are transferred from the mesh bags to the compartmentalized tray. Set this tray of bivalves into a tub containing clean water. It is essential that the bivalves be submerged prior to measurement. They must NOT contain any air between their valves. Begin the length and weight measurements, measuring one individual at a time and recording the data both electronically and manually. After the individual is measured, place it into a compartmentalized tray; this tray is not placed in a tub containing clean water. Again, retain order of individuals. For dead or missing individuals, the cell for that individual on the Excel spreadsheet is left blank; note on the hard copy data sheets “M” or “D” for these individuals. It is important to make the distinction between missing and dead for the percent survival calculations.

After all animals of an care are measured and weighed, begin the tissue removal process as described above. Shuck the tissues and then weigh the soft tissues for each individual. Place empty shells, in order, on the foil-lined tray. After all tissues have been weighed and transferred to the appropriate sample container, weigh each of

the shells, recording data both electronically and manually to the data sheets. Discard shells after weight measurements are complete. **Additional endpoints could be gained by measuring the thickness of the shell and relating that to other metrics but this is a very time-consuming process and may not be very cost-effective.**

11.10 Analysis of Tissues for Background Contamination— Analysis of the test organisms for the contaminants of concern as well as other chemicals to which they may have been exposed should be conducted. Bivalves may be used without analysis of chemical concentration if the bivalves are obtained from an area that is monitored for chemical contamination and known to be free of toxicants or if the tissues of those bivalves have been monitored regularly as in culture facilities. Bivalves from contaminated areas should not be used in field bioassays unless the experimental design specifically requires use of that population. This is most likely to occur where the purpose of the study is to rank sites with respect to relative exposure and bioeffects.

11.11 Collection and Preparation of Bivalve Tissues for Chemical Analysis—All equipment used in sample collection should be thoroughly cleaned before each sample (i.e., chemical replicate) is processed. All instruments should be of corrosion resistant stainless steel, anodized aluminum, or borosilicate glass. If corrosion resistant stainless steel is unavailable, use regular stainless steel products, carefully checking gear before each use for signs of rust, pitting, or corrosion. Do not use gear if rust, pitting, or corrosion is evident. Before each use, all instruments should be cleaned according to the following process: wash with Alconox, hot tap water rinse, deionized/distilled water rinse.

Upon retrieval of caged bivalves from the collection site, inspect outside of shells for sediment, oily sheen, or other debris. While still in their mesh netting, rinse bivalves several times with clean water (i.e., the same water to be used for holding bivalves during growth measurements). If foreign material is still present, blot shells with clean paper towels to remove.

During tissue collection, the order of bivalves must be maintained; tissue weights are recorded by individual and will be paired with whole-animal wet-weights and other size metrics. Use the compartmentalized trays for holding bivalves prior to shucking, and maintain order after tissues are removed.

It is not necessary to keep bivalves in water once the growth measurements are made. Therefore, after performing the growth measurements, place bivalves in compartmentalized trays; do not put these compartmentalized trays in larger tubs containing water. It may be necessary to use a grid, or other device, to aid in maintaining order of tissues and shells during the shucking and weighing process.

Cover cutting boards with aluminum foil; rinse work surface of foil with 95% ethanol,

allow to air dry.

If gloves are worn during the shucking process, ensure that they are powder free. Wash hands thoroughly with Alconox or replace gloves between chemical replicates.

Take first individual of the chemical replicate and place on covered cutting board. Slide the knife blade between bivalve shells, severing posterior and anterior adductor muscles. Spread the shells apart to reveal soft tissues.

If preparing bivalve tissues, it may be necessary to notch the shell prior to inserting knife blade between bivalve shells. Use a separate knife designated only for the purposes of shell notching. Be sure that none of this shell material is combined with the soft tissue material.

Using tip of knife blade, separate tissue from shell, scraping as much of adductor muscle from points of attachment as possible.

Holding tissues to shell, tip shell to drain excess liquid . (Note: it may be necessary to use paper towels to dam a work space on the foil-covered cutting board to prevent bivalve fluids from flooding work area.)

Keep tissues in shell after complete separation. Use shell as a “holding dish” until tissue weights are made. Place shucked bivalve on a tray lined with aluminum foil, keeping bivalves in order and sufficient space between individuals to prevent the shell of one from touching the soft tissue of another. Minimize exposure of tissue to hands, aluminum foil, and any other surface other than the interior of the specimen’s original shell.

Repeat process until all bivalves constituting a “chemical replicate” are shucked.

Prepare a weighing pan from aluminum foil, rinse with 95% ethanol, and place on electronic balance. Tare balance.

Pick up first specimen, and using shucking knife blade tip, slide tissue onto weigh pan. Allow balance to stabilize. Record weight electronically to Excel spreadsheet and by hand to hard copy. Tare material on balance.

Continue adding tissues, one at a time, recording weights of each individual. Tare after each addition.

When all tissues of a “chemical replicate” have been weighed, transfer tissues from weigh pan to prepared sample jar by gently sliding them off the foil. Tightly cap sample jar, affix prepared label, and place collected tissues in freezer.

Discard foil from cutting board and weigh pan. Decon all sampling equipment before proceeding to next sample.

11.12 *Quality Assurance/Quality Control Procedures*—The quality assurance/quality control (QA/QC) procedures for the bivalve measurements will involve remeasuring 5 percent animals. These QA/QC measurements are performed during the initial measurement process. QA/QC length measurements and whole-animal wet-weight measurements within ± 5 percent of the original measurements will be considered to be within acceptable error measurements.

Precision and accuracy are fundamental to obtaining reliable, usable data. Precision is a measure of the reproducibility among individual measurements under similar conditions; it is the ability of the same measurements to be made time after time. Precision is assessed by performing multiple measurements for the parameters. The following approach will be used to determine the precision of the measurements made on the individual animals. At test initiation, 5 percent of the bivalves will be remeasured for shell length and whole animal wet-weight. The remeasuring of animal length and weight occurs throughout the measurement process as each series of bags is processed to ensure that all measurements are within the acceptable limits. **A 1.0 mm (± 0.5 mm) variance in length and a 0.5 g (± 0.25 g) variance in weight are the recommended limits.** If the results of the remeasurements fall outside of these limits, the previous batch of 100 individuals will be remeasured. The hard copy data sheets contain a separate row for the QA/QC data. These QA/QC measurements should be made on the last “row” of bivalves to be entered into a series of bags.

Accuracy is an expression of the degree to which a measured or computed value represents the true value; the ability of the measuring device to provide the true value. The accuracy of the measuring devices will be determined according to the standard operating procedures for each measuring device. For the balance, this involves calibrating the instrument with a standard weight (200 g). After every 100 measurements made on the balance, the standard weight will be applied to the balance. If the balance is off by more than 1 percent (2 g), the balance will be recalibrated and the previous batch of 100 individuals reweighed. The accuracy of the calipers will be checked by completely closing the device and recording the displayed measurement, which should be 0.000 mm. If the caliper displays a value greater than 0.5 mm, the unit will be re-zeroed and the previous batch of 100 individuals remeasured.

As part of the standard methodology, bivalve weight and length measurements are recorded both electronically onto a computer disk and by hand into a laboratory notebook. This serves two purposes: 1) the electronic data are cross-checked later for accuracy; and 2) as a backup for the electronic record.

The primary procedure used to assess the condition of the test animals is complete

closure of the shell upon light stimulation. Bivalves that do not completely close their shells upon movement or light touching of the shell are considered unhealthy and will not be used in the study. In addition, animals that have broken shells or holes in their shells will not be used. If, during the measurement and distribution process, individual bivalves are "floating," these individuals will not be measured and weighed until they have purged the air trapped between their shells.

11.13 *Sample Containers, Handling, and Preservation*—Precleaned sample containers will be purchased from a supplier or provided by the analytical laboratories. Each jar will be sealed, affixed with a completed label, assigned a unique tag number, and stored under appropriate conditions. Sample labels will be made of waterproof material and will be self-adhering; an indelible pen will be used to fill out each label. Each sample label will contain the project number, sample identification, preservation technique, analyses, date and time of collection, and initials of the person(s) preparing the sample. A completed sample label will be affixed to each sample container. In addition, a unique numbered tag will be affixed to each sample container. Tissue samples will be frozen prior to analysis.

11.14 *Logistics*—Weather and time of year can have a major impact of a successful study. The logistics of obtaining test animals, reaching the field stations, and safely conducting the study should be carefully addressed prior to the onset of any field work. All options for reducing travel time (i.e., air, boat, or auto travel) should be considered; the final decision should have a contingency plan to ensure meeting project schedules.

12.0 Ancillary Measurements

12.1 *Temperature*—Marine and freshwater species should be selected to match the site-specific temperatures in the area of concern. Ideally, if species are naturally found in the area or have been found in the area in the past, it is a good indication that temperature tolerances are appropriate. Since temperature could influence bioaccumulation and growth, it is important to monitor temperature during the course of the test using *in-situ* temperature monitors.

12.2 *Food*—As with temperature, if indigenous populations of the bivalves of choice are found in the area of concern, it is a good indication that there is adequate food to support caged bivalves in the area. Since food could also influence bioaccumulation and growth, it is helpful to measure parameters such as chlorophyll a, particulate organic carbon and suspended solids during the course of the test.

13.0 Acceptability of Test

13.1 Survival of bivalves at the control site during the test is an indication of the health of the population and other factors. If a mean or greater than 20% mortality occurs in

the controls, or if individual replicate control mortality values exceed 30%, test results must be interpreted with caution. Similarly if significant growth is not measured during the exposure period, it could suggest that animals were unhealthy and the relative concentration of contaminants should also be interpreted with caution.

13.2 Mean survival among all stations should be 80 percent or greater.

14.0 Interpretation of Results

15.0 Report

15.1. A record of the results of an acceptable caged bivalve exposure and effects test should include the following information either directly or by reference to existing publications.

15.1.1 Names of test and investigator(s), name and location of laboratory, and dates of initiation and termination of test;

15.1.1 Source of test animals, scientific name and how verified, initial whole-animal wet-weights, lengths, and estimates of tissue weights as well as end-of-test whole animal wet-weights, lengths, and estimates of tissue weights. Means, ranges, and standard deviations of all measurements will be included. Length is measured as the distance from the tip of the umbo to the distal valve edge.

15.1.2 Description of the experimental design and cages, including any attached instrumentation and predator deterring devices, water depth and depth of cages, the number of animals per test site, station coordinates, and any other outstanding features of the area to assist in station-finding.

15.1.3 Mean, range and standard deviation of dissolved oxygen and how it was measured.

15.1.4 Averages and ranges of the acclimation temperature during the measurement and distribution process as well as the time spent out of water while in transit to the measurement location at the beginning of the test and while in transit to the deployment locations at the beginning and end of the test.

15.1.5 Percentage of test animals that died, showed signs of disease, stress, or other adverse effects.

15.1.6 Reproductive state of the test animals including degree of gonad development or if any animals spawned either during the measurement or deployment phases of the test.

15.1.7 Description of water, tissue and sediment samples analyzed, and methods used to obtain, prepare, and store them.

15.1.8. Methods used for, and results (with standard deviations or confidence limits) of, chemical analyses of water quality and concentration of chemicals in water, sediment, and tissues, including validation studies and reagent blanks.

15.1.9. Methods used for, and results of, measurements of lipids or fats.

15.1.10 A table of data on concentrations of chemicals (and lipids or fats if available) in water, sediment, and tissues in sufficient detail to allow independent statistical analyses.

15.1.11 A table of data on growth rate and survival data in sufficient detail to allow independent statistical analyses.

15.1.12 Ratio of wet to dry tissue weights to allow more accurate conversions of wet versus dry weights and provide comparability with other data.

15.1.13 Anything unusual about the test, any deviation from these procedures, and any other relevant information.

15.1.14 Published reports should contain enough information to clearly identify the methodology used and the quality of the results.

16.0 Keywords

field bioassay *in-situ* exposure effects bivalve bioaccumulation growth

17.0 Annexes

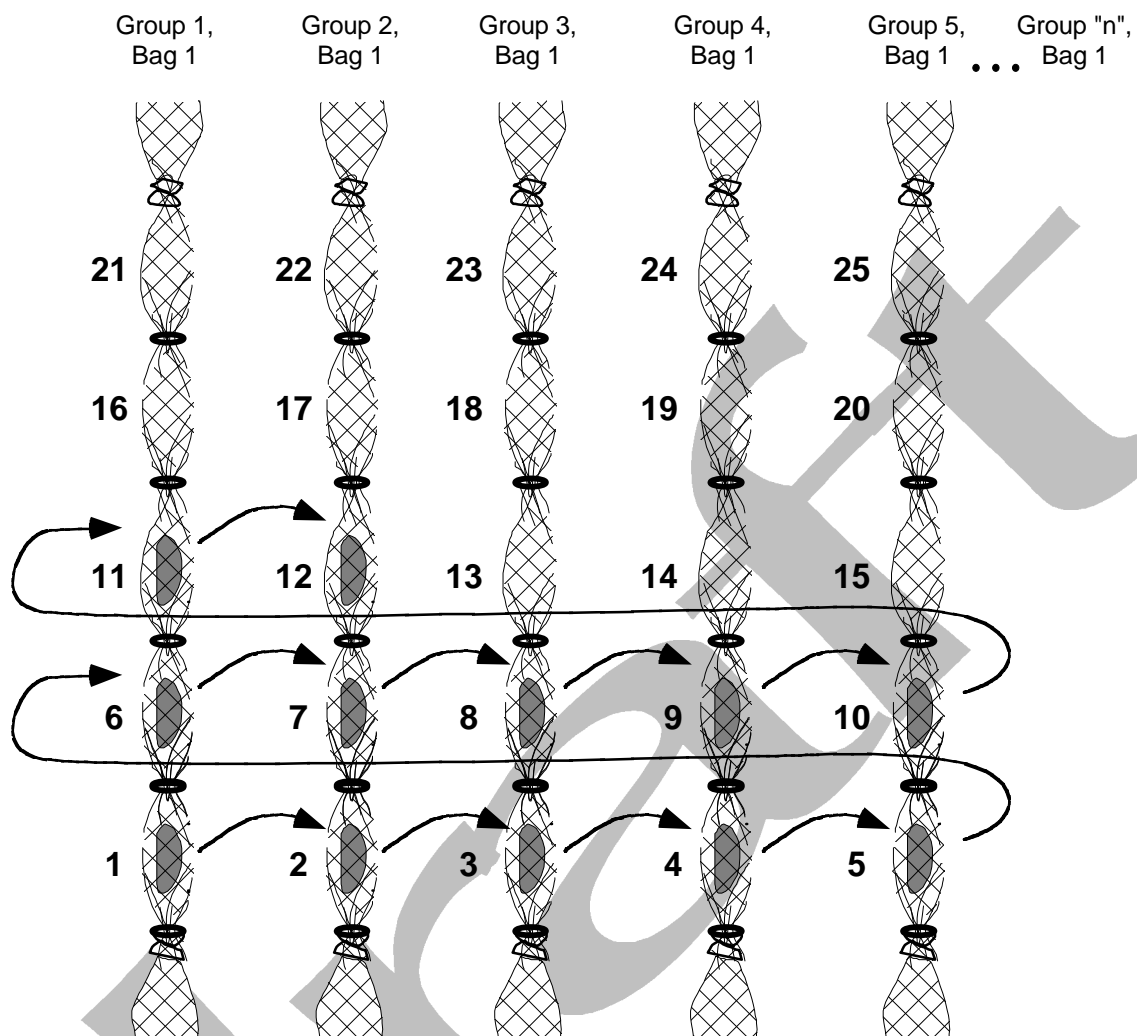


Figure 1. Distribution process used to ensure similar sizes of bivalves among treatments.

APPENDIX B
TISSUE CHEMISTRY LABORATORY REPORTS

TOTAL MERCURY

Sheet1

<u>BR ID Number</u>	<u>Station</u>	<u>Replicate</u>	<u>Cage No.</u>
97BR135-02	Initial	3	32
97BR135-03	Initial	2	29
97BR135-04	Initial	4	36
97BR135-05	Initial	1	7
97BR185-01	8	4	44
97BR185-02	8	3	33
97BR185-03	6	4	41
97BR185-04	6	3	26
97BR185-05	3	1	2
97BR185-06	3	3	30
97BR185-07	5	4	42
97BR185-08	5	2	18
97BR185-09	2	2	15
97BR185-10	2	3	24
97BR185-11	5	1	4
97BR185-12	5	3	27
97BR185-13	4	2	17
97BR185-14	4	3	23
97BR185-15	1	1	13
97BR185-16	1	3	25
97BR185-17	10	3	31
97BR185-18	10	2	12
97BR185-19	2	4	35
97BR185-20	2	1	5
97BR185-21	7	3	20
97BR185-22	7	2	9
97BR185-23	9	4	39
97BR185-24	9	3	21
97BR185-25	10	4	40
97BR185-26	10	1	6
97BR185-27	4	1	3
97BR185-28	4	4	34
97BR185-29	3	2	11
97BR185-30	3	4	37
97BR185-31	6	2	19
97BR185-32	6	1	14
97BR185-33	9	2	10
97BR185-34	9	1	8
97BR185-35	1	4	43
97BR185-36	1	2	22
97BR185-37	7	1	1
97BR185-38	7	4	38
97BR185-39	8	1	16
97BR185-40	8	2	28

Analyte: Hg
 Matrix: biota, filter
 Method: BR-0002

Prep. Date: 9/30/97
 Analysis Date: 10/2/97

QA RESULTS**Calibration Data**

Initial Calibration

pg	PA		
100	178		
500	841	Corr. Coef.:	0.9999
2500	4177	Calib. Coef.:	0.5990
7500	12284	RSD:	1.7%

Calibration Verification

known pg	meas. pg	% recovery
500	525	104.9%
500	531	106.3%
500	533	106.6%

Certified Reference Material

ID	units	Known	measured	% recovery
DORM-2	ug/g	4.64	4.51	97.3%

Method Blanks

ID	ng/blank
MB-1	0.140

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR185-01MS	ng/g	489	446	91.2%

Method Duplicate

ID	Native ng/g (wet)	Duplicate ng/g (wet)	Average ng/g (wet)	RPD %
97BR185-01	155	133	144	15.3%

BRL Data Summary

Batch #: 97-258

Analyte: Hg
 Matrix: biota, filter
 Method: BR-0002

Prep. Date: 9/30/97
 Analysis Date: 10/2/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR135-02	0.159	15.0%	1.06	
97BR135-03	0.258	15.5%	1.66	
97BR135-04	0.204	15.3%	1.34	
97BR135-05	0.149	15.0%	0.993	
97BR185-01	0.155	15.0%	1.03	
97BR185-01	0.133	15.0%	0.887	D
97BR185-02	0.124	15.7%	0.792	
97BR185-03	0.110	16.3%	0.675	
97BR185-04	0.111	16.4%	0.678	
97BR185-05	0.128	15.4%	0.830	
97BR185-06	0.126	14.6%	0.862	
97BR185-07	0.143	14.0%	1.02	
97BR185-08	0.160	15.6%	1.03	
97BR185-09	0.113	14.7%	0.771	
97BR185-10	0.132	15.1%	0.877	
97BR185-11	0.141	15.1%	0.932	
97BR185-12	0.178	14.2%	1.26	
97BR185-13	0.151	15.2%	0.995	
97BR185-14	0.159	16.2%	0.981	
97BR185-15	0.175	14.5%	1.21	
	ng/filter			
97BR135-01	0.718			

BRL Data Summary

Batch #: 97-258

Analyte: Hg
 Matrix: blota, filter
 Method: BR-0002

Prep. Date: 9/30/97
 Analysis Date: 10/2/97

QA RESULTS**Calibration Data**

Initial Calibration

pg	PA		
100	178		
500	841	Corr. Coef.:	0.9999
2500	4177	Calib. Coef.:	0.5990
7500	12284	RSD:	1.7%

Calibration Verification

known pg	meas. pg	% recovery
500	525	104.9%
500	531	106.3%
500	533	106.6%

Certified Reference Material

ID	units	Known	measured	% recovery
DORM-2	ug/g	4.64	4.51	97.3%

Method Blanks

ID	ng/blank
MB-1	0.140

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR185-01MS	ng/g	489	446	91.2%

Method Duplicate

ID	Native ng/g (wet)	Duplicate ng/g (wet)	Average ng/g (wet)	RPD %
97BR185-01	155	133	144	15.3%

BRL Data Summary

Batch #: 97-259

Analyte: Hg
 Matrix: biota
 Method: BR-0002

Prep. Date: 10/3/97
 Analysis Date: 10/7/97

QA RESULTS**Calibration Data**

Initial Calibration

pg	PA		
100	180		
500	873	Corr. Coef.:	0.9999
2500	4306	Calib. Coef.:	0.5857
8000	13278	RSD:	2.0%

Calibration Verification

known pg	meas. pg	% recovery
500	518	103.6%
500	517	103.4%
500	518	103.6%

Certified Reference Material

ID	units	Known	measured	% recovery
DORM-2	ug/g	4.64	4.62	99.6%

Method Blanks

ID	ng/blank
MB-1	0.181

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR185-17MS	ng/g	488	540	110.8%

Method Duplicate

ID	Native ng/g (wet)	Duplicate ng/g (wet)	Average ng/g (wet)	RPD %
97BR185-17	128	128	128	0.2%

Analyte: Hg
 Matrix: biota, filter
 Method: BR-0002

Prep. Date: 10/7/97
 Analysis Date: 10/8/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR185-36	0.149	17.4%	0.858	
97BR185-37	0.109	16.9%	0.644	
97BR185-38	0.139	17.2%	0.810	
97BR185-39	0.115	16.5%	0.697	
97BR185-40	0.168	15.4%	1.09	
97BR185-40	0.135	15.4%	0.877	D
	ng/filter			
97BR185-41	1.61			
97BR185-42	0.842			

QA RESULTS**Calibration Data****Initial Calibration**

pg	PA	Corr. Coef.:	1.0000
100	178	Calib. Coef.:	0.5893
500	870	RSD:	2.0%
2500	4179		
7500	12501		

Calibration Verification

known pg	meas. pg	% recovery
500	519	103.8%
500	505	101.0%
500	526	105.2%

Certified Reference Material

ID	units	Known	measured	% recovery
DORM-2	ug/g	4.64	4.51	97.3%

Method Blanks

ID	ng/blank
MB-1	0.134
MB-2	0.122

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR185-40MS	ng/g	485	520	107.0%

Method Duplicate

ID	Native ng/g (wet)	Duplicate ng/g (wet)	Average ng/g (wet)	RPD %
97BR185-40	168	135	152	21.8%

Analyte: Hg

Matrix: water (homogenization blanks)

Prep. Date: 9/24/97

Method: EPA1631

Analysis Date: 9/25/97

SAMPLE RESULTS

BRL Sample ID	Result ng/L	Qualifier	ng/equipment rinse
97BR185-43	0.14	T	0.035
97BR185-44	0.05	K	0.013
97BR185-45	0.08	K	0.020

QA RESULTS

Calibration Data

Initial Calibration

pg	PA		
50	97		
100	174		
500	817	low std. recovery:	107%
2500	4045	Calib. Coef.:	0.6023
8000	13128	RSD:	3.9%

Calibration Verification

known pg	meas. pg	% recovery
500	483	96.6%
500	493	98.6%

Certified Reference Material

ID	units	Known	measured	% recovery
1641c	ng/L*	7.35	6.95	94.6%

*after BRL dilution

Method Blanks

ID	ng/blank
MB-1	0.015

Matrix Spike Recovery and Precision - other clients' samples

ID	units	Known	measured	% recovery
97BR173-01MS	ng/L	20.0	18.9	94.5%
97BR173-01MSD	ng/L	19.8	19.5	98.5%
			Average:	96.5%
			RPD:	4.1%
97BR177-06MS	ng/L	20.0	20.7	103.5%
97BR177-06MSD	ng/L	19.8	20.0	101.0%
			Average:	102.3%
			RPD:	2.4%

METHYLMERCURY

2575380001 -
Disk 160**Analyte: MMHg**

Matrix: water (homogenization blanks)

Method: BR-0011

Prep. Date: 9/29/97

Analysis Date: 9/30/97

SAMPLE RESULTS

BRL Sample ID	Result ng/L	Qualifier	ng/equipment rinse
97BR185-43	0.0449	T	0.011
97BR185-44	0.0031	K	0.001
97BR185-45	0.0431	T	0.011

QA RESULTS**Calibration Data**

Initial Calibration

pg	PA	Corr. Coef.:	0.9996
5	33	Calib. Coef.:	0.1798
10	57	RSD:	10.1%
50	247		
100	525		
500	2987		

Calibration Verification

known pg	meas. pg	% recovery
50.0	44.6	89.2%
50.0	52.1	104.3%
50.0	50.3	100.7%
50.0	45.3	90.6%
50.0	46.7	93.5%
50.0	55.4	110.8%
50.0	45.8	91.7%

Method Blanks

ID	ng/L
MB-1	0.013
MB-2	0.031

BRL Data Summary

Batch #: 97-255

Analyte: MMHg
 Matrix: biota
 Method: BR-0011

Prep. Date: 9/30/97
 Analysis Date: 10/1/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR135-02	0.0400	15.0%	0.267	
97BR135-03	0.0378	15.6%	0.243	
97BR135-04	0.0410	15.3%	0.269	
97BR135-05	0.0382	15.0%	0.255	
97BR185-01	0.0185	15.0%	0.123	
97BR185-02	0.0159	15.7%	0.102	
97BR185-02	0.0189	15.7%	0.121	D
97BR185-03	0.0163	16.3%	0.100	
97BR185-04	0.0185	16.4%	0.113	
97BR185-05	0.0236	15.4%	0.153	
97BR185-06	0.0199	14.6%	0.136	
97BR185-07	0.0211	14.0%	0.151	
97BR185-08	0.0194	15.6%	0.124	
97BR185-09	0.0113	14.7%	0.0771	
97BR185-10	0.0140	15.1%	0.0930	
97BR185-11	0.0231	15.1%	0.153	
97BR185-12	0.0279	14.2%	0.197	
97BR185-13	0.0273	15.2%	0.180	
97BR185-14	0.0254	16.2%	0.157	
97BR185-15	0.0217	14.5%	0.149	

BRL Data Summary

Batch #: 97-255

Analyte: MMHg
 Matrix: biota
 Method: BR-0011

Prep. Date: 9/30/97
 Analysis Date: 10/1/97

QA RESULTS**Calibration Data**

Initial Calibration

pg	PA		
10	55	Corr. Coef.:	0.9998
50	289	Calib. Coef.:	0.1733
100	553	RSD:	6.8%
500	3142		
1000	6089		

Calibration Verification

known pg	meas. pg	% recovery
50	43.2	86.3%
50	43.5	87.0%
50	44.4	88.7%

Certified Reference Material

ID	units	Known	measured	% recovery
DORM-2	ug/g	4.47	3.43	76.6%

Method Blanks

ID	meas. ng
MB-1	0.56

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR185-02MS	ng/g	96.2	96.6	100%

Method Duplicate

ID	Native ng/g (wet)	Duplicate ng/g (wet)	Average ng/g (wet)	RPD %
97BR185-02	15.9	18.9	17.4	17.2%

BRL Data Summary

Batch #: 97-256

Analyte: MMHg
 Matrix: biota
 Method: BR-0011

Prep. Date: 10/3/97
 Analysis Date: 10/6/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR185-16	0.0290	14.4%	0.201	
97BR185-16	0.0274	14.4%	0.190	D
97BR185-17	0.0196	15.0%	0.131	
97BR185-18	0.0202	15.0%	0.135	
97BR185-19	0.0158	15.0%	0.105	
97BR185-20	0.0176	14.5%	0.121	
97BR185-21	0.0246	15.5%	0.159	
97BR185-22	0.0228	15.6%	0.146	
97BR185-23	0.0221	16.1%	0.137	
97BR185-24	0.0231	16.1%	0.143	
97BR185-25	0.0200	14.9%	0.134	
97BR185-26	0.0193	15.5%	0.125	
97BR185-27	0.0282	16.5%	0.171	
97BR185-28	0.0328	14.7%	0.223	
97BR185-29	0.0273	16.9%	0.162	
97BR185-30	0.0283	16.1%	0.176	
97BR185-31	0.0229	16.0%	0.143	
97BR185-32	0.0237	16.2%	0.146	
97BR185-33	0.0227	16.1%	0.141	
97BR185-34	0.0219	15.7%	0.139	
97BR185-35	0.0267	14.4%	0.185	

Analyte: MMHg
 Matrix: biota
 Method: BR-0011

Prep. Date: 10/3/97
 Analysis Date: 10/6/97

QA RESULTS**Calibration Data**

Initial Calibration

pg	PA		
10	58	Corr. Coef.:	0.9995
50	283	Calib. Coef.:	0.1819
100	555	RSD:	4.9%
500	2760		
1000	5900		

Calibration Verification

known pg	meas. pg	% recovery
50	54.8	109.5%
50	53.3	106.6%
50	50.9	101.8%

Certified Reference Material

ID	units	Known	measured	% recovery
DORM-2	ug/g	4.47	4.30	96.1%

Method Blanks

ID	meas. ng
MB-1	0.809

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR185-16MS	ng/g	99.6	112.0	112%

Method Duplicate

ID	Native ng/g (wet)	Duplicate ng/g (wet)	Average ng/g (wet)	RPD %
97BR185-16	29.0	27.4	28.2	5.7%

Analyte: MMHg
 Matrix: biota
 Method: BR-0011

Prep. Date: 9/22/97
 Analysis Date: 9/25/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR185-36	0.0183	17.4%	0.105	D
97BR185-36	0.0192	17.4%	0.111	
97BR185-37	0.0197	16.9%	0.116	
97BR185-38	0.0176	17.2%	0.103	
97BR185-39	0.0141	16.5%	0.0855	
97BR185-40	0.0149	15.4%	0.0958	

QA RESULTS**Calibration Data****Initial Calibration**

pg	PA	Corr. Coef.:	0.9950
5	32	Calib. Coef.:	0.1844
10	57	RSD:	8.6%
50	288		
100	531		
500	2850		
1000	4890		

Calibration Verification

known pg	meas. pg	% recovery
50	45.6	91.3%

Certified Reference Material

ID	units	Known	measured	% recovery
DORM-2	ug/g	4.47	3.26	72.9%
DORM-2	ug/g	4.47	3.23	72.3%

Method Blanks

ID	meas. ng
MB-1	<1
MB-2	<1

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR185-36MS	ng/g	98.9	95.3	96.3%

Method Duplicate

ID	Native ng/g (wet)	Duplicate ng/g (wet)	Average ng/g (wet)	RPD %
97BR185-36	18.3	19.2	18.8	4.8%

BRL Data Summary

Batch #: 97-271

Analyte: MMHg
 Matrix: filters
 Method: BR-0011

Prep. Date: 10/7/97
 Analysis Date: 10/8/97

SAMPLE RESULTS

BRL Sample ID	Result ng/filter	Qualifier
97BR135-01	0.0117	
97BR185-41	0.00481	
97BR185-42	0.00801	

QA RESULTS**Calibration Data**

Initial Calibration

pg	PA	Corr. Coef.:	0.9993
10	54	Calib. Coef.:	0.178
50	263	RSD:	7.0%
500	2829		
1000	6118		

Calibration Verification

known pg	meas. pg	% recovery
50	45.9	91.8%
50	47.0	94.0%

Certified Reference Material

ID	units	Known	measured	% recovery
IAEA-356	ng/g	5.46	5.40	98.8%
IAEA-356	ng/g	5.46	5.82	106.6%

Method Blanks

ID	pg/sample
MB-1	0.7
MB-2	1.4

Method Duplicate -other client's sample

ID	Native ng/g (wet)	Duplicate ng/g (wet)	Average ng/g (wet)	RPD %
97BR187-13	0.320	0.292	0.306	9.2%

LEAD

BRL Data Summary

Batch #: 97-273

Analyte: Pb
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 9/25/97
 Analysis Date: 10/7/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR135-02	<0.05	15.0%	<0.33	U
97BR135-02	<0.05	15.0%	<0.33	U, D
97BR135-03	0.004	15.5%	0.026	K
97BR135-04	<0.05	15.3%	<0.33	U
97BR135-05	0.093	15.0%	0.620	T
97BR185-01	0.230	15.0%	1.53	T
97BR185-02	0.354	15.7%	2.26	
97BR185-03	0.190	16.3%	1.17	T
97BR185-04	0.144	16.4%	0.879	T
97BR185-05	0.120	15.4%	0.778	T
97BR185-06	0.0810	14.6%	0.554	T
97BR185-07	0.190	14.0%	1.36	T
97BR185-08	0.270	15.6%	1.73	
97BR185-09	0.130	14.7%	0.887	T
97BR185-10	0.150	15.1%	0.997	T
97BR185-11	0.220	15.1%	1.45	T
97BR185-12	0.310	14.2%	2.19	
97BR185-13	0.420	15.2%	2.77	
97BR185-14	0.150	16.2%	0.925	T
97BR185-15	0.130	14.5%	0.895	T
	ug/filter	Qualifier		
97BR135-01	<0.3	U		

Analyte: Pb
 Matrix: bioa
 Method: EPA 200.9

Prep. Date: 9/25/97
 Analysis Date: 10/7/97

QA RESULTS**Calibration Data**

Initial Calibration

ug/L	Absorbance		
0	-0.001		
5	0.013	Corr. Coef.:	0.99977
10	0.027	Slope:	0.0023
25	0.060	Intercept:	0.002
50	0.118		
100	0.228		

Calibration Verification

Known ug/L	meas. ug/L	% recovery
40	38.8	97.0%
40	36.9	92.3%
40	36.1	90.3%
40	36.6	91.5%

Certified Reference Material

ID	units	Known	measured	% recovery
ERA 6970*	ug/L	66.0	64.8	98.2%
TORT-1	ug/g	10.4	13.0	125.0%

*1:2 dilution of 132 ug/L certified concentration

Method Blanks

ID	meas. ug/L
LRB-1	<1
LRB-2	<1

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR135-02MS	ug/g	2.37	2.33	98.6%

Method Duplicate

ID	Native ug/g (wet)	Duplicate ug/g (wet)	Average ug/g (wet)	RPD %
97BR135-02	<0.05	<0.05	<0.05	NA

BRL Data Summary

Batch #: 97-274

Analyte: Pb
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 9/29/97
 Analysis Date: 10/10/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR185-16	0.110	14.4%	0.764	T
97BR185-16	0.114	14.4%	0.792	T, D
97BR185-17	0.160	15.0%	1.07	T
97BR185-18	0.146	15.0%	0.973	T
97BR185-19	0.138	15.0%	0.920	T
97BR185-20	0.227	14.5%	1.57	T
97BR185-21	0.140	15.5%	0.903	T
97BR185-22	0.136	15.6%	0.872	T
97BR185-23	0.160	16.1%	0.994	T
97BR185-24	0.159	16.1%	0.998	T
97BR185-25	0.120	14.9%	0.805	T
97BR185-26	0.128	15.5%	0.826	T
97BR185-27	0.132	16.5%	0.800	T
97BR185-28	0.154	14.7%	1.05	T
97BR185-29	0.072	16.9%	0.426	T
97BR185-30	0.130	16.1%	0.807	T
97BR185-31	0.233	16.0%	1.46	T
97BR185-32	0.092	16.2%	0.568	T
97BR185-33	0.113	16.1%	0.702	T
97BR185-34	0.129	15.7%	0.822	T
97BR185-35	0.090	14.4%	0.625	T

Analyte: Pb
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 9/29/97
 Analysis Date: 10/10/97

QA RESULTS**Calibration Data**

Initial Calibration

ug/L	Absorbance		
0	0.000		
5	0.013	Corr. Coef.:	0.99995
10	0.025	Slope:	0.0024
25	0.063	Intercept:	0.001
50	0.124		
100	0.243		

Calibration Verification

Known ug/L	meas. ug/L	% recovery	
40	38.9	97.3%	
40	39.8	99.5%	
40	39.7	99.3%	
40	35.0	87.5%	*repoured and reanalyzed
40	38.6	96.5%	

Certified Reference Material

ID	units	Known	measured	% recovery
ERA 9970*	ug/L	66	65.4	99.1%
TORT-1	ug/g	10.4	13.3	128%

*1:2 dilution of 132 ug/L certified concentration

Method Blanks

ID	meas. ug/L
LRB-1	<1
LRB-2	<1

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR185-16MS	ug/g	2.45	2.51	102.4%

Method Duplicate

ID	Native ug/g (wet)	Duplicate ug/g (wet)	Average ug/g (wet)	RPD %
97BR185-16	0.110	0.114	0.112	3.6%

Analyte: Pb
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 10/9/97
 Analysis Date: 10/13/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR185-36	0.080	17.4%	0.460	T
97BR185-36	0.070	17.4%	0.402	T, D
97BR185-37	0.112	16.9%	0.663	T
97BR185-38	0.120	17.2%	0.698	T
97BR185-39	0.145	16.5%	0.879	T
97BR185-40	0.120	15.4%	0.779	T
	ug/filter	Qualifier		
97BR185-41	<0.3	U		
97BR185-42	<0.3	U		
	ug/L	Qualifier	ug/equipment rinse	
97BR185-43	<1	U	<0.25	
97BR185-44	<1	U	<0.25	
97BR185-45	<1	U	<0.25	

Analyte: Pb
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 10/9/97
 Analysis Date: 10/13/97

QA RESULTS**Calibration Data****Initial Calibration**

ug/L	Absorbance		
0	-0.018		
5	0.011	Corr. Coef.:	0.99969
10	0.022	Slope:	0.0021
25	0.055	Intercept:	0.002
50	0.106		
100	0.206		

Calibration Verification

Known ug/L	meas. ug/L	% recovery
40	40.7	101.8%
40	41.0	102.5%
40	40.0	100.1%

Certified Reference Material

ID	units	Known	measured	% recovery
ERA 9970*	ug/L	66.0	65.3	98.9%
TORT-1	ug/g	10.4	8.00	76.9%

*1:2 dilution of 132 ug/L certified concentration

Method Blanks

ID	meas. ug/L
LRB-1	<1

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR185-36MS	ug/g	2.58	2.53	98.0%

Method Duplicate

ID	Native ug/g (wet)	Duplicate ug/g (wet)	Average ug/g (wet)	RPD %
97BR185-36	0.080	0.070	0.075	13.3%

CHROMIUM

BRL Data Summary

Batch #: 97-276

Analyte: Cr
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 9/25/97
 Analysis Date: 10/15/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR135-02	0.436	15.0%	2.92	
97BR135-02	0.430	15.0%	2.88	D
97BR135-03	0.430	15.5%	2.77	
97BR135-04	0.443	15.3%	2.90	
97BR135-05	0.357	15.0%	2.38	
97BR185-01	6.77	15.0%	45.1	
97BR185-02	15.8	15.7%	101	
97BR185-03	3.69	16.4%	22.6	
97BR185-04	3.21	16.4%	19.6	
97BR185-05	2.74	15.4%	17.8	
97BR185-06	2.56	14.0%	17.5	
97BR185-07	8.00	14.0%	57.3	
97BR185-08	12.4	15.6%	79.2	
97BR185-09	0.685	14.7%	4.68	
97BR185-10	0.857	15.1%	5.69	
97BR185-11	9.41	15.1%	62.2	
97BR185-12	11.7	14.2%	82.2	
97BR185-13	4.98	15.2%	32.8	
97BR185-14	1.48	16.2%	9.10	
97BR185-15	0.945	14.5%	6.51	
	ug/filter	Qualifier		
97BR135-01	0.717			

Analyte: Cr
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 9/25/97
 Analysis Date: 10/15/97

QA RESULTS**Calibration Data**

Initial Calibration

ug/L	Absorbance		
0	0.000		
1	0.013	Corr. Coef.:	0.99941
5	0.068	Slope:	0.0126
10	0.137	Intercept:	0.000
25	0.334		
50	0.626		

Calibration Verification

Known ug/L	meas. ug/L	% recovery
20	20.56	102.8%
20	20.92	104.6%
20	21.06	105.3%
20	20.82	104.1%
20	20.77	103.9%
20	21.03	105.2%

Certified Reference Material

ID	units	Known	measured	% recovery
ERA 9970*	ug/L	24.1	24.2	100.6%
TORT-1	ug/g	2.40	2.01	83.9%

*1:10 dilution of 241 ug/L certified concentration

Method Blanks

ID	meas. ug/L
LRB-1	0.62
LRB-2	0.62

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR135-02MS	ug/g	2.37	2.37	100.3%

Method Duplicate

ID	Native ug/g (wet)	Duplicate ug/g (wet)	Average ug/g (wet)	RPD %
97BR135-02	0.436	0.430	0.433	1.4%

BRL Data Summary

Batch #: 97-277a

Analyte: Cr
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 9/29/97
 Analysis Date: 10/9/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR185-16	1.88	14.4%	13.0	
97BR185-16	1.79	14.4%	12.4	D
97BR185-17	2.20	15.0%	14.7	
97BR185-18	1.07	15.0%	7.12	

QA RESULTS

Calibration Data

Initial Calibration

ug/L	Absorbance	Corr. Coef.:	0.99986
0	-0.009	Slope:	0.0122
1	0.011	Intercept:	0.001
5	0.063		
10	0.123		
25	0.313		
50	0.606		

Calibration Verification

Known ug/L	meas. ug/L	% recovery
20	19.66	99.3%
20	19.27	96.4%

Certified Reference Material

ID	units	Known	measured	% recovery
ERA 9970*	ug/L	24.1	23.1	95.9%
TORT-1	ug/g	2.4	2.02	84.2%

*1:10 dilution of 241 ug/L certified concentration

Method Blanks

ID	meas. ug/L
LRB-1	<0.2
LRB-2	<0.2

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR185-16MS	ug/g	2.45	2.14	87.3%

Method Duplicate

ID	Native ug/g (wet)	Duplicate ug/g (wet)	Average ug/g (wet)	RPD %
97BR185-16	1.88	1.79	1.83	4.8%

BRL Data Summary

Batch #: 97-277b

Analyte: Cr
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 9/29/97
 Analysis Date: 10/9/97

QA RESULTS**Calibration Data**

Initial Calibration

ug/L	Absorbance		
0	-0.002		
1	0.008	Corr. Coef.:	0.9998
5	0.051	Slope:	0.0104
10	0.105	Intercept:	0.000
25	0.268		
50	0.516		

Calibration Verification

Known ug/L	meas. ug/L	% recovery
20	20.63	103.2%
20	19.25	96.3%
20	19.06	95.3%

Certified Reference Material

ID	units	Known	measured	% recovery
ERA 9970*	ug/L	24.1	24.07	99.9%

*1:10 dilution of 241 ug/L. certified concentration

Method Blanks

see 97-277a

Matrix Spike Recovery

see 97-277a

Method Duplicate

see 97-277a

BRL Data Summary

Batch #: 97-278

Analyte: Cr
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 10/9/97
 Analysis Date: 10/13/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR185-35	0.779	17.4%	4.48	
97BR185-36	0.809	17.4%	4.65	D
97BR185-37	4.43	16.9%	26.2	
97BR185-38	3.04	17.2%	17.7	
97BR185-39	5.67	16.5%	34.3	
97BR185-40	2.96	15.4%	19.2	
	ug/filter	Qualifier		
97BR185-41	0.546			
97BR185-42	0.414			
	ug/L	Qualifier	ug/equipment rinse	
97BR185-43	<0.02	U	<0.005	
97BR185-44	<0.02	U	<0.005	
97BR185-45	<0.02	U	<0.005	

BRL Data Summary

Batch #: 97-278

Analyte: Cr
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 10/9/97
 Analysis Date: 10/13/97

QA RESULTS

Calibration Data

Initial Calibration

ug/L	Absorbance		
0	-0.026		
1	0.006	Corr. Coef.:	0.99986
5	0.053	Slope:	0.0124
10	0.115	Intercept:	-0.005
25	0.310		
50	0.612		

Calibration Verification

Known ug/L	meas. ug/L	% recovery
20	19.6	97.9%
20	20.1	100.6%
20	19.5	97.6%

Certified Reference Material

ID	units	Known	measured	% recovery
LFB	ug/L	50.0	46.6	93.2%
TORT-1	ug/g	2.40	1.90	79.1%

Method Blanks

ID	meas. ug/L
LRB-1	0.13

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR165-36MS	ug/g	2.58	2.66	102.9%

Method Duplicate

ID	Native ug/g (wet)	Duplicate ug/g (wet)	Average ug/g (wet)	RPD %
97BR165-36	0.779	0.809	0.794	3.8%

CADMIUM

BRL Data Summary

Batch #: 97-279a

2575380001
Disk 160Analyte: Cd
Matrix: biota
Method: EPA 200.9Prep. Date: 9/25/97
Analysis Date: 10/8/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR135-05	0.479	15.0%	3.19	
97BR185-01	0.522	15.0%	3.48	
97BR185-02	0.621	15.7%	3.97	
97BR185-03	0.650	16.4%	3.97	
97BR185-04	0.461	16.4%	2.81	
97BR185-05	0.478	15.4%	3.10	
97BR185-06	0.440	14.6%	3.01	
97BR185-07	0.440	14.0%	3.15	
97BR185-08	0.411	15.6%	2.63	
97BR185-09	0.491	14.7%	3.35	
97BR185-10	0.549	15.1%	3.64	
97BR185-11	0.369	15.1%	2.44	
97BR185-12	0.413	14.2%	2.91	
97BR185-13	0.394	15.2%	2.60	
97BR185-14	0.364	16.2%	2.25	
97BR185-15	0.379	14.5%	2.61	

QA RESULTS

Calibration Data

Initial Calibration

ug/L	Absorbance	Corr. Coef.:	0.9981
0.00	-0.001	Slope:	0.0217
0.50	0.013	Intercept:	0.005
1.00	0.027		
2.00	0.053		
5.00	0.122		
10.00	0.218		

Calibration Verification

Known ug/L	meas. ug/L	% recovery
4.00	4.10	102.6%
4.00	4.00	100.0%
4.00	3.80	97.5%

Certified Reference Material

see 97-279b

Method Blanks

see 97-279b

Matrix Spike Recovery

see 97-279b

Method Duplicate

see 97-279b

BRL Data Summary

Batch #: 97-279b

Analyte: Cd
Matrix: biota
Method: EPA 200.9

Prep. Date: 9/25/97
Analysis Date: 10/11/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR135-02	0.410	15.0%	2.74	
97BR135-02	0.460	15.0%	3.07	D
97BR135-03	0.490	15.5%	3.15	
97BR135-04	0.480	15.3%	3.15	
	ug/filter	Qualifier		
97BR135-01	<0.03	U		

BRL Data Summary

Batch #: 97-279b

Analyte: Cd
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 9/25/97
 Analysis Date: 10/11/97

QA RESULTS

Calibration Data

Initial Calibration

ug/L	Absorbance		
0.00	0.000		
0.50	0.012	Corr. Coef.:	0.99854
1.00	0.023	Slope:	0.0206
2.00	0.047	Intercept:	0.002
5.00	0.104		

Calibration Verification

Known ug/L	meas. ug/L	% recovery
4.00	4.00	100.0%
4.00	3.90	97.5%
4.00	4.10	102.5%

Certified Reference Material

ID	units	Known	measured	% recovery
ERA 9970*	ug/L	4.80	4.60	95.9%
TORT-1	ug/g	25.3	25.0	95.1%

*1:20 dilution of 95.9 ug/L certified concentration

Method Blanks

ID	meas. ug/L
LRB-1	<0.1
LRB-2	<0.1

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR135-02MS	ug/g	2.37	2.79	118%

Method Duplicate

ID	Native ug/g (wet)	Duplicate ug/g (wet)	Average ug/g (wet)	RPD %
97BR135-02	0.410	0.460	0.435	11.5%

Analyte: Cd
Matrix: biota
Method: EPA 200.9

Prep. Date: 9/29/97
Analysis Date: 10/9/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR185-16	0.351	14.4%	2.44	
97BR185-16	0.337	14.4%	2.34	D
97BR185-17	0.478	15.0%	3.19	
97BR185-18	0.423	15.0%	2.82	
97BR185-19	0.439	15.0%	2.93	
97BR185-20	0.407	14.5%	2.81	
97BR185-21	0.390	15.5%	2.52	
97BR185-22	0.386	15.6%	2.47	
97BR185-23	0.410	16.1%	2.55	
97BR185-24	0.408	16.1%	2.53	
97BR185-25	0.405	14.9%	2.72	
97BR185-26	0.438	15.5%	2.83	
97BR185-27	0.315	16.5%	1.91	
97BR185-28	0.336	14.7%	2.29	
97BR185-29	0.339	16.9%	2.01	
97BR185-30	0.380	16.1%	2.36	
97BR185-31	0.335	16.0%	2.09	
97BR185-32	0.322	16.2%	1.99	
97BR185-33	0.349	16.1%	2.17	
97BR185-34	0.388	15.7%	2.47	
97BR185-35	0.300	14.4%	2.06	

Analyte: Cd
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 9/29/97
 Analysis Date: 10/9/97

QA RESULTS**Calibration Data****Initial Calibration**

ug/L	Absorbance		
0	0.000		
0.5	0.014	Corr. Coef.:	0.99601
1	0.028	Slope:	0.0224
2	0.057	Intercept:	0.007
5	0.131		
10	0.223		

Calibration Verification

Known ug/L	meas. ug/L	% recovery
4.00	4.30	107.5%
4.00	3.80	95.0%
4.00	3.90	97.5%
4.00	3.80	95.0%

Certified Reference Material

ID	units	Known	measured	% recovery
ERA 9970*	ug/L	4.80	5.00	104%
TORT-1	ug/g	26.3	26.9	102%

*1:20 dilution of 95.9 ug/L certified concentration

Method Blanks

ID	meas. ug/L
LRB-1	<0.01
LRB-2	<0.01

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR185-16MS	ug/g	2.45	2.49	101.7%

Method Duplicate

ID	Native ug/g (wet)	Duplicate ug/g (wet)	Average ug/g (wet)	RPD %
97BR185-16	0.351	0.337	0.344	4.1%

BRL Data Summary

Batch #: 97-281

Analyte: Cd
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 10/9/97
 Analysis Date: 10/13/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR185-36	0.310	17.4%	1.78	
97BR185-36	0.310	17.4%	1.78	D
97BR185-37	0.430	16.9%	2.54	
97BR185-38	0.440	17.2%	2.56	
97BR185-39	0.482	16.5%	2.92	
97BR185-40	0.496	15.4%	3.22	
	ug/filter	Qualifier		
97BR185-41	<0.03	U		
97BR185-42	<0.03	U		
	ug/L	Qualifier	ug/equipment rinse	
97BR185-43	<0.1	U	<0.025	
97BR185-44	<0.1	U	<0.025	
97BR185-45	<0.1	U	<0.025	

Analyte: Cd
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 10/9/97
 Analysis Date: 10/13/97

QA RESULTS**Calibration Data****Initial Calibration**

ug/L	Absorbance
0	0.000
0.5	0.011
1	0.022
2	0.043
5	0.094
10	0.156

Corr. Coef.: 0.9999
 Slope: 0.0233
 non-linear fit used

Calibration Verification

Known ug/L	meas. ug/L	% recovery
4	4.2	105.0%
4	4.3	107.5%
4	4.4	110.0%

Certified Reference Material

ID	units	Known	measured	% recovery
ERA 9970*	ug/L	4.80	4.9	102.2%
TORT-1	ug/g	26.3	25.3	96.2%

*1:20 dilution of 95.9 ug/L certified concentration

Method Blanks

ID	meas. ug/L
LRB-1	<0.1

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR185-36MS	ug/g	2.58	2.54	98.4%

Method Duplicate

ID	Native ug/g (wet)	Duplicate ug/g (wet)	Average ug/g (wet)	RPD %
97BR185-36	0.310	0.310	0.310	0.0%

ARSENIC

BRL Data Summary

Batch #: 97-282

Analyte: As
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 9/25/97
 Analysis Date: 10/4/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR135-02	0.992	15.0%	6.56	
97BR135-02	0.891	15.0%	5.95	D
97BR135-03	0.971	15.5%	6.25	
97BR135-04	0.934	15.3%	6.12	
97BR135-05	0.910	15.0%	6.07	
97BR185-01	0.939	15.0%	6.26	
97BR185-02	1.02	15.7%	6.52	
97BR185-03	0.964	16.4%	5.90	
97BR185-04	0.980	16.4%	5.98	
97BR185-05	0.887	15.4%	5.75	
97BR185-06	0.875	14.6%	5.99	
97BR185-07	0.910	14.0%	6.52	
97BR185-08	0.855	15.6%	5.48	
97BR185-09	0.880	14.7%	6.01	
97BR185-10	0.837	15.1%	5.56	
97BR185-11	0.706	15.1%	4.67	
97BR185-12	0.917	14.2%	6.47	
97BR185-13	0.821	15.2%	5.41	
97BR185-14	0.811	16.2%	5.00	
97BR185-15	0.884	14.5%	6.09	
	ug/filter	Qualifier		
97BR135-01	<0.3	U		

BRL Data Summary

Batch #: 97-282

Analyte: As
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 9/25/97
 Analysis Date: 10/4/97

QA RESULTS**Calibration Data****Initial Calibration**

ug/L	Absorbance		
0	0.000		
5	0.014	Corr. Coef.:	0.99933
10	0.024	Slope:	0.0023
25	0.064	Intercept:	0.003
50	0.123		
100	0.232		

Calibration Verification

Known ug/L	meas. ug/L	% recovery
40	39.77	99.4%
40	39.36	98.4%
40	38.46	96.2%
40	37.65	94.1%

Certified Reference Material

ID	units	Known	measured	% recovery
ERA 9970	ug/L	76.5	79.1	103.5%
DORM-2	ug/g	18.0	12.8	71.1%

Method Blanks

ID	meas. ug/L
LRB-1	<1
LRB-2	<1

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR135-02MS	ug/g	2.37	1.64	69.2%

Method Duplicate

ID	Native ug/g (wet)	Duplicate ug/g (wet)	Average ug/g (wet)	RPD %
97BR135-02	0.982	0.891	0.937	9.7%

Analyte: As
Matrix: biota
Method: EPA 200.9

Prep. Date: 9/29/97
Analysis Date: 10/10/97

SAMPLE RESULTS

BRL Sample ID	Result ug/g (wet)	% solids	Result ug/g (dry)	Qualifier
97BR185-16	0.839	14.4%	5.82	
97BR185-16	0.808	14.4%	5.61	D
97BR185-17	0.805	15.0%	5.37	
97BR185-18	0.799	15.0%	5.33	
97BR185-19	0.812	15.0%	5.41	
97BR185-20	0.678	14.5%	4.68	
97BR185-21	0.821	15.5%	5.30	
97BR185-22	0.738	15.6%	4.73	
97BR185-23	0.840	16.1%	5.22	
97BR185-24	0.874	16.1%	5.43	
97BR185-25	0.767	14.9%	5.15	
97BR185-26	0.846	15.5%	5.45	
97BR185-27	0.763	16.5%	4.63	
97BR185-28	0.760	14.7%	5.17	
97BR185-29	0.766	16.9%	4.53	
97BR185-30	0.788	16.1%	4.89	
97BR185-31	0.799	16.0%	5.00	
97BR185-32	0.781	16.2%	4.82	
97BR185-33	0.716	16.1%	4.45	
97BR185-34	0.791	15.7%	5.04	
97BR185-35	0.834	14.4%	5.79	

Analyte: As
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 9/29/97
 Analysis Date: 10/10/97

QA RESULTS**Calibration Data**

Initial Calibration

ug/L	Absorbance		
0	-0.001		
5	0.017	Corr. Coef.:	0.99958
10	0.037	Slope:	0.0033
25	0.088	Intercept:	0.003
50	0.176		
100	0.334		

Calibration Verification

Known ug/L	meas. ug/L	% recovery
40	36.51	91.3%
40	37.18	93.0%
40	38.64	91.6%
40	35.08	90.2%

Certified Reference Material

ID	units	Known	measured	% recovery
ERA 9970	ug/L	76.5	71.7	93.7%
TORT-1	ug/g	24.6	22.1	89.8%

Method Blanks

ID	meas. ug/L
LRB-1	<1
LRB-2	<1

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR185-16MS	ug/g	2.45	2.01	81.9%

Method Duplicate

ID	Native ug/g (wet)	Duplicate ug/g (wet)	Average ug/g (wet)	RPD %
97BR185-16	0.839	0.808	0.823	3.7%

BRL Data Summary

Batch #: 97-284

Analyte: As
 Matrix: biota
 Method: EPA 200.9

Prep. Date: 10/9/97
 Analysis Date: 10/14/97

QA RESULTS**Calibration Data**

Initial Calibration

ug/L	Absorbance		
0	0.000		
5	0.017	Corr. Coef.:	0.99975
10	0.033	Slope:	0.003
25	0.079	Intercept:	0.003
50	0.154		
100	0.296		

Calibration Verification

Known ug/L	meas. ug/L	% recovery
40	39.6	99.1%
40	40.6	101.6%
40	41.0	102.4%

Certified Reference Material

ID	units	Known	measured	% recovery
ERA 9970	ug/L	76.5	78.0	99.3%
TORT-1	ug/g	24.6	24.3	98.7%

Method Blanks

ID	meas. ug/L
LRB-1	0.53

Matrix Spike Recovery

ID	units	Known	measured	% recovery
97BR185-36MS	ug/g	2.58	2.41	93.4%

Method Duplicate

ID	Native ug/g (wet)	Duplicate ug/g (wet)	Average ug/g (wet)	RPD %
97BR185-36	0.831	0.834	0.833	0.4%

PERCENT LIPIDS

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Analyte: % Lipids
 Matrix: biota
 Method: Bligh-Dyer

Wet Wt. Date: 10/10/97
 Dry Wt. Date: 10/10/97

SAMPLE RESULTS

BRL Sample ID	% Lipids	Qualifier
97BR135-02	1.08%	
97BR135-03	1.40%	
97BR135-04	1.42%	
97BR135-05	1.23%	
97BR185-01	1.21%	
97BR185-02	1.69%	
97BR185-02	1.61%	D
97BR185-03	1.49%	
97BR185-04	1.34%	
97BR185-05	1.55%	
97BR185-05	1.46%	D
97BR185-06	1.41%	
97BR185-07	1.24%	
97BR185-08	1.30%	
97BR185-09	1.22%	
97BR185-10	0.82%	R
97BR185-11	1.34%	
97BR185-12	1.72%	
97BR185-13	1.06%	
97BR185-14	1.82%	
97BR185-15	1.11%	

QA RESULTS**Method Blanks**

ID	wet wt. (g)	dry wt. (g)	diff. (g)
MB-1	0.9438	0.9439	0.0001
MB-2	0.9384	0.9363	-0.0001

Method Duplicate

ID	Native % lipids	Duplicate % lipids	Average % lipids	RPD %
97BR185-02	1.69%	1.61%	1.65%	4.8%
97BR185-05	1.55%	1.46%	1.51%	6.0%

Analyte: % Lipids
 Matrix: biota
 Method: Bligh-Dyer

Wet Wt. Date: 10/14/97
 Dry Wt. Date: 10/14/97

SAMPLE RESULTS

BRL Sample ID	% Lipids	Qualifier
97BR185-10	1.21%	
97BR185-21	1.45%	
97BR185-11	1.27%	D
97BR185-25	1.24%	D
97BR185-30	1.44%	D
97BR185-38	1.38%	D

QA RESULTS*Inter-Batch Method Duplicates*

ID	% lipids	Native from Batch #	Duplicate % lipids	Average % lipids	RPD %
97BR185-11	1.34%	97-268a	1.27%	1.31%	5.4%
97BR185-25	1.15%	97-269	1.24%	1.20%	7.5%
97BR185-30	1.56%	97-269	1.44%	1.50%	8.0%
97BR185-38	1.66%	97-270	1.38%	1.52%	18.4%

PERCENT SOLIDS

Analyte: % Solids

Matrix: biota

Method: BR-1501

Wet Wt. Date: 9/30/97

Dry Wt. Date: 10/1/97

SAMPLE RESULTS

BRL Sample ID	% solids	Qualifier
97BR135-02	15.0%	
97BR135-03	15.5%	
97BR135-04	15.3%	
97BR135-05	15.0%	
97BR185-01	15.0%	
97BR185-02	15.7%	
97BR185-03	16.1%	
97BR185-03	16.6%	D
97BR185-04	16.4%	
97BR185-05	15.4%	
97BR185-06	14.6%	
97BR185-07	14.0%	
97BR185-08	15.6%	
97BR185-09	14.7%	
97BR185-10	15.1%	
97BR185-11	15.1%	
97BR185-12	14.2%	
97BR185-13	15.2%	
97BR185-14	16.2%	
97BR185-15	14.5%	

QA RESULTS*Method Blanks*

ID	wet wt. (g)	dry wt. (g)	diff. (g)
MB-1	0.943	0.943	0.000
MB-2	0.940	0.939	-0.001

Method Duplicate

ID	Native % solids	Duplicate % solids	Average % solids	RPD %
97BR185-03	16.1%	16.6%	16.3%	3.1%

Analyte: % Solids
 Matrix: biota
 Method: BR-1501

Wet Wt. Date: 10/2/97
 Dry Wt. Date: 10/3/97

SAMPLE RESULTS

BRL Sample ID	% solids	Qualifier
97BR185-16	14.4%	
97BR185-17	15.0%	
97BR185-18	15.0%	
97BR185-19	14.9%	
97BR185-10	15.1%	D
97BR185-20	14.5%	
97BR185-21	15.5%	
97BR185-22	15.6%	
97BR185-23	16.1%	
97BR185-24	16.1%	
97BR185-25	14.9%	
97BR185-26	15.5%	
97BR185-27	16.5%	
97BR185-28	14.7%	
97BR185-29	16.9%	
97BR185-30	16.1%	
97BR185-31	16.0%	
97BR185-32	16.2%	
97BR185-33	15.1%	
97BR185-34	15.7%	
97BR185-35	14.4%	

QA RESULTS**Method Blanks**

ID	wet wt. (g)	dry wt. (g)	diff. (g)
MB-1	0.937	0.935	-0.002
MB-2	0.938	0.937	-0.001

Method Duplicate

ID	Native % solids	Duplicate % solids	Average % solids	RPD %
97BR185-19	14.9%	15.1%	15.0%	1.3%

Analyte: % Solids

Matrix: biota
Method: BR-1501

Wet Wt. Date: 10/6/97
Dry Wt. Date: 10/7/97

SAMPLE RESULTS

BRL		
Sample ID	% solids	Qualifier
97BR185-36	17.4%	
97BR185-37	16.9%	
97BR185-38	17.2%	
97BR185-39	16.5%	
97BR185-40	15.3%	
97BR185-40	15.5%	D

QA RESULTS**Method Blanks**

ID	wet wt. (g)	dry wt. (g)	diff. (g)
MB-1	0.933	0.933	0.000
MB-2	0.944	0.944	0.000

Method Duplicate

ID	Native % solids	Duplicate % solids	Average % solids	RPD %
97BR185-40	15.3%	15.5%	15.4%	1.6%

APPENDIX C
LABORATORY STANDARD OPERATING PROCEDURES

SOP #BR-0011

Determination of Methylmercury by Aqueous Phase Ethylation, Trapping Pre-Collection, Isothermal GC Separation, and CVAFS Detection

Brooks Rand, Ltd.

Revision 003
Revised 8/95

Reviewed

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8/23/95
Date

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8/23/95
Date

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Senior Scientist

8/23/95
Date

Determination of Methylmercury by Aqueous Phase Ethylation, Trapping Pre-Collection, Isothermal GC Separation, and CVAFS Detection

1. DESCRIPTION

1.1. Mono-methylmercury (MMHg) is determined by an improved method (Liang, Bloom, and Horvat 1994). The MMHg is first ethylated with sodium tetraethylborate (BEt_4^-) and collected by purging with dry, Hg free Nitrogen onto a column filled with either Carbotrap™ or Tenax. The ethyl mercury derivatives are then thermally desorbed and transferred to a GC column held in an oven at 96° C, and the species are chromatographically separated by the GC column. The organo-Hg compounds are decomposed at 900° C to Hg^0 , then quantified by a cold vapor atomic fluorescence spectrometer (CVAFS). The detection limits (DL, as Hg) for the technique are about 0.6 pg for MMHg. The method can be applied for the determination of MMHg in a variety of samples and it has been demonstrated as being a very sensitive, precise, and accurate method. Very good results were obtained for the determination of MMHg in reference standard materials and hair, blood, and brain intercalibration samples (Liang, Bloom, and Horvat 1994).

2. APPARATUS AND MATERIAL

2.1. Cold vapor atomic fluorescence spectrometer (CVAFS) made at Brooks Rand, Ltd.

2.2. Chromatographic peak integrator (Lab Data Control I-400)

2.3. Reaction and purge vessels: A 150 mL flat bottom bottle with 24/40 tapered fitting is used as the reaction vessel. A special 4-way valve sparging-tube cap-assembly is used. This valve assembly allows the water sample to react initially with the ethylating reagent, without bubbling, then to be purged onto the trapping column, and finally to be bypassed, so that water vapor adsorbed onto the column may be evaporated by the direct flow of dry carrier gas.

2.4. Trapping column: A column for the collection of purged organomercury species is constructed from a 10 cm length of 6.4 mm outside diameter x 4.0 mm inside diameter silanized quartz tubing with a coarse quartz frit 2.5 cm from one end. The column is prepared by packing either 180 mg of Carbotrap™ or 80 mg of Tenax TA, using silanized glass wool to hold the packing in place (see figure 1). The layer of glass wool to the end A should be thin, just for blocking up grains of filling material, while the layer to the end B should be packed in a manner that makes a glass wool stopper about

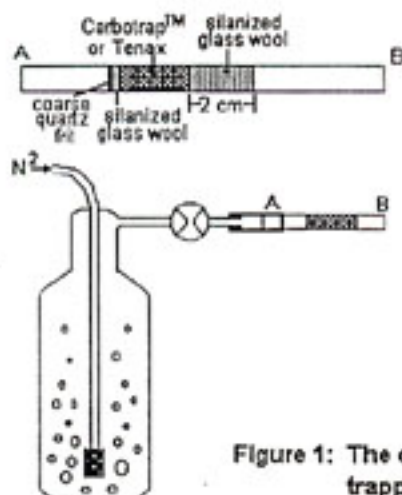


Figure 1: The construction of trapping column and its connection with a reaction vessel

2 cm length, and then placed into the quartz tubing as tightly as possible. Compress the packing again, carefully making filling grains tight, but do not crush them. Figure 1 also shows the connection of the column and a reaction vessel.

2.5. Isothermal gas chromatography system: Illustrated in figure 2 is a schematic diagram. A GC column is prepared by packing 65 cm length of preconditioned 15% OV-3 on chromasorb W-AW-DMCS, 60/80 mesh into a silanized 80 cm total length 6.4 mm outside diameter x 4.0 mm inside diameter borosilicate glass chromatography U-tube within a sealed glass sheath, and the OV-3 column is held in place with silanized glass wool plugs. Under a 50 mL/min flow of high purity helium, organomercury species desorbed from a trapping column were carried by gas passing through a GC column held at 96° C in a cylindrical oven and eluted. Separated species were decomposed in a thermal decomposition tube and finally detected by CVAFS.

3. REAGENTS, GASES, AND WATER

3.1. MMHg Standard solutions

- a) Stock solution: 1 mg/mL MMHg, as Hg. Dissolve 0.1252 g CH₃HgCl (95%+) in 100 mL of isopropanol.
- b) Intermediate stock solution: 1 µg/mL MMHg, as Hg. Dilute 1.00 mg/mL stock solution in isopropanol. This solution is stable at least for one year if stored in refrigerator.

- c) Working solution. 1 ng/mL MMHg, as Hg. Dilute 1.00 ng/mL stock solution in 1% HCl. This solution is stable for at least 3 weeks when stored out of direct light at room temperature.

3.2. Sodium tetraethylborate (NaBEt_4) solution: Dissolve one gram of NaBEt_4 in 100 mL of 2% NaOH solution stored previously in refrigerator. The solution is then divided into several smaller Teflon small mouth bottles. These small bottles are stored frozen. Since this reagent is extremely air sensitive, the preparation must be performed quickly. Defrost the solution prior to use. Frozen aliquots may lose effectiveness after 2 weeks.

3.3. Sodium acetate buffer: A 2M acetate buffer is prepared by dissolving 272 g of reagent grade sodium acetate and 118 mL of glacial acetic acid in DDW to a final volume of 1 L. This solution is purified of trace mercury by the addition of 5 g of 1 N HCl-rinsed sulthydoxyl chelating resin (Sumitomo Q-10R) to the bottle and agitation. The solution is stored in a Teflon FEP bottle and filtered prior to use.

3.4. Potassium hydroxide methanol solution: Dissolve 250 g of reagent grade KOH pellets in high purity methanol to a final volume of 1 L. The solution is stored in a Teflon FEP bottle.

3.5. Gases: Helium used as a GC carrier gas is laboratory grade. Nitrogen used as a purge gas for sweeping derivatives from a bubbler is also laboratory grade. Both are passed through a gold-coated sand trap to remove traces of mercury prior to use.

3.6. Water: Double Deionized Water (DDW) from a Millipore System was used throughout.

4. ANALYSIS

Standards, typically 0, 10, 50, 100, 500 pg for MMHg, and samples (for sample preparation see section 6) to be analyzed are added into reaction vessels containing 50-100 mL of DDW and 200 μl of 2M acetate buffer. An aliquot of 50 μl of NaBEt_4 is added, the 4-way valve-cap inserted and the vessel swirled to rinse. The mixture is allowed to react without purging for 12 minutes. A trapping column is placed in an orientation shown in Figure 1, and then is purged with N_2 at a flow rate of $250 \text{ mL}\cdot\text{min}^{-1}$ for 12 minutes. The organomercury compounds are swept and collected onto the trapping column. Then the valve is switched to pass dry gas over the column for 5 minutes, to remove residual water condensation from the trap. The trapping column is then connected in-line with the GC column (Fig. 2).

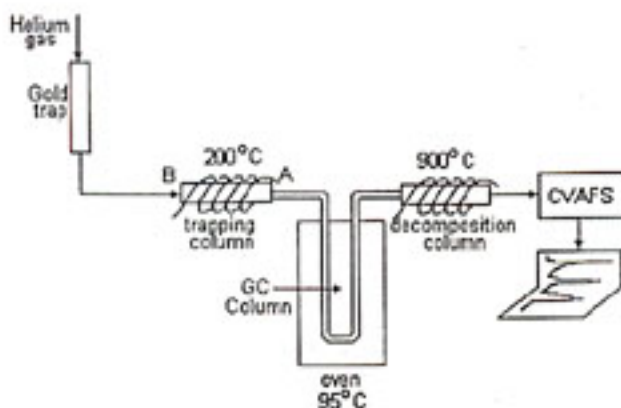


FIGURE 2: A schematic diagram of isothermal gas chromatograph system

When a carbotrap is used, special attention must be paid to the orientation of the trap shown in Figure 2. The trap is placed so that the end facing the bubbler output is now facing the GC column input to avoid the organomercury species passing through the entire length of the heating trap column and decomposing to Hg^0 (Liang, Bloom, and Bloom 1994). Under a helium flow rate of 80 mL-min the column is heated to reach 200° C from room temperature within 30 seconds, controlled by switching on a timer connected in-line, while turning on the integrator or chart recorder. The organomercury species were desorbed and carried to pass through the GC column held in an oven at 96° C. The species are eluted in an order of increasing molecular weight and carried through the thermal (900° C) decomposition tube where all organomercury species are converted into Hg^0 and detected by CVAFS, and fluorescence signals are recorded by an integrator as peak area or by a chart recorder as peak heights, and are measured manually with a millimeter ruler.

5. CALCULATIONS

Calculations may be made by reading off the (linear) standard curve, or by the following method, which is functionally the same.

Calculate a mean (B) "peak height (mm) of the calibration (bubbler) blank".

Calculate a mean coefficient (C)

$$C = \frac{\text{pgHg}}{\text{PH} - B}$$

where PH is a peak height of aliquot of standard in mm.

Calculate the concentration of each species in sample by the following formula:

For aqueous samples:

$$\text{ng of Hg/L} = \{[C \cdot (S-B) \cdot V_2 / V_1] - MB\} / V_3$$

where S is the peak height of sample aliquot in mm, V_1 is the analyzed sample aliquot size in mL, V_2 is the final dilution volume of the distillate in mL, MB is the total picograms of the method blank and V_3 is the original sample volume distilled in mL.

$$MB = C \cdot (S-B) \cdot V_2 / V_1$$

where S is the peak height of method blank in mm, V_1 is the analyzed method blank aliquot size in mL, and V_2 is the final dilution volume of the method blank distillate in mL.

For solid samples:

Solid samples are calculated in the same manner as above except that V_3 is the original sample weight digested or distilled in mg, with the result being in ng/g

6. SAMPLE PREPARATION

Depending on the purposes and definitions of investigations of mercury biogeochemistry cycling, samples are prepared in the following methods prior to analysis.

6.1. The following two isolation methods, distillation and solvent extraction, have been used in our labs for the determination of MMHg in aqueous samples. Good agreement was obtained in the comparison of the two methods for most water samples studied: for organic rich and/or high level sulfide containing samples, the distillation showed some advantages over the solvent extraction method with higher recoveries ($85 \pm 4\%$, Horvat, Bloom, and Liang, 1993). In addition, extraction consumes a lot of organic solvent and results in environmental contamination. Therefore, distillation is preferred.

6.1.1. Distillation:

Reagents: 20% KCl in L-Cysteine, 8M H_2SO_4 , 0.05% $\text{NH}_2\text{OH}\cdot\text{HCl}$

Distillation devices: Vials and caps for distillation and distillate collection are made of Teflon obtained by Savillex Corporation, USA. Caps have 1/8" ports for friction fit 1/8" Teflon tubing. Instead of Teflon, a glass distillation still may also be used (Horvat and Stoepler, 1988).

Distillation procedures: An aliquot of water sample, typically 45 mL, is transferred into a 60 mL Teflon vial (for high MMHg concentration samples, small sample size should be used, but bring the final volume to a known volume with DDW). Add 0.2 mL of 20% KCl and 0.5 mL of 8M H_2SO_4 . Start the distillation immediately after addition of reagents at a nitrogen flow rate of $60 \text{ mL}\cdot\text{min}^{-1}$ and at a heating

block temperature of 145° C. The distillate is collected into a 60 mL Teflon vial containing 3-5 mL of 0.05% $\text{NH}_2\text{OH}\cdot\text{HCl}$ in DDW, which is cooled in an ice-water bath. The distillation is finished when approximately 85% of distillate is collected after taking 3-4 hours. Bring the final volume to 58 mL with DDW in receiving vial. Depending on its MMHg concentration, the whole or an aliquot of the distillate is added into the methylation reaction vessel for analysis as described in section 4. Some acid can be carried over during distillation. Adjust pH in the bubbler to 3.5-5.5 by adding 20% KOH and/or 1:1 HAC solutions before adding buffer.

6.1.2. Solvent extraction

Reagent: 30% KCl (saturated), methylene chloride (large blanks in MMHg determination occasionally result from this solvent. Therefore, different brands and lot numbers should be examined to minimize this contamination.)

Extraction procedure: An extraction procedure described by Bloom (1989) was used. Depending on its concentration, weigh an approximate volume of the sample acidified to a pH of 2-5, typically 50 mL into a 125 mL Teflon bottle. If a smaller sample size is used, bring the final volume to 50 mL with DDW. Add 5 mL of 30% KCl, and swirl the bottle to mix. Add 40 mL of methylene chloride. Shake the bottle for 1-2 h with a mechanical shaker to reach a distribution equilibrium of MMHg between aqueous and solvent phases, then allow the two phases to separate. Remove the upper phase (aqueous phase) by pipetting. Add about 50 mL of DDW to the methylene chloride, and place the bottle in a hot water bath at 60° C until all of the CH_2Cl_2 has boiled away. The water is then purged for 2-3 minutes at $250 \text{ mL}\cdot\text{min}^{-1}$ with N_2 to remove any residual solvent. The MMHg is transferred to the DDW matrix, which is ready for ethylation as described above. At least 2 reagent blanks and 2 spikes are run each day of extraction/analysis. Usually, 10% of samples are used for spike recovery evaluation. The mean recovery is calculated, which is used to correct all sample results.

6.2. Determination of MMHg and Hg(II) in biological materials and sediments

6.2.1. Alkaline digestion: About one gram of biological materials or sediments (wet, homogenous) is weighed into a 30 mL Teflon vial. 10 mL of 25% KOH methanol solution is then added to the vial, which is then tightly closed with a cap. The sample is digested in an oven at 65° C for 3-4 hours. After digestion, bring the final volume to 25.6 mL with methanol prior to analysis. Analyze an appropriate aliquot, depending on the sample's concentration of MMHg and Hg(II).

6.2.2. Distillation: If the MMHg concentration compared to Hg(II) is low, matrix interference on ethylation reaction caused by using large volumes of alkaline

digestate will occur. This interference is avoided by distillation (Horvat, Bloom, and Liang, 1993). A sediment sample can be distilled directly by weighing an appropriate amount into a 30 mL Teflon vial and adding 10 mL of DDW, followed by the distillation procedure mentioned above (6.1.1). For biological samples (Liang, Bloom, and Horvat 1994) the MMHg bound on protein must be distilled out completely; therefore, a sample should be distilled after alkaline digestion by taking 0.5 mL of alkaline digestion, adding 10 mL DDW into a 30 mL vial, and following section 6.2.1.

7. SAMPLE COLLECTION, STORAGE, AND HANDLING, AQUEOUS, SEDIMENTS, AND BIOLOGICAL MATERIALS.

7.1. Water

7.1.1. Samples should be collected only into rigorously cleaned Teflon bottles. Under no circumstances should ordinary plastic (i.e., polyethylene, polypropylene, or vinyl) containers be used, as they are very diffusive to gaseous Hg^0 from the air. Ashed or rigorously acid cleaned Borosilicate or quartz glass bottles with Teflon caps may be used as well. It is critical that the bottles have very tightly sealing caps to avoid diffusion of atmospheric Hg through the threads (Gill and Fitzgerald, 1985). As an added precaution, clean bottles are filled with high purity 1% HCl solution and dried, capped, and double-bagged in new zip-loc bags in the clean-room, and stored in wooden or plastic boxes until use.

7.1.2. Samples are collected using rigorous ultra-clean protocols (Gill and Fitzgerald, 1985; and EPA Method 1669 "Sampling Ambient Water for Trace Metals At EPA Water Quality Criteria Levels", April 1995) which are summarized as follows:

- a) At least two persons wearing fresh clean-room gloves at all times, are required on a sampling crew.
- b) One person ("dirty hands") pulls a bagged bottle from the box, and opens the outer, dirty bag, avoiding touching inside that bag.
- c) The other person ("clean hands") reaches in, opens the inner bag, and pulls out the sample bottle.
- d) The bottle is opened with a plastic shrouded dedicated wrench, and the acidified water is discarded downstream of the sampling site.
- e) The bottle is rinsed once with sample water, and then filled.
- f) Preservative (i.e.; 0.8% by volume of high purity HCl) may be added at this time, or within several hours after receipt at the clean laboratory.

- g) The cap is replaced with the wrench, and the bottle rebagged in the opposite order from which it was removed.
- h) Clean-room gloves are changed between samples and whenever something not known to be clean is touched.
- i) Water samples are best obtained by surface grab, using gloved hands, and facing into a flowing body of water (i.e.; looking upstream or of the bow of a moving boat). If samples are to be taken from depth, the only non-contaminating method generally available is pumping. Two methods have been found to work in this regard. The first is to use rigorously acid-cleaned Teflon tubing, and a peristaltic pump with *freshly cleaned* (heating to 70° C in 5% HCl + CH₃COOH) silicon tubing. Beware that once cleaned, silicon tubing quickly absorbs Hg from the air. The other method involves high-volume pumping (i.e.; 50 L·min⁻¹) through neoprene hose. If this method is used, it is best to clean the system first by pumping several hundred liters of 5% HCl solution, and then pumping clean water for several hours. This second technique works largely because the rate of flow is so fast that the contamination becomes imperceptibly diluted.
- j) DISCRETE SAMPLERS, i.e.; Niskin, GoFlo, and Kemerer BOTTLES, ARE TO BE AVOIDED, AS EVEN UNDER THE BEST OF CONDITIONS THEY ARE OFTEN FOUND TO GROSSLY CONTAMINATE SAMPLES AT THE ng·L⁻¹ LEVEL.

7.1.3. Samples may be preserved by adding 8 mL·L⁻¹ of concentrated HCl (if only total methylmercury is to be analyzed), or frozen if labile and methylmercury are to be analyzed. Samples may also be sent back to the laboratory unpreserved if they are 1) collected in Teflon bottles, 2) filled to the top with no head space, and 3) sent at 1° C by overnight mail. The samples should be preserved and analyzed soon after arrival at the laboratory (within 24 hours). FREEZING IS NOT AN ACCEPTABLE TECHNIQUE FOR TOTAL INORGANIC Hg, AS UPON THAWING, MUCH Hg(II) IS CONVERTED TO VOLATILE Hg⁰.

7.1.4. All handling of the samples in the lab is to occur by clean-room gloved personnel in a class-100 clean room station with mercury removal filters, after rinsing the outside of the bottles in low Hg water, and drying in the clean air hood.

7.2. Solids

7.2.1. Samples should be collected only into rigorously cleaned Teflon containers or glass containers with Teflon lined lids. Under no circumstances should polyethylene, polypropylene, or vinyl containers be used.

7.2.2. Samples are to be frozen at $<-10^{\circ}\text{C}$ (standard freezer on coldest setting) until use. A holding time of 1 year at $<-10^{\circ}\text{C}$ is recommended.

7.2.3. All dissection, homogenization, and other handling of the samples is to occur by clean-room gloved personnel in a class-100 clean room station with mercury removal filters.

8. QUALITY CONTROL

8.1. All quality control data should be maintained and available for easy reference or inspection.

8.2. Calibration data must be composed of a minimum of 3 calibration (or bubbler) blanks and 3 standards (preferably four of each). Such a calibration should be run at least once per day, or every 20 samples, whichever comes first. If work performed is research level, more than 20 samples may be analyzed in a batch at the discretion of the lab director.

8.3. Samples containing high analyte concentrations may be run either following dilution, or on a separate run at lower instrumental sensitivity provided the instrument is calibrated at this sensitivity. All peak areas obtained for samples must ultimately fall below the peak area obtained from the highest standard analyzed in the calibration curve and above the lowest standard if possible.

8.4. Calibration checks must be analyzed after instrument calibration, after every ten samples and at the end of the analytical batch. Calibration checks shall consist of a mid-level standard and a bubbler blank. The calibration check standard must be within 20% of the calibration and the calibration check blank must be within 100% of the calibration blanks.

8.5. A minimum of 2 method blanks per batch of 20 samples must be run. To obtain a meaningful value for the reporting limits of detection, the standard deviation must be estimated from at least 7 sets of method blanks. Method blanks should consist of all reagents used for a sample and should be carried through the entire method as a sample. To estimate the standard deviation from multiple sets of duplicate method blanks, the following formula is used:

$$\text{Estimated Standard Deviation} = \sqrt{[\sum(d \cdot d)]/2m}$$

where d is the difference between within batch determinations of the method blanks and m is the number of duplicate blank determinations.

8.6. Analysis of split samples should be run once every 10 samples or once per batch, whichever comes first. Split samples are defined as a homogeneous sample that is split into two aliquots, and then each aliquot is carried through the entire preparation and analytical procedure. Criteria for split sample results are determined by control charts. If

control charts are not available then the split sample results must have a relative percent difference of 25% or less for water and 35% or less for solids for the analysis to be considered valid. Sample results not meeting this criteria shall be reprepared and analyzed or qualified at the discretion of the lab director.

8.7. NRC or NBS certified reference materials for mercury in tissues and sediments should be analyzed at a frequency of once per 10 samples or once per batch, whichever comes first. Criteria for CRMs are determined by control charts. If control charts are not available then CRM results should be within 25% of the certified value for the analysis to be considered valid. CRM sample results not meeting this criteria shall be reprepared and analyzed or qualified at the discretion of the lab director.

8.8. Procedural spike recoveries are analyzed at the request of the client, or in the absence of a suitable certified sample as determined by the lab director.

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- EPA Method 1669 (April 1995) "Sampling Ambient Water for Trace Metals At EPA Water Quality Criteria Levels."

SOP #BR-0002

Determination of Total Mercury in Solids by Cold Vapor Atomic Fluorescence Spectrophotometry (CVAFS)

Brooks Rand, Ltd.

Revision 003
Revised 12/94

Reviewed

D J Brook
President

12/5/94
Date

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12.02.94
Date

Total Mercury In Solids By Cold Vapor Atomic Fluorescence Spectrophotometry

1. SCOPE AND APPLICATION

1.1. Method BR-0002 is a peer-reviewed, published procedure for the determination of total mercury in a wide range of biological and geological matrices. All samples must be subject to an appropriate digestion step prior to analysis.

2. SUMMARY OF METHOD

2.1. Prior to analysis, the solid samples must be prepared according to the procedure discussed in this method.

2.2. Method BR-0002 is a cold vapor atomic fluorescence technique, based upon the emission of 253.7 nm radiation by excited Hg^0 atoms in an inert gas stream. Mercuric ions in the oxidized sample are reduced to Hg^0 with SnCl_2 , and then purged onto gold-coated sand traps as a means of preconcentration. Mercury vapor is thermally desorbed into the fluorescence cell. Fluorescence (peak height or area) is measured as a function of total mercury collected, which is converted to concentration by the size of the aliquot purged.

2.3. The typical detection limit for this method is $1 \text{ ng}\cdot\text{g}^{-1}$ as Hg (or 1 ppb) calculated as 3 times the standard deviation of complete method blanks.

3. INTERFERENCES

3.1. Due to the strong oxidation step there are no observed interferences with this method.

3.2. The potential exists for destruction of the gold traps (and consequently, low values) if free halogens are purged onto them, or if they are overheated ($>500^\circ \text{C}$). When these instructions are followed accurately, neither of these outcomes is likely.

3.3. Water vapor may collect in the gold traps, and be released into the fluorescence cell where it condenses, giving a false peak due to scattering of the excitation radiation. This can be avoided with the use of a soda lime pre trap.

3.4. As always with atomic fluorescence, the fluorescent intensity is strongly dependent upon the inertness of the carrier gas. It is the analyst's responsibility to ensure high purity inert carrier gas and a leak-free analytical train.

4. APPARATUS AND MATERIALS

4.1. Atomic fluorescence spectrophotometer or equivalent. To achieve the low detection levels and small, interference-free aliquots claimed by this method, a very sensitive CVAFS detector is required. Such systems are built at Brooks Rand, Ltd. (BRL Model II and Model III) based on the principals discussed by Bloom and Fitzgerald(1988). Other mercury specific detectors such as atomic absorption or plasma emission may be used, but detection limits would be 10-100 times higher. The CVAFS detector contains the four major components:

4.1.1. Four watt low pressure mercury vapor lamp

4.1.2. Far UV quartz flow-through fluorescence cell 12 mm x 12 mm x 45 mm long, with a 10 mm path length.

4.1.3. UV Visible photomultiplier: Sensitive to <230 nm. This PMT is isolated from outside light with a 254 nm interference filter.

4.1.4. Flowmeter: flowmeter with needle valve capable of reproducibly keeping carrier gas flow at 30 mL·min⁻¹.

4.2. Flow meter/needle valve: Capable of controlling and measuring gas flow to the purge vessel at 200-500 mL·min⁻¹.

4.3. Teflon® fittings: Connections between components and traps are made using 3.2 mm O.D. precleaned Teflon® FEP tubing, and Teflon® friction-fit or threaded tubing connectors.

4.4. Acid-fume and moisture pretrap: A 10 cm x 0.9 cm diameter Teflon® tube containing 2-3 grams of reagent grade, non-indicating 8-12 mesh soda lime, packed in between wads of silanized glass wool. This trap is purged of Hg by placing on the output of a clean cold vapor generator, filled with double deionized water (DDW), and purging for 20 minutes with N₂ at 100 mL·min⁻¹.

4.5. Cold vapor generator: A 250 mL or 125 mL florence flask with standard taper 24/40 neck, fitted with a sparging stopper having a coarse glass frit which extends to within 0.2 cm of the flask bottom.

4.6. Gold-coated sand traps: Made from 10 cm lengths of 6.5 mm O.D. x 4 mm I.D. quartz tubing, with a circular indentation 2.0 cm from one end. The tube is filled with 2.5 cm of gold-coated ashed (800° C for 6 hours) quartz sand (60/80 mesh). The end is then plugged with quartz wool. Gold is applied to the sand as a coating several atoms thick using an ion discharge gilding apparatus such as is employed to coat electron microscopy samples. Traps are heated to 450°-500° C (a barely visible red glow when the room is darkened) with a coil consisting of 78.75 cm of 22 ga nichrome wire at a potential of 10

VAC. Potential is applied and finely adjusted with an autotransformer. Traps should be heated for 5 minutes and cooled, after construction and before their first use.

4.7. Recorder: Any integrator with 0.1-5.000 mV input.

4.8. Pipettors: All plastic pneumatic fixed volume and variable pipettors in the range of 10 μ L to 5.0 mL.

4.9. Refluxing digestion flask. 100 mL volumetric flasks with acid-cleaned 1 inch diameter glass marbles over the mouth. When the flasks are placed on a hot plate (about 125°-150° C) the contents will reflux, the marbles acting as pressure relief valves. Loosely capped Teflon® vials can be used instead of volumetric flasks.

5. REAGENTS

5.1. Water: 18 megohm ultrapure deionized water (ASTM type I) starting from a pre-purified (distilled, R.O., etc.) source. As a final mercury and organic removal step, the activated carbon cartridge on the 18 megohm system is placed between the final ion exchange bed and the 0.2 μ M filter. Water should be monitored for Hg -- especially after ion exchange beds are changed.

5.2. Nitric/sulfuric acid: Carefully add 300 mL of pre-analyzed low mercury (<10 ng·L⁻¹ Hg) concentrated sulfuric acid to 700 mL pre-analyzed, low mercury (<10 ng·L⁻¹ Hg) concentrated nitric acid in a Teflon bottle, with constant stirring.

Caution: This mixture gets hot and emits caustic fumes!

5.3. Stannous Chloride: A solution containing 200 g of SnCl₂·2H₂O and 200 mL concentrated HCl is brought to 1.0 L with high purity water. This solution is purged overnight with mercury-free N₂ at 500 mL·min⁻¹ to remove all traces of Hg.

5.4. Bromine monochloride: 27 g of KBr are added to a 2.5 L bottle of concentrated pre-analyzed HCl found to be low in Hg (<5 ng·L⁻¹ Hg). A clean magnetic stir bar is placed in the bottle, and it is stirred for 1 hour in a fume hood. Next, 38 g of pre-analyzed, low Hg KBrO₃ are slowly added to the acid with stirring.

Caution: This process generates copious quantities of free Cl₂ which are released from the bottle. Add the KBrO₃ slowly and in a well operating fume hood! The fumes from this reagent, like chlorine or bromine, are very irritating and corrosive.

When all of the KBrO₃ has been added, the solution should have gone from yellow to red to orange. Loosely cap the bottle, and allow to stir another hour before tightening the lid. Store tightly capped, and in the dark. This reagent usually has a Hg concentration in the range of 25-40 ng/L.

5.5. Stock mercury standard: A commercially available $1000 \text{ mg}\cdot\text{L}^{-1}$ mercury atomic absorption standard that is traceable to NIST is used. Alternatively, 0.1354 g of high purity HgCl_2 may be dissolved in 75 mL of water, 5 mL of bromine monochloride solution added, and the volume brought to 100.0 mL in a class A volumetric flask. This stock standard should be replaced by the manufacturer's expiration date.

5.6. Intermediate mercury standard solution: 0.100 mL of the stock solution is diluted to 100.0 mL of water containing 5 mL of bromine monochloride. This solution contains $1.00 \mu\text{g}\cdot\text{mL}^{-1} \text{ Hg}$. Keep in a tightly closed Teflon® bottle. This solution should be replaced yearly.

5.7. Mercury working standards: 1.00 mL of the intermediate mercury standard is diluted to 100.0 mL with high purity water containing 1% by volume bromine monochloride solution, to make a $10.0 \text{ ng}\cdot\text{mL}^{-1}$ working solution. Also, a $1.00 \text{ ng}\cdot\text{mL}^{-1}$ working standard should be made with 0.100 mL of the intermediate mercury standard diluted to 100.0 mL with high purity water containing 1% by volume BrCl solution. Both working standards should be replaced monthly.

5.8. Nitrogen: Grade 4.5 (standard laboratory grade) nitrogen which has been further purified by the removal of Hg using a gold-coated sand trap.

5.9. Helium or argon: Grade 5.0 (ultra high purity, G.C. grade) inert gas which has been further purified by the removal of Hg using a gold-coated sand trap.

6. SAMPLE COLLECTION, PRESERVATION, AND HANDLING

6.1. Samples should be collected into acid-cleaned Teflon® container or glass containers with Teflon® lids. Under no circumstances should polyethylene, polypropylene, or vinyl containers be used.

6.2. Samples are to be frozen at $<-10^\circ \text{ C}$ (standard freezer on coldest setting) until use. A maximum holding time of 1 year at $<-10^\circ \text{ C}$ is recommended.

6.3. All dissection, homogenization, and other handling of the samples is to occur by clean-room gloved personnel in either a class-100 clean station with mercury removal filters or in a clean room atmosphere.

7. PROCEDURE

7.1. Sample Preparation: Dissect and/or homogenize the sample or a greater than 10 g aliquot (if available) with acid-washed stainless steel tools. An approximately 1.0 gram aliquot of the homogenized sample is weighed directly into the volumetric flask. If necessary, up to $2\text{-}3 \text{ mL}$ of high purity water may be used to rinse the sample down to the bottom. 10.0 mL of the $\text{HNO}_3/\text{H}_2\text{SO}_4$ mixture are pipetted in, and the sample swirled. The marble is placed over the mouth, and the samples are allowed to predigest at room

temperature for about 1 hour. Samples are next placed on a hot plate, and brought up to a refluxing boil in temperature increments. This is to avoid excessive foaming, especially common with tissue samples. Samples are digested at 105° C (hot plate temperature) for an hour and then refluxed at a hot plate temperature 150° C for 2 hours, or until all organic matter is dissolved, the solution looks substantially colorless or light yellow, and the brown gas above the liquid has almost disappeared. Sediment samples, especially sandy ones, may take less time. The samples are allowed to cool on the hot plate, and the marbles collected and rinsed in a beaker of water. Samples are diluted to the 100.0 mL mark with high purity water containing 1.0% BrCl. The original volumetric flask caps are replaced, and the samples thoroughly homogenized prior to analysis. Experience and numerous intercalibrations show that undigested rock material or animal fat does not affect the accuracy of this digestion for Hg, because these fractions are both very low in initial Hg content, and are effectively leached by the boiling acid. As a substitute, 25.6 Teflon® vials may be used instead. If Teflon® vials are used the caps should be loosened about 1/4 turn after the threads make good contact before heating, to allow the samples to vent. After digestion the vials should be allowed to cool, and 0.5 mL of BrCl should be added and the volume brought up to 25.6 mL.

7.2. Analysis: The sequence of steps for analysis is shown graphically in Figure 1. 100 mL of water is placed in the bubblers, and 1.0 mL of SnCl₂ solution added. The bubbler is purged with N₂ at 300 mL·min⁻¹ for 20 minutes, and then a gold-coated sand trap is connected to the soda lime pretrap and purged for another 12 minutes. This value is the bubbler blank or calibration blank used for calibration. To analyze samples, 0.5 mL of SnCl₂ and an aliquot of the digestate, usually in the range of 0.25-1.0 mL, are pipetted into each bubbler. The caps are replaced, the vessel gently swirled, and gold-coated sand traps placed onto the soda lime pretrap outlet, and the sample bubbled for 12 minutes. New samples may then be added to the bubblers, with additional aliquots of SnCl₂. After 10 samples standards should be analyzed and then bubbler blanks should be measured. Then the water in the bubblers is replaced with fresh ultrapure water, and the above sequence is repeated.

To analyze the mercury contained on a gold trap, the nichrome wire coil is placed around the trap, and the trap is inserted in between the incoming Hg-free argon (or helium) and the analyzer. Electrical current (10 VAC) is then applied to the coil for 2.5 minutes (or 1 minute after returning to the base line), thermally desorbing the Hg as Hg⁰, which is carried by the He to the analyzer. At the same time the data acquisition device (integrator) is turned on.

Following the recording of the peak, the coil on the gold trap is turned off, and the cooling fan directed at it. The gold trap is now removed from the gas stream, and the Teflon® end plugs replaced until it is needed to collect another sample. The next sample trap is placed in line, and the procedure repeated.

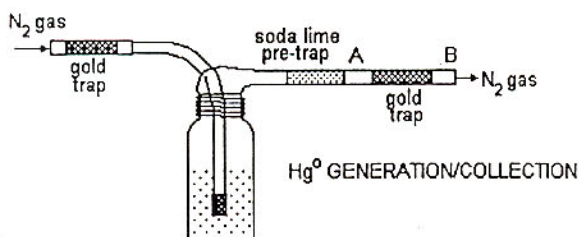
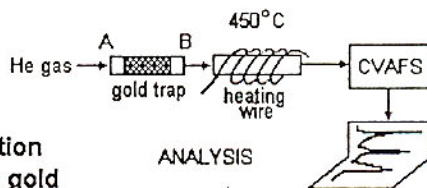


Figure 1:
Schematic diagram of
 Hg^0 generation/collection
and analysis by single gold
amalgamation/CVAFS



Peaks generated using this technique should be very sharp and almost symmetrical. The peak comes off at approximately 1 minute, and has a half-height width of about 5 seconds. Broad or asymmetrical peaks are indicative of an analytical problem, possibly including: low gas flow, water vapor on the trap, or the trap being damaged by chemical fumes or overheating. The last possibility is definitely the case if following a sharp peak, a secondary small broad peak is observed. If the gold trap has been damaged, it and the Teflon® tubing downstream from it should be discarded, due to the possibility of gold migration on downstream surfaces.

7.3. Cold Vapor Atomic Fluorescence for mercury is linear over at least 5 orders of magnitude (Bloom and Fitzgerald, 1988). However, it is required that at least a 3 point calibration curve be prepared each day prior to analysis to verify linearity. Standards to be analyzed for calibration should include one standard at 100 pg, one at 500 or 1000 pg and one at 5000 pg.

7.4. To run standards, aliquots of working standard solution are injected into a purged bubbler containing a fresh 0.5 mL aliquot of SnCl_2 , and the analysis run as a sample.

7.5. Gold-coated sand traps should be tracked by unique identifiers, so that any trap producing poor results can be quickly recognized and discarded. A log book should be maintained documenting initial trap testing and any questionable trap behavior. Occasionally due to inadvertent contact with halogen fumes, bubbler solution, organic fumes, or overheating, a sampling trap will become damaged, giving low and irreproducible results. Suspect traps should be checked with at least two consecutive standard runs before continued use.

7.6. The major cause of analytical problems with this method is from using the soda lime pretraps too long. These traps should be purged for at least 20 minutes as described and

then used for only one day's analytical work. Longer use risks irreproducibility, as the traps may begin retarding the flow of Hg^0 . Also, as they become very wet, there is a risk of NaOH-saturated water drops coming out onto the gold trap. If sample aliquots with much acid (i.e. 5 mL) are being analyzed, it is recommended that the soda lime pretraps are changed every two or three samples. The acid fumes in combination with water vapor, when trapped in soda lime pretraps seem to start trapping Hg^0 and therefore low recoveries may result.

7.7. Duplicates, spiked samples, method blanks and check standards should be routinely analyzed, as discussed in section 8.

7.8. Calculations are made by the following method:

a) Divide each standard amount (pg of Hg) by each net standard result (peak area of standard minus mean peak area of bubbler blanks or CB) in the calibration, to yield the "pg Hg/peak area." Pool all of the "pg Hg/peak area" values for a given calibration, to obtain a mean "pg Hg/peak area" value called the calibration coefficient (C). (C) is also functionally the equal to the slope of the regression of the standard curve. Linear regression is used to calculate a correlation coefficient (r). The r value should be greater than 0.995 for sample analysis to commence.

b) Pool the calibration blank values to obtain a mean "calibration blank peak area" (CB).

c) To calculate the amount of total mercury measured in the sample aliquot analyzed (P), employ the following formula:

$$P = \text{Hg (in pg)} = C(A - \text{CB})$$

Where A is the gross sample area. If blank correction is not desired by a customer, CB is not subtracted out.

d) To determine the concentration of total mercury in a sample, the calculation is performed as follows:

$$\text{Hg (in ng/g or ppb)} = [(P/v)V - p]/M$$

Where V is the final dilution volume of the digestate in mL (in this case, 100 mL) v is the volume of digestate analyzed in mL, M is the digested sample mass, in milligrams and p is the mean pg from the preparation of the method blanks. If blank correction is not desired by a customer, p is not subtracted out.

e) To determine the pg from the preparation of the method blanks (p), use the following formula for each method blank:

$$p = [(MB - \text{CB})C \cdot V]/v$$

Where MB is the peak area of the method blank, V is the final dilution volume of the method blank and v is the volume of the method blank analyzed.

d) The limit of detection is considered to be 3 times the standard deviation of the picograms in the entire method blanks. The picograms in the method blanks is calculated in the following manner:

$$\text{Hg in method blank (in pg)} = (\text{MB} \cdot \text{C} \cdot \text{V}) / \text{v}$$

To determine if a sample is detectable, the limit of detection should be multiplied by V and divided by v using volume amounts specific for that sample. If a sample is below the detection limit it should be qualified as such.

8. QUALITY CONTROL

8.1. All quality control data should be maintained and available for easy reference or inspection.

8.2. Calibration data must be composed of a minimum of 3 calibration (or bubbler) blanks and 3 standards (preferably four of each). Such a calibration should be run at least once per day, or every 20 samples, whichever comes first. If work performed is research level, more than 20 samples may be analyzed in a batch at the discretion of the lab director.

8.3. Samples containing high analyte concentrations may be run either following dilution, or on a separate run at lower instrumental sensitivity provided the instrument is calibrated at this sensitivity. All peak areas obtained for samples must ultimately fall below the peak area obtained from the highest standard analyzed in the calibration curve.

8.4. Calibration checks must be analyzed after instrument calibration, after every ten samples and at the end of the analytical batch. Calibration checks shall consist of a mid-level standard (500 or 1000 pg) and a bubbler blank. The calibration check standard must be within 20% of the calibration and the calibration check blank must be within 100% of the calibration blanks.

8.5. A minimum of 2 method blanks per batch of 20 samples must be run. To obtain a meaningful value for the reporting limits of detection, the standard deviation must be estimated from at least 7 sets of method blanks. Method blanks should consist of all reagents used for a sample and should be carried through the entire method as a sample. To estimate the standard deviation from multiple sets of duplicate method blanks, the following formula is used:

$$\text{Estimated Standard Deviation} = \sqrt{[\sum(d \cdot d)] / 2m}$$

where d is the difference between within batch determinations of the method blanks and m is the number of duplicate blank determinations.

8.6. Analysis of split samples should be run once every 10 samples or once per batch, whichever comes first. Split samples are defined as a homogeneous sample that is split into two aliquots, and then each aliquot is carried through the entire preparation and analytical procedure. Criteria for split sample results are determined by control charts. If control charts are not available then the split sample results must have a relative percent difference of 35% or less for the analysis to be considered valid. Sample results not meeting this criteria shall be reprepared and analyzed or qualified at the discretion of the lab director.

8.7. NRC or NBS certified reference materials for mercury in tissues and sediments should be analyzed at a frequency of once per 10 samples or once per batch, whichever comes first. Criteria for CRMs are determined by control charts. If control charts are not available then CRM results should be within 25% of the certified value for the analysis to be considered valid. CRM sample results not meeting this criteria shall be reprepared and analyzed or qualified at the discretion of the lab director.

8.8. Procedural spike recoveries are analyzed at the request of the client, or in the absence of a suitable certified sample as determined by the lab director.

9. REFERENCES

- Bloom, N.S. and Crecelius, E.A. (1983). "Determination of Mercury in Seawater at Subnanogram per Liter Levels." *Mar. Chem.* 14:49.
- Bloom, N.S. and Fitzgerald, W.F. (1988). "Determination of Volatile Mercury Species at the Picogram Level by Low-Temperature Gas Chromatography with Cold-Vapour Atomic Fluorescence Detection." *Anal. Chim. Acta.* 208:151.
- Fitzgerald, W.F. and Gill, G.A. (1979). "Sub-Nanogram Determination of Mercury by Two-Stage Gold Amalgamation and Gas Phase Detection Applied to Atmospheric Analysis." *Anal. Chem.* 15:1714.
- Liang, L. and Bloom, N.S. (1992). "Determination of Total Hg by Single-Stage Gold Amalgamation with Cold Vapor Atomic Spectrometric Detection." *JAAS.* June 8:001

SOP #BR-1501

Dry Weight Determination

Brooks Rand, Ltd.

Written 2/19/93

Revision 000

Reviewed _____



President

2/25/93

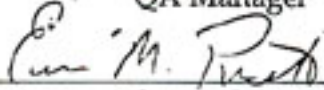
Date



QA Manager

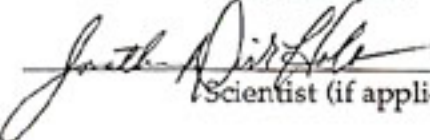
2/25/93

Date



Senior Scientist

Date



Scientist (if applicable)

2.24.93

Date

Dry Weight Determination

1. DESCRIPTION

A. Definition: Dry weight determination (defined as): determining the percent dry weight of the gross weight solid sample.

B. Scope: The scope of dry weight determination is to determine the contribution of any mercury or contaminate due to the moisture content of a sample.

C. Summary: A solid sample is mixed to a homogenous state and an aliquot is measured into a vessel (gross), dried in an oven overnight, weighed again and a dry weight is recorded.

2. MATERIALS

2.1 Needed: samples in labeled containers, disposable weighing dishes, top-loading balance with accuracy to 0.001 g, thermostatically controlled drying oven capable of temperature of at least 110°C, and data entry sheets to record weights (Exhibit A).

3. PROCEDURE

3.1 First, record the current date, name of operator, and project name onto the data entry sheet (Exhibit A). With an indelible marker, write the number or tag letters of the labeled sample vessel onto the tab of the disposable weighing dish and also into the entry sheet. Place the dish on the balance and record the dish weight as the tare weight. At this point, tare the dish and place an aliquot of homogenous sample (preferably 9.8-10.2 grams of stirred sample) onto the dish trying as best as possible to obtain uniform composition. Record this weight as the wet weight (net wt). Place the dish with sample into the drying oven at a temperature of 100-110°C overnight.

3.2 The following day, the samples can be removed from the oven and re-weighed. This weight is recorded as the dry weight. Subtract the tare weight (dish weight) from the dry weight and record this weight as the net dry weight. You can now calculate the percent moisture of the solid sample and record it into the data entry sheet. Sign or initial the entry upon completion of calculations.

4. QUALITY ASSURANCE

4.1 For every set of ten samples a triplicate should be done. Also each day the balance and oven should be checked and calibrated as referred to in BR-1200.

Appendix D
Statistical Results

Chemistry

Tissue Chemistry Concentration Data, Including Reference Stations 1 and 2	D-1
Tissue Chemistry Concentration Data, Excluding Reference Station 1	D-16
Tissue Chemistry Content Data, Including Reference Stations 1 and 2	D-31
Tissue Chemistry Content Data, Excluding Reference Station 1	D-47

Growth

Beginning-of-Test (T ₀) ANOVA: By Cage and Station	D-62
Binomial Multiple Comparison on Percent Survival	D-64
Clam Growth Metrics: Tissue Weight, Whole-animal Wet-Weight and Growth Rate	D-66
Percent Solids and Percent Lipids	D-72
Water, Sediment and Tissue Chemistry Correlations	D-77

STATISTICAL RESULTS
TISSUE CHEMISTRY CONCENTRATION DATA
INCLUDING REFERENCE STATIONS 1 AND 2

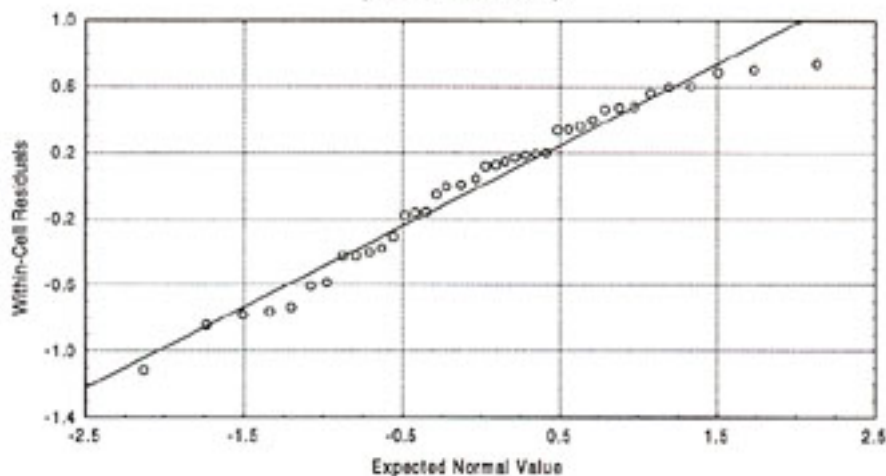
Tissue Chemistry Concentration Statistical Results (including both Reference stations 1 and 2)

Means

	AS	CD	CR	PB	HG	MEHG
1	5.620000	2.227500	8.190000	.686000	1.074500	.160000
2	5.415000	3.182500	5.887500	1.093500	.833500	.099025
3	5.290000	2.620000	17.300000	.641250	.865500	.156750
4	5.052500	2.262500	25.200000	1.386250	.975250	.182750
5	5.785000	2.782500	70.225000	1.682500	1.060500	.156250
6	5.425000	2.715000	18.550000	1.019250	.756000	.125500
7	5.105000	2.522500	19.450000	.784000	.813750	.131000
8	5.920000	3.397500	49.900000	1.362000	.902250	.101825
9	5.035000	2.430000	14.857500	.876500	1.099750	.140000
10	5.325000	2.890000	9.467500	.918500	.858250	.131250

Arsenic

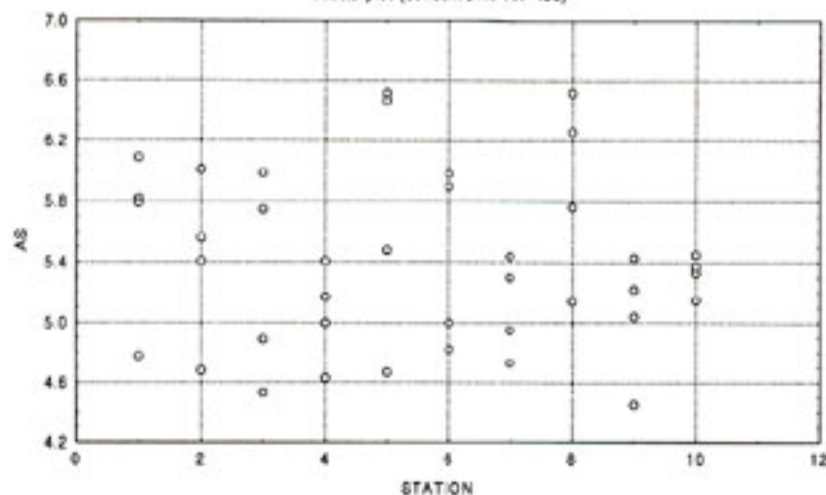
Normal Probability Plot of Residuals
variable: AS
 $y = -1.494e-6 + 0.489 * x + \text{eps}$



Correlation

	AS_X	AS_Y	
AS_X	1.000000	.984365	- normal
AS_Y	.984365	1.000000	

Scatterplot (concn. STA 14v*43c)



ANOVA

Effect	Sum of Squares	df	Mean Square	F	p-level
Effect	3.306123	9	.367347	1.210492	.325171
Error	9.104075	30	.303469		

Bonferroni contrasts - arsenic (with both Reference stations)

As

Rets 1 and 2 vs:

3	-0.6743861
4	-1.3784155
5	0.7929595
6	-0.2742009
7	-1.222768
8	1.1831446
9	-1.4302914
10	-0.5706344

critical value = 1.697

Newman-Keuls test - arsenic

	3	4	5	6	7	8	9	10
3		.814270	.584874	.935425	.637188	.495301	.911501	.928815
4	.814270		.430691	.869236	.893374	.311926	.964431	.894614
5	.584874	.430691		.361812	.420663	.730462	.476945	.471481
6	.935425	.869236	.361812		.841382	.420587	.910960	.798480
7	.637188	.893374	.420663	.841382		.317988	.982237	.838171
8	.495301	.311926	.730462	.420587	.317988		.340642	.432228
9	.911501	.964431	.476945	.910960	.982237	.340642		.942486
10	.928815	.894614	.471481	.798480	.838171	.432228	.942486	

Dunnett's contrasts - all stations vs. initial concentrations - arsenic
 If the value of q is greater than 2.878 then the P value is less than 0.05.

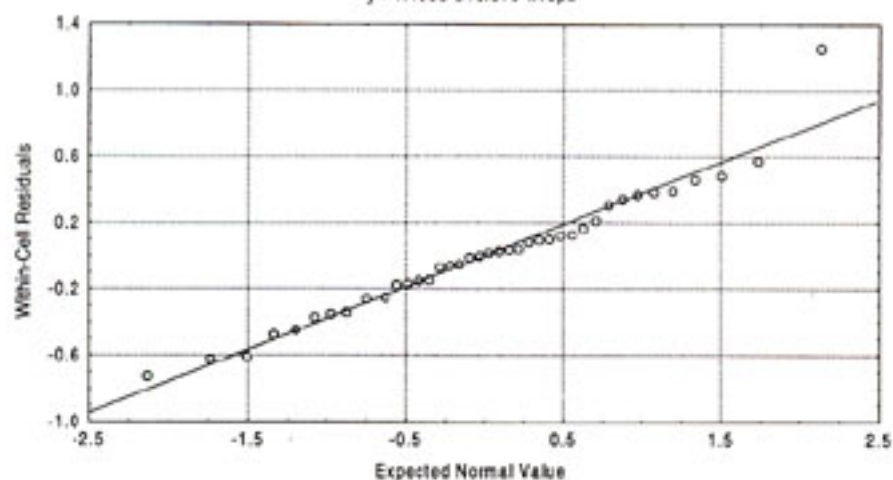
Comparison	Mean		P value
	Difference	q	
Initial vs Station 1	0.630	1.683	ns P>0.05
Initial vs Station 2	0.835	2.230	ns P>0.05
Initial vs Station 3	0.960	2.564	ns P>0.05
Initial vs Station 4	1.198	3.199	* P<0.05
Initial vs Station 5	0.465	1.242	ns P>0.05
Initial vs Station 6	0.825	2.204	ns P>0.05
Initial vs Station 7	1.145	3.059	* P<0.05
Initial vs Station 8	0.330	0.881	ns P>0.05
Initial vs Station 9	1.215	3.246	* P<0.05
Initial vs Station 10	0.9250	2.471	ns P>0.05

Cadmium

Normal Probability Plot of Residuals

variable: CD

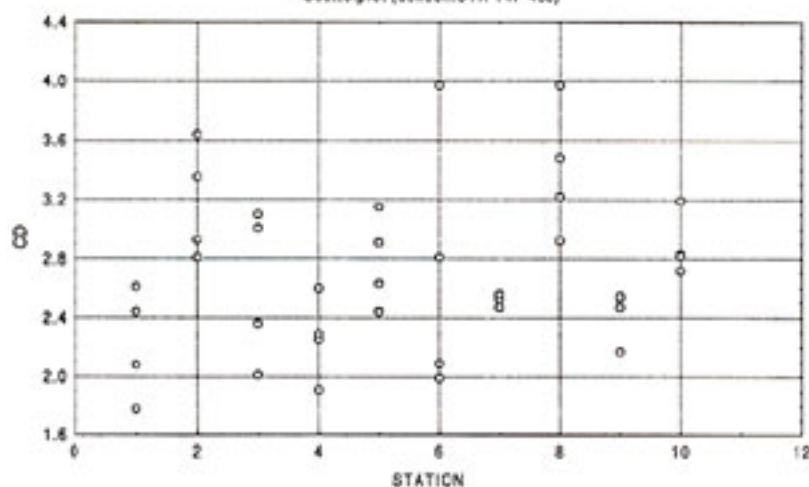
$$y = -1.195e-5 + 0.378 * x + \text{eps}$$



Correlation

	CD_X	CD_Y	
CD_X	1.000000	.975568	- normal
CD_Y	.975568	1.000000	

Scatterplot (concen.STA 14r*43c)



ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	5.151290	9	.572366	3.107108	.009284
Error	5.526350	30	.184212		

Bonferroni contrasts - cadmium (with both Reference stations)

Cd

Refs 1 and 2 vs:

3	-0.3234032
4	-1.6635991
5	0.2948676
6	0.0380474
7	-0.6943657
8	2.634785
9	-1.0463045
10	0.7038770

critical value = 1.697

Newman-Keuls test - cadmium

	3	4	5	6	7	8	9	10
3		.665661	.862052	.763521	.757503	.126046	.816730	.822549
4	.665661		.565403	.602881	.686484	.02436*	.596451	.433798
5	.862052	.565403		.830683	.838204	.141291	.789479	.733573
6	.763521	.602881	.830683		.812403	.155535	.797992	.841996
7	.757503	.686484	.838204	.812403		.091184	.769555	.763650
8	.126046	.024362	.141291	.155535	.091184		.063363	.117045
9	.816730	.596451	.789479	.797992	.769555	.063363		.683025
10	.822549	.433798	.733573	.841996	.763650	.117045	.683025	

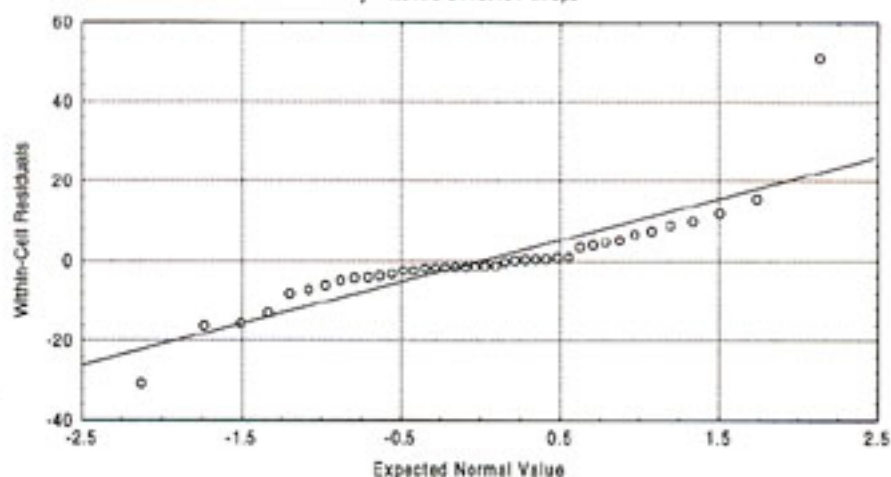
Dunnett's contrasts - all stations vs. initial concentrations - cadmium

If the value of q is greater than 2.878 then the P value is less than 0.05.

Comparison	Mean Difference	q	P value
Initial vs Station 1	0.8300	2.834	ns P>0.05
Initial vs Station 2	-0.1250	0.427	ns P>0.05
Initial vs Station 3	0.4375	1.494	ns P>0.05
Initial vs Station 4	0.7950	2.714	ns P>0.05
Initial vs Station 5	0.2750	0.939	ns P>0.05
Initial vs Station 6	0.3425	1.169	ns P>0.05
Initial vs Station 7	0.5350	1.827	ns P>0.05
Initial vs Station 8	-0.3400	1.161	ns P>0.05
Initial vs Station 9	0.6275	2.142	ns P>0.05
Initial vs Station 10	0.1675	0.572	ns P>0.05

Chromium

Normal Probability Plot of Residuals
variable: CR
 $y = -4.9176 \cdot 8 + 10.401 \cdot x + \epsilon$

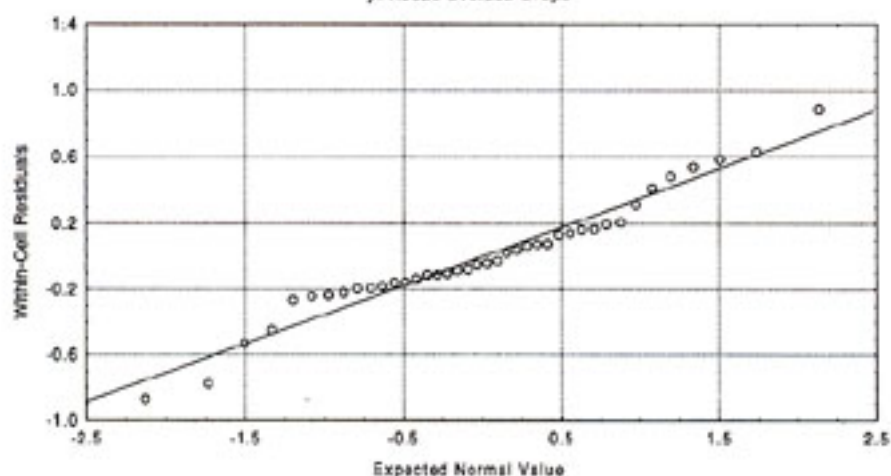


Correlation

	CR_X	CR_Y	
CR_X	1.000000	.872784	- not normal
CR_Y	.872784	1.000000	

Log-transformed Chromium

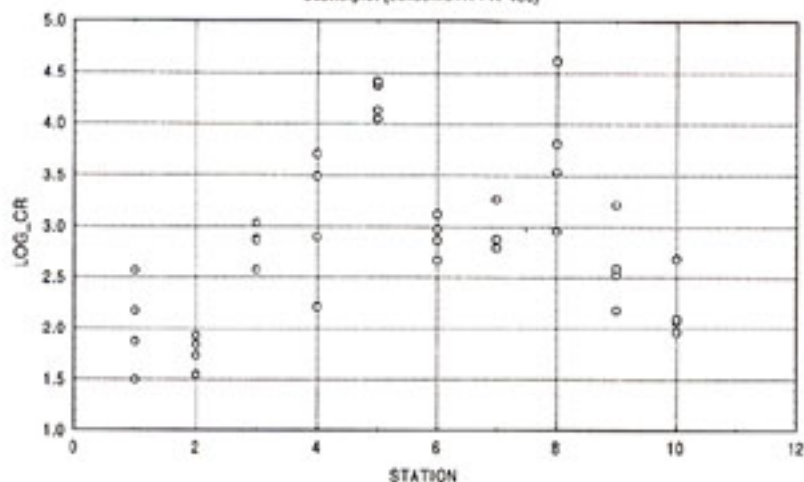
Normal Probability Plot of Residuals
variable: LOG_CR
 $y = 1.262 \cdot 8 + 0.353 \cdot x + \epsilon$



Correlation

	LGCR_X	LGCR_Y	
LGCR_X	1.000000	.978941	- normal
LGCR_Y	.978941	1.000000	

Scatterplot (concen.STA 14x43c)



ANOVA

Effect	Sum of Squares	df	Mean Square	F	p-level
Effect	20.37051	9	2.263390	14.13056	.000000
Error	4.80531	30	.160177		

Bonferroni contrasts - log chromium (with both Reference stations)

log Cr

Refs 1 and 2 vs:

3	1.6695467
	2.0923207
	4.1551691
6	1.7939711
7	1.8686436
8	3.2409011
9	1.2945549
10	0.5473012

critical value = 1.697

Newman-Keuls test - log chromium

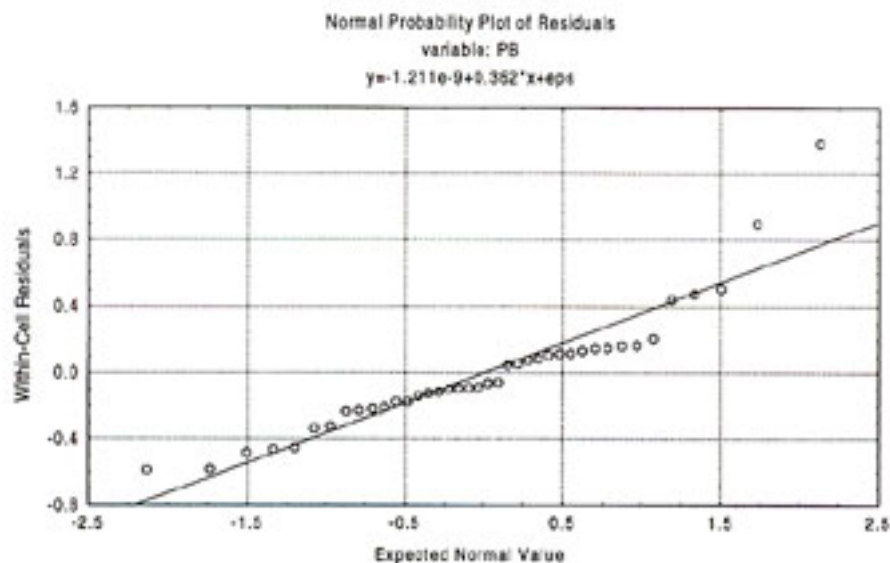
	3	4	5	6	7	8	9	10
3		.846750	.00100*	.812555	.922308	.04041*	.476774	.098294
4	.846750		.00166*	.834543	.670226	.03548*	.549013	.063644
5	.001002	.001664		.00122*	.00113*	.093466	.00032*	.00015*
6	.812555	.834543	.001225		.886829	.04532*	.606781	.103420
7	.922308	.670226	.001132	.886829		.03528*	.688880	.113172
8	.040409	.035477	.093466	.045318	.035279		.01085*	.00056*
9	.476774	.549013	.000323	.606781	.688880	.010854		.162674
10	.098294	.063644	.000152	.103420	.113172	.000556	.162674	

Dunnnett's contrasts - all stations vs. initial concentrations - log-transformed chromium

If the value of q is greater than 2.878 then the P value is less than 0.05.

Comparison	Mean Difference	q	P value
Initial vs Station 1	-0.4437	3.776	** P<0.01
Initial vs Station 2	-0.3289	2.799	ns P>0.05
Initial vs Station 3	-0.7955	6.769	** P<0.01
Initial vs Station 4	-0.8991	7.651	** P<0.01
Initial vs Station 5	-1.405	11.953	** P<0.01
Initial vs Station 6	-0.8260	7.029	** P<0.01
Initial vs Station 7	-0.8443	7.184	** P<0.01
Initial vs Station 8	-1.183	10.063	** P<0.01
Initial vs Station 9	-0.7036	5.987	** P<0.01
Initial vs Station 10	-0.5204	4.429	** P<0.01

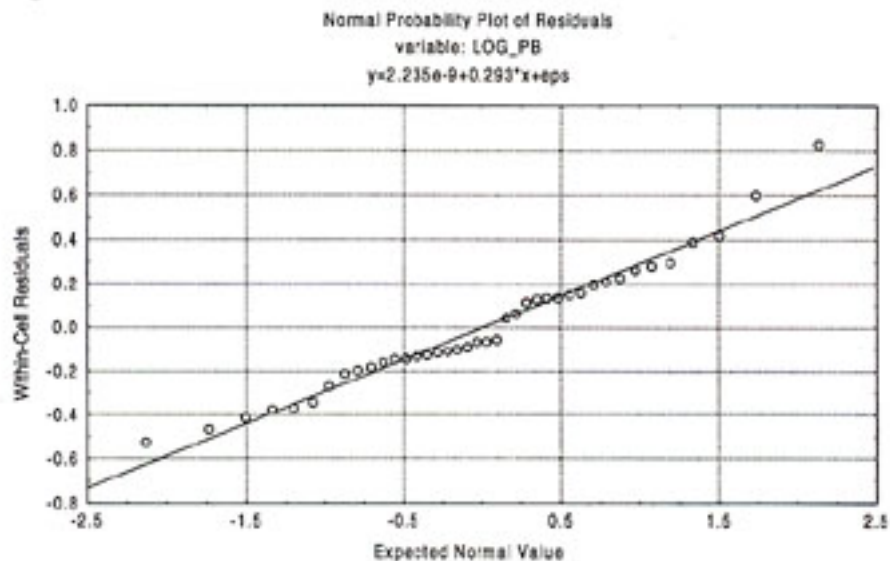
Lead



Correlation

	PB_X	PB_Y	
PB_X	1.000000	.937043	- not normal
PB_Y	.937043	1.000000	

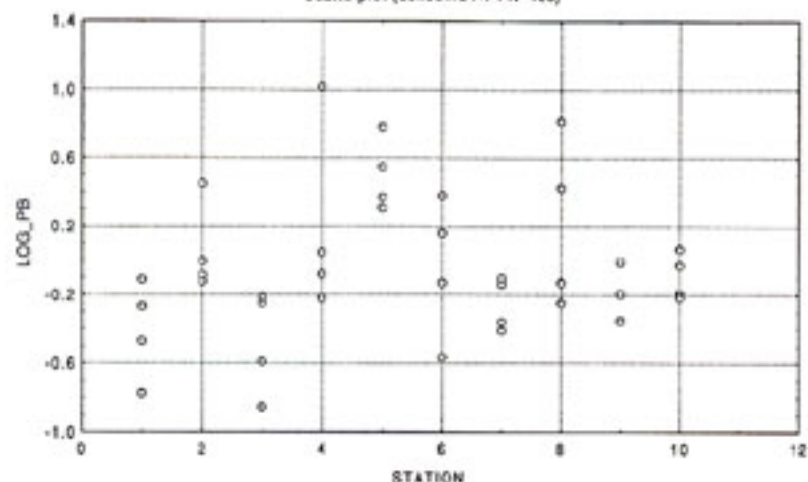
Log-transformed Lead



Correlation

	LGPB_X	LGPB_Y	
LGPB_X	1.000000	.984107	- normal
LGPB_Y	.984107	1.000000	

Scatterplot (conces. STA 14v*45c)



ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	3.230086	9	.358898	3.297433	.006575
Error	3.265254	30	.108842		

Bonferroni contrasts - log lead (with both Reference stations)
log Pb

Refs 1 and 2 vs:

3	-0.6548039
	0.7832666
	1.4521014
6	0.2857827
7	-0.1712093
8	0.8345283
9	0.0661068
10	0.173666

critical value = 1.697

Newman-Keuls test - log lead

	3	4	5	6	7	8	9	10
3		.098554	.00935*	.391874	.361751	.102810	.363678	.401195
4	.098554		.416405	.348370	.377600	.922398	.523952	.480659
5	.009350	.416405		.140419	.060593	.246678	.119946	.134218
6	.391874	.348370	.140419		.815750	.550275	.906747	.831228
7	.361751	.377600	.060593	.815750		.407054	.652333	.786808
8	.102810	.922398	.246678	.550275	.407054		.585958	.589559
9	.363678	.523952	.119946	.906747	.652333	.585958		.837986
10	.401195	.480659	.134218	.831228	.786808	.589559	.837986	

Dunnnett's contrasts - all stations vs. initial concentrations - log-transformed lead

If the value of q is greater than 2.878 then the P value is less than 0.05.

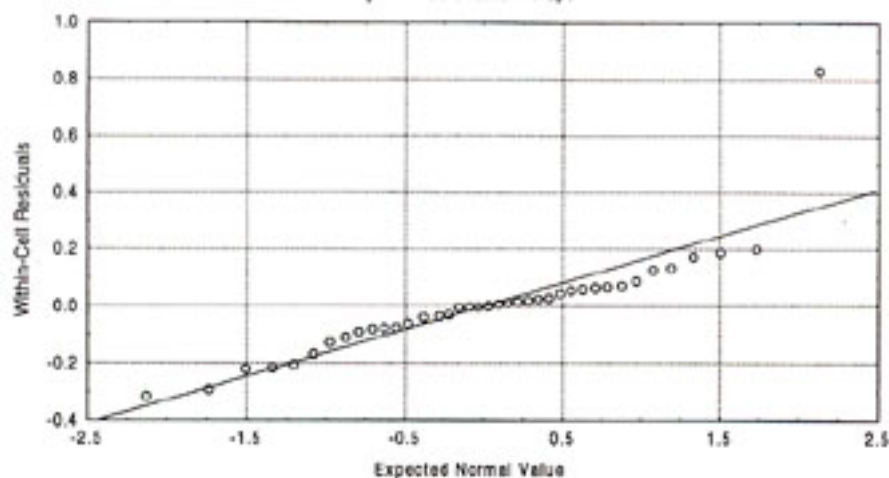
Comparison	Mean		P value
	Difference	q	
Initial vs Station 1	-0.6628	4.287	** P<0.01
Initial vs Station 2	-0.8660	5.602	** P<0.01
Initial vs Station 3	-0.6321	4.089	** P<0.01
Initial vs Station 4	-0.9226	5.968	** P<0.01
Initial vs Station 5	-1.058	6.842	** P<0.01
Initial vs Station 6	-0.8221	5.318	** P<0.01
Initial vs Station 7	-0.7298	4.721	** P<0.01
Initial vs Station 8	-0.9330	6.035	** P<0.01
Initial vs Station 9	-0.7778	5.031	** P<0.01
Initial vs Station 10	-0.7995	5.171	** P<0.01

Mercury

Normal Probability Plot of Residuals

variable: HG

$$y = -1.752e-6 + 0.164 * x + \text{eps}$$



Correlation

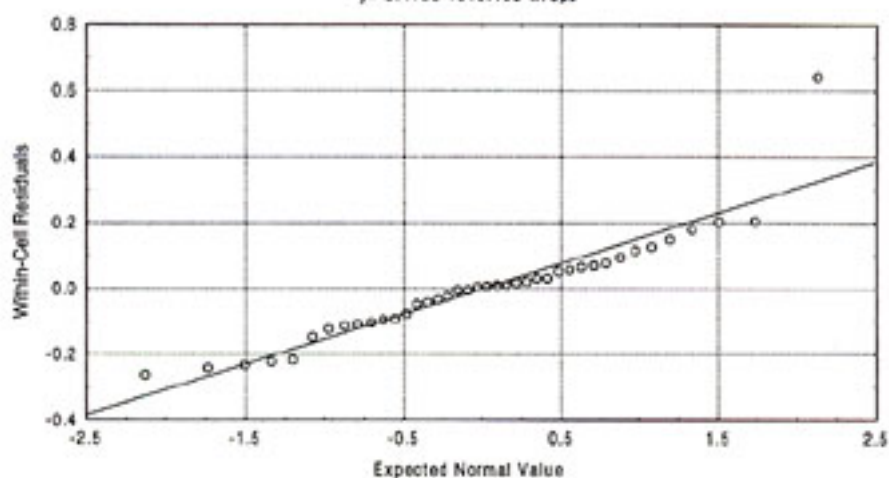
	HG_X	HG_Y	
HG_X	1.000000	.881520	- not normal
HG_Y	.881520	1.000000	

Log-transformed Mercury

Normal Probability Plot of Residuals

variable: LOG_HG

$$y = -5.413e-10 + 0.153 * x + \text{eps}$$



Correlation

	LGHG_X	LGHG_Y	
LGHG_X	1.000000	.934478	- not normal
LGHG_Y	.934478	1.000000	

Rank-it transformed Mercury

ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	15.70109	9	1.744566	2.422993	.033332
Error	21.60014	30	.720004		

Bonferroni contrasts -rank mercury (with both Reference stations) rank Hg

Refs 1 and 2 vs:

3	-0.3305049
	0.1303898
	0.4400372
6	-0.8790729
7	-0.6139864
8	-0.2320628
9	0.3028256
10	-0.3691711

critical value = 1.697

Newman-Keuls test - ranked mercury

	3	4	5	6	7	8	9	10
3		.728777	.494554	.438258	.585298	.994971	.932098	.752391
4	.728777		.560977	.181286	.352135	.564255	.502584	.658985
5	.494554	.560977		.069875	.162117	.385769	.424959	.399499
6	.438258	.181286	.069875		.602263	.552391	.435239	.460747
7	.585298	.352135	.162117	.602263		.748399	.660360	.504001
8	.994971	.564255	.385769	.552391	.748399		.728451	.943398
9	.932098	.502584	.424959	.435239	.660360	.728451		.904760
10	.752391	.658985	.399499	.460747	.504001	.943398	.904760	

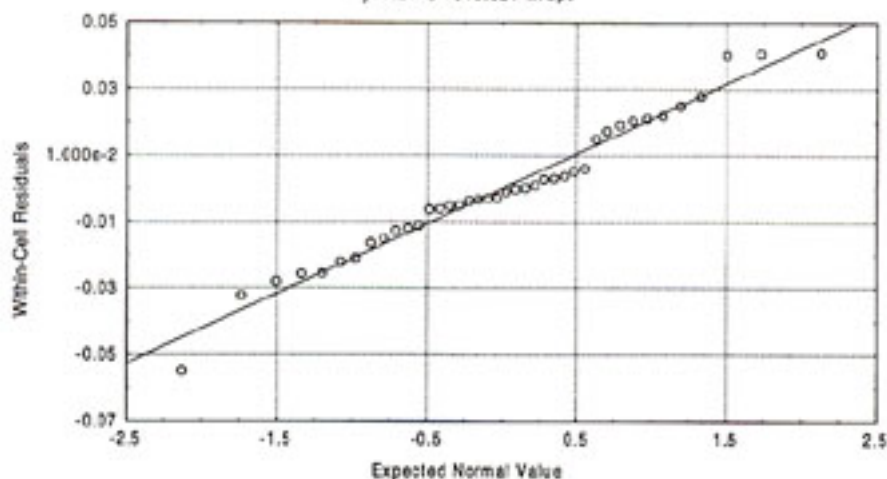
Dunnnett's contrasts - all stations vs. initial concentrations - rank-transformed mercury

If the value of q is greater than 2.878 then the P value is less than 0.05.

Comparison	Mean Difference	q	P value
Initial vs Station 1	0.383	0.672	ns P>0.05
Initial vs Station 2	1.691	2.967	* P<0.05
Initial vs Station 3	1.352	2.372	ns P>0.05
Initial vs Station 4	0.755	1.325	ns P>0.05
Initial vs Station 5	0.440	0.773	ns P>0.05
Initial vs Station 6	2.251	3.950	** P<0.01
Initial vs Station 7	1.952	3.424	* P<0.05
Initial vs Station 8	1.343	2.356	ns P>0.05
Initial vs Station 9	1.075	1.887	ns P>0.05
Initial vs Station 10	1.542	2.704	ns P>0.05

Methylmercury

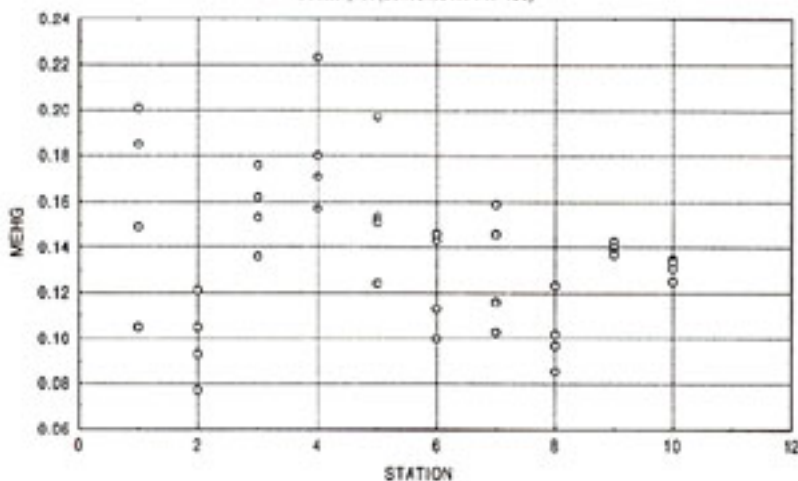
Normal Probability Plot of Residuals
variable: MEHG
 $y = 1.244e-10 + 0.021 * x + \epsilon$



Correlation

	MEHG_X	MEHG_Y
MEHG_X	1.000000	.986249 - normal
MEHG_Y	.986249	1.000000

Scatterplot (concn.STA 14*43c)



ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	.025007	9	.002779	4.941215	.000417
Error	.016870	30	.000562		

Bonferroni contrasts - methylmercury (with both Reference stations)

MeHg

Refs 1 and 2 vs:

3	1.8762187
	3.6571938
	1.8417768
6	-0.2763957
7	0.1024644
8	-1.9072163
9	0.7224174
10	0.1196864

critical value = 1.697

Newman-Keuls test - methylmercury

	3	4	5	6	7	8	9	10
3		.089930	.973275	.308626	.423846	.01550*	.500263	.329013
4	.089930		.190474	.01073*	.01939*	.00039*	.03636*	.01444*
5	.973275	.190474		.256465	.337308	.01273*	.280296	.225946
6	.308626	.010730	.256465		.711838	.120665	.758777	.919554
7	.423846	.019387	.337308	.711838		.138031	.815107	.986674
8	.015496	.000389	.012729	.120665	.138031		.103081	.215748
9	.500263	.036357	.280296	.758777	.815107	.103081		.557576
10	.329013	.014437	.225946	.919554	.986674	.215748	.557576	

Dunnett's contrasts - all stations vs. initial concentrations - methylmercury

If the value of q is greater than 2.878 then the P value is less than 0.05.

Comparison	Mean		q	P value
	Difference			
Initial vs Station 1	0.0985		6.083	** P<0.01
Initial vs Station 2	0.1595		9.849	** P<0.01
Initial vs Station 3	0.1018		6.284	** P<0.01
Initial vs Station 4	0.0757		4.678	** P<0.01
Initial vs Station 5	0.1023		6.315	** P<0.01
Initial vs Station 6	0.1330		8.214	** P<0.01
Initial vs Station 7	0.1275		7.874	** P<0.01
Initial vs Station 8	0.1567		9.676	** P<0.01
Initial vs Station 9	0.1185		7.318	** P<0.01
Initial vs Station 10	0.1273		7.859	** P<0.01

STATISTICAL RESULTS
TISSUE CHEMISTRY CONCENTRATION DATA
EXCLUDING REFERENCE STATION 1

Tissue Chemistry Concentration Statistical Results (excluding Reference Station 1)

Means

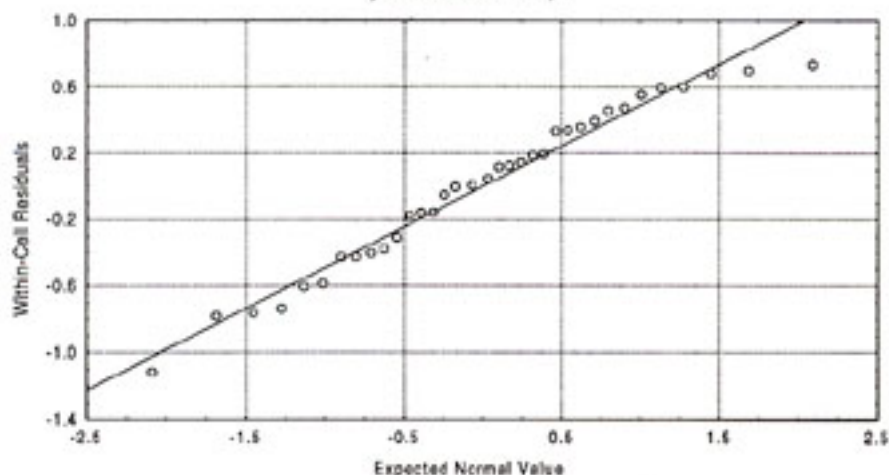
	ARSENIC	CADMIUM	CHROMIUM	LEAD	MERCURY	METHMERC
2	5.415000	3.182500	5.88750	1.093500	.833500	.099025
3	5.290000	2.620000	17.30000	.641250	.865500	.156750
4	5.052500	2.262500	25.20000	1.386250	.975250	.182750
5	5.785000	2.782500	70.22500	1.682500	1.060500	.156250
6	5.425000	2.715000	18.55000	1.019250	.756000	.125500
7	5.105000	2.522500	19.45000	.784000	.813750	.131000
8	5.920000	3.397500	49.90000	1.362000	.902250	.101825
9	5.035000	2.430000	14.85750	.876500	1.099750	.140000
10	5.325000	2.890000	9.46750	.918500	.858250	.131250

Arsenic concentration

Normal Probability Plot of Residuals

variable: AS

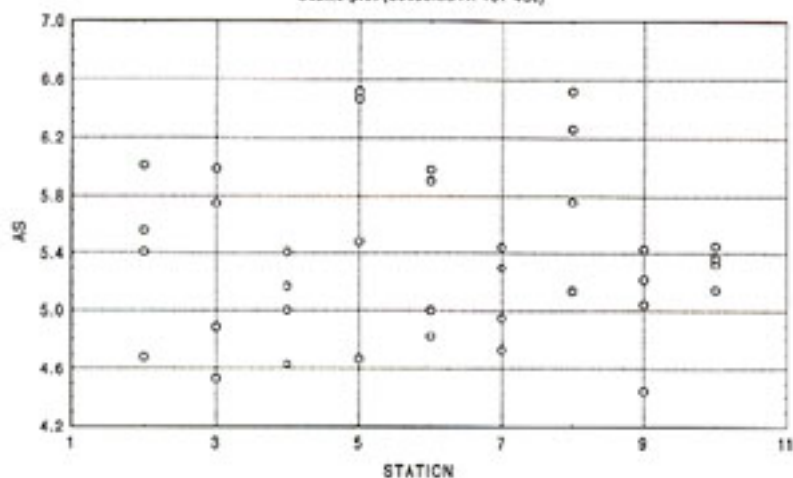
$$y = -1.1238e-6 + 0.49x + \epsilon$$



Correlation

	ARS_X	ARS_Y	
ARS_X	1.000000	.981876	- normal
ARS_Y	.981876	1.000000	

Scatter plot (coscen.STA 13r*43c)



ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	3.085600	8	.385700	1.284291	.292630
Error	8.108675	27	.300321		

Dunnett's contrasts - treatment stations vs. reference (w/o Reference 1) - arsenic

If the value of q is greater than 2.840 then the P value is less than 0.05.

Comparison	Mean Difference	q	P value
Station 2 vs Station 3	0.1250	0.3226	ns P>0.05
Station 2 vs Station 4	0.3625	0.9355	ns P>0.05
Station 2 vs Station 5	-0.3700	0.9548	ns P>0.05
Station 2 vs Station 6	-0.0100	0.0258	ns P>0.05
Station 2 vs Station 7	0.3100	0.8000	ns P>0.05
Station 2 vs Station 8	-0.5050	1.303	ns P>0.05
Station 2 vs Station 9	0.3800	0.9806	ns P>0.05
Station 2 vs Station 10	0.0900	0.2323	ns P>0.05

Newman-Keuls test - arsenic

	3	4	5	6	7	8	9	10
3		.814270	.584874	.935425	.637188	.495301	.911501	.928815
4	.814270		.430691	.869236	.893374	.311926	.964431	.894614
5	.584874	.430691		.361812	.420663	.730462	.476945	.471481
6	.935425	.869236	.361812		.841382	.420587	.910960	.798480
7	.637188	.893374	.420663	.841382		.317988	.982237	.838171
8	.495301	.311926	.730462	.420587	.317988		.340642	.432228
9	.911501	.964431	.476945	.910960	.982237	.340642		.942486
10	.928815	.894614	.471481	.798480	.838171	.432228	.942486	

Dunnett's contrasts - Reference station 2 and treatment stations vs. initial concentrations - arsenic
 If the value of q is greater than 2.860 then the P value is less than 0.05.

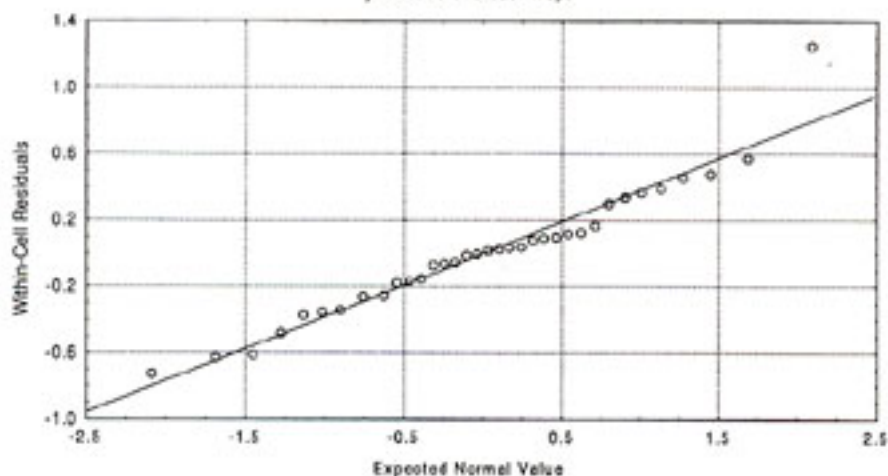
Comparison	Mean		
	Difference	q	P value
Initial vs Station 2	0.835	2.251	ns P>0.05
Initial vs Station 3	0.960	2.588	ns P>0.05
Initial vs Station 4	1.198	3.229	* P<0.05
Initial vs Station 5	0.465	1.254	ns P>0.05
Initial vs Station 6	0.825	2.224	ns P>0.05
Initial vs Station 7	1.145	3.087	* P<0.05
Initial vs Station 8	0.330	0.890	ns P>0.05
Initial vs Station 9	1.215	3.276	* P<0.05
Initial vs Station 10	0.925	2.494	ns P>0.05

Cadmium concentration

Normal Probability Plot of Residuals

variable: CD

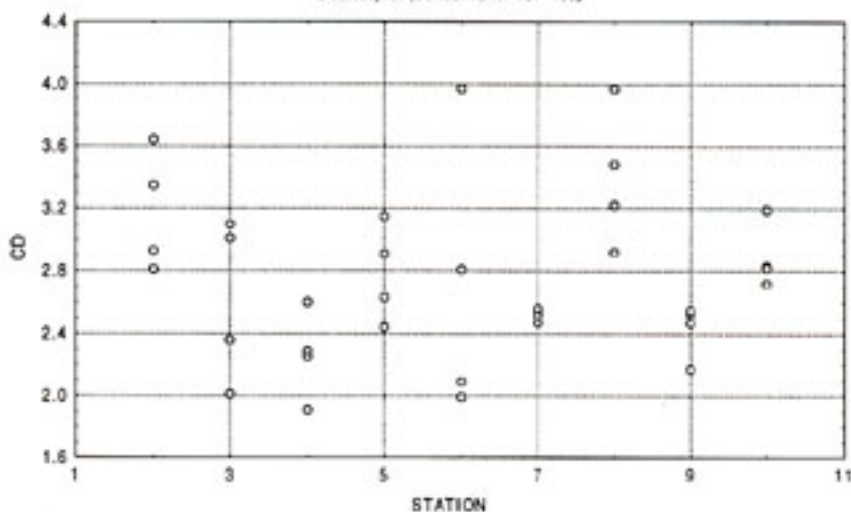
$$y = -1.698e-5 + 0.383 * x + \text{eps}$$



Correlation

	CAD_X	CAD_Y	
CAD_X	1.000000	.958257	- normal
CAD_Y	.958257	1.000000	

Scatterplot (concn.STA 13r*43c)



ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	4.146400	8	.518300	2.737031	.023770
Error	5.112875	27	.189366		

Dunnett's contrasts - treatment stations vs. reference (w/o Reference 1) - cadmium

If the value of q is greater than 2.840 then the P value is less than 0.05.

Comparison	Mean		P value
	Difference	q	
Station 2 vs Station 3	0.5625	1.828	ns P>0.05
Station 2 vs Station 4	0.9200	2.990	* P<0.05
Station 2 vs Station 5	0.4000	1.300	ns P>0.05
Station 2 vs Station 6	0.4675	1.519	ns P>0.05
Station 2 vs Station 7	0.6600	2.145	ns P>0.05
Station 2 vs Station 8	-0.2150	0.699	ns P>0.05
Station 2 vs Station 9	0.7525	2.446	ns P>0.05
Station 2 vs Station 10	0.2925	0.951	ns P>0.05

Newman-Keuls test - cadmium

	3	4	5	6	7	8	9	10
3		.665661	.862052	.763521	.757503	.126046	.816730	.822549
4	.665661		.565403	.602881	.686484	.02436*	.596451	.433798
5	.862052	.565403		.830683	.838204	.141291	.789479	.733573
6	.763521	.602881	.830683		.812403	.155535	.797992	.841996
7	.757503	.686484	.838204	.812403		.091184	.769555	.763650
8	.126046	.024362	.141291	.155535	.091184		.063363	.117045
9	.816730	.596451	.789479	.797992	.769555	.063363		.683025
10	.822549	.433798	.733573	.841996	.763650	.117045	.683025	

Dunnett's contrasts - Reference station 2 and treatment stations vs. initial concentrations - cadmium

If the value of q is greater than 2.860 then the P value is less than 0.05.

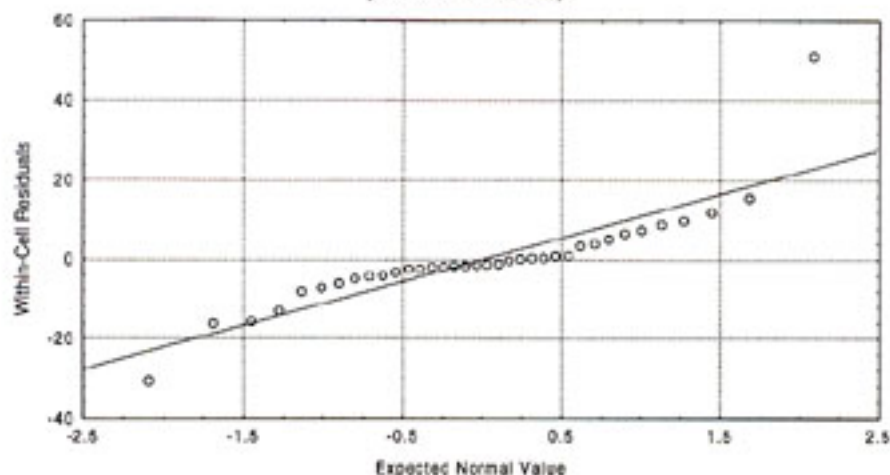
Comparison	Mean		P value
	Difference	q	
Initial vs Station 2	-0.1250	0.423	ns P>0.05
Initial vs Station 3	0.4375	1.479	ns P>0.05
Initial vs Station 4	0.7950	2.688	ns P>0.05
Initial vs Station 5	0.2750	0.930	ns P>0.05
Initial vs Station 6	0.3425	1.158	ns P>0.05
Initial vs Station 7	0.5350	1.809	ns P>0.05
Initial vs Station 8	-0.3400	1.150	ns P>0.05
Initial vs Station 9	0.6275	2.122	ns P>0.05
Initial vs Station 10	0.1675	0.567	ns P>0.05

Chromium

Normal Probability Plot of Residuals

variable: CR

$$y = -5.2986 \cdot 8 + 11.06 \cdot x + \text{eps}$$



Correlation

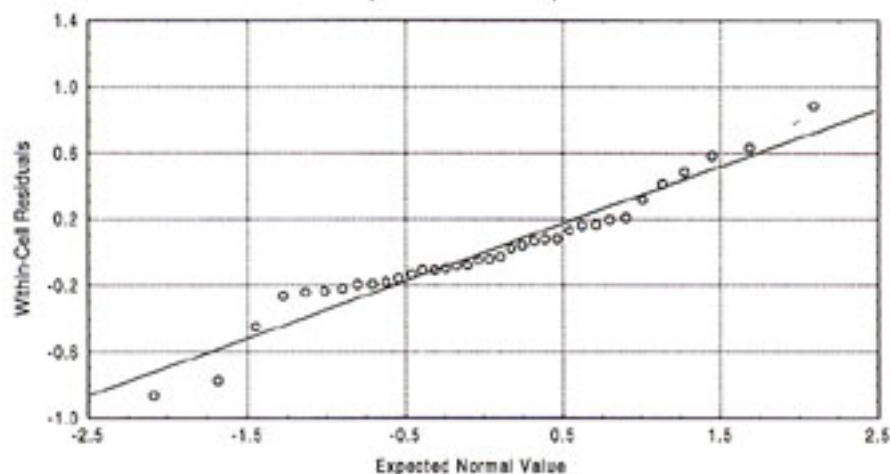
	CHROM_X	CHROM_Y	
CHROM_X	1.000000	.823525	- not normal
CHROM_Y	.823525	1.000000	

Log-transformed Chromium

Normal Probability Plot of Residuals

variable: LOG_CR

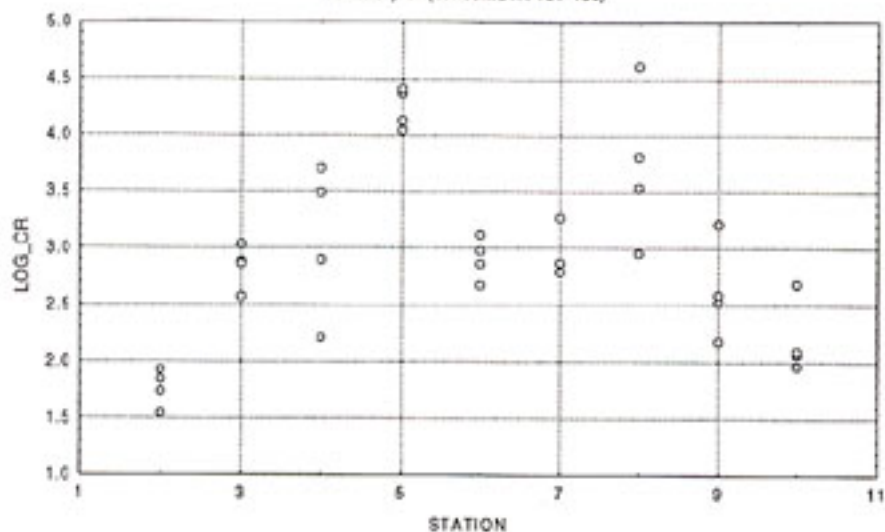
$$y = 1.4356 \cdot 8 + 0.346 \cdot x + \text{eps}$$



Correlation

	LGCHRM_X	LGCHRM_Y	
LGCHRM_X	1.000000	.969138	- normal
LGCHRM_Y	.969138	1.000000	

Scatterplot (concn.STA 13v43c)



ANOVA

Effect	Sum of Squares	df	Mean Square	F	p-level
Effect	17.46519	8	2.183149	14.05679	.000000
Error	4.19335	27	.155309		

Dunnett's contrasts - treatment stations vs. reference (w/o Reference 1) - log-transformed chromium
 If the value of q is greater than 2.840 then the P value is less than 0.05.

Comparison	Mean Difference	q	P value
Station 2 vs Station 3	-0.4666	3.856	** P<0.01
Station 2 vs Station 4	-0.5702	4.712	** P<0.01
Station 2 vs Station 5	-1.076	8.889	** P<0.01
Station 2 vs Station 6	-0.4971	4.108	** P<0.01
Station 2 vs Station 7	-0.5154	4.259	** P<0.01
Station 2 vs Station 8	-0.8537	7.054	** P<0.01
Station 2 vs Station 9	-0.3747	3.096	* P<0.05
Station 2 vs Station 10	-0.1916	1.583	ns P>0.05

Newman-Keuls test - log chromium

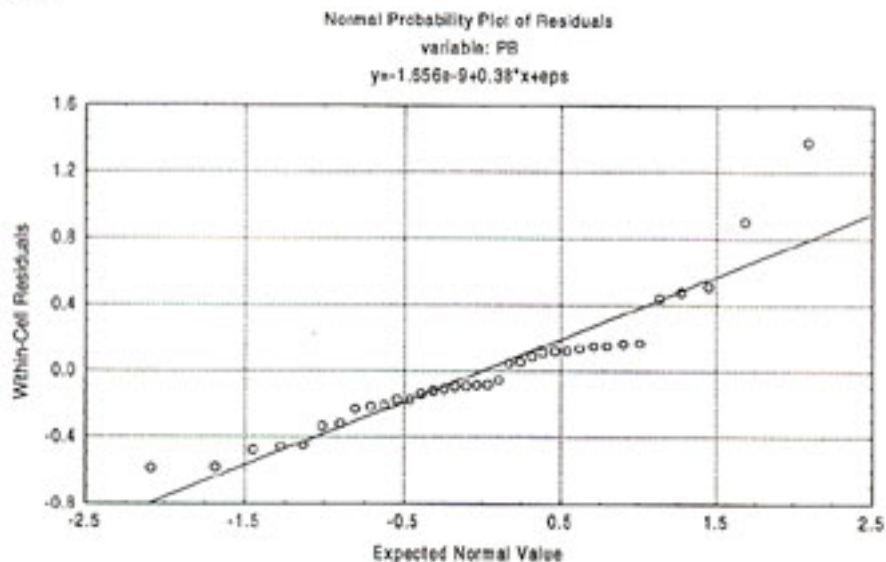
	3	4	5	6	7	8	9	10
3		.846750	.00100*	.812555	.922308	.04041*	.476774	.098294
4	.846750		.00166*	.834543	.670226	.03548*	.549013	.063544
5	.001002	.001664		.00122*	.00113*	.093466	.00032*	.00015*
6	.812555	.834543	.001225		.886829	.04532*	.506781	.103420
7	.922308	.670226	.001132	.886829		.03528*	.688880	.113172
8	.040409	.035477	.093466	.045318	.035279		.01085*	.00056*
9	.476774	.549013	.000323	.606781	.688880	.010854		.162674
10	.098294	.063544	.000152	.103420	.113172	.000556	.162674	

Dunnett's contrasts - Reference station 2 and treatment stations vs. initial concentrations - log-transformed chromium

If the value of q is greater than 2.860 then the P value is less than 0.05.

Comparison	Mean Difference	q	P value
Initial vs Station 2	-0.3289	2.855	ns P>0.05
Initial vs Station 3	-0.7955	6.906	** P<0.01
Initial vs Station 4	-0.8991	7.806	** P<0.01
Initial vs Station 5	-1.405	12.195	** P<0.01
Initial vs Station 6	-0.8260	7.171	** P<0.01
Initial vs Station 7	-0.8443	7.330	** P<0.01
Initial vs Station 8	-1.183	10.267	** P<0.01
Initial vs Station 9	-0.7036	6.108	** P<0.01
Initial vs Station 10	-0.5204	4.518	** P<0.01

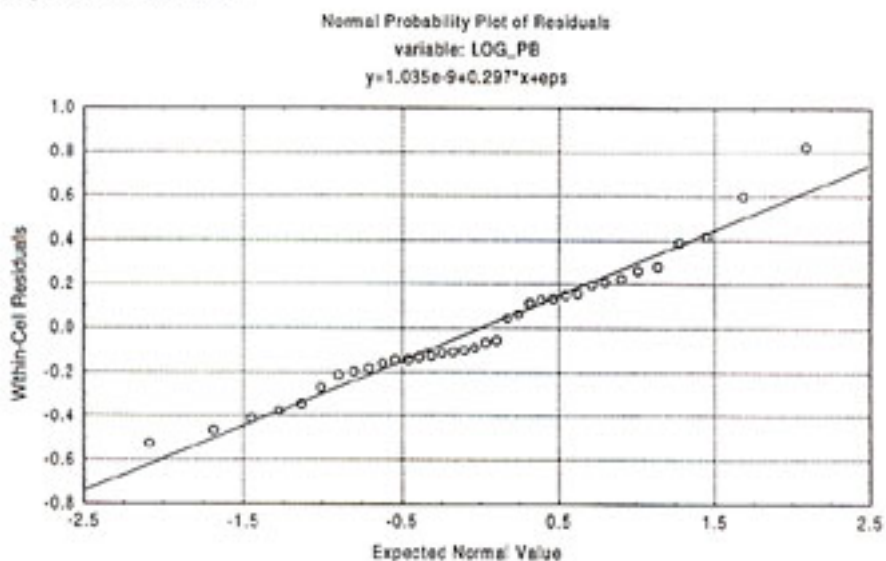
Lead



Correlation

	LEAD_X	LEAD_Y	
LEAD_X	1.000000	.928758	- not normal
LEAD_Y	.928758	1.000000	

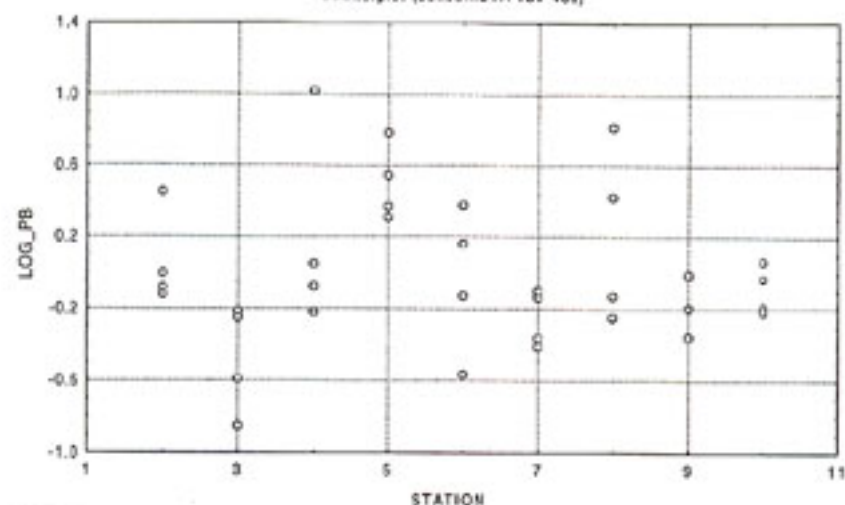
Log-transformed Lead



Correlation

	LGLD_X	LGLD_Y	
LGLD_X	1.000000	.977602	- normal
LGLD_Y	.977602	1.000000	

Scatterplot (concen.STA 13x*43c)



ANOVA

Effect	Sum of Squares	df	Mean Square	F	p-level
Effect	2.645220	8	.330653	2.958041	.016370
Error	3.018085	27	.111781		

Dunnett's contrasts - treatment stations vs. reference (w/o Reference 1) - log-transformed lead

If the value of q is greater than 2.840 then the P value is less than 0.05.

Comparison	Mean		
	Difference	q	P value
Station 2 vs Station 3	0.2339	2.278	ns P>0.05
Station 2 vs Station 4	-0.0566	0.552	ns P>0.05
Station 2 vs Station 5	-0.1918	1.868	ns P>0.05
Station 2 vs Station 6	0.0439	0.427	ns P>0.05
Station 2 vs Station 7	0.1362	1.326	ns P>0.05
Station 2 vs Station 8	-0.0670	0.653	ns P>0.05
Station 2 vs Station 9	0.0882	0.859	ns P>0.05
Station 2 vs Station 10	0.0665	0.648	ns P>0.05

Newman-Keuls test - log lead

	3	4	5	6	7	8	9	10
3		.098554	.00935*	.391874	.361751	.102810	.363678	.401195
4			.416405	.348370	.377600	.922398	.523952	.480659
5				.140419	.060593	.246678	.119946	.134218
6					.815750	.550275	.906747	.831228
7						.407054	.652333	.786808
8							.585958	.589559
9								.837986
10								

Dunnett's contrasts - Reference station 2 and treatment stations vs. initial concentrations - log-transformed lead

If the value of q is greater than 2.860 then the P value is less than 0.05.

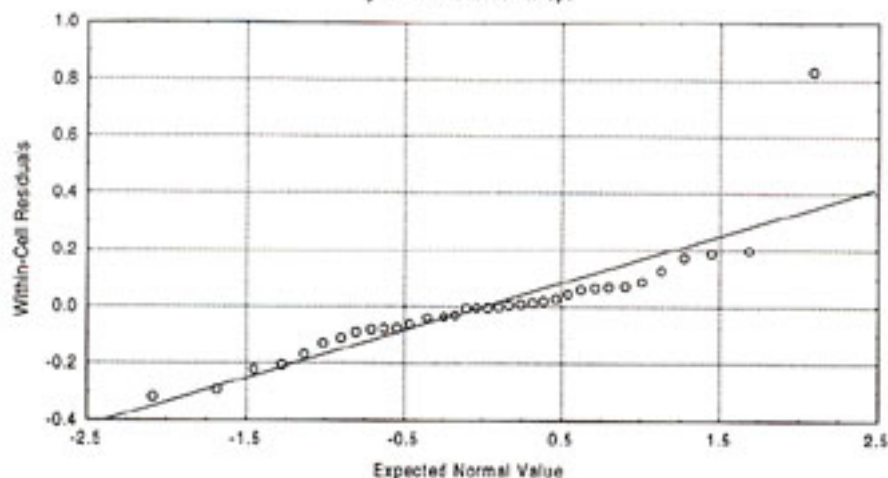
Comparison	Mean Difference	q	P value
Initial vs Station 2	-0.8660	5.422	** P<0.01
Initial vs Station 3	-0.6321	3.957	** P<0.01
Initial vs Station 4	-0.9226	5.776	** P<0.01
Initial vs Station 5	-1.058	6.622	** P<0.01
Initial vs Station 6	-0.8221	5.147	** P<0.01
Initial vs Station 7	-0.7298	4.569	** P<0.01
Initial vs Station 8	-0.9330	5.841	** P<0.01
Initial vs Station 9	-0.7778	4.869	** P<0.01
Initial vs Station 10	-0.7995	5.005	** P<0.01

Mercury

Normal Probability Plot of Residuals

variable: HG

$$y = -2.203e-6 + 0.167x + \epsilon$$



Correlation

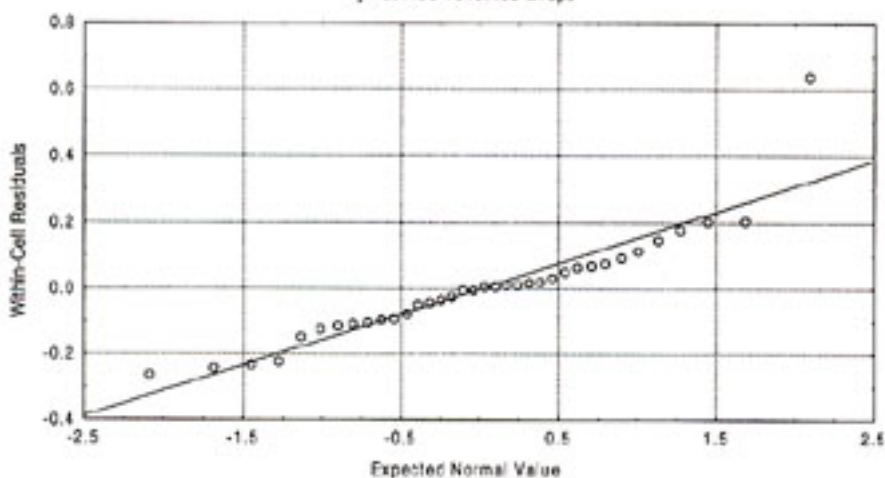
	MERC_X	MERC_Y	
MERC_X	1.000000	.824963	- not normal
MERC_Y	.824963	1.000000	

Log-transformed Mercury

Normal Probability Plot of Residuals

variable: LOG_HG

$$y = -9.119e-10 + 0.155x + \epsilon$$



Correlation

	LGMERC_X	LGMERC_Y	
LGMERC_X	1.000000	.903945	- not normal
LGMERC_Y	.903945	1.000000	

Rank-it transformed Mercury

ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	1.324614	8	.165577	2.740183	.023643
Error	1.631486	27	.060425		

Dunnett's contrasts - treatment stations vs. reference (w/o Reference 1) - rank-transformed mercury

If the value of q is greater than 2.840 then the P value is less than 0.05.

Comparison	Mean Difference	q	P value
Station 2 vs Station 3	-0.3554	0.5884	ns P>0.05
Station 2 vs Station 4	-0.9976	1.652	ns P>0.05
Station 2 vs Station 5	-1.362	2.255	ns P>0.05
Station 2 vs Station 6	0.5880	0.9736	ns P>0.05
Station 2 vs Station 7	0.2615	0.4329	ns P>0.05
Station 2 vs Station 8	-0.3594	0.5951	ns P>0.05
Station 2 vs Station 9	-0.5767	0.9547	ns P>0.05
Station 2 vs Station 10	-0.1580	0.2616	ns P>0.05

Newman-Keuls test - ranked mercury

	3	4	5	6	7	8	9	10
3		.728777	.494554	.438258	.585298	.994971	.932098	.752391
4	.728777		.560977	.181286	.352135	.564255	.502584	.658985
5	.494554	.560977		.069875	.162117	.385769	.424959	.399499
6	.438258	.181286	.069875		.602263	.552391	.435239	.460747
7	.585298	.352135	.162117	.602263		.748399	.660360	.504001
8	.994971	.564255	.385769	.552391	.748399		.728451	.943398
9	.932098	.502584	.424959	.435239	.660360	.728451		.904760
10	.752391	.658985	.399499	.460747	.504001	.943398	.904760	

Dunnett's contrasts - Reference station 2 and treatment stations vs. initial concentrations - rank-transformed mercury

If the value of q is greater than 2.860 then the P value is less than 0.05.

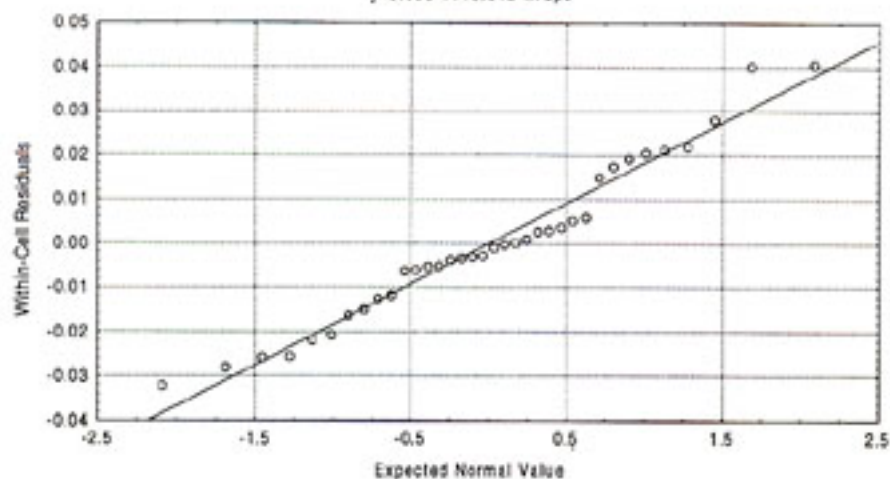
Comparison	Mean Difference	q	P value
Initial vs Station 2	1.691	2.943	* P<0.05
Initial vs Station 3	1.352	2.353	ns P>0.05
Initial vs Station 4	0.755	1.314	ns P>0.05
Initial vs Station 5	0.440	0.7664	ns P>0.05
Initial vs Station 6	2.251	3.917	** P<0.01
Initial vs Station 7	1.952	3.396	* P<0.05
Initial vs Station 8	1.343	2.336	ns P>0.05
Initial vs Station 9	1.075	1.871	ns P>0.05
Initial vs Station 10	1.542	2.682	ns P>0.05

Methyl Mercury

Normal Probability Plot of Residuals

variable: MEHG

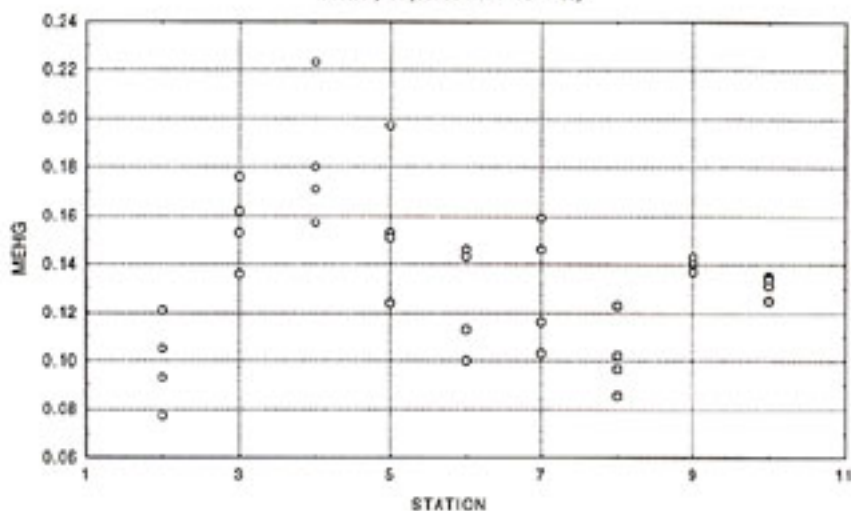
$$y = 8.65e-11 + 0.018 * x + \text{eps}$$



Correlation

	METH_X	METH_Y	
METH_X	1.000000	.982805	- normal
METH_Y	.982805	1.000000	

Scatterplot (concern STA 13r*43c)



ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	.022940	8	.002868	6.780954	.000071
Error	.011418	27	.000423		

Dunnnett's contrasts - treatment stations vs. reference (w/o Reference 1) - methylmercury

If the value of q is greater than 2.840 then the P value is less than 0.05.

Comparison	Mean		P value
	Difference	q	
Station 2 vs Station 3	-0.05773	3.970	** P<0.01
Station 2 vs Station 4	-0.08373	5.758	** P<0.01
Station 2 vs Station 5	-0.05723	3.935	** P<0.01
Station 2 vs Station 6	-0.02648	1.821	ns P>0.05
Station 2 vs Station 7	-0.03198	2.199	ns P>0.05
Station 2 vs Station 8	-0.00280	0.193	ns P>0.05
Station 2 vs Station 9	-0.04098	2.818	ns P>0.05
Station 2 vs Station 10	-0.03223	2.216	ns P>0.05

Newman-Keuls test - methylmercury

	3	4	5	6	7	8	9	10
3		.089930	.973275	.308626	.423846	.01550*	.500263	.329013
4	.089930		.190474	.01073*	.01939*	.00039*	.03636*	.01444*
5	.973275	.190474		.256465	.337308	.01273*	.280296	.225946
6	.308626	.010730	.256465		.711838	.120665	.758777	.919554
7	.423846	.019387	.337308	.711838		.138031	.815107	.986674
8	.015496	.000389	.012729	.120665	.138031		.103081	.215748
9	.500263	.036357	.280296	.758777	.815107	.103081		.557576
10	.329013	.014437	.225946	.919554	.986674	.215748	.557576	

Dunnnett's contrasts - Reference station 2 and treatment stations vs. initial concentrations - methylmercury

If the value of q is greater than 2.860 then the P value is less than 0.05.

Comparison	Mean		P value
	Difference	q	
Initial vs Station 2	0.1595	11.346	** P<0.01
Initial vs Station 3	0.1018	7.239	** P<0.01
Initial vs Station 4	0.07575	5.389	** P<0.01
Initial vs Station 5	0.1023	7.275	** P<0.01
Initial vs Station 6	0.1330	9.463	** P<0.01
Initial vs Station 7	0.1275	9.071	** P<0.01
Initial vs Station 8	0.1567	11.147	** P<0.01
Initial vs Station 9	0.1185	8.431	** P<0.01
Initial vs Station 10	0.1273	9.054	** P<0.01

STATISTICAL RESULTS
TISSUE CHEMISTRY CONTENT DATA
INCLUDING REFERENCE STATIONS 1 AND 2

Tissue Chemistry Content Statistical Results (including both Reference stations 1 and 2)

Means

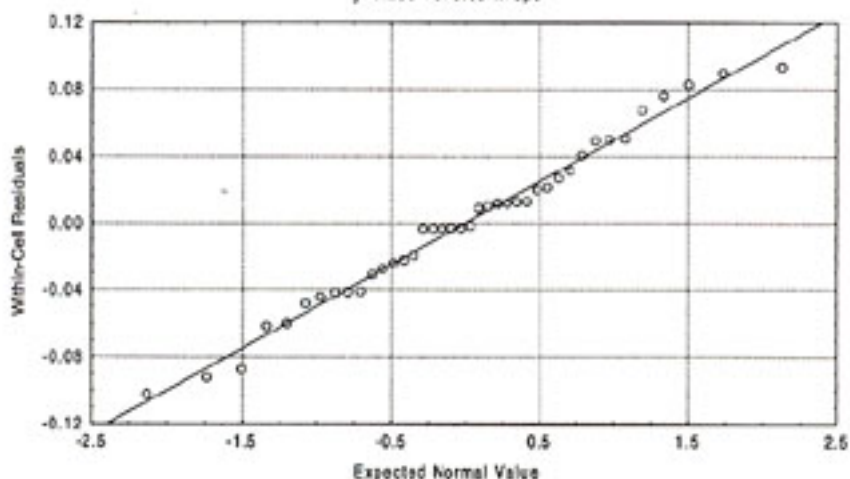
	AS	CD	CR	PB	HG	MEHG
1	.624777	.246354	.893316	.075154	.119008	.017597
2	.674566	.396493	.733056	.136177	.103809	.012330
3	.763298	.376461	2.526446	.092369	.125976	.022878
4	.685925	.306608	3.313383	.184683	.132399	.024677
5	.682629	.328843	8.356944	.199552	.125534	.018445
6	.786685	.390658	2.682702	.147712	.110264	.018343
7	.734344	.362907	2.814472	.112101	.116259	.018706
8	.821944	.472016	6.960159	.188801	.124610	.014096
9	.706854	.341081	2.073355	.122996	.155017	.019651
10	.670644	.363786	1.190796	.115398	.108097	.016526

Arsenic

Normal Probability Plot of Residuals

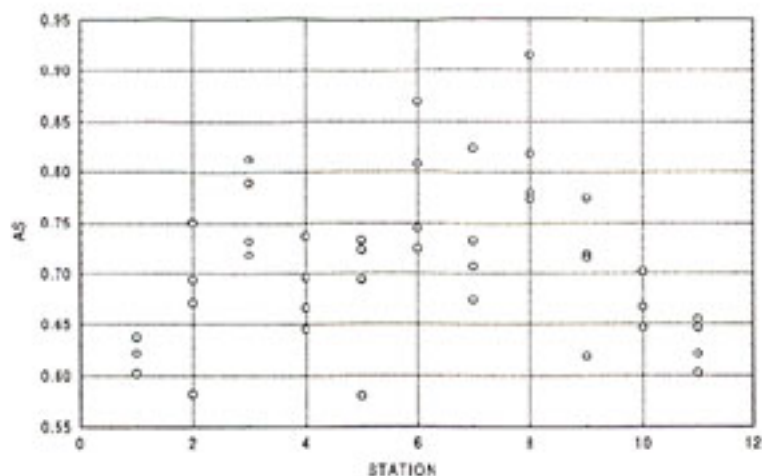
variable: AS

$$y = 3.26e-10 + 0.05 * x + \text{eps}$$



Correlation

	AS_X	AS_Y	
AS_X	1.000000	.993642	- normal
AS_Y	.993642	1.000000	



ANOVA

Effect	Sum of Squares	df	Mean Square	F	p-level
Effect	.131938	9	.014660	4.706110	.000603
Error	.093451	30	.003115		

Bonferroni contrasts - arsenic (with both Reference stations)

As

Refs 1 and 2 vs:

3	3.3245609
4	1.0607320
5	0.9642981
6	4.0088396
7	2.4774196
8	5.0404706
9	1.6730882
10	0.6136364

critical value = 1.697

Newman-Keuls test - arsenic

	3	4	5	6	7	8	9	10
3		.246178	.294896	.567017	.479323	.329379	.356169	.232615
4	.246178		.935554	.123708	.463488	.02673*	.608212	.924048
5	.294896	.935554		.140279	.581636	.02905*	.820743	.768725
6	.567017	.123708	.140279		.409248	.390203	.222626	.099445
7	.479323	.463488	.581636	.409248		.159087	.501585	.522781
8	.329379	.026735	.029055	.390203	.159087		.060453	.01858*
9	.356169	.608212	.820743	.222626	.501585	.060453		.805475
10	.232615	.924048	.768725	.099445	.522781	.018585	.805475	

Dunnnett's contrasts - all stations vs. initial contents - arsenic

If the value of q is greater than 2.878 then the P value is less than 0.05.

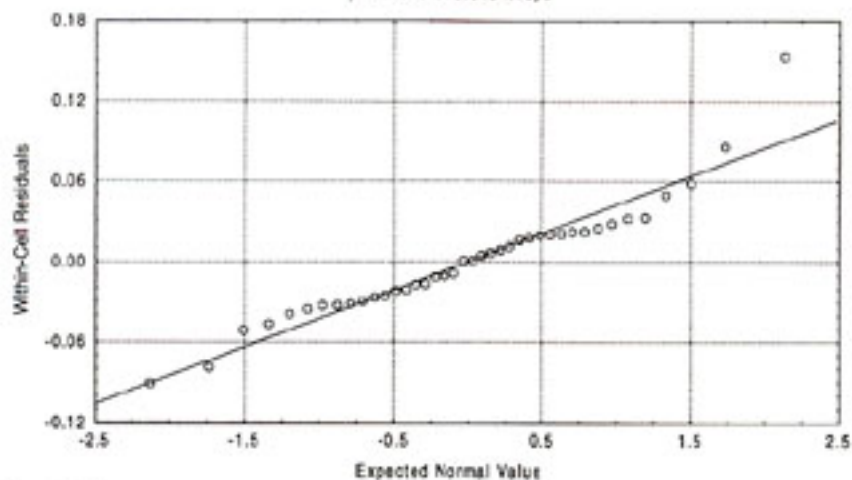
Comparison	Mean		P value
	Difference	q	
Initial vs Station 1	0.0066	0.173	ns P>0.05
Initial vs Station 2	-0.0432	1.138	ns P>0.05
Initial vs Station 3	-0.1319	3.474	* P<0.05
Initial vs Station 4	-0.0546	1.437	ns P>0.05
Initial vs Station 5	-0.0513	1.350	ns P>0.05
Initial vs Station 6	-0.1553	4.090	** P<0.01
Initial vs Station 7	-0.1030	2.712	ns P>0.05
Initial vs Station 8	-0.1906	5.018	** P<0.01
Initial vs Station 9	-0.0755	1.988	ns P>0.05
Initial vs Station 10	-0.0393	1.034	ns P>0.05

Cadmium

Normal Probability Plot of Residuals

variable: CD

$$y = -1.404e-9 + 0.043 * x + \text{eps}$$



Correlation

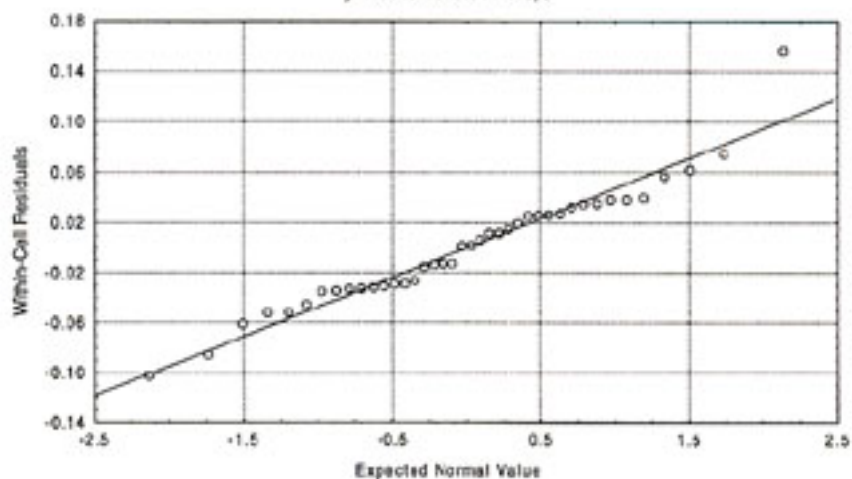
	CD_X	CD_Y	
CD_X	1.000000	.958236	- not normal
CD_Y	.958236	1.000000	

Log-transformed Cadmium Content

Normal Probability Plot of Residuals

variable: LOG_CD

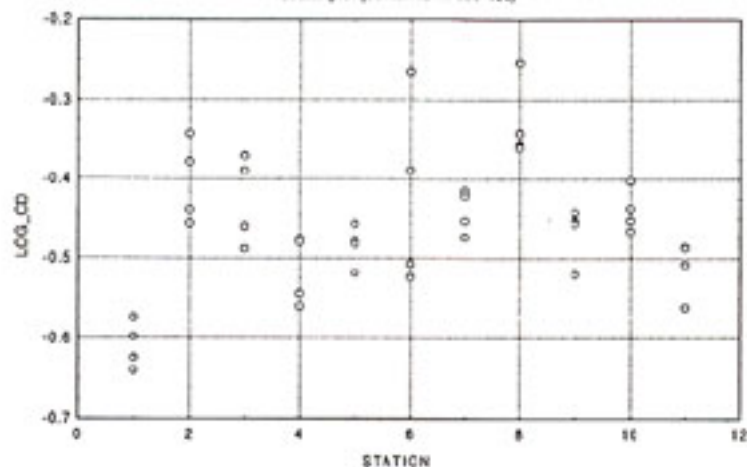
$$y = 7.014e-10 + 0.047 * x + \text{eps}$$



Correlation

	LGCD_X	LGCD_Y
LGCD_X	1.000000	.972382
LGCD_Y	.972382	1.000000

Scatterplot (content STA 17V45c)



ANOVA

Effect	Sum of Squares	df	Mean Square	F	p-level
Effect	.197397	9	.021933	7.518413	.000011
Error	.087517	30	.002917		

Bonferroni contrasts – log-transformed cadmium (with both Reference stations)
log Cd

Refs 1 and 2 vs:

3	1.0465158
4	-0.1100018
5	0.3036268
6	1.1240911
7	0.8644192
8	2.3423149
9	0.5056177
10	0.8779706

critical value = 1.697

Newman-Keuls test – log-transformed cadmium

	3	4	5	6	7	8	9	10
3		.271655	.623085	.883704	.935928	.052864	.732871	.750743
4	.271655		.438111	.260652	.272000	.00216*	.479574	.352153
5	.623085	.438111		.627829	.541491	.01082*	.703402	.695554
6	.883704	.260652	.627829		.959430	.02906*	.762610	.886242
7	.935928	.272000	.541491	.959430		.065513	.500424	.979693
8	.052864	.002158	.010825	.029061	.065513		.02008*	.04653*
9	.732871	.479574	.703402	.762610	.500424	.020076		.759936
10	.750743	.352153	.695554	.886242	.979693	.046531	.759936	

Dunnnett's contrasts - all stations vs. initial contents - log-transformed cadmium
 If the value of q is greater than 2.878 then the P value is less than 0.05.

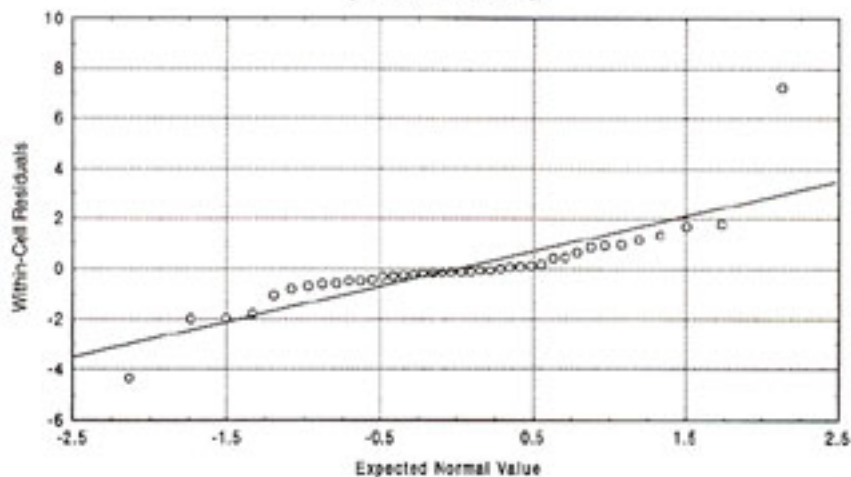
Comparison	Mean		P value
	Difference	q	
Initial vs Station 1	0.0981	2.636	ns P>0.05
Initial vs Station 2	-0.1069	2.873	ns P>0.05
Initial vs Station 3	-0.0841	2.261	ns P>0.05
Initial vs Station 4	0.0040	0.107	ns P>0.05
Initial vs Station 5	-0.0275	0.740	ns P>0.05
Initial vs Station 6	-0.0900	2.419	ns P>0.05
Initial vs Station 7	-0.0702	1.888	ns P>0.05
Initial vs Station 8	-0.1828	4.913	** P<0.01
Initial vs Station 9	-0.0429	1.154	ns P>0.05
Initial vs Station 10	-0.0713	1.916	ns P>0.05

Chromium

Normal Probability Plot of Residuals

variable: CR

$$y = 2.827x - 6 + 1.397z + \epsilon$$



Correlation

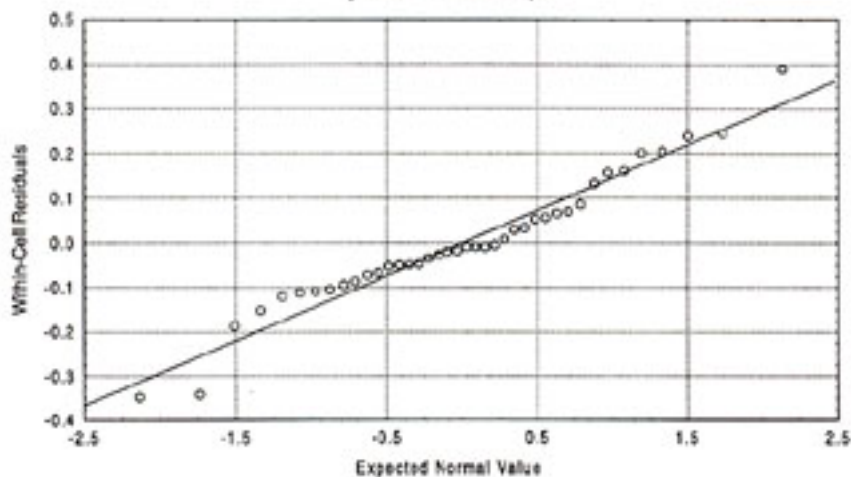
	CR_X	CR_Y	
CR_X	1.000000	.852850	- not normal
CR_Y	.852850	1.000000	

Log-transformed Chromium

Normal Probability Plot of Residuals

variable: LOG_CR

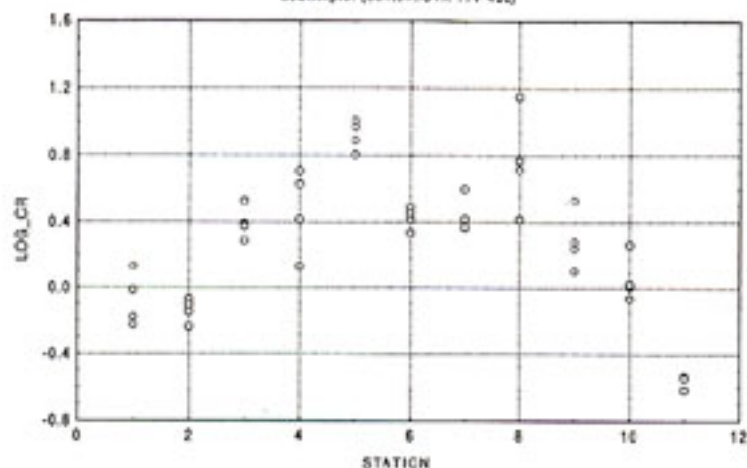
$$y = 5.716x - 9 + 0.146z + \epsilon$$



Correlation

	LGCR_X	LGCR_Y	
LGCR_X	1.000000	.977398	- normal
LGCR_Y	.977398	1.000000	

Scatterplot (content:STA 17v45c)



ANOVA

Effect	Sum of Squares	df	Mean Square	F	p-level
Effect	4.103900	9	.455989	16.54177	.000000
Error	.826977	30	.027566		

Bonferroni contrasts - log chromium (with both Reference stations)
log Cr

Refs 1 and 2 vs:

3	2.132132
4	2.4526544
5	4.3606848
6	2.2657771
7	2.3228278
8	3.7077686
9	1.6780957
10	0.6948919

critical value = 1.697

Newman-Keuls test - log chromium

	3	4	5	6	7	8	9	10	
3		.929033	.00375*	.802568	.931000	.04635*	.398803	.03103*	
4		.929033		.00395*	.933628	.808083	.02598*	.593180	.02991*
5		.003750	.003950		.00485*	.00404*	.228600	.00072*	.00015*
6		.802568	.933628	.004854		.915009	.053327	.516024	.03141*
7		.931000	.808083	.004038	.915009		.03847*	.620460	.03736*
8		.046350	.025985	.228600	.053327	.038475		.00914*	.00025*
9		.398803	.593180	.000720	.516024	.620460	.009141		.075181
10		.031033	.029912	.000152	.031406	.037359	.000253	.075181	

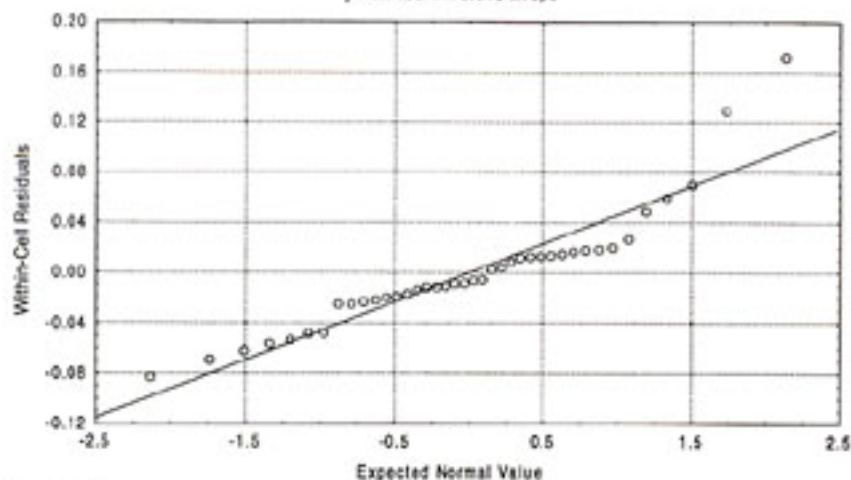
Dunnnett's contrasts - all stations vs. initial contents - log-transformed chromium

If the value of q is greater than 2.878 then the P value is less than 0.05.

Comparison	Mean Difference	q	P value
Initial vs Station 1	-0.4871	4.341	** P<0.01
Initial vs Station 2	-0.4199	3.742	** P<0.01
Initial vs Station 3	-0.9526	8.490	** P<0.01
Initial vs Station 4	-1.028	9.159	** P<0.01
Initial vs Station 5	-1.474	13.139	** P<0.01
Initial vs Station 6	-0.9839	8.769	** P<0.01
Initial vs Station 7	-0.9973	8.888	** P<0.01
Initial vs Station 8	-1.322	11.777	** P<0.01
Initial vs Station 9	-0.8463	7.542	** P<0.01
Initial vs Station 10	-0.6162	5.491	** P<0.01

Lead

Normal Probability Plot of Residuals
variable: PB
 $y = -1.7469 \cdot 11 + 0.0467 \cdot x + \text{eps}$

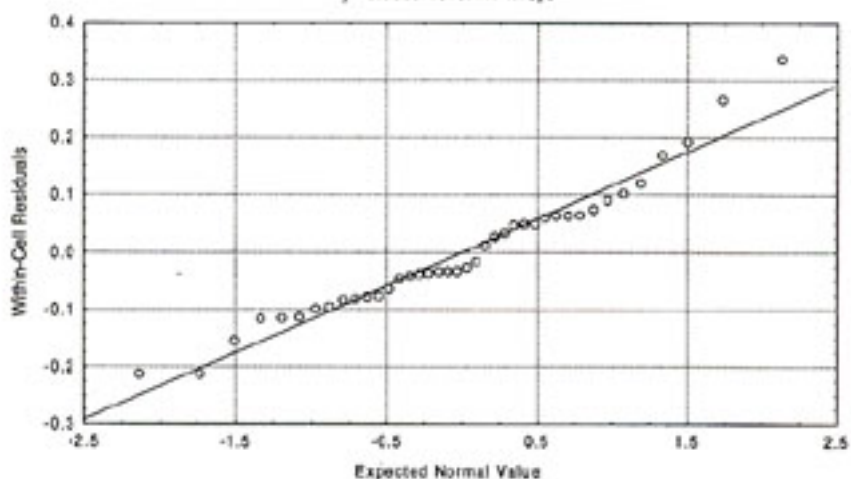


Correlation

	PB_X	PB_Y	
PB_X	1.000000	.931464	- not normal
PB_Y	.931464	1.000000	

Log-transformed Lead

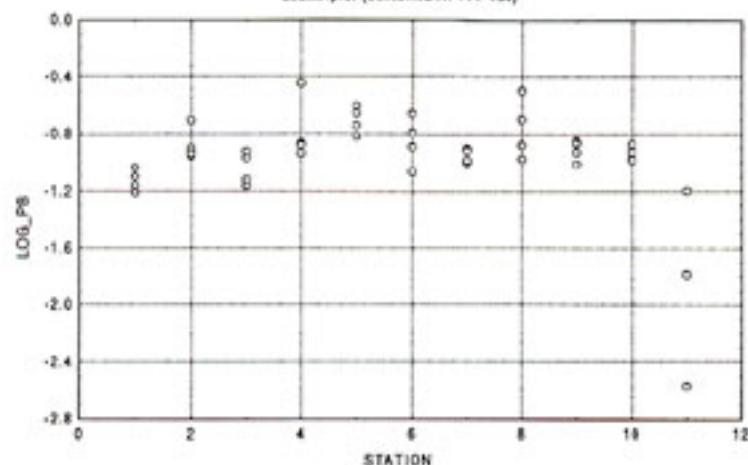
Normal Probability Plot of Residuals
variable: LOG_PB
 $y = -3.9589 \cdot 10 + 0.117 \cdot x + \text{eps}$



Correlation

	LGPB_X	LGPB_Y	
LGPB_X	1.000000	.977251	- normal
LGPB_Y	.977251	1.000000	

Scatterplot (content: STA 17v45c)



ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	.599370	9	.066597	3.796937	.002725
Error	.526187	30	.017540		

Bonferroni contrasts - log lead (with both Reference stations)
log Pb

Refs 1 and 2 vs:

3	-0.226136
4	1.1761614
5	1.5844088
6	0.7852211
7	0.2743369
8	1.2871453
9	0.47626
10	0.3407437

critical value = 1.697

Newman-Keuls test - log lead

	3	4	5	6	7	8	9	10
3		.124241	.03979*	.330186	.354026	.104362	.555812	.540986
4	.124241		.724440	.479289	.451652	.835989	.397792	.410296
5	.039790	.724440		.459243	.213493	.580128	.256272	.214819
6	.330186	.479289	.459243		.760396	.628120	.552991	.671570
7	.354026	.451652	.213493	.760396		.419832	.923403	.901421
8	.104362	.835989	.580128	.628120	.419832		.435976	.404338
9	.555812	.397792	.256272	.552991	.923403	.435976		.800440
10	.540986	.410296	.214819	.671570	.901421	.404338	.800440	

Dunnnett's contrasts - all stations vs. initial contents - log-transformed lead

If the value of q is greater than 2.878 then the P value is less than 0.05.

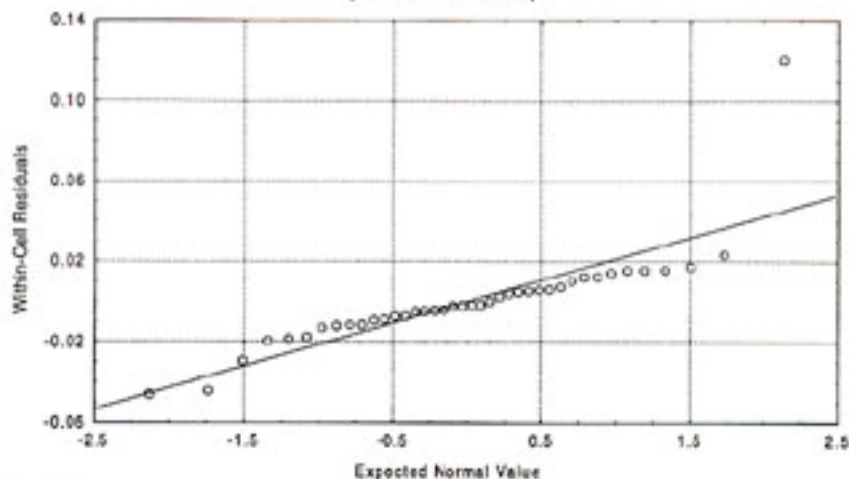
Comparison	Mean		
	Difference	q	P value
Initial vs Station 1	-0.7061	4.719	** P<0.01
Initial vs Station 2	-0.9570	6.395	** P<0.01
Initial vs Station 3	-0.7893	5.274	** P<0.01
Initial vs Station 4	-1.051	7.025	** P<0.01
Initial vs Station 5	-1.127	7.534	** P<0.01
Initial vs Station 6	-0.9801	6.549	** P<0.01
Initial vs Station 7	-0.8828	5.899	** P<0.01
Initial vs Station 8	-1.072	7.163	** P<0.01
Initial vs Station 9	-0.9205	6.151	** P<0.01
Initial vs Station 10	-0.8952	5.982	** P<0.01

Mercury

Normal Probability Plot of Residuals

variable: HG

$$y = 1.426e-9 + 0.021^*x + \text{eps}$$



Correlation

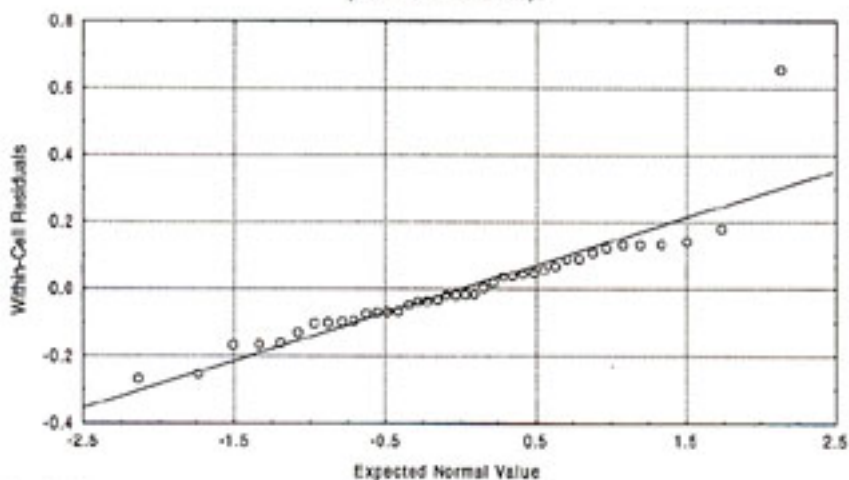
	HG_X	HG_Y	
HG_X	1.000000	.839532	- not normal
HG_Y	.839532	1.000000	

Log-transformed Mercury

Normal Probability Plot of Residuals

variable: LOG_HG

$$y = 1.979e-9 + 0.142^*x + \text{eps}$$



Correlation

	LGHG_X	LGHG_Y	
LGHG_X	1.000000	.911263	- not normal
LGHG_Y	.911263	1.000000	

Rank-it transformed Mercury**ANOVA**

	Sum of Squares	df	Mean Square	F	p-level
Effect	12.42416	9	1.380462	1.797922	.110228
Error	23.03430	30	.767810		

Bonferroni contrasts -rank mercury (with both Reference stations)
rank-it Hg

Refs 1 and 2 vs:

3	1.6498871
4	2.3949827
5	1.5866748
6	-0.3560980
7	0.6063342
8	1.5002635
9	1.4410801
10	-0.3274251

critical value = 1.697

Newman-Keuls test - ranked mercury

	3	4	5	6	7	8	9	10
3		.592114	.961570	.647329	.905831	.999189	.997012	.630697
4	.592114		.825743	.384487	.720227	.959687	.925465	.382022
5	.961570	.825743		.599712	.844918	.996174	.979763	.565254
6	.647329	.384487	.599712		.711649	.438136	.520619	.921914
7	.905831	.720227	.844918	.711649		.469784	.710685	.495380
8	.999189	.959687	.996174	.438136	.469784		.953808	.343351
9	.997012	.925465	.979763	.520619	.710685	.953808		.461216
10	.630697	.382022	.565254	.921914	.495380	.343351	.461216	

Dunnnett's contrasts - all stations vs. initial contents - rank-transformed mercury

If the value of q is greater than 2.878 then the P value is less than 0.05.

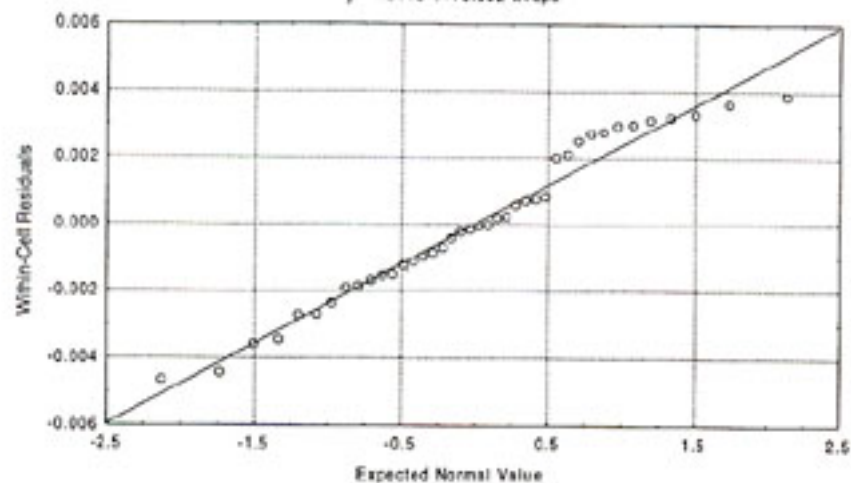
Comparison	Mean Difference	q	P value
Initial vs Station 1	0.1577	0.239	ns P>0.05
Initial vs Station 2	1.242	1.887	ns P>0.05
Initial vs Station 3	-0.1795	0.273	ns P>0.05
Initial vs Station 4	-0.5449	0.828	ns P>0.05
Initial vs Station 5	-0.1466	0.223	ns P>0.05
Initial vs Station 6	0.9369	1.423	ns P>0.05
Initial vs Station 7	0.4043	0.614	ns P>0.05
Initial vs Station 8	-0.0898	0.136	ns P>0.05
Initial vs Station 9	-0.1293	0.196	ns P>0.05
Initial vs Station 10	0.8702	1.322	ns P>0.05

Methylmercury

Normal Probability Plot of Residuals

variable: MEHG

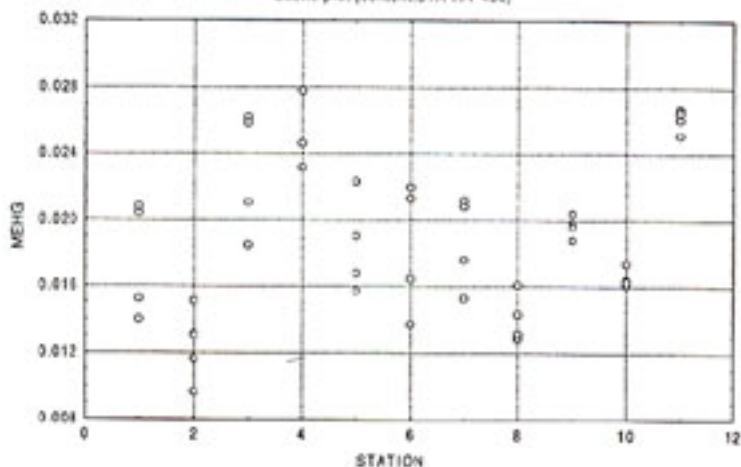
$$y = -4.311e-11 + 0.302 \cdot x \text{eeps}$$



Correlation

	MEHG_X	MEHG_Y	
MEHG_X	1.000000	.985603	- normal
MEHG_Y	.985603	1.000000	

Scatter plot (content STA 17v45c)



ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	.000482	9	.000054	7.475855	.000012
Error	.000215	30	.000007		

Bonferroni contrasts - methylmercury (with both Reference stations)

MeHg

Refs 1 and 2 vs:

3	4.8849731
4	5.9950515
5	2.1486453
6	2.0860654
7	2.3095711
8	-0.5352647
9	2.8928054
10	0.9643596

critical value = 1.697

Newman-Keuls test - methylmercury

	3	4	5	6	7	8	9	10
3		.338606	.102697	.133255	.080469	.00140*	.092543	.02270*
4	.338606		.01893*	.02323*	.01710*	.00027*	.03042*	.00305*
5	.102697	.018931		.956651	.888703	.112302	.791600	.558412
6	.133255	.023231	.956651		.979007	.074222	.892308	.333662
7	.080469	.017105	.888703	.979007		.123403	.612682	.642834
8	.001397	.000274	.112302	.074222	.123403		.058875	.199605
9	.092543	.030422	.791600	.892308	.612682	.058875		.454670
10	.022699	.003050	.558412	.333662	.642834	.199605	.454670	

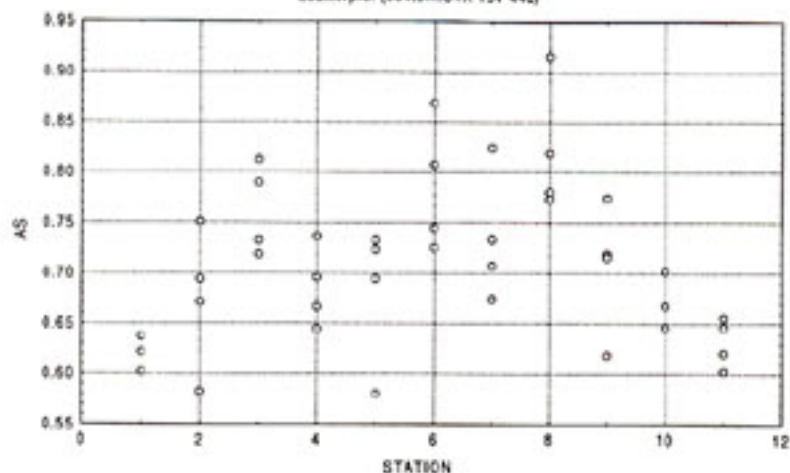
Dunnett's contrasts - all stations vs. initial contents - methylmercury

If the value of q is greater than 2.878 then the P value is less than 0.05.

Comparison	Mean		
	Difference	q	P value
Initial vs Station 1	0.00850	4.693	** P<0.01
Initial vs Station 2	0.01377	7.601	** P<0.01
Initial vs Station 3	0.00322	1.777	ns P>0.05
Initial vs Station 4	0.00142	0.784	ns P>0.05
Initial vs Station 5	0.00765	4.225	** P<0.01
Initial vs Station 6	0.00775	4.281	** P<0.01
Initial vs Station 7	0.00739	4.081	** P<0.01
Initial vs Station 8	0.01200	6.626	** P<0.01
Initial vs Station 9	0.00644	3.559	** P<0.01
Initial vs Station 10	0.00957	5.284	** P<0.01

STATISTICAL RESULTS
TISSUE CHEMISTRY CONTENT DATA
EXCLUDING REFERENCE STATION 1

Scatterplot (content:STA 15V44c)



ANOVA

Effect	Sum of Squares	df	Mean Square	F	p-level
Effect	.095625	8	.011953	3.484553	.006904
Error	.092619	27	.003430		

Dunnett's contrasts - treatment stations vs. reference (w/o Reference 1) - arsenic content
 If the value of q is greater than 2.840 then the P value is less than 0.05.

Comparison	Mean Difference	q	P value
Station 2 vs Station 3	-0.0887	2.143	ns P>0.05
Station 2 vs Station 4	-0.0114	0.274	ns P>0.05
Station 2 vs Station 5	-0.0081	0.195	ns P>0.05
Station 2 vs Station 6	-0.1121	2.707	ns P>0.05
Station 2 vs Station 7	-0.0598	1.443	ns P>0.05
Station 2 vs Station 8	-0.1474	3.559	** P<0.01
Station 2 vs Station 9	-0.0323	0.780	ns P>0.05
Station 2 vs Station 10	0.0039	0.095	ns P>0.05

Newman-Keuls test - arsenic content

	3	4	5	6	7	8	9	10
3		.246178	.294896	.567017	.479323	.329379	.356169	.232615
4			.935554	.123708	.463488	.02673*	.608212	.924048
5				.140279	.581636	.02905*	.820743	.768725
6					.409248	.390203	.222626	.099445
7						.159087	.501585	.522781
8							.060453	.01858*
9								.805475
10								

Dunnnett's contrasts - Reference station 2 and treatment stations vs. initial consent - arsenic
 If the value of q is greater than 2.860 then the P value is less than 0.05.

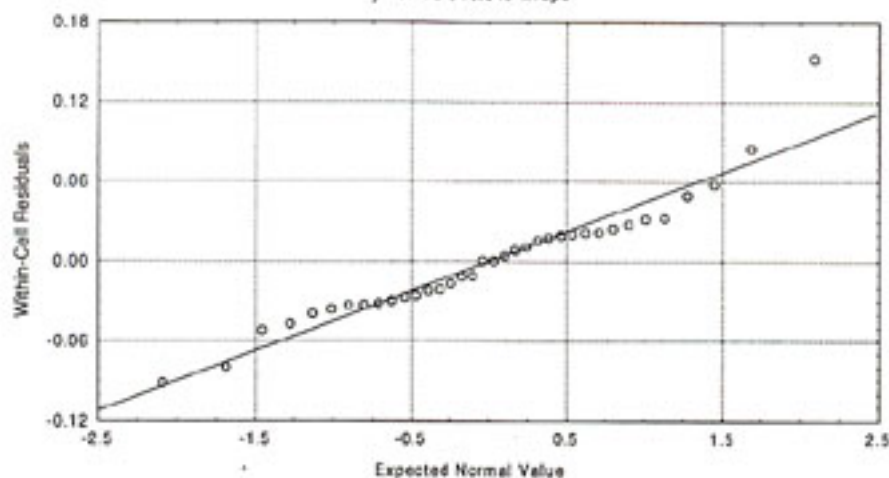
Comparison	Mean Difference	q	P value
Initial vs Station 2	-0.0432	1.090	ns P>0.05
Initial vs Station 3	-0.1319	3.327	* P<0.05
Initial vs Station 4	-0.0546	1.376	ns P>0.05
Initial vs Station 5	-0.0513	1.293	ns P>0.05
Initial vs Station 6	-0.1553	3.917	** P<0.01
Initial vs Station 7	-0.1030	2.597	ns P>0.05
Initial vs Station 8	-0.1906	4.806	** P<0.01
Initial vs Station 9	-0.0755	1.904	ns P>0.05
Initial vs Station 10	-0.0393	0.991	ns P>0.05

Cadmium content

Normal Probability Plot of Residuals

variable: CD

$$y = -1.47E-9 + 0.045 * x + \epsilon$$

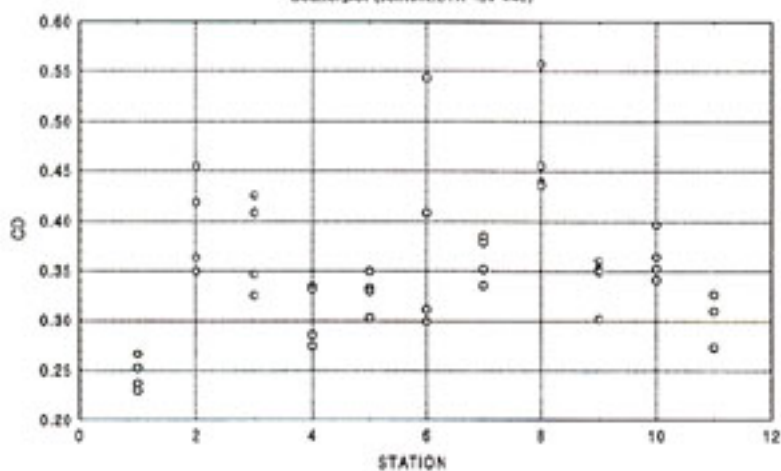


Correlation

N=36

	CD_X	CD_Y	
CD_X	1.000000	.961241	- normal
CD_Y	.961241	1.000000	

Scatterplot (content.STA '5*'44c)



ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	.072826	8	.009103	3.426452	.007580
Error	.071733	27	.002657		

Dunnett's contrasts - treatment stations vs. reference (w/o Reference 1) - cadmium content

If the value of q is greater than 2.840 then the P value is less than 0.05.

Comparison	Mean		
	Difference	q	P value
Station 2 vs Station 3	0.02003	0.550	ns P>0.05
Station 2 vs Station 4	0.08988	2.466	ns P>0.05
Station 2 vs Station 5	0.06765	1.856	ns P>0.05
Station 2 vs Station 6	0.00583	0.160	ns P>0.05
Station 2 vs Station 7	0.03359	0.921	ns P>0.05
Station 2 vs Station 8	-0.07552	2.072	ns P>0.05
Station 2 vs Station 9	0.05541	1.520	ns P>0.05
Station 2 vs Station 10	0.03271	0.897	ns P>0.05

Newman-Keuls test - cadmium content

	3	4	5	6	7	8	9	10	
3		.423938	.694952	.702284	.927837	.03987*	.770663	.732849	
4			.550284	.288414	.433541	.00319*	.621133	.536677	
5				.554067	.627993	.01048*	.741698	.777155	
6					.873089	.03642*	.663062	.746933	
7							.04716*	.557576	.981203
8								.01725*	.03305*
9									.811352
10									

Dunnett's contrasts - Reference station 2 and treatment stations vs. initial content - cadmium

If the value of q is greater than 2.860 then the P value is less than 0.05.

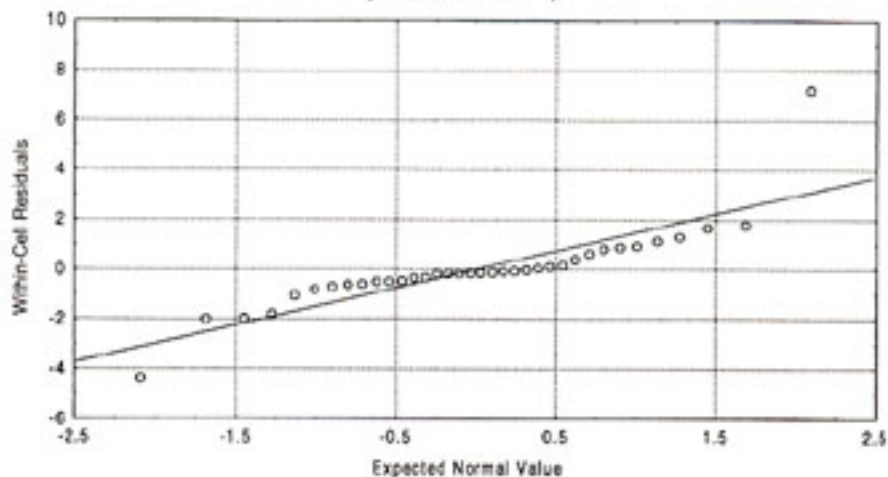
Comparison	Mean		
	Difference	q	P value
Initial vs Station 2	-0.08748	2.498	ns P>0.05
Initial vs Station 3	-0.06745	1.926	ns P>0.05
Initial vs Station 4	0.00241	0.069	ns P>0.05
Initial vs Station 5	-0.01983	0.566	ns P>0.05
Initial vs Station 6	-0.08164	2.332	ns P>0.05
Initial vs Station 7	-0.05389	1.539	ns P>0.05
Initial vs Station 8	-0.1630	4.655	** P<0.01
Initial vs Station 9	-0.03207	0.916	ns P>0.05
Initial vs Station 10	-0.05477	1.564	ns P>0.05

Chromium Content

Normal Probability Plot of Residuals

variable: CR

$$y = 3.161 \times 10^{-8} + 1.492 \times x + \text{eps}$$



Correlation

N=36

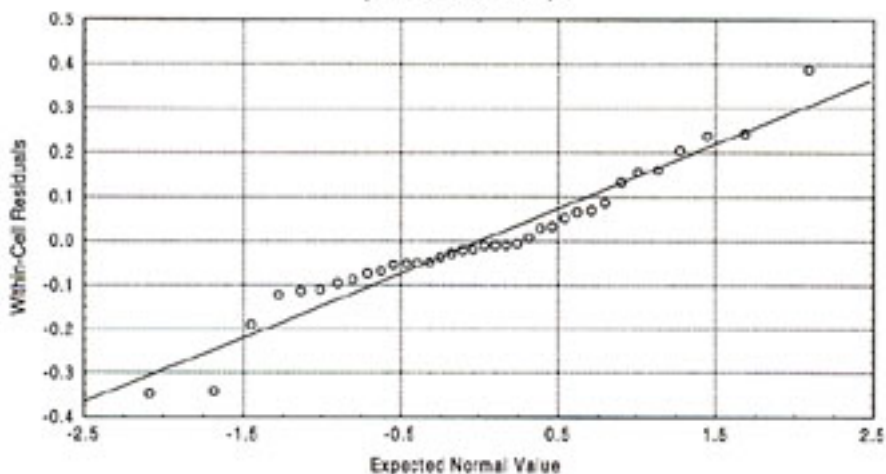
	CR_X	CR_Y	
CR_X	1.000000	.862783	- not normal
CR_Y	.862783	1.000000	

Log-transformed Chromium Content

Normal Probability Plot of Residuals

variable: LOG_CR

$$y = 6.041 \times 10^{-9} + 0.146 \times x + \text{eps}$$

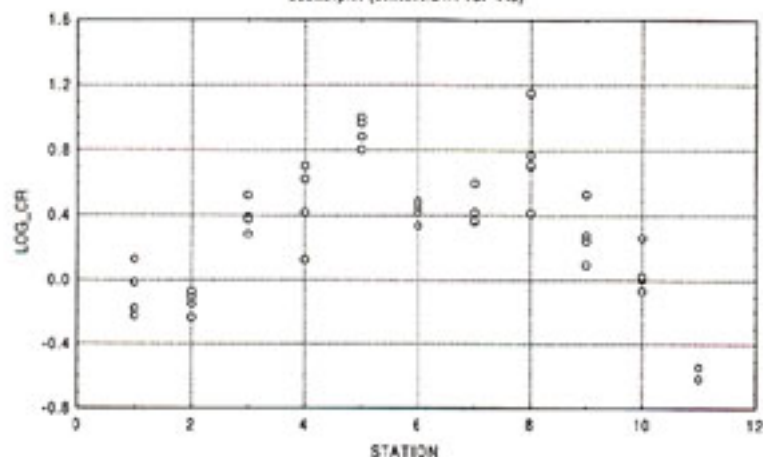


Correlation

N=36

	LGCR_X	LGCR_Y	
LGCR_X	1.000000	.970282	- normal
LGCR_Y	.970282	1.000000	

Scatterplot (content STA 15v44c)



ANOVA

Effect	Sum of Squares	df	Mean Square	F	p-level
Effect	3.298850	8	.412356	14.85963	.000000
Error	.749253	27	.027750		

Dunnett's contrasts - treatment stations vs. reference (w/o Reference 1) - log-transformed chromium content

If the value of q is greater than 2.840 then the P value is less than 0.05.

Comparison	Mean Difference	q	P value
Station 2 vs Station 3	-0.5328	4.523	** P<0.01
Station 2 vs Station 4	-0.6078	5.160	** P<0.01
Station 2 vs Station 5	-1.054	8.952	** P<0.01
Station 2 vs Station 6	-0.5640	4.788	** P<0.01
Station 2 vs Station 7	-0.5774	4.902	** P<0.01
Station 2 vs Station 8	-0.9016	7.654	** P<0.01
Station 2 vs Station 9	-0.4265	3.620	** P<0.01
Station 2 vs Station 10	-0.1963	1.666	ns P>0.05

Newman-Keuls test - log chromium content

	3	4	5	6	7	8	9	10	
3		.929033	.00375*	.802568	.931000	.04635*	.398803	.03103*	
4		.929033		.00395*	.933628	.808083	.02598*	.593180	.02991*
5		.003750	.003950		.00485*	.00404*	.228600	.00072*	.00015*
6		.802568	.933628	.004854		.915009	.053327	.516024	.03141*
7		.931000	.808083	.004038	.915009		.03847*	.620460	.03736*
8		.046350	.025985	.228600	.053327	.038475		.00914*	.00025*
9		.398803	.593180	.000720	.516024	.620460	.009141		.075181
10		.031033	.029912	.000152	.031406	.037359	.000253	.075181	

Dunnnett's contrasts - Reference station 2 and treatment stations vs. initial content - log-transformed chromium

If the value of q is greater than 2.860 then the P value is less than 0.05.

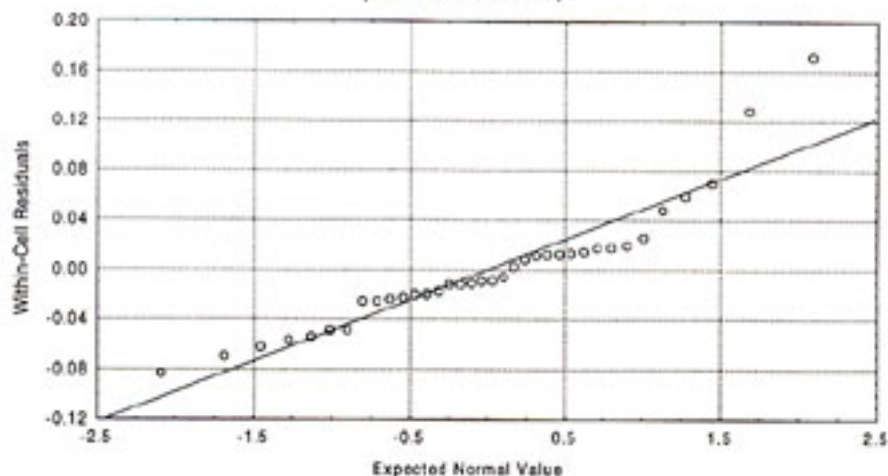
Comparison	Mean Difference	q	P value
Initial vs Station 2	-0.420	3.747	** P<0.01
Initial vs Station 3	-0.953	8.502	** P<0.01
Initial vs Station 4	-1.028	9.172	** P<0.01
Initial vs Station 5	-1.474	13.158	** P<0.01
Initial vs Station 6	-0.984	8.781	** P<0.01
Initial vs Station 7	-0.997	8.900	** P<0.01
Initial vs Station 8	-1.321	11.794	** P<0.01
Initial vs Station 9	-0.846	7.553	** P<0.01
Initial vs Station 10	-0.616	5.499	** P<0.01

Lead Content

Normal Probability Plot of Residuals

variable: PB

$$y = 8.488e-11 + 0.049 * x + \text{eps}$$



Correlation

N=36

PB_X

PB_Y

PB_X 1.000000

.937261

- not normal

PB_Y .937261

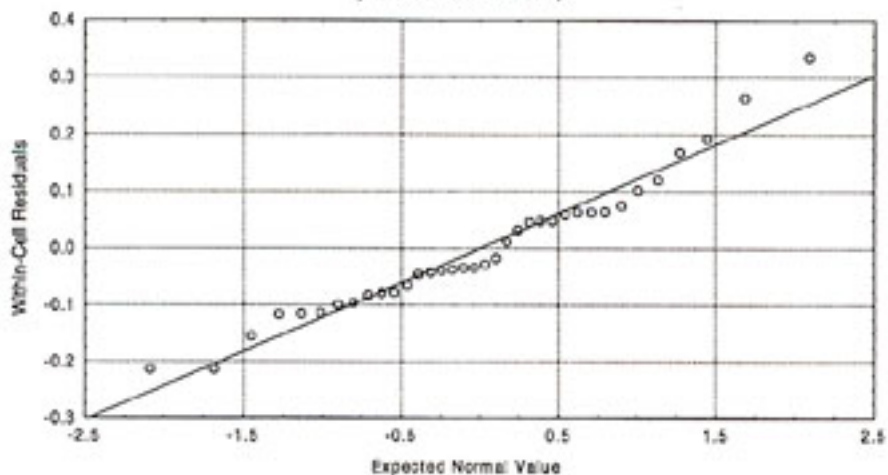
1.000000

Log-transformed Lead Content

Normal Probability Plot of Residuals

variable: LOG_PB

$$y = 4.915e-10 + 0.122 * x + \text{eps}$$



Correlation

N=36

LGPB_X

LGPB_Y

LGPB_X 1.000000

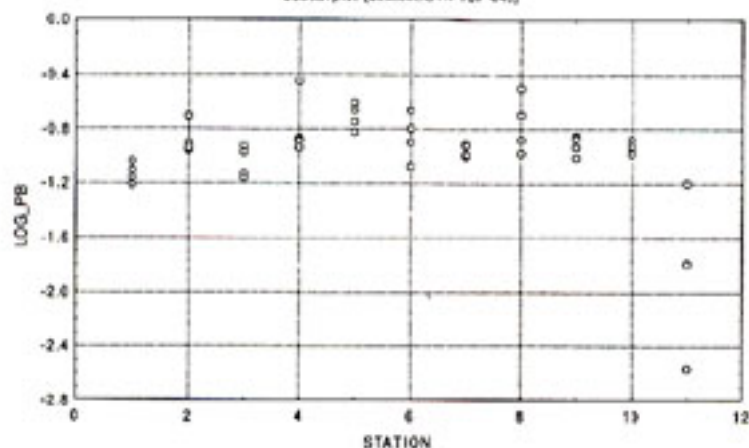
.977419

- normal

LGPB_Y .977419

1.000000

Scatterplot (eastest.STA 10*44)



ANOVA

Effect	Sum of Squares	df	Mean Square	F	p-level
Effect	.360126	8	.045016	2.386342	.043432
Error	.509326	27	.018864		

Dunnett's contrasts - treatment stations vs. reference (w/o Reference 1) - log-transformed lead content
 If the value of q is greater than 2.840 then the P value is less than 0.05.

Comparison	Mean Difference	q	P value
Station 2 vs Station 3	0.1677	1.727	ns P>0.05
Station 2 vs Station 4	-0.0942	0.970	ns P>0.05
Station 2 vs Station 5	-0.1704	1.755	ns P>0.05
Station 2 vs Station 6	-0.0231	0.238	ns P>0.05
Station 2 vs Station 7	0.0742	0.764	ns P>0.05
Station 2 vs Station 8	-0.1149	1.183	ns P>0.05
Station 2 vs Station 9	0.0365	0.376	ns P>0.05
Station 2 vs Station 10	0.0618	0.636	ns P>0.05

Newman-Keuls test - log lead content

	3	4	5	6	7	8	9	10
3		.124241	.03979*	.330186	.354026	.104362	.555812	.540986
4			.724440	.479289	.451652	.835989	.397792	.410296
5				.459243	.213493	.580128	.256272	.214819
6					.760396	.628120	.552991	.671570
7						.419832	.923403	.901421
8							.435976	.404338
9								.800440
10								

Dunnnett's contrasts - Reference station 2 and treatment stations vs. initial content - log-transformed lead

If the value of q is greater than 2.860 then the P value is less than 0.05.

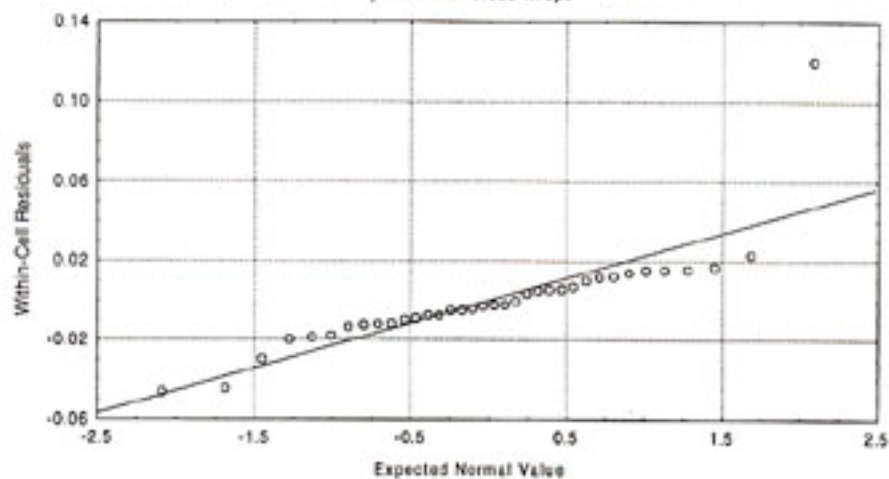
Comparison	Mean Difference	q	P value
Initial vs Station 2	-0.957	6.133	** P<0.01
Initial vs Station 3	-0.789	5.058	** P<0.01
Initial vs Station 4	-1.051	6.736	** P<0.01
Initial vs Station 5	-1.127	7.225	** P<0.01
Initial vs Station 6	-0.980	6.280	** P<0.01
Initial vs Station 7	-0.883	5.657	** P<0.01
Initial vs Station 8	-1.072	6.869	** P<0.01
Initial vs Station 9	-0.920	5.899	** P<0.01
Initial vs Station 10	-0.895	5.737	** P<0.01

Mercury Content

Normal Probability Plot of Residuals

variable: HG

$$y = 1.567e-9 + 0.023 * x + \text{eps}$$



Correlation

N=36

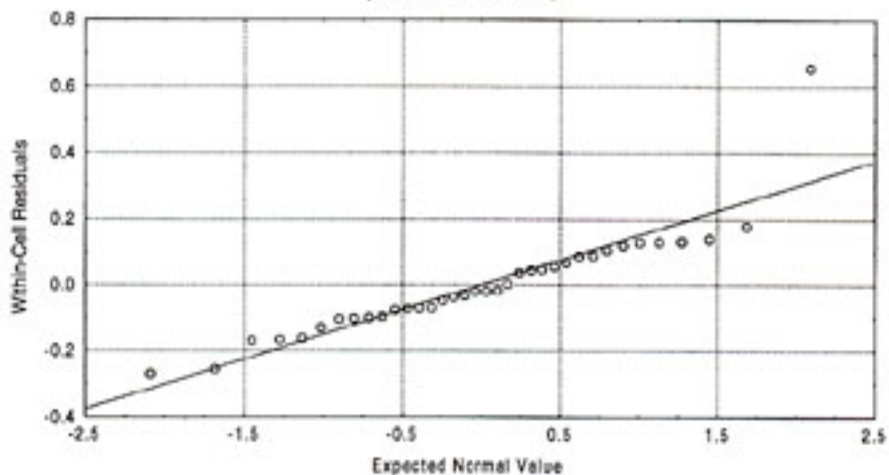
	HG_X	HG_Y	
HG_X	1.000000	.847530	- not normal
HG_Y	.847530	1.000000	

Log-transformed Mercury Content

Normal Probability Plot of Residuals

variable: LOG_HG

$$y = 2.251e-9 + 0.151 * x + \text{eps}$$



Correlation

N=36

	LGHG_X	LGHG_Y
LGHG_X	1.000000	.914646
LGHG_Y	.914646	1.000000

Rank-it transformed Mercury Content

ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	12.38452	8	1.548065	1.824603	.115942
Error	22.90786	27	.848439		

Dunnett's contrasts - treatment stations vs. reference (w/o Reference 1) - rank-transformed mercury content

If the value of q is greater than 2.840 then the P value is less than 0.05.

Comparison	Mean Difference	q	P value
Station 2 vs Station 3	-1.457	2.178	ns P>0.05
Station 2 vs Station 4	-1.868	2.792	ns P>0.05
Station 2 vs Station 5	-1.423	2.126	ns P>0.05
Station 2 vs Station 6	-0.350	0.524	ns P>0.05
Station 2 vs Station 7	-0.882	1.318	ns P>0.05
Station 2 vs Station 8	-1.375	2.054	ns P>0.05
Station 2 vs Station 9	-1.343	2.006	ns P>0.05
Station 2 vs Station 10	-0.367	0.548	ns P>0.05

Newman-Keuls test - ranked mercury

	3	4	5	6	7	8	9	10
3		.592114	.961570	.647329	.905831	.999189	.997012	.630697
4	.592114		.825743	.384487	.720227	.959687	.925465	.382022
5	.961570	.825743		.599712	.844918	.996174	.979763	.565254
6	.647329	.384487	.599712		.711649	.438136	.520619	.921914
7	.905831	.720227	.844918	.711649		.469784	.710685	.495380
8	.999189	.959687	.996174	.438136	.469784		.953808	.343351
9	.997012	.925465	.979763	.520619	.710685	.953808		.461216
10	.630697	.382022	.565254	.921914	.495380	.343351	.461216	

Dunnett's contrasts - Reference station 2 and treatment stations vs. initial content - rank-transformed mercury

If the value of q is greater than 2.860 then the P value is less than 0.05.

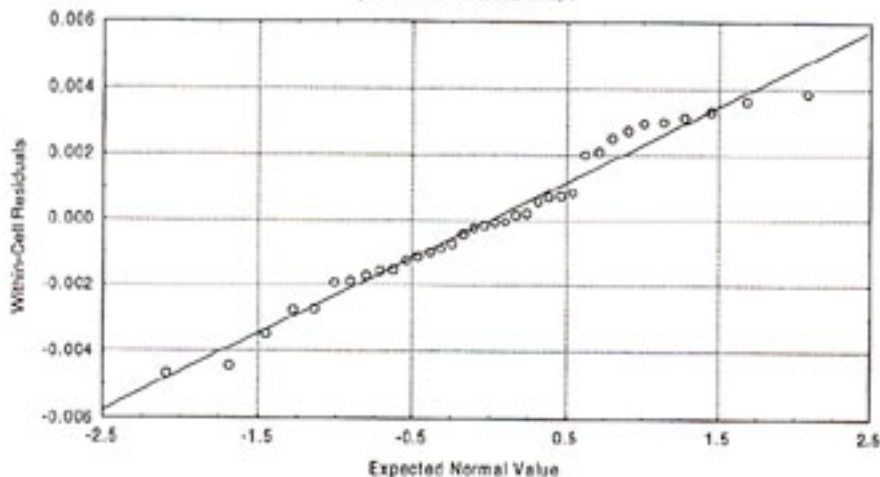
Comparison	Mean Difference	q	P value
Initial vs Station 2	1.245	1.768	ns P>0.05
Initial vs Station 3	-0.2122	0.301	ns P>0.05
Initial vs Station 4	-0.6232	0.885	ns P>0.05
Initial vs Station 5	-0.1773	0.252	ns P>0.05
Initial vs Station 6	0.8946	1.270	ns P>0.05
Initial vs Station 7	0.3634	0.516	ns P>0.05
Initial vs Station 8	-0.1297	0.184	ns P>0.05
Initial vs Station 9	-0.0975	0.138	ns P>0.05
Initial vs Station 10	0.8784	1.247	ns P>0.05

Methyl Mercury Content

Normal Probability Plot of Residuals

variable: MEHG

$$y = -2.2030e-11 + 0.002 * x \text{eeps}$$

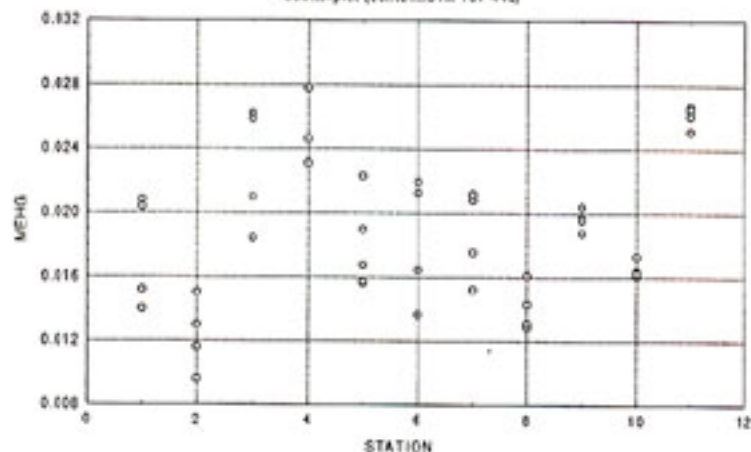


Correlation

N=36

	MEHG_X	MEHG_Y
MEHG_X	1.000000	.988075
MEHG_Y	.988075	1.000000

Scatterplot (content: STA 16v44c)



ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	.000480	8	.000060	9.077078	.000006
Error	.000178	27	.000007		

Dunnnett's contrasts - treatment stations vs. reference (w/o Reference 1) - methylmercury content

If the value of q is greater than 2.840 then the P value is less than 0.05.

Comparison	Mean		P value
	Difference	q	
Station 2 vs Station 3	-0.01055	5.803	** P<0.01
Station 2 vs Station 4	-0.01235	6.792	** P<0.01
Station 2 vs Station 5	-0.00611	3.364	* P<0.05
Station 2 vs Station 6	-0.00601	3.308	* P<0.05
Station 2 vs Station 7	-0.00638	3.507	* P<0.05
Station 2 vs Station 8	-0.00177	0.972	ns P>0.05
Station 2 vs Station 9	-0.00732	4.027	** P<0.01
Station 2 vs Station 10	-0.00420	2.308	ns P>0.05

Newman-Keuls test - methylmercury content

	3	4	5	6	7	8	9	10
3		.338606	.102697	.133255	.080469	.00140*	.092543	.02270*
4	.338606		.01893*	.02323*	.01710*	.00027*	.03042*	.00305*
5	.102697	.018931		.956651	.888703	.112302	.791600	.558412
6	.133255	.023231	.956651		.979007	.074222	.892308	.333662
7	.080469	.017105	.888703	.979007		.123403	.612682	.642834
8	.001397	.000274	.112302	.074222	.123403		.058875	.199605
9	.092543	.030422	.791600	.892308	.612682	.058875		.454670
10	.022699	.003050	.558412	.333662	.642834	.199605	.454670	

Dunnnett's contrasts - Reference station 2 and treatment stations vs. initial content - methylmercury

If the value of q is greater than 2.860 then the P value is less than 0.05.

Comparison	Mean		P value
	Difference	q	
Initial vs Station 2	0.01377	7.951	** P<0.01
Initial vs Station 3	0.00322	1.859	ns P>0.05
Initial vs Station 4	0.00142	0.820	ns P>0.05
Initial vs Station 5	0.00765	4.419	** P<0.01
Initial vs Station 6	0.00775	4.478	** P<0.01
Initial vs Station 7	0.00739	4.269	** P<0.01
Initial vs Station 8	0.01200	6.931	** P<0.01
Initial vs Station 9	0.00645	3.723	** P<0.01
Initial vs Station 10	0.00957	5.527	** P<0.01

STATISTICAL RESULTS
CLAM GROWTH DATA

Anova: Single Factor

SUMMARY

Groups	Count	Sum	Average	Variance
Cage 1	75	417.23	5.563067	0.847773
Cage 2	75	406.12	5.414933	0.738993
Cage 3	75	402.09	5.3612	0.623873
Cage 4	75	412.55	5.500667	0.724855
Cage 5	75	415.53	5.5404	0.736823
Cage 6	75	402.8	5.370667	0.710563
Cage 7	75	410.55	5.474	0.667246
Cage 8	75	420.4	5.605333	0.672526
Cage 9	75	418.34	5.578667	0.733698
Cage 10	75	406.06	5.400667	0.773058
Cage 11	75	414.73	5.529733	0.702505
Cage 12	75	415.44	5.5392	0.54171
Cage 13	75	412.91	5.505467	0.767985
Cage 14	75	421.75	5.623333	0.703639
Cage 15	75	417.72	5.5696	0.674334
Cage 16	75	407.76	5.4368	0.638722
Cage 17	75	415.79	5.543867	0.905221
Cage 18	75	405.67	5.408933	0.582483
Cage 19	75	418.84	5.584533	0.580803
Cage 20	75	425.09	5.667867	0.760167
Cage 21	75	417.53	5.567067	0.743145
Cage 22	75	412.85	5.504667	0.627474
Cage 23	75	439.07	5.854267	0.77663
Cage 24	75	412.18	5.495733	0.708765
Cage 25	75	415.1	5.534667	0.702067
Cage 26	75	419.7	5.596	0.834727
Cage 27	75	416.99	5.559867	0.571318
Cage 28	75	417.89	5.571867	0.72254
Cage 29	75	404.42	5.392267	0.730656
Cage 30	75	420.77	5.610267	0.761469
Cage 31	75	410.02	5.466933	0.637210
Cage 32	75	410.02	5.466933	0.691457
Cage 33	75	416.69	5.555867	0.600781
Cage 34	75	417.82	5.570933	0.693663
Cage 35	75	409.56	5.4608	0.677856
Cage 37	75	412.61	5.501467	0.808034
Cage 38	75	412.79	5.503867	0.737429
Cage 39	75	403.06	5.374133	0.666757
Cage 40	75	425.18	5.669067	0.75576
Cage 41	75	405.13	5.401733	0.653639
Cage 42	75	410.47	5.472933	0.606770
Cage 43	75	418.09	5.574533	0.717449
Cage 44	75	395.11	5.268133	0.570978

ANOVA Results

H₀: No Significant differences among cages

Source of Variation	SS	df	MS	F	P-value	F crit
Between Groups	32.24341	42	0.7677	1.093392	0.314455	1.387843
Within Groups	2234.168	3182	0.702127			
Total	2266.411	3224				

Anova: Single Factor

SUMMARY

Groups	Count	Sum	Average	Variance
Station 1	300	1658.95	5.529833	0.697503
Station 2	300	1654.99	5.516633	0.70886
Station 3	300	1657.23	5.5241	0.767434
Station 4	300	1674.77	5.582567	0.773542
Station 5	300	1645.68	5.4856	0.618066
Station 6	300	1665.42	5.5514	0.693938
Station 7	300	1673.45	5.578167	0.772933
Station 8	300	1637.45	5.458167	0.641711
Station 9	300	1646.04	5.4868	0.717117
Station 10	300	1653.44	5.511467	0.686571
Initial (T0)	300	1634.55	5.4485	0.685942

ANOVA Results

H₀: No Significant differences among Stations

Source of Variation	SS	df	MS	F	P-value	F crit
Between Groups	5.851184	10	0.585118	0.831173	0.595455	1.833573
Within Groups	2315.347	3289	0.703967			
Total	2321.199	3299				

Binomial Multiple Comparison Worksheet for Percent Survival

Number of Sites:	1	2	3	4	5	6	7	8	9	10
Station	0.92	0.93	0.91	0.9	0.87	0.95	0.92	0.95	0.94	0.93
P	0.000255	0.000233	0.0003	0.000333	0.000433	0.000167	0.000268	0.000167	0.000201	0.000235
denom	277	280	273	270	261	284	275	284	280	277
N										

denom=B6*(1-B6)/B8
z=ABS(B6-C6)/sqrt(B7+C7)

	z	p	k	P
1 v. 2	0.448019	0.6541	36	0.032727 FAIL TO REJECT
1 v. 3	0.420441	0.6742	40	0.036354 FAIL TO REJECT
1 v. 4	0.817152	0.4138	30	0.027273 FAIL TO REJECT
1 v. 5	1.891123	0.0586	9	0.008182 FAIL TO REJECT
1 v. 6	1.441779	0.1494	15	0.013636 FAIL TO REJECT
1 v. 7		1.0000	43	0.039091 FAIL TO REJECT
1 v. 8	1.441779	0.1494	16	0.014545 FAIL TO REJECT
1 v. 9	0.925358	0.3548	27	0.024545 FAIL TO REJECT
1 v. 10	0.446891	0.6550	38	0.034545 FAIL TO REJECT
2 v. 3	0.865703	0.3861	29	0.026384 FAIL TO REJECT
2 v. 4	1.26118	0.2072	20	0.018182 FAIL TO REJECT
2 v. 5	2.325244	0.0201	5	0.004545 FAIL TO REJECT
2 v. 6	1.000308	0.3172	23	0.020909 FAIL TO REJECT
2 v. 7	0.447153	0.6546	37	0.033636 FAIL TO REJECT
2 v. 8	1.000308	0.3172	24	0.021818 FAIL TO REJECT
2 v. 9	0.460055	0.6312	34	0.030909 FAIL TO REJECT
2 v. 10		1.0000	44	0.04 FAIL TO REJECT
3 v. 4	0.39736	0.6911	42	0.038182 FAIL TO REJECT
3 v. 5	1.477098	0.1396	14	0.012727 FAIL TO REJECT
3 v. 6	1.850477	0.0642	11	0.01 FAIL TO REJECT
3 v. 7	0.419725	0.6747	41	0.037273 FAIL TO REJECT
3 v. 8	1.850477	0.0642	12	0.010909 FAIL TO REJECT
3 v. 9	1.339728	0.1803	19	0.017273 FAIL TO REJECT
3 v. 10	2.481039	0.0131	4	0.003636 FAIL TO REJECT

4 v. 5	1.083473	0.2786	22	0.02	FAIL TO REJECT
4 v. 6	2.234757	0.0254	7	0.006384	FAIL TO REJECT
4 v. 7	0.815838	0.4146	31	0.028182	FAIL TO REJECT
4 v. 8	2.234757	0.0254	8	0.007273	FAIL TO REJECT
4 v. 9	1.729735	0.0837	13	0.011818	FAIL TO REJECT
4 v. 10	1.258383	0.2083	21	0.019091	FAIL TO REJECT
5 v. 6	3.26439	0.0011	1	0.000909	FAIL TO REJECT
5 v. 7	1.888515	0.0590	10	0.009091	FAIL TO REJECT
5 v. 8	3.26439	0.0011	2	0.001818	REJECT
5 v. 9	2.776366	0.0055	3	0.002727	FAIL TO REJECT
5 v. 10	2.320859	0.0203	6	0.005455	FAIL TO REJECT
6 v. 7	1.438572	0.1503	17	0.015455	FAIL TO REJECT
6 v. 8	0	1.0000	45	0.040909	FAIL TO REJECT
6 v. 9	0.520804	0.6025	32	0.029091	FAIL TO REJECT
6 v. 10	0.997173	0.3187	25	0.022727	FAIL TO REJECT
7 v. 8	1.438572	0.1503	18	0.016364	FAIL TO REJECT
7 v. 9	0.92345	0.3558	28	0.025455	FAIL TO REJECT
7 v. 10	0.446031	0.6556	39	0.035455	FAIL TO REJECT
8 v. 9	0.520804	0.6025	33	0.03	FAIL TO REJECT
8 v. 10	0.997173	0.3187	26	0.023636	FAIL TO REJECT
9 v. 10	0.478663	0.6322	35	0.031818	FAIL TO REJECT

Statistics for Clam Growth Metrics

Tissue Weight

Means

	TISSUE
1	.739350
2	.841690
3	.921825
4	.869852
5	.807241
6	.899049
7	.882582
8	.890947
9	.877429
10	.834043

ANOVA (including both Reference stations)

	Sum of Squares	df	Mean Square	F	p-level
Effect	7.01611	9	.779568	35.49254	0.00
Error	60.55554	2757	.021964		

Planned Comparisons

Reference stations 1 & 2 vs Station 3

	Mean sq Effect	Mean sq Error	F	p-level
TISSUES	3.173694	.021693	146.3025	0.000000

Reference stations 1 & 2 vs Station 4

	Mean sq Effect	Mean sq Error	F	p-level
TISSUES	1.147089	.021693	52.87908	.000000

Reference stations 1 & 2 vs Station 5

	Mean sq Effect	Mean sq Error	F	p-level
TISSUES	.049802	.021693	2.295793	.129828

Reference stations 1 & 2 vs Station 6

	Mean sq Effect	Mean sq Error	F	p-level
TISSUES	2.220723	.021693	102.3720	.000000

Reference stations 1 & 2 vs Station 7

	Mean sq Effect	Mean sq Error	F	p-level
TISSUES	1.563956	.021693	72.09605	.000000

Reference stations 1 & 2 vs Station 8

	Mean sq Effect	Mean sq Error	F	p-level
TISSUES	1.905976	.021693	87.86263	.000000

Reference stations 1 & 2 vs Station 9

	Mean sq	Mean sq		
	Effect	Error	F	p-level
TISSUES	1.410672	.021693	65.02986	.000000

Reference stations 1 & 2 vs Station 10

	Mean sq	Mean sq		
	Effect	Error	F	p-level
TISSUES	.351251	.021693	16.19213	.000059

Reference stations 1 & 2 vs Initial Measurements

	Mean sq	Mean sq		
	Effect	Error	F	p-level
TISSUES	3.092628	.021693	142.5656	0.000000

Dunnett Multiple Comparisons Test for Reference station 2 versus treatment stations
 If the value of q is greater than 2.720 then the P value is less than 0.05.

Comparison	Mean Difference	q		P value
Station 2 vs Station 1	0.1023	8.177	**	P<0.01
Station 2 vs Station 3	-0.08013	6.385	**	P<0.01
Station 2 vs Station 4	-0.02816	2.236	ns	P>0.05
Station 2 vs Station 5	0.03445	2.711	*	P<0.05
Station 2 vs Station 6	-0.05736	4.612	**	P<0.01
Station 2 vs Station 7	-0.04089	3.261	**	P<0.01
Station 2 vs Station 8	-0.04926	3.964	**	P<0.01
Station 2 vs Station 9	-0.03574	2.863	*	P<0.05
Station 2 vs Station 10	0.00765	0.611	ns	P>0.05

Newman-Keuls test for significance between treatment stations

	3	4	5	6	7	8	9	10
3		.00072*	.00003*	.075583	.01181*	.04229*	.00485*	.00003*
4	.000723		.00002*	.151994	.581178	.352838	.554438	.00523*
5	.000032	.000024		.00003*	.00002*	.00002*	.00001*	.03653*
6	.075583	.151994	.000026		.403761	.527323	.330604	.00002*
7	.011813	.581178	.000017	.403761		.513972	.687648	.00090*
8	.042293	.352838	.000020	.527323	.513972		.542322	.00010*
9	.004855	.554438	.000008	.330604	.687648	.542322		.00207*
10	.000026	.005226	.036527	.000025	.000896	.000102	.002066	

Dunnett Multiple Comparisons Test for End-of-Test Tissue Weights versus Initial Tissue Weights
 If the value of q is greater than 2.720 then the P value is less than 0.05.

Comparison	Mean Difference	q		P value
Initial vs Station 1	-0.0746	6.080	**	P<0.01
Initial vs Station 2	-0.1770	14.512	**	P<0.01
Initial vs Station 3	-0.2571	20.889	**	P<0.01
Initial vs Station 4	-0.2051	16.602	**	P<0.01
Initial vs Station 5	-0.1425	11.431	**	P<0.01
Initial vs Station 6	-0.2343	19.216	**	P<0.01
Initial vs Station 7	-0.2178	17.717	**	P<0.01
Initial vs Station 8	-0.2262	18.568	**	P<0.01
Initial vs Station 9	-0.2127	17.379	**	P<0.01
Initial vs Station 10	-0.1693	13.796	**	P<0.01

Log-transformed End-of-Test Whole-Animal Wet-Weight

Means

	<u>BOT_WAWW</u>
1	5.556968
2	5.617429
3	5.712784
4	5.722630
5	5.580766
6	5.762923
7	5.760691
8	5.581444
9	5.700214
10	5.630433

ANOVA (including both Reference stations)

	Sum of Squares	df	Mean Square	F	p-level
Effect	.45020	9	.050022	2.384048	.010987
Error	57.72134	2751	.020982		

Planned Comparisons

Reference stations 1 & 2 vs Station 3

	Sum of Squares	df	Mean Square	F	p-level
Effect	.09706	1	.097063	4.577153	.032489
Error	58.42231	2755	.021206		

Reference stations 1 & 2 vs Station 4

	Sum of Squares	df	Mean Square	F	p-level
Effect	.11443	1	.114428	5.396035	.020255
Error	58.42231	2755	.021206		

Reference stations 1 & 2 vs Station 5

	Sum of Squares	df	Mean Square	F	p-level
Effect	.00013	1	.000128	.006034	.938089
Error	58.42231	2755	.021206		

Reference stations 1 & 2 vs Station 6

	Sum of Squares	df	Mean Square	F	p-level
Effect	.20138	1	.201379	9.496341	.002079
Error	58.42231	2755	.021206		

Reference stations 1 & 2 vs Station 7

	Sum of Squares	df	Mean Square	F	p-level
Effect	.17823	1	.178226	8.404531	.003772
Error	58.42231	2755	.021206		

Reference stations 1 & 2 vs Station 8

	Sum of Squares	df	Mean Square	F	p-level
Effect	69.918	1	69.91766	86.89794	.000000
Error	2216.660	2755	.80460		

Reference stations 1 & 2 vs Station 9

	Sum of Squares	df	Mean Square	F	p-level
Effect	232.485	1	232.4848	288.9463	0.00
Error	2216.660	2755	.8046		

Reference stations 1 & 2 vs Station 10

	Sum of Squares	df	Mean Square	F	p-level
Effect	55.349	1	55.34949	68.79173	.000000
Error	2216.660	2755	.80460		

Dunnett Multiple Comparisons Test for Reference station 2 versus treatment stations

If the value of q is greater than 2.690 then the P value is less than 0.05.

Comparison	Mean			P value
	Difference	q		
Station 2 vs Station 1	0.6518	8.661	**	P<0.01
Station 2 vs Station 3	-0.5061	6.700	**	P<0.01
Station 2 vs Station 4	-0.2076	2.741	*	P<0.05
Station 2 vs Station 5	0.3273	4.284	**	P<0.01
Station 2 vs Station 6	-0.8566	11.454	**	P<0.01
Station 2 vs Station 7	-0.6209	8.236	**	P<0.01
Station 2 vs Station 8	-0.3029	4.050	**	P<0.01
Station 2 vs Station 9	-0.8276	11.027	**	P<0.01
Station 2 vs Station 10	-0.2487	3.304	**	P<0.01

Newman-Keuls test for significance between treatment stations

	3	4	5	6	7	8	9	10
3		.00072*	.00002*	.00004*	.139430	.00892*	.00012*	.00266*
4			.00001*	.00003*	.00002*	.437565	.00002*	.597145
5				.00003*	.00002*	.00001*	.00003*	.00002*
6					.00683*	.00002*	.708783	.00002*
7						.00014*	.00782*	.00002*
8							.00001*	.485304
9								.00002*
10								

Rank-it transformed Growth Rate*Means*

	<u>GROWTH</u>
1	5.16255
2	14.49019
3	22.48600
4	17.92480
5	9.56880
6	28.04358
7	24.26093
8	19.24972
9	27.24464
10	18.55577

ANOVA (including both Reference stations)

	Sum of Squares	df	Mean Square	F	p-level
Effect	135380.9	9	15042.32	71.83776	0.00
Error	576040.0	2751	209.39		

*Planned Comparisons***Reference stations 1 & 2 vs Station 3**

	Sum of Squares	df	Mean Square	F	p-level
Effect	117.803	1	117.8034	146.4132	0.00
Error	2216.660	2755	.8046		

Reference stations 1 & 2 vs Station 4

	Sum of Squares	df	Mean Square	F	p-level
Effect	46.809	1	46.80931	58.17747	.000000
Error	2216.660	2755	.80460		

Reference stations 1 & 2 vs Station 5

	Sum of Squares	df	Mean Square	F	p-level
Effect	.027	1	.027100	.033681	.854400
Error	2216.660	2755	.804595		

Reference stations 1 & 2 vs Station 6

	Sum of Squares	df	Mean Square	F	p-level
Effect	245.298	1	245.2981	304.8715	0.00
Error	2216.660	2755	.8046		

Reference stations 1 & 2 vs Station 7

	Sum of Squares	df	Mean Square	F	p-level
Effect	153.167	1	153.1665	190.3647	0.00
Error	2216.660	2755	.8046		

Reference stations 1 & 2 vs Station 8

	Sum of Squares	df	Mean Square	F	p-level
Effect	.00020	1	.000203	.009589	.922000
Error	58.42231	2755	.021206		

Reference stations 1 & 2 vs Station 9

	Sum of Squares	df	Mean Square	F	p-level
Effect	.08105	1	.081046	3.821853	.050689
Error	58.42231	2755	.021206		

Reference stations 1 & 2 vs Station 10

	Sum of Squares	df	Mean Square	F	p-level
Effect	.01729	1	.017289	.815287	.366641
Error	58.42231	2755	.021206		

Dunnett Multiple Comparisons Test for Reference station 2 versus treatment stations

If the value of q is greater than 2.690 then the P value is less than 0.05.

Comparison	Mean Difference	q		P value
Station 2 vs Station 1	0.00862	0.7006	ns	P>0.05
Station 2 vs Station 3	-0.01868	1.514	ns	P>0.05
Station 2 vs Station 4	-0.02075	1.676	ns	P>0.05
Station 2 vs Station 5	0.00346	0.2771	ns	P>0.05
Station 2 vs Station 6	-0.02837	2.322	ns	P>0.05
Station 2 vs Station 7	-0.02677	2.173	ns	P>0.05
Station 2 vs Station 8	0.00327	0.2675	ns	P>0.05
Station 2 vs Station 9	-0.01652	1.347	ns	P>0.05
Station 2 vs Station 10	-0.00535	0.4349	ns	P>0.05

Newman-Keuls test for significance between treatment stations

	3	4	5	6	7	8	9	10
3		.867246	.377873	.861547	.789735	.284385	.861222	.526827
4	.867246		.365780	.810651	.625932	.293884	.937562	.597062
5	.377873	.365780		.164255	.179095	.987677	.368545	.755777
6	.861547	.810651	.164255		.896708	.137959	.873297	.424607
7	.789735	.625932	.179095	.896708		.145318	.840497	.412874
8	.284385	.293884	.987677	.137959	.145318		.244659	.485442
9	.861222	.937562	.368545	.873297	.840497	.244659		.365668
10	.526827	.597062	.755777	.424607	.412874	.485442	.365668	

Statistical Results for Percent Solids and Percent Lipids

Means

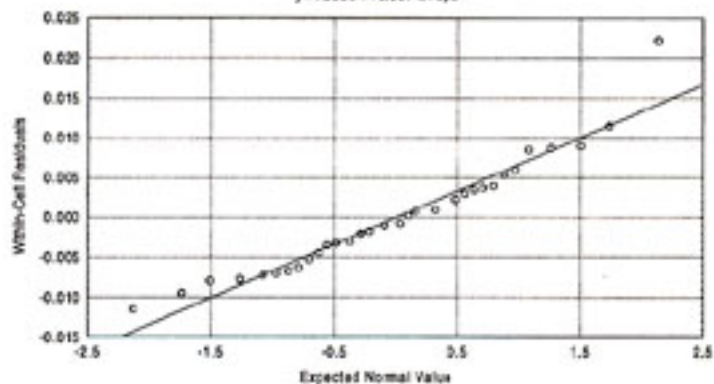
	<u>% SOLIDS</u>	<u>% LIPIDS</u>
1	.151750	1.360000
2	.148000	1.350000
3	.157500	1.555000
4	.156500	1.390000
5	.147250	1.400000
6	.161750	1.502500
7	.163000	1.482500
8	.156250	1.425000
9	.160000	1.720000
10	.151000	1.370000

Percent Solids

Normal Probability Plot of Residuals

variable: %_SOLIDS

$$y = 4.355e-7 + 0.007^*x + \text{eps}$$

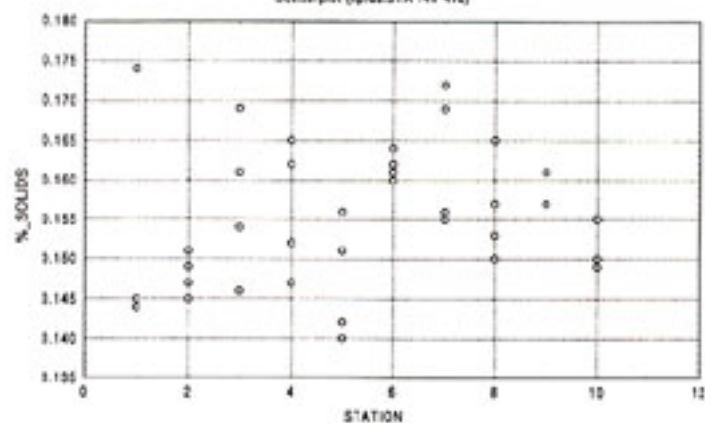


Correlation

N=40

	<u>SOLID_X</u>	<u>SOLID_Y</u>	
SOLID_X	1.000000	.971485	- normal
SOLID_Y	.971485	1.000000	

Scatterplot (ipids.STA 14w41c)



ANOVA

Effect	Sum of Squares	df	Mean Square	F	p-level
Effect	.001117	9	.000124	2.124738	.058955
Error	.001753	30	.000058		

Bonferroni contrasts - Percent Solids (with both Reference Stations 1 and 2)
% Solids

Refs 1 and 2 vs:

3	1.6349716
4	1.4205491
5	-0.5020591
6	2.5462679
7	2.8142054
8	1.3669435
9	2.1710279
10	0.2412253

critical value = 1.697

Newman-Keuls test - Percent Solids

	3	4	5	6	7	8	9	10
3		.834347	.225505	.646079	.654861	.962322	.601823	.526351
4			.232043	.686619	.648643	.958376	.742218	.485736
5				.067887	.04795*	.159345	.112709	.435463
6					.793791	.771365	.714562	.242913
7						.710338	.802691	.189968
8							.856783	.277800
9								.342190
10								

Dunnnett's multiple comparisons for initial against treatment stations – Percent Solids

If the value of q is greater than 2.878 then the P value is less than 0.05.

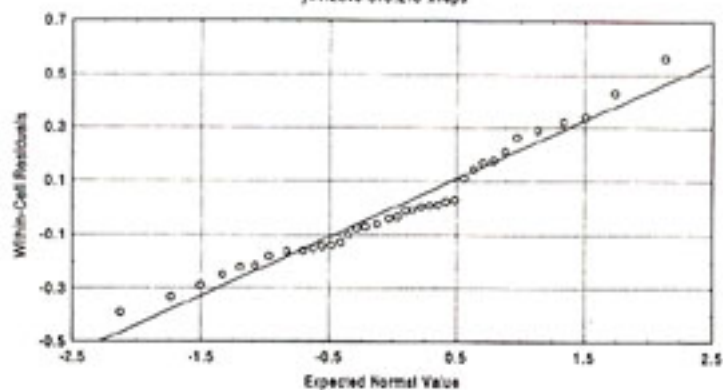
Comparison	Mean Difference	q	P value
Initial vs Station 1	0.00025	0.048	ns P>0.05
Initial vs Station 2	0.00400	0.772	ns P>0.05
Initial vs Station 3	-0.00550	1.062	ns P>0.05
Initial vs Station 4	-0.00450	0.869	ns P>0.05
Initial vs Station 5	0.00475	0.917	ns P>0.05
Initial vs Station 6	-0.00975	1.882	ns P>0.05
Initial vs Station 7	-0.01100	2.124	ns P>0.05
Initial vs Station 8	-0.00425	0.820	ns P>0.05
Initial vs Station 9	-0.00800	1.544	ns P>0.05
Initial vs Station 10	0.00100	0.193	ns P>0.05

Percent Lipids

Normal Probability Plot of Residuals

variable: %_LIPIDS

$y = 1.224e-5 + 0.218 * x$

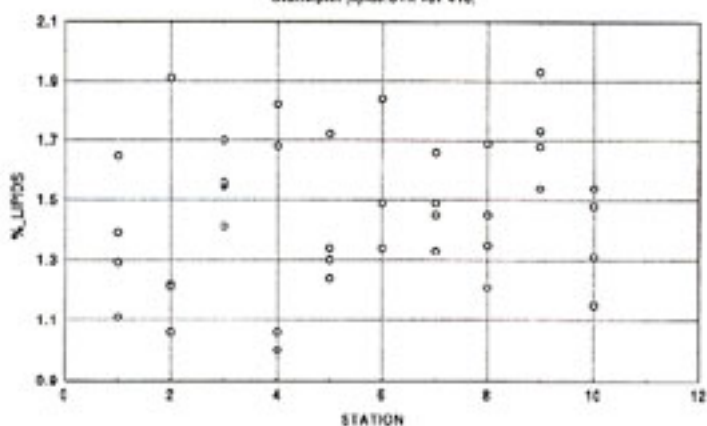


Correlation

N=40

	LIPID_X	LIPID_Y
LIPID_X	1.000000	.981625
LIPID_Y	.981625	1.000000

Scatterplot (lipids STA 16v41e)



ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	.474640	9	.052738	.870763	.560862
Error	1.816950	30	.060565		

Bonferroni contrasts - Percent Lipids (with both Reference Stations 1 and 2)
 % Lipids

Refs 1 and 2 vs:

3	1.3270995
4	0.2322424
5	0.2985974
6	0.9787359
7	0.646026
8	0.4644648
9	2.4219567
10	0.0695325

critical value = 1.697

Newman-Keuls test - Percent Lipids

	3	4	5	6	7	8	9	10
3		.902962	.866733	.745944	.893682	.848253	.313136	.903733
4	.902962		.950793	.953924	.937862	.974102	.405374	.901736
5	.866733	.950793		.917972	.864730	.877328	.372000	.980931
6	.745944	.953924	.917972		.901736	.879546	.378010	.959420
7	.893682	.937862	.864730	.901736		.722749	.462647	.953924
8	.848253	.974102	.877328	.879546	.722749		.373886	.985781
9	.313136	.405374	.372000	.378010	.462647	.373886		.393714
10	.903733	.901736	.980931	.959420	.953924	.985781	.393714	

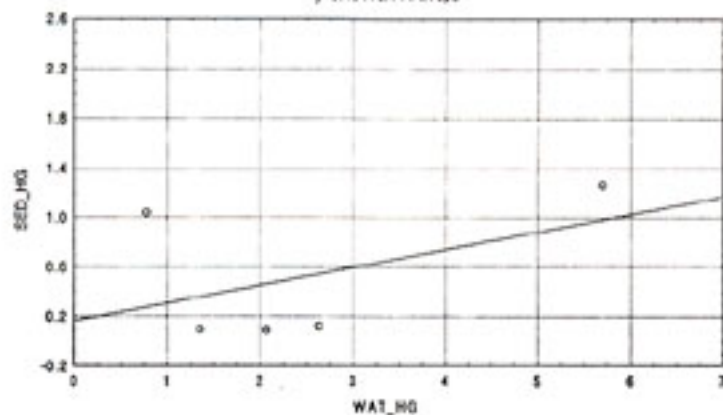
Dunnnett's multiple comparisons for initial clams against treatment stations

If the value of q is greater than 2.878 then the P value is less than 0.05.

Comparison	Mean Difference	q	P value
Initial vs Station 1	-0.0625	0.367	ns P>0.05
Initial vs Station 2	-0.0525	0.309	ns P>0.05
Initial vs Station 3	-0.2575	1.514	ns P>0.05
Initial vs Station 4	-0.0925	0.544	ns P>0.05
Initial vs Station 5	-0.1025	0.602	ns P>0.05
Initial vs Station 6	-0.2050	1.205	ns P>0.05
Initial vs Station 7	-0.1850	1.087	ns P>0.05
Initial vs Station 8	-0.1275	0.749	ns P>0.05
Initial vs Station 9	-0.4225	2.483	ns P>0.05
Initial vs Station 10	-0.0725	0.426	ns P>0.05

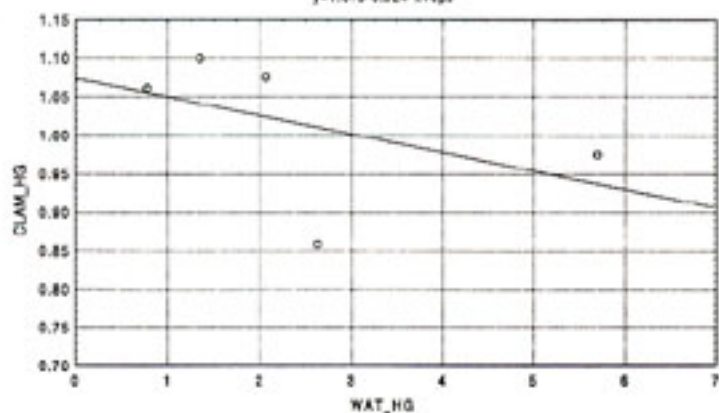
Water, sediment, and tissue chemistry correlations:

Scatterplot (watersed.STA 20v*10c)
 $y=0.154+0.144*x+eps$



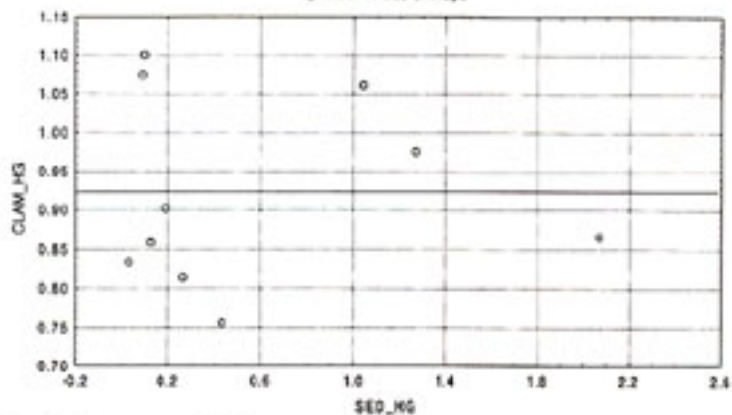
Correlation	N=5	
	WAT_HG	SED_HG
WAT_HG	1.000000	.474903
SED_HG	.474903	1.000000

Scatterplot (watersed.STA 20v*10c)
 $y=1.073-0.024*x+eps$



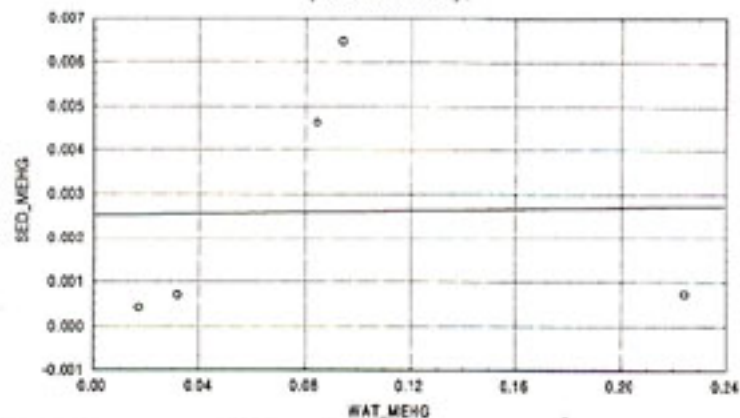
Correlation	N=5	
	WAT_HG	CLAM_HG
WAT_HG	1.000000	-.462263
CLAM_HG	-.462263	1.000000

Scatterplot (watershed STA 20v10c)
 $y=0.024+3.22e-5*x+eps$



Correlation	N=10	
	SED_HG	CLAM_HG
SED_HG	1.000000	.000181
CLAM_HG	.000181	1.000000

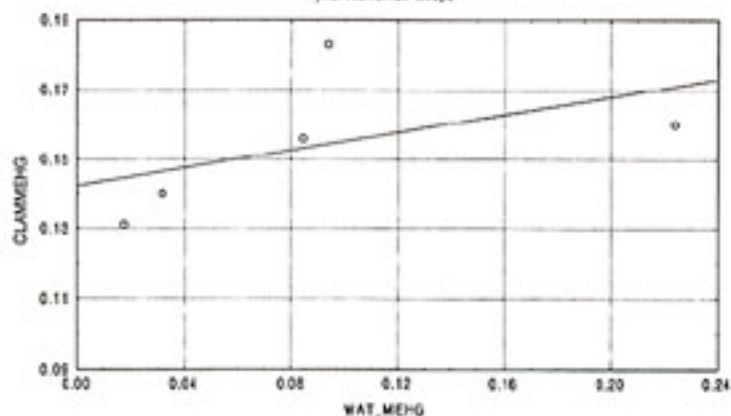
Scatterplot (watershed STA 20v*10c)
 $y=0.003+8.878e-4*x$



Correlation N=5

	WAT_MEHG	SED_MEHG
WAT_MEHG	1.000000	.026072
SED_MEHG	.026072	1.000000

Scatterplot (watershed STA 20v*10c)
 $y=0.143+0.127*x$

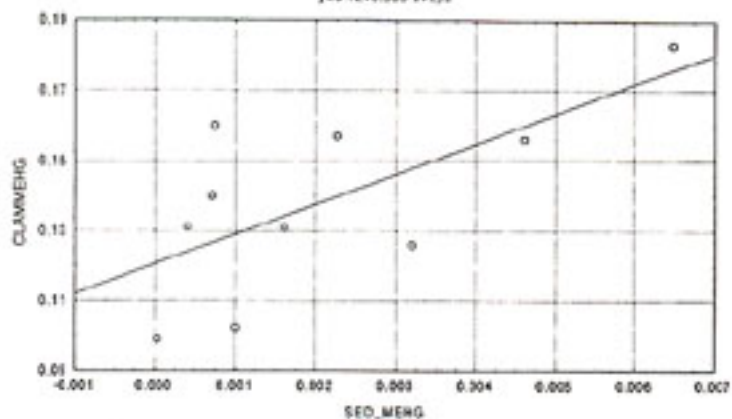


Correlation N=5

	WAT_MEHG	CLAMMEHG
WAT_MEHG	1.000000	.518423
CLAMMEHG	.518423	1.000000

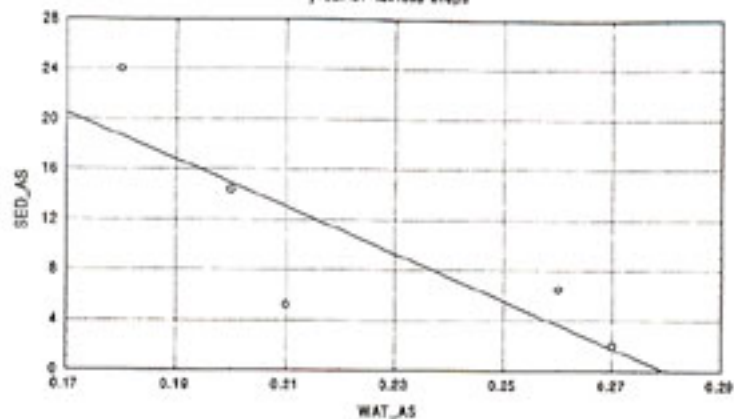
Scatterplot (watered STA 20v100)

$y = 0.12 + 4.563 * x + eps$



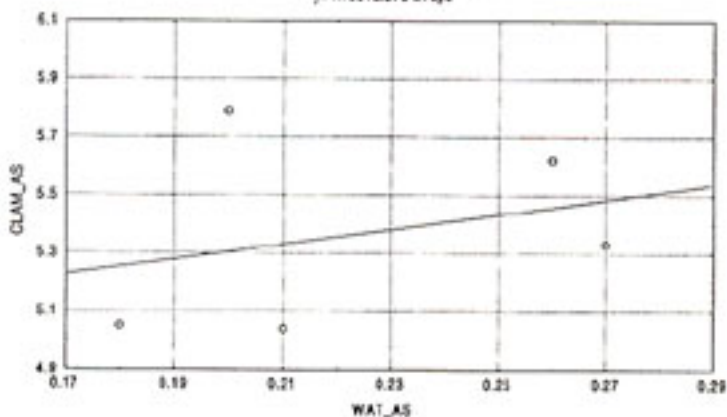
Correlation	N=10	
	<u>SED_MENHG</u>	<u>CLAMMEHG</u>
<u>SED_MENHG</u>	1.000000	.676960
<u>CLAMMEHG</u>	.676960	1.000000

Scatterplot (watersed.STA 20v*10c)
 $y = 62.457 - 187.683 * x + egs$



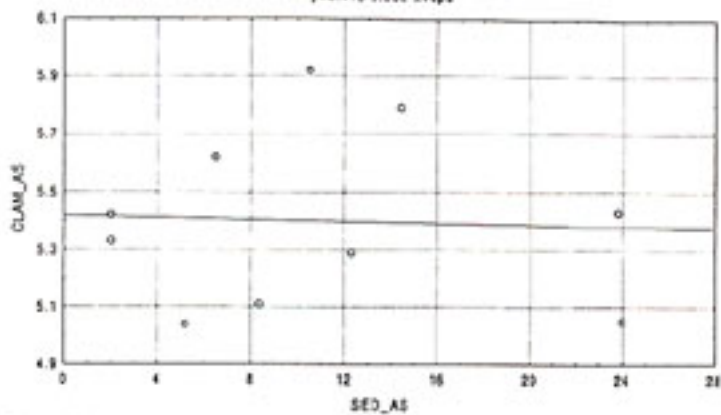
Correlation	N=5	
	<u>WAT_AS</u>	<u>SED_AS</u>
WAT_AS	1.000000	-.828647
SED_AS	-.828647	1.000000

Scatterplot (watersed.STA 10v*10c)
 $y = 4.750 + 2.578 * x + egs$



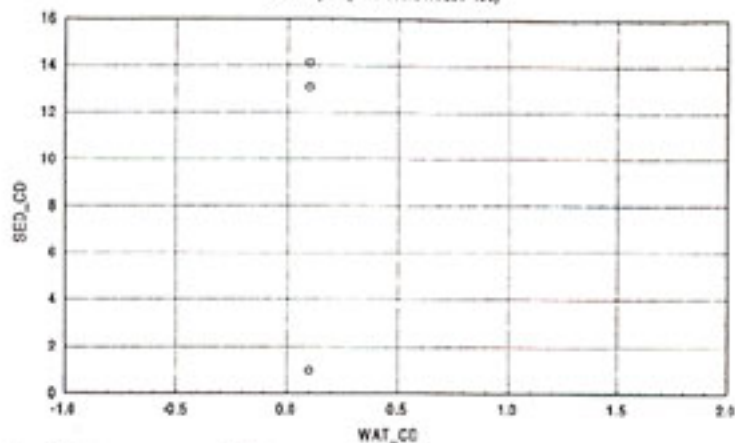
Correlation	N=5	
	<u>WAT_AS</u>	<u>CLAM_AS</u>
WAT_AS	1.000000	.300121
CLAM_AS	.300121	1.000000

Scatterplot (waterread.STA 20v10q)
 $y=5.418-0.003*x_{sed}$



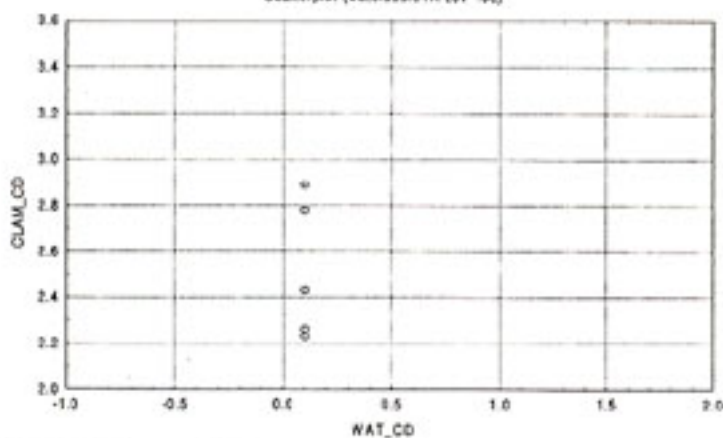
Correlation	N=10	
	<u>SED_AS</u>	<u>CLAM_AS</u>
<u>SED_AS</u>	1.000000	-.042809
<u>CLAM_AS</u>	-.042809	1.000000

Scatterplot (watersed.STA 10v*10c)



Correlation	N=5	
	WAT_CD	SED_CD
WAT_CD	1.000000	--
SED_CD	--	1.000000

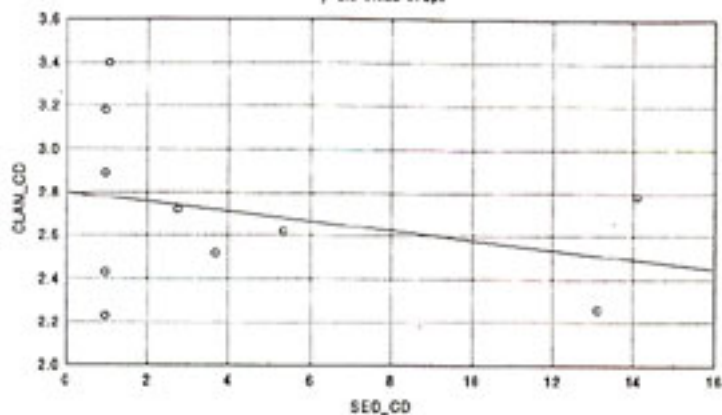
Scatterplot (watersed.STA 10v*10c)



Correlation	N=5	
	WAT_CD	CLAM_CD
WAT_CD	1.000000	--
CLAM_CD	--	1.000000

Scatterplot (wateraed.DTA 20v10c)

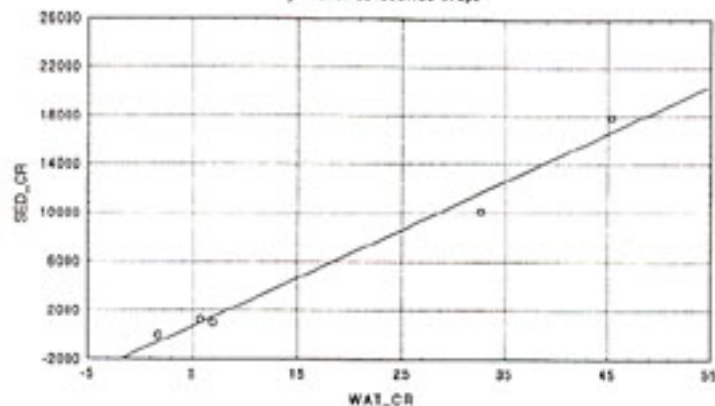
$$y = 2.8 - 0.022 * x \text{ exp}$$



Correlation	N=10	
	SED_CD	CLAM_CD
SED_CD	1.000000	-.296137
CLAM_CD	-.296137	1.000000

Scatterplot (watersed STA 20v*10c)

$$y = 1276.703 + 295.189 * x + \text{eps}$$



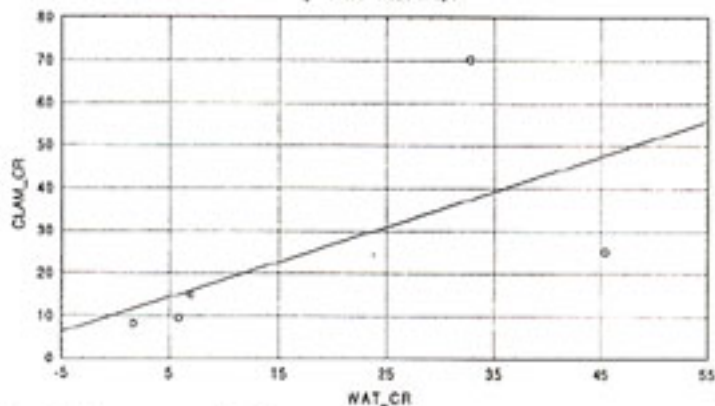
Correlation

N=5

	WAT_CR	SED_CR
WAT_CR	1.000000	.990882
SED_CR	.990882	1.000000

Scatterplot (watersed STA 20v*10c)

$$y = 10.259 + 1.628 * x + \text{eps}$$



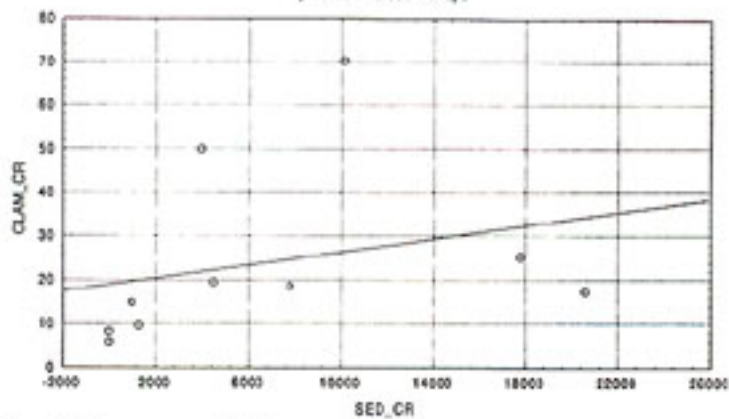
Correlation

N=5

	WAT_CR	CLAM_CR
WAT_CR	1.000000	.621165
CLAM_CR	.621165	1.000000

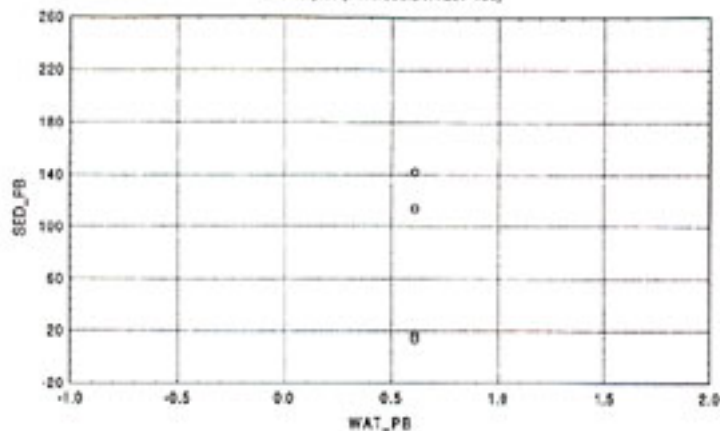
Scatterplot (watershed.STA 20V10c)

$$y = 18.884 + 7.488e-4 * x + eps$$



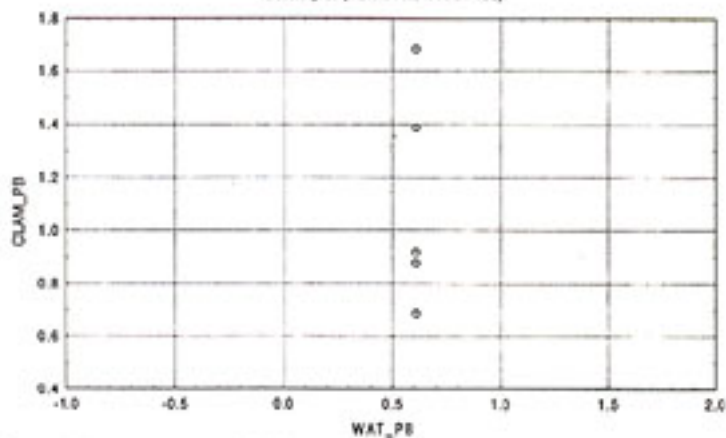
Correlation	N=10	
	SED_CR	CLAM_CR
SED_CR	1.000000	.270382
CLAM_CR	.270382	1.000000

Scatterplot (watersed STA 20v10c)



Correlation		N=5	
	WAT_PB	SED_PB	
WAT_PB	1.000000	--	
SED_PB	--	1.000000	

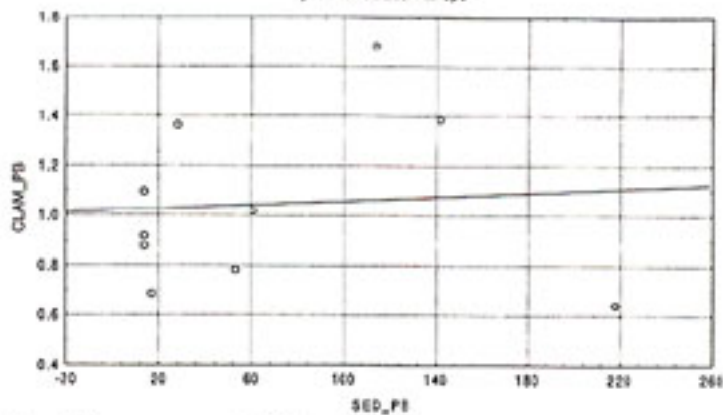
Scatterplot (watersed STA 20v10c)



Correlation		N=5	
	WAT_PB	CLAM_PB	
WAT_PB	1.000000	--	
CLAM_PB	--	1.000000	

Scatterplot (watered.STA 20v'10c)

$$y=1.018+3.322e-4*x+eps$$



Correlation

N=10

	<u>SED_PB</u>	<u>CLAM_PB</u>
<u>SED_PB</u>	1.000000	.080533
<u>CLAM_PB</u>	.080533	1.000000

APPENDIX E
CLAM MEASUREMENT DATA

1997 Cannelton Clam Biomonitoring Study Initial Whole-Animal Wet-Weights (g) by Station

mean	5.53	5.52	5.52	5.58	5.49	5.55	5.58	5.46	5.49	5.51	5.45
min	4.02	4.04	4.01	4.02	4.1	4.07	4.04	4.02	4.01	4.02	4.01
max	7.9	7.93	7.92	7.95	7.79	7.89	7.91	7.75	7.75	7.85	7.79
stdev	0.84	0.84	0.88	0.88	0.79	0.83	0.88	0.80	0.85	0.82	0.83
N	300	300	300	300	300	300	300	300	300	300	300

Cage #s:	13,22,25,43	5,15,24, 35	2,11,30,37	3,17,23,34	4,18,27,42	14,19,26,41	1,9,20,38	16,28,33,44	8,10,21,39	6,12,31,40	7,29,32,36
	<u>Sta 1</u>	<u>Sta 2</u>	<u>Sta 3</u>	<u>Sta 4</u>	<u>Sta 5</u>	<u>Sta 6</u>	<u>Sta 7</u>	<u>Sta 8</u>	<u>Sta 9</u>	<u>Sta 10</u>	<u>Initial (T0)</u>
Rep 1 - 1	4.87	5.62	6.02	6.46	7.79	6.61	7.54	4.72	6.22	5.78	6.50
2	5.99	6.30	4.15	5.27	7.33	5.28	4.77	5.96	5.68	4.90	4.67
3	4.91	5.54	4.90	5.09	5.83	4.85	5.96	7.15	5.75	6.45	4.92
4	6.00	5.41	6.34	6.90	6.20	6.12	4.76	4.35	5.45	4.82	5.66
5	5.34	4.38	5.84	6.54	5.04	4.64	4.52	4.95	5.61	5.83	5.22
6	4.56	6.04	4.66	4.32	5.39	4.62	4.40	5.69	4.02	7.47	6.62
7	6.36	4.46	7.04	5.17	6.37	6.59	6.17	4.24	6.52	4.68	5.79
8	7.90	4.34	4.50	5.27	5.20	6.39	4.28	5.84	4.87	5.40	4.59
9	4.10	4.65	6.07	4.14	5.47	4.91	4.99	5.09	5.71	4.73	6.42
10	5.94	5.61	4.82	4.29	5.60	5.00	5.03	6.10	7.75	4.80	4.90
11	4.54	5.40	4.86	4.75	5.94	4.91	5.40	6.49	6.26	5.61	5.40
12	6.02	5.17	4.47	4.56	4.10	4.57	7.66	5.97	4.63	4.31	5.70
13	4.63	5.90	4.36	5.01	4.62	5.86	4.37	5.02	5.43	4.41	4.64
14	4.16	5.42	5.86	4.39	4.87	4.87	5.26	5.49	4.71	5.05	4.25
15	5.40	5.31	5.18	5.28	4.54	4.68	4.80	4.30	6.02	5.14	4.47
16	6.18	4.49	7.11	6.23	6.27	4.32	5.23	4.20	5.79	4.81	5.92
17	5.79	5.60	4.86	5.11	4.65	6.43	5.03	5.48	4.79	6.12	4.68
18	5.73	5.08	4.44	4.46	5.04	5.04	4.08	4.78	4.52	5.47	4.64
19	6.57	7.48	6.83	6.88	7.51	6.54	6.15	6.43	5.50	7.17	6.20
20	4.80	4.37	4.25	4.46	4.58	5.29	4.96	5.18	5.88	4.85	4.57
21	5.86	5.89	5.05	6.12	5.84	5.35	5.34	5.17	4.95	5.12	5.39
22	4.77	5.79	5.80	5.77	5.33	5.66	5.13	4.57	4.98	4.92	5.73
23	6.01	5.96	5.08	5.37	4.70	5.69	5.83	6.05	5.44	5.46	4.74
24	5.47	5.79	4.85	5.60	4.45	5.62	5.51	4.76	5.78	4.19	4.39
25	4.59	7.11	5.16	5.23	6.46	4.77	5.77	5.62	5.26	4.24	5.64
26	6.74	5.11	7.55	5.62	5.65	5.41	7.09	6.23	5.12	4.44	4.78
27	6.27	5.14	5.28	5.31	6.11	5.65	4.94	5.54	6.32	5.94	5.07
28	7.07	5.71	6.64	6.91	6.60	5.44	7.36	6.43	5.64	5.87	7.08
29	4.04	5.59	5.28	4.68	6.09	4.24	5.62	4.91	4.87	5.51	5.60
30	5.34	6.94	6.39	5.56	5.40	5.16	5.57	5.90	4.84	6.23	7.04
31	4.73	4.64	4.72	5.62	6.27	4.52	6.65	4.13	5.06	5.52	4.58
32	4.46	4.16	5.79	4.68	4.60	4.19	6.24	5.24	5.11	4.49	5.28
33	4.74	6.78	4.16	5.23	4.61	5.09	4.36	4.61	4.62	4.76	5.34
34	4.71	4.07	4.17	4.51	4.38	4.44	4.49	5.41	4.12	4.06	4.61
35	5.64	5.24	5.01	4.44	5.34	6.68	4.81	4.48	6.81	7.16	5.53
36	5.07	5.55	6.48	5.01	7.53	7.32	6.40	4.78	5.87	4.58	6.14
37	5.01	5.28	4.62	6.10	4.66	4.47	5.46	5.40	4.09	4.67	6.16
38	4.68	4.20	6.18	5.49	5.84	5.95	5.36	4.75	5.05	4.53	4.75
39	4.33	5.55	5.51	5.40	6.90	6.32	6.50	5.11	5.46	6.53	5.14
40	5.68	5.43	5.86	5.75	6.00	5.30	6.05	6.06	5.50	5.77	4.22
41	6.07	4.91	6.11	4.97	4.30	5.35	7.26	6.22	4.06	5.04	4.52
42	5.75	6.51	6.09	6.21	5.33	6.57	5.74	5.16	5.82	4.49	5.77
43	6.06	6.18	5.32	5.23	4.91	4.07	5.29	6.78	6.49	4.34	4.68
44	4.57	4.27	4.98	4.15	4.67	6.49	5.21	4.23	5.78	5.72	6.44
45	4.40	5.20	4.62	5.80	5.57	7.39	6.10	4.37	5.19	6.68	6.33
46	6.05	5.37	5.41	5.39	4.10	4.70	6.55	5.06	4.68	5.14	4.53
47	6.43	5.46	6.15	4.48	5.20	4.83	5.63	6.04	6.69	4.94	4.88

**1997 Cannelton Clam Biomonitoring Study
Initial Whole-Animal Wet-Weights (g) by Station**

	48	5.15	4.68	5.30	4.50	5.01	6.79	4.48	4.46	6.95	4.45	6.95
	49	4.88	4.77	5.26	6.41	5.71	5.09	5.55	5.85	6.04	5.68	4.50
	50	5.39	5.17	5.04	4.35	5.34	6.35	4.57	5.77	5.68	6.38	4.25
	51	4.70	6.31	5.44	6.29	5.80	6.23	7.35	6.24	4.39	5.85	4.94
	52	6.35	5.86	4.29	5.85	5.88	6.18	4.61	6.67	6.03	5.86	7.79
	53	5.34	5.38	4.77	5.36	4.47	5.98	5.35	4.46	5.83	5.05	4.90
	54	5.51	6.46	5.58	5.53	5.32	4.69	5.93	5.48	7.71	6.01	6.81
	55	4.04	4.98	6.21	4.80	5.19	6.90	4.24	6.59	6.18	4.63	4.61
	56	5.35	5.36	4.67	4.68	5.04	5.36	5.71	4.65	4.90	4.81	4.83
	57	4.23	6.41	5.69	5.98	6.11	6.25	6.02	5.60	5.32	4.73	5.12
	58	5.37	4.66	4.79	6.13	5.92	5.32	4.91	6.39	7.21	4.34	5.03
	59	6.33	7.12	5.66	5.73	6.70	6.55	5.27	6.67	5.72	4.53	6.27
	60	6.24	4.96	6.14	5.02	5.51	6.88	5.68	6.72	6.69	4.80	6.23
	61	5.36	5.39	4.84	4.27	4.55	7.00	4.43	4.25	6.56	5.98	5.77
	62	5.85	5.77	4.98	4.48	5.12	6.37	6.83	4.19	6.53	5.83	6.13
	63	6.26	6.17	6.62	6.82	5.86	5.76	6.76	5.28	5.49	6.36	5.30
	64	6.77	5.19	6.92	4.84	5.08	6.12	6.30	5.50	6.25	5.46	6.18
	65	7.16	6.15	4.74	5.95	4.43	4.17	6.27	5.24	4.44	5.15	5.24
	66	5.06	5.42	4.31	4.16	5.03	6.55	4.55	5.30	5.49	5.11	5.64
	67	7.17	6.70	6.84	5.42	5.93	6.43	6.99	6.02	4.93	5.98	5.78
	68	7.27	7.91	7.64	7.29	7.03	5.62	7.82	5.46	6.06	7.85	5.69
	69	6.69	5.72	6.42	5.41	4.18	6.00	5.34	6.23	5.92	5.51	5.25
	70	5.46	6.25	5.89	6.69	5.83	4.97	5.75	7.28	6.03	5.27	6.98
	71	4.19	4.55	4.40	4.35	5.49	6.21	4.50	4.88	4.88	4.02	6.27
	72	5.79	7.83	5.87	5.47	5.96	5.83	4.47	4.43	5.54	5.93	6.45
	73	6.25	4.57	5.83	6.30	6.34	6.11	5.13	5.72	6.86	6.41	5.43
	74	4.96	4.81	5.13	4.74	4.68	5.77	5.52	6.11	5.53	6.26	6.20
	75	5.46	6.58	5.03	6.06	5.86	6.08	5.28	5.88	6.53	6.42	5.89
Rep	2	4.70	5.52	5.23	4.48	5.12	6.31	5.88	5.70	6.96	4.91	5.29
1	2	5.52	6.61	5.40	6.44	5.10	5.17	5.80	5.05	6.06	6.39	4.01
	3	5.78	5.55	6.33	6.54	6.80	4.63	5.25	4.42	4.81	5.63	6.28
	4	4.85	5.26	6.46	4.25	4.61	6.12	4.33	7.75	5.03	6.34	7.33
	5	5.63	7.62	6.57	7.74	5.85	5.05	6.16	6.61	4.72	5.91	4.24
	6	4.95	4.49	5.66	5.03	4.85	4.67	5.89	5.79	5.26	5.26	5.71
	7	6.00	5.73	7.13	4.47	5.86	4.65	6.02	6.64	5.70	4.84	5.36
	8	5.44	4.82	5.90	5.84	4.59	5.81	5.27	4.73	4.80	4.48	4.97
	9	5.33	5.47	5.87	5.06	4.89	5.32	6.25	4.04	4.59	4.66	4.92
	10	4.39	6.05	6.92	4.49	4.58	6.37	6.08	5.79	5.52	6.21	4.80
	11	5.67	6.42	5.77	4.38	4.28	5.52	4.25	4.68	5.12	5.79	5.54
	12	5.32	4.48	6.63	4.17	5.98	6.42	5.12	6.74	4.74	5.10	4.70
	13	5.19	6.56	4.93	7.45	4.97	5.22	6.12	5.68	6.36	5.24	4.41
	14	4.59	5.19	4.56	4.13	4.75	6.63	4.23	4.52	4.68	5.68	6.76
	15	4.84	4.77	5.71	5.42	4.58	4.88	6.98	5.53	5.42	4.73	4.76
	16	5.43	6.07	5.07	5.35	6.37	5.52	4.11	5.37	4.31	4.59	5.15
	17	5.29	6.10	4.39	5.57	4.51	5.91	4.68	4.09	4.45	4.29	5.29
	18	5.91	4.88	4.06	4.62	4.15	4.59	4.58	4.58	4.56	4.85	5.77
	19	5.54	7.10	5.72	5.63	6.75	7.18	6.62	6.14	7.58	6.43	5.12
	20	4.85	5.74	4.56	5.35	4.18	5.45	4.16	4.43	5.09	5.01	4.29
	21	4.67	5.83	6.16	4.18	4.35	5.42	5.71	4.37	5.86	4.78	5.06
	22	5.90	4.25	4.66	5.60	4.26	6.03	6.13	4.65	4.49	5.09	6.45
	23	4.70	4.32	4.30	5.41	4.60	4.35	6.25	4.76	4.82	6.29	5.72
	24	5.91	6.36	5.33	5.14	5.34	5.52	5.69	7.28	4.16	5.27	6.60
	25	5.35	6.11	4.55	4.10	4.81	4.11	6.11	4.36	4.83	5.90	5.57
	26	6.94	5.31	7.11	7.35	5.48	5.61	5.27	4.98	5.46	6.38	6.70
	27	5.77	5.66	5.84	4.97	4.74	6.61	5.74	5.07	5.38	6.46	4.83

**1997 Cannelton Clam Biomonitoring Study
Initial Whole-Animal Wet-Weights (g) by Station**

28	6.90	6.54	7.03	5.58	5.96	5.26	5.62	5.65	5.26	5.86	4.92	
29	5.03	4.61	4.92	4.44	4.50	4.21	4.77	5.94	4.94	5.26	4.17	
30	5.41	6.46	6.37	4.68	6.51	7.22	5.88	4.63	6.50	5.02	4.71	
31	6.27	5.09	5.30	7.01	5.28	5.40	7.30	5.68	5.22	5.00	4.27	
32	5.17	5.71	4.01	4.33	4.99	5.91	6.38	6.64	4.13	4.89	6.18	
33	4.21	4.15	5.15	4.59	5.36	5.09	5.07	4.55	6.35	5.75	4.06	
34	5.12	5.96	5.15	5.19	5.20	6.32	4.51	5.95	4.38	6.16	5.08	
35	5.23	6.67	5.32	5.11	7.15	5.69	5.03	5.56	6.57	6.58	5.62	
36	4.17	5.72	5.22	4.06	5.11	5.31	5.72	5.36	7.14	6.47	4.32	
37	6.65	5.10	5.23	7.83	5.69	4.81	5.37	5.09	5.07	5.46	5.32	
38	6.71	5.15	5.86	5.00	5.76	4.33	5.38	6.07	5.50	4.50	4.86	
39	6.01	4.36	5.06	5.29	6.69	4.84	4.96	6.47	5.35	5.52	4.96	
40	5.14	6.32	5.63	6.59	4.89	6.13	6.02	4.57	6.26	6.65	5.40	
41	4.53	5.64	4.43	5.67	4.37	4.41	6.55	4.91	5.69	6.94	6.91	
42	5.86	6.67	5.91	6.10	5.41	5.63	6.13	4.92	4.21	5.63	4.59	
43	6.38	5.87	6.05	4.87	5.20	4.91	5.51	5.61	4.94	6.78	5.18	
44	4.74	6.26	4.52	6.15	5.83	4.75	5.87	4.62	5.21	5.83	5.58	
45	4.98	4.92	5.30	6.02	4.63	5.53	4.63	5.15	4.92	5.66	5.33	
46	4.02	4.80	5.33	5.16	5.38	5.73	4.78	5.59	4.01	4.17	5.73	
47	5.73	6.22	4.07	4.85	4.83	5.74	5.97	6.39	4.33	4.39	4.48	
48	4.90	4.21	4.49	5.57	5.76	5.09	5.12	7.12	6.13	4.71	4.29	
49	6.94	6.42	4.43	5.15	4.91	5.64	4.07	6.42	5.04	5.14	4.79	
50	4.71	4.96	5.45	6.07	5.02	7.22	4.13	4.24	4.27	5.99	5.52	
51	5.71	5.37	6.18	5.02	5.45	6.41	4.99	6.56	4.90	5.85	5.41	
52	5.26	4.77	6.29	6.57	5.70	5.39	6.78	5.43	6.22	6.69	4.99	
53	5.03	5.18	5.75	6.41	5.91	7.11	7.37	5.60	6.64	6.14	5.01	
54	4.76	6.51	7.00	6.51	6.06	5.34	6.65	4.68	6.57	5.18	5.19	
55	6.40	5.65	5.04	5.10	5.59	4.99	4.72	6.89	6.14	7.02	5.41	
56	6.59	5.00	4.69	5.46	5.75	6.52	5.22	5.80	4.79	4.70	6.21	
57	6.94	6.53	6.41	6.95	7.52	6.71	5.49	5.75	5.07	6.48	6.18	
58	6.15	4.27	5.07	5.49	4.90	4.78	6.59	6.69	6.90	5.98	7.54	
59	6.63	4.81	5.20	4.50	5.94	6.70	6.34	5.03	4.34	5.31	4.48	
60	5.19	5.22	6.36	6.97	6.37	5.87	7.43	5.60	5.98	7.12	7.01	
61	5.34	6.18	5.92	5.18	5.88	6.31	5.43	6.06	5.40	5.12	4.08	
62	5.59	4.59	4.55	4.41	5.30	5.73	7.36	6.03	4.45	5.25	4.73	
63	4.05	6.53	5.24	6.31	5.57	5.83	6.25	4.99	5.31	5.54	4.04	
64	5.81	5.28	5.20	5.59	5.32	6.29	5.61	6.65	5.24	5.56	6.71	
65	4.61	6.85	5.88	6.14	5.63	5.09	5.62	6.02	5.06	6.23	6.71	
66	5.50	4.84	5.08	5.79	5.03	5.12	5.01	6.11	7.25	5.30	5.59	
67	5.63	5.62	4.65	6.60	5.74	5.56	5.07	5.52	5.96	6.38	5.58	
68	4.80	5.57	7.02	6.00	6.05	4.56	6.48	5.00	6.03	5.26	5.57	
69	6.67	4.48	7.11	7.38	5.84	5.28	5.99	5.09	6.24	5.87	6.30	
70	5.92	6.54	5.72	5.98	6.64	6.58	4.97	7.26	5.44	5.64	5.61	
71	4.31	4.74	4.40	6.29	5.10	5.07	4.11	6.25	4.32	4.30	6.44	
72	7.24	5.43	6.89	5.13	4.91	5.35	4.11	5.93	6.62	5.18	5.49	
73	6.23	4.83	6.47	7.11	5.56	5.60	6.20	5.83	5.43	4.59	5.89	
74	7.16	5.56	5.59	5.29	5.72	5.61	5.35	5.81	7.61	4.93	7.02	
75	6.06	7.29	5.97	5.14	7.41	6.80	5.75	6.43	4.96	4.95	5.33	
Rep 1	3	4.92	5.08	4.39	5.79	5.42	5.84	5.08	6.02	4.68	6.68	6.33
	2	6.29	5.40	5.18	5.55	6.11	4.65	5.22	5.47	5.60	4.60	4.75
	3	4.72	4.87	5.19	6.63	4.85	4.44	5.49	5.65	7.47	5.19	5.18
	4	4.66	5.36	4.25	5.25	4.78	4.27	5.49	7.41	4.46	6.54	5.77
	5	4.40	4.79	5.76	4.85	5.22	5.46	4.82	4.85	5.94	5.65	4.36
	6	4.59	5.47	5.17	4.27	4.99	4.83	6.18	4.92	4.94	5.32	4.42
	7	5.10	5.08	4.79	4.31	5.03	7.08	5.38	7.28	5.78	5.03	7.05

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8	4.76	4.98	6.61	6.73	4.74	5.47	5.60	5.83	4.09	5.83	6.09
9	5.01	5.21	5.99	4.92	5.80	4.44	5.15	4.46	5.67	4.50	4.73
10	5.93	5.82	4.48	5.37	5.95	5.50	5.60	4.27	4.96	4.71	5.70
11	5.03	4.44	6.49	5.32	4.47	6.60	5.59	5.10	5.67	4.71	5.97
12	4.45	6.05	5.33	5.45	5.94	6.16	4.32	4.21	5.08	6.92	5.56
13	6.09	4.75	6.91	6.01	6.20	5.76	5.73	4.41	5.52	4.76	5.02
14	5.39	6.03	5.64	6.13	5.84	5.51	4.28	4.84	4.05	4.34	4.87
15	5.31	5.71	4.97	5.20	5.03	7.89	5.02	6.15	5.98	5.78	5.02
16	4.54	4.77	5.79	5.67	6.02	5.26	4.95	5.43	4.37	5.37	4.70
17	5.02	5.38	4.43	5.43	6.26	5.14	5.13	4.71	6.31	5.16	4.92
18	6.93	6.43	7.48	5.65	5.14	5.33	5.48	4.45	4.64	6.07	4.34
19	4.98	4.14	5.08	6.22	4.41	4.92	6.75	5.19	7.05	6.36	4.58
20	4.33	5.16	4.45	5.19	5.03	4.29	4.79	4.11	6.08	4.86	6.28
21	6.20	4.04	5.20	5.05	4.58	4.23	4.45	5.67	5.58	4.84	5.79
22	5.65	5.23	7.84	5.37	4.41	6.19	6.06	5.70	5.82	6.78	5.88
23	5.79	4.43	5.03	5.29	4.82	5.07	4.52	4.81	5.22	4.32	5.77
24	5.37	5.87	5.01	5.75	5.34	4.31	5.04	4.48	5.95	5.40	5.11
25	5.62	6.87	4.96	6.26	6.86	5.89	5.77	6.65	6.09	4.31	4.46
26	5.06	7.39	6.60	6.23	5.19	5.71	6.72	5.89	6.11	4.98	6.69
27	5.54	5.67	5.09	4.88	6.22	5.52	6.79	5.87	6.07	5.80	4.06
28	6.22	4.98	4.28	5.48	5.11	6.01	6.95	6.39	5.77	5.91	5.29
29	5.05	5.86	5.50	6.38	5.69	5.29	4.63	4.60	4.60	5.80	6.59
30	4.54	6.35	5.74	6.57	5.07	5.33	5.47	4.86	6.73	4.67	4.58
31	4.29	6.71	4.75	4.65	5.98	5.58	6.08	5.82	6.08	4.33	5.28
32	5.01	5.41	6.29	7.69	5.17	5.57	6.24	5.15	6.04	5.45	6.05
33	6.76	4.07	4.05	5.05	6.11	4.20	4.31	6.15	4.39	4.40	4.80
34	4.79	5.43	6.89	5.78	5.39	4.70	6.95	4.81	5.63	4.79	4.94
35	6.32	5.47	7.12	6.61	5.26	7.01	6.34	6.73	6.50	5.96	4.46
36	7.36	4.44	6.72	4.96	7.35	6.10	7.82	6.17	6.55	5.41	6.12
37	5.79	5.83	4.76	5.14	6.89	4.85	7.24	5.96	4.95	6.29	4.49
38	5.62	4.53	6.43	7.47	5.65	5.10	5.65	5.18	6.28	5.46	4.92
39	4.71	5.09	6.58	6.07	5.84	4.86	4.70	4.66	6.23	5.60	6.57
40	5.44	5.68	6.13	5.50	4.81	5.46	4.24	5.34	5.85	5.21	6.69
41	5.19	5.32	4.86	7.59	6.73	6.23	4.28	5.36	4.26	5.22	5.56
42	4.37	4.39	5.63	6.20	5.03	4.96	5.02	5.31	4.46	6.18	6.84
43	4.69	6.31	5.05	7.36	5.76	5.62	5.34	5.98	5.28	5.90	5.99
44	6.17	4.74	4.87	6.88	4.77	6.36	4.25	5.05	5.07	7.64	5.41
45	4.72	5.15	4.60	4.44	6.42	4.44	7.91	6.67	5.09	4.89	6.91
46	5.00	6.07	5.74	4.66	5.84	6.04	5.06	5.31	4.76	4.48	4.40
47	5.12	5.74	5.20	4.96	4.21	6.98	5.63	6.26	6.48	5.43	4.55
48	7.18	4.39	5.26	5.27	5.49	4.85	6.13	6.19	6.15	4.65	4.63
49	5.61	5.03	7.05	5.41	5.83	4.78	5.17	5.36	7.41	5.63	6.48
50	4.70	6.03	5.51	5.72	6.87	7.08	5.45	5.92	4.53	4.89	5.05
51	5.55	5.78	5.96	5.18	4.66	7.38	6.29	5.26	5.46	5.68	6.59
52	7.45	5.10	4.99	5.71	5.98	5.42	7.14	5.23	4.91	4.71	4.50
53	4.64	5.33	6.70	5.70	5.17	7.09	5.51	4.71	5.56	5.35	6.41
54	5.71	6.16	5.05	6.16	5.67	5.59	5.05	6.91	4.68	6.23	4.89
55	4.84	4.10	5.79	5.70	5.14	4.77	7.19	6.64	5.47	4.88	5.68
56	4.73	4.68	4.64	7.65	5.64	6.93	6.31	5.38	6.69	7.62	4.35
57	6.22	5.78	6.87	7.28	5.90	5.33	6.58	5.53	5.12	5.25	5.51
58	5.83	6.48	4.61	6.30	5.34	5.97	5.61	5.56	5.58	4.56	5.64
59	5.70	4.65	5.98	5.15	4.26	5.56	5.81	4.46	6.19	5.09	4.94
60	4.51	5.17	5.96	6.45	7.23	4.76	5.63	6.14	4.61	6.61	5.52
61	5.67	6.36	5.66	7.39	4.47	7.12	6.07	5.81	5.99	6.34	6.43
62	6.39	6.59	5.49	6.30	6.50	5.77	5.81	6.95	4.28	6.14	5.60
63	5.25	6.51	7.08	5.29	5.95	7.23	6.17	6.29	5.28	6.53	5.95

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64	5.92	6.70	5.27	6.74	5.56	7.51	4.98	5.27	6.93	6.65	5.83
65	6.55	7.93	6.51	5.09	5.62	4.89	5.13	5.42	4.52	4.29	5.13
66	6.07	5.19	4.10	7.45	6.34	5.64	7.31	4.74	7.15	5.00	5.04
67	6.51	5.94	5.09	7.80	6.02	6.01	5.18	5.50	4.80	6.23	6.60
68	6.09	6.68	6.33	6.10	5.81	5.86	5.72	5.58	4.75	6.20	4.88
69	6.51	5.24	5.84	6.48	7.69	4.36	6.29	6.50	5.57	4.72	4.59
70	6.46	5.58	5.83	6.48	6.23	5.66	6.02	5.95	5.87	5.80	4.45
71	5.91	5.84	5.31	4.54	4.91	7.12	5.11	6.76	5.08	4.50	6.12
72	7.70	5.30	6.19	5.48	5.90	4.38	4.75	6.78	4.54	5.12	5.07
73	6.81	7.92	7.28	6.24	4.83	4.74	5.51	4.82	7.68	5.24	6.97
74	4.90	4.53	6.04	4.98	4.67	6.36	7.58	5.74	5.88	6.45	5.71
75	6.85	5.20	5.08	6.82	5.58	5.09	6.08	5.70	6.67	5.83	7.62
Rep 4-	1	4.88	7.66	4.47	6.47	6.31	4.89	5.65	5.60	4.96	4.94
	2	4.58	4.90	4.34	4.88	5.43	4.82	4.36	5.17	4.30	6.16
	3	6.69	6.58	5.19	4.91	5.72	4.83	4.47	4.02	4.14	5.66
	4	4.74	5.88	4.33	6.13	4.44	4.39	4.60	5.31	5.28	4.94
	5	6.52	4.98	4.77	6.36	5.17	5.52	4.08	4.98	5.80	4.82
	6	6.25	5.09	5.70	4.86	5.29	4.66	6.23	6.33	4.83	4.43
	7	5.29	4.44	4.33	4.72	6.25	4.88	5.42	6.08	6.47	5.30
	8	4.39	5.26	5.76	4.02	5.62	6.00	5.60	4.03	5.23	6.23
	9	5.71	6.56	5.20	5.00	4.81	5.33	7.64	5.37	6.06	4.28
	10	7.59	5.93	4.31	5.02	4.76	5.19	4.67	6.73	4.13	5.44
	11	4.80	4.55	5.15	5.24	6.18	5.67	5.42	5.09	4.72	4.53
	12	6.05	5.94	6.20	5.10	4.84	4.48	4.50	4.76	4.08	5.99
	13	5.09	5.36	4.79	4.07	5.53	5.08	6.05	5.55	6.95	5.49
	14	5.58	4.73	5.75	4.61	5.67	4.53	4.96	4.31	4.82	4.14
	15	6.01	4.49	4.29	5.21	4.55	5.22	6.44	4.51	5.43	5.14
	16	4.29	4.87	7.45	4.57	4.13	5.45	5.03	4.31	4.20	4.72
	17	5.71	5.95	7.40	4.51	4.27	5.63	5.00	5.04	5.98	4.62
	18	5.55	4.96	4.73	4.36	4.52	5.66	6.47	5.54	4.77	6.55
	19	5.49	4.41	5.98	5.42	5.01	4.30	5.63	4.02	5.95	6.01
	20	5.10	4.97	5.41	4.77	6.25	4.79	4.31	4.12	4.31	5.78
	21	5.07	5.87	5.21	5.99	6.71	5.86	4.40	4.34	6.16	5.29
	22	5.70	4.78	6.38	5.83	5.84	5.61	4.91	4.57	4.92	4.46
	23	6.41	5.33	5.91	6.41	6.24	6.30	4.39	5.51	4.62	4.34
	24	4.65	4.93	4.84	5.20	5.46	4.08	5.54	4.88	5.02	5.06
	25	5.44	5.67	5.46	6.39	5.61	4.81	5.95	4.61	4.72	7.70
	26	6.46	6.72	5.52	5.73	5.62	4.81	5.00	5.68	5.15	5.18
	27	5.01	5.72	4.96	5.29	5.76	5.24	5.96	5.52	4.83	7.28
	28	4.18	6.54	4.66	5.57	4.21	5.04	5.25	5.08	6.38	6.28
	29	4.98	5.73	6.67	4.40	7.05	4.64	5.64	6.08	6.42	6.13
	30	4.20	4.94	6.76	5.86	5.11	5.62	4.67	5.54	6.09	6.56
	31	5.91	5.55	4.80	4.80	5.19	5.75	6.81	5.92	5.49	6.02
	32	5.95	5.79	5.54	6.41	6.79	4.35	5.33	5.24	4.76	4.76
	33	6.60	5.43	5.23	6.54	5.33	6.94	7.28	5.06	5.47	5.21
	34	6.51	4.63	6.37	5.87	4.20	4.93	5.49	4.31	5.14	5.00
	35	5.29	5.89	4.71	5.63	6.28	4.11	4.62	6.38	5.63	5.18
	36	4.98	5.95	4.22	5.96	4.23	5.31	5.13	5.73	4.92	5.43
	37	5.51	4.97	4.46	5.21	5.67	4.17	5.67	4.55	4.52	5.91
	38	5.58	6.45	6.55	6.63	5.37	6.45	7.84	6.30	6.88	5.88
	39	4.83	4.47	5.27	5.03	6.41	6.51	4.53	4.90	6.81	5.43
	40	5.20	4.32	6.61	4.33	5.58	6.30	5.20	5.27	6.38	6.99
	41	5.30	4.05	4.63	5.90	5.59	5.46	5.68	6.65	4.60	5.84
	42	4.40	4.26	5.43	5.87	5.07	4.70	4.32	5.89	4.56	7.22
	43	5.86	6.93	7.73	6.79	5.65	5.94	5.00	5.05	5.39	5.88
	44	5.41	7.18	5.90	6.48	5.76	4.70	5.98	4.98	5.59	4.47

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45	5.29	5.26	5.82	7.04	4.22	5.59	5.69	6.28	4.78	4.66	5.31
46	4.34	4.97	4.15	4.77	4.64	5.12	4.56	5.85	5.02	4.63	4.38
47	4.43	5.47	5.11	4.98	4.64	4.59	5.17	4.61	4.83	6.19	5.13
48	6.43	5.96	5.78	4.83	5.83	6.22	6.57	4.53	5.94	7.21	7.63
49	4.75	6.82	4.27	6.84	4.81	6.60	4.92	5.28	5.04	5.13	5.26
50	4.84	4.64	6.74	5.53	5.24	4.72	7.24	4.71	5.43	5.91	5.38
51	6.09	5.38	5.27	6.88	6.33	6.46	6.05	4.33	6.33	7.43	5.58
52	6.36	4.31	4.57	4.57	6.04	4.90	4.04	7.16	7.13	6.08	4.62
53	5.35	4.27	6.05	5.45	6.39	6.24	5.29	5.09	5.39	5.02	5.94
54	4.99	4.75	4.88	6.06	6.08	4.40	6.05	4.50	4.53	4.48	5.02
55	4.42	5.30	5.03	6.62	4.37	7.13	6.00	5.52	5.77	5.27	5.46
56	4.55	5.71	5.24	7.95	7.64	7.10	4.60	5.88	5.63	7.07	5.46
57	5.52	4.60	4.74	4.98	5.08	6.03	4.94	6.41	6.55	6.43	5.65
58	5.93	5.05	6.00	5.16	5.07	6.05	4.81	4.48	5.67	5.81	6.18
59	5.20	6.37	5.01	5.02	4.74	6.55	4.25	4.69	4.29	5.63	6.64
60	5.78	6.50	5.10	6.40	4.67	6.36	6.60	4.61	4.88	6.10	5.22
61	7.08	5.90	7.56	6.85	6.03	7.13	4.56	5.49	4.43	5.84	4.19
62	6.91	5.80	5.89	4.67	4.60	6.50	6.51	5.38	5.33	5.48	6.67
63	6.92	4.58	6.96	5.57	6.11	4.49	6.06	5.46	4.44	7.14	6.61
64	6.00	5.40	7.17	5.89	5.98	5.03	6.26	7.20	4.91	7.63	7.50
65	7.09	5.88	4.68	5.79	7.13	5.60	5.74	4.71	4.57	5.07	6.65
66	6.36	5.12	6.59	7.27	5.06	5.90	6.42	5.42	4.96	6.89	7.07
67	7.44	5.58	5.35	5.64	4.94	5.17	5.91	5.01	6.89	5.51	6.57
68	6.70	4.63	7.92	5.24	5.97	7.12	5.82	5.83	5.65	5.26	6.05
69	4.87	4.38	6.11	5.89	5.74	5.24	6.05	4.15	7.05	5.07	4.65
70	5.87	5.15	5.57	5.26	6.56	5.48	5.36	6.68	5.66	6.50	5.34
71	4.68	4.63	4.36	5.70	4.84	4.51	5.89	5.28	5.11	5.41	4.25
72	4.72	6.87	5.56	6.27	5.74	5.53	5.32	5.33	5.68	5.43	5.78
73	6.53	6.03	5.60	6.58	5.95	4.53	5.94	5.12	6.61	6.33	5.07
74	5.96	7.81	5.29	4.49	4.70	4.71	6.45	6.03	6.86	6.25	5.38
75	6.95	6.83	4.87	5.28	5.85	5.18	6.60	5.18	4.84	5.65	5.48

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mean	5.56	5.62	5.71	5.72	5.58	5.76	5.76	5.58	5.70	5.63
min	3.98	4.03	4.2	4.15	4.03	4.12	4.15	4.13	3.44	4.3
max	7.98	8.11	8.06	8.06	7.95	7.83	8.09	7.77	8.28	8.29
stdev	0.82	0.81	0.86	0.85	0.79	0.83	0.88	0.79	0.86	0.81
N	277	280	273	270	261	284	275	284	280	277

Cage #s:	13,22,25,43	5,15,24, 35	2,11,30,37	3,17,23,34	4,18,27,42	14,19,26,41	1,9,20,38	16,28,33,44	8,10,21,39	6,12,31,40
	<u>Sta 1</u>	<u>Sta 2</u>	<u>Sta 3</u>	<u>Sta 4</u>	<u>Sta 5</u>	<u>Sta 6</u>	<u>Sta 7</u>	<u>Sta 8</u>	<u>Sta 9</u>	<u>Sta 10</u>
Rep 1 - 1	4.88	5.78		6.57	7.95	6.84	7.60	4.90	6.32	5.92
2	5.97	6.41	4.38	5.41	7.50	5.49	5.09	6.25	6.00	5.09
3	4.93	5.65	4.98	5.35	5.92	5.16	6.06	7.32	6.06	6.63
4	5.96	5.66	6.51	6.98	6.34	6.29	4.90	4.60	5.78	4.99
5	5.32	4.58	5.94	6.63	5.04	4.71	4.70	4.97	5.91	6.00
6	4.58	6.29	4.90	4.48	5.43		4.73		3.44	7.56
7	6.39		7.37	5.44	6.53	6.75		4.35	6.55	4.83
8	7.98	4.53	4.81	5.38	5.32	6.59	4.45	6.54	5.19	5.56
9	4.12	4.91	6.18	4.29	5.58	5.18	5.33	5.21	5.92	4.82
10	5.95	5.86	4.85	4.59	5.77	5.11	5.11	6.16	8.28	5.07
11	4.68	5.50	5.16	4.84	6.17	5.36	5.56	5.91	6.34	5.83
12	6.05	5.21	4.59	4.87	4.18	5.04	7.88	6.11	4.83	4.56
13	4.61	6.01	4.68	5.04	4.61		4.40	5.39		4.87
14	4.29	5.73	6.03	4.64	4.95	5.20	5.14	5.69	4.94	5.06
15	5.42		5.46	5.38	4.58	4.92	4.99	4.62	6.40	5.26
16		4.76	7.13	6.28	6.37	4.50	5.40	4.32	6.09	4.90
17		5.68	5.07	5.26	4.73	6.70	5.08	5.62	4.85	6.30
18	5.79	5.34	4.68	4.90	5.18	5.19	4.30	5.13	4.71	5.80
19	6.57		7.03	6.97	7.54	6.73	6.18	6.67	5.71	7.22
20	4.68	4.55	4.46	4.90	4.59	5.54	5.11	5.28	6.11	5.05
21	5.97	6.08	5.27	6.28	5.97	5.60	5.33	5.38	5.18	5.31
22	4.83		6.05	5.96	5.39			4.68	5.14	4.98
23	6.00	6.19	5.19	5.52	4.94	6.06	5.95	6.15	5.84	5.69
24	5.46	5.19	5.00	5.76	4.71	5.79	5.66	4.93	6.00	4.42
25	4.63	7.31	5.32	5.29	6.62	4.86	5.71	6.00		4.34
26	6.79	5.24	7.75	5.73	5.78	5.77	7.33	6.39	5.27	4.58
27	6.36	5.28	5.62	5.59	6.30	5.78		5.70	6.64	6.16
28	7.11	5.81	6.68	7.29	6.72		7.65	6.51	5.82	6.12
29	4.02	5.67	5.58	4.79		4.31		5.01	5.10	5.76
30		7.03	6.19	5.43	5.47	5.42	5.85	6.07	5.16	6.33
31	4.72	4.82	4.67	5.76	6.33	4.64	6.83	4.28	5.16	5.59
32	4.47	4.28	5.81	5.04	4.72	4.32	6.54	5.52	5.27	4.64
33	4.94	6.68		5.33	4.82	5.33	4.68	4.96	4.66	4.89
34	4.78	4.34	4.58	4.70		4.63	4.87	5.54	4.29	4.33
35	5.76	5.33	5.15	4.62	5.41	6.85	5.13	4.65	7.07	7.33
36	4.93	5.70	6.86	5.09	7.66	7.83	6.59	4.89	6.08	4.62
37	5.28	5.40	4.89	6.20	4.77	4.78	5.80	5.53	4.53	4.92
38	4.67	4.51	6.33	5.80	5.87	6.21	5.58	5.12	5.35	4.67
39	4.36	5.67	5.65		6.86	6.44	6.68	5.25	5.43	6.49
40	5.71	5.37	5.96	5.46	6.06	5.61		6.32	5.69	5.96
41	6.15	5.18	6.31	5.02	4.43	5.86	7.45	6.30	4.40	4.99
42	5.77	6.66	6.19	6.41	5.44	6.83	5.56	5.32	6.07	4.57
43		6.28	5.55	5.63	5.22	4.33	5.56		6.66	4.47
44	4.70	4.48	5.35	4.44	4.88	6.75	5.40	4.32	6.21	5.89
45	4.56		4.71	5.97	5.76	7.58	6.37	4.68	5.36	6.87
46	6.03	5.58	5.47	5.62	4.29	4.87	6.72	5.30	4.83	5.31
47	6.53	5.53		4.62	5.30	5.24	5.80	6.18	6.69	

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48	5.13	4.91	5.47	4.72	5.07	6.77	4.68	4.64	7.08	4.70
49		4.86	5.50	6.52	5.75	5.03	5.72	5.83	6.39	5.79
50		5.33	5.29	4.51	5.28	6.50	4.78	5.96	5.86	
51	4.72	6.54	5.62	6.59		6.59	7.59	6.34	4.52	
52	6.47	5.98	4.44	6.00	5.89	6.23	4.86	7.03	6.23	5.97
53		5.39		5.52	4.56	6.06	5.46	4.43	6.01	5.17
54		6.53	5.76	5.66	5.45	4.82	6.19	5.71	7.98	6.07
55	4.09	5.19	6.53	5.14	5.32	7.06	4.54	6.70	6.61	4.97
56	5.39	5.48	4.89	4.93	5.23	5.66	5.92	4.99	5.22	5.02
57	4.34	6.59	5.99	6.09	6.20	6.71	6.24	5.80	5.46	4.94
58	5.35	4.77	4.96	6.21	6.09	5.34		6.54	7.38	4.59
59	6.32	7.35	5.91		6.93	6.88	5.40	6.81	6.04	4.71
60	6.28	5.10	6.22	5.10	5.69		5.68		6.95	5.09
61		5.70	5.00	4.43	4.72	7.46	4.63	4.54	6.80	6.32
62	5.94	5.93	5.06	4.65	5.23	6.61	6.91	4.43	6.81	6.00
63	6.36	6.29	6.68	7.18	5.97	6.15	7.08	5.34	5.76	6.52
64	6.76	5.36	6.96	4.85	5.29	6.42	6.22	5.73	6.36	5.71
65	7.27	6.29	4.85	6.09	4.39	4.40	6.44	5.55		5.36
66	5.22	5.43	4.46	4.41	5.25	6.80	4.86	5.46	5.71	5.19
67	7.23	6.99	6.75	5.68	6.08	6.74	7.05		5.21	6.17
68		8.11	7.84		7.10	6.15	8.09	5.73	6.32	8.29
69	6.66	5.95	6.65	5.51	4.32	6.34	5.52	6.33		5.67
70		6.37	6.12	6.74	5.97	5.18	5.87	7.41	6.20	5.50
71	4.17	4.85	4.58	4.62	5.73	6.54		5.08	5.25	4.30
72	5.61	8.06	6.05	5.70	6.08	6.13	4.84	4.89	5.71	6.25
73	6.30	4.72	6.11	6.38	6.58	6.44	5.41	5.87	7.20	6.55
74	5.00	5.02	5.14	5.08	4.72	6.02	5.79	6.24	5.77	6.53
75	5.37	6.71	5.14	6.32	5.97	6.37	5.42	6.04	7.07	6.70
Rep 2 1	4.85	5.75	5.36	4.61		6.60	6.07	6.01	7.01	5.02
2	5.68	6.60	5.52	6.62	5.17	5.47	5.86	5.18	6.25	
3	5.78	5.54	6.48	6.54	6.98	4.67	5.40	4.53		5.89
4	4.95	5.37	6.81	4.41	4.80	6.31	4.49	7.77	5.08	6.49
5	5.63	7.51	6.63		5.88	5.28	6.21	6.68	4.88	5.97
6	5.15	4.62	5.80		4.95	4.87	5.93	5.83	5.43	5.34
7	5.94	5.89	7.29		6.01	5.03	6.24	6.67	5.98	4.92
8	5.60	4.88	6.22	5.97	4.78	6.00	5.52	4.94	5.09	4.67
9	5.49	5.51	6.01	5.16	5.13	5.61	6.47	4.22	4.98	4.95
10	4.54	6.23	7.18	4.73	4.70	6.64	6.37		5.71	6.37
11	5.69	6.62	5.92		4.33	5.70	4.44	5.04	5.45	5.94
12	5.34	4.63		4.24	6.20	6.68	5.35	7.03	4.94	5.27
13	5.22	6.65	5.29	7.46		5.38	6.17	6.08	6.54	5.41
14	4.70	5.37	4.90	4.32	4.88	6.82	4.74	4.80	4.80	5.85
15	4.99	4.89		5.55	4.74	5.05	7.22	5.72	5.69	4.94
16	5.43	6.22	5.35	5.43	6.45	5.76	4.41	5.64	4.37	4.67
17	5.34	6.31	4.74	5.59	4.60	6.27	5.03	4.38	4.68	4.54
18		5.01	4.52	4.77	4.54	4.90	4.67	4.91	4.87	4.99
19	5.55	7.11		5.70		7.34	6.79		7.74	6.53
20	4.73	5.91		5.46	4.27	5.63	4.35	4.52	5.35	5.15
21	4.70	5.96	6.64	4.38	4.59	5.58		4.66	6.09	4.92
22	5.91	4.52	4.75	5.90	4.33	6.26		4.80	4.91	5.31
23	4.86	4.53	4.57	5.64	4.75	4.48	6.50	5.14	4.96	6.45
24	5.93	6.41	5.68	5.31	5.44	5.71	6.12	7.18		5.37
25	5.39	6.33	4.86	4.22	5.13	4.23	6.30	4.73	5.13	6.01
26	7.04	5.27	7.29	7.44	5.53	5.79	5.38	4.99	5.70	6.23
27	6.02	5.49	5.82		4.51	6.78	5.99	5.34	5.56	6.63
28	7.07	6.66	7.11	5.62	6.02	5.37	5.69		5.32	5.98

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29	5.31	4.69	5.09	4.50	4.62	4.48	5.02	6.09	5.24	5.47
30	5.46	6.43	6.17	4.71	6.65	7.43	6.12	4.72		4.96
31	6.53	5.12	5.15	7.20	5.34	5.36	7.39	5.81	5.43	4.95
32		5.79	4.20	4.47		6.02	6.60	6.71	4.26	5.03
33	4.47	4.32	5.27	4.71	5.56	5.21	5.29	4.63	6.56	5.86
34	5.21	6.04	5.46	5.19	5.44	6.47	4.79	6.01	4.59	6.29
35	5.22	6.40	5.38	5.17	7.33	5.84	5.16	5.62	6.91	6.72
36	4.25	5.75	5.35		5.34	5.46	5.91	5.29	7.36	6.59
37	6.62		5.40	7.91	6.03	5.12	5.69	5.46	5.28	5.47
38	6.77	5.27	6.10	5.10	5.79		5.50	6.33	5.76	4.77
39	6.03	4.49	5.10	5.39	6.78	4.96	4.98	6.80	5.62	
40	5.21	6.40	5.81	6.68	4.91	6.27	6.54	4.63	6.41	6.92
41	4.62	5.72	4.82	5.89	4.59	4.81	6.69	4.90	5.99	7.06
42	5.91	6.77	6.24	6.26	5.58	6.13	6.27	5.16	4.43	5.73
43	6.40	5.99			5.50	5.08		5.80	5.02	
44	4.74		5.09	6.28	6.05	4.90	6.19	4.76	5.53	6.02
45	5.09	4.96	5.48	5.94	4.65	5.76	4.74	5.18	5.22	5.85
46		4.91	5.48	5.30	5.51	5.98	4.86	5.80	4.14	4.37
47	5.85		4.42	4.87	5.08	5.86	6.14	6.60	4.58	4.48
48	5.05	4.42	4.76	5.59	5.69	5.28	5.19	7.45	6.20	4.78
49	7.01	6.66	4.55	5.16	4.95	5.84	4.23	6.64	5.27	5.27
50	4.77	5.04		6.13	5.11	7.54	4.32	4.34	4.20	6.09
51	5.84	5.46	6.34		5.69	6.73	5.15	6.67	5.11	6.01
52	5.32	4.86	6.58	6.70	5.81	5.71	7.00	5.43	6.31	6.82
53	5.02	5.26		6.39	5.84	7.30	7.57	5.79	6.82	6.19
54	4.78	6.40	7.23	6.56	6.15	5.48		4.74	6.67	5.27
55	6.40	5.70	5.44	5.05	5.72	5.05	4.92		6.29	6.96
56	6.59	5.06	4.98	5.61			5.68	6.00	5.00	4.92
57	6.88	6.55	6.38		7.62	6.82	5.77	5.88	5.28	6.70
58	6.16	4.23	5.16	5.55	4.91	5.06	6.71	6.60	7.18	
59	6.70		5.42	4.77	5.97	6.87		5.30	4.50	5.46
60	5.22	5.24	6.59	7.17	6.40	6.17	7.98	5.74	6.17	7.21
61	5.26	6.32	6.26	5.28	5.91	6.50	5.59	6.24	5.58	
62	5.71	4.67	4.76	4.78	5.51	5.85	7.65	5.93	4.63	
63	3.98	6.29	5.62	6.43	5.39	6.17	6.43	5.22		5.68
64	5.83	5.36	5.21	5.70	5.37	6.67	5.86	6.87	5.57	
65	4.64	6.98	6.18	6.26	5.65	5.38	5.89	6.02	5.39	6.43
66	5.58	5.08	5.16	5.93	5.15	5.30	5.50	6.30	7.25	5.35
67	5.62	5.73	5.09	6.74	5.87	5.70	5.27	5.66	6.05	6.53
68	4.90	5.77	7.22		6.15	4.65		4.98	6.18	5.41
69	6.65	4.52	7.32	7.24	5.97	5.41	6.14	5.22	6.38	5.98
70	5.95	6.62		6.13	6.38	6.61	5.13	7.33	5.54	5.80
71	4.35	4.93		6.38	5.22	5.15	4.33	6.39	4.58	4.52
72	7.47	5.53	7.06	5.19	5.06	5.62	4.29	6.01	6.82	5.26
73	6.14	4.94	6.68	7.22	5.68	5.76	6.41	5.94	5.65	4.76
74	7.31	5.70	5.69	5.38	5.81	5.82	5.60	5.88	7.65	5.06
75	6.21	7.49	6.29	5.21	7.33	7.18	5.92	6.45	5.17	5.02
Rep 3 1	4.91	5.15		6.04	5.04	5.88		5.98	4.80	6.68
2	6.09	5.51	5.31	5.94	6.10	4.78	5.51	5.61	5.83	4.68
3	4.79	4.89	5.29	6.80		4.83	5.81	5.02	7.54	5.31
4	4.72	5.46	4.34	5.46	4.85	4.68	5.63	7.62		6.53
5	4.43	4.80	5.99		5.28	5.84	4.95	5.03	6.24	5.76
6	4.60	5.60	5.38	4.55	5.12	5.07	6.25	5.35	5.30	5.51
7	5.05	4.93	4.84	4.36	5.01	7.23	5.59	7.51	6.09	5.10
8	4.88	5.13	6.79	6.91	4.83	5.69	5.74	5.96	4.67	6.00
9	5.09	5.29	6.19	5.07	5.88	4.68	5.38	4.64	5.77	

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10	6.00	6.11	4.72	5.64	6.10	5.76	5.80	4.53	5.16	4.85
11	5.04	4.63	6.83	5.50	4.63	6.88	5.77	5.27	6.12	4.86
12	4.44	6.13		5.66	5.94	6.43	4.61	4.40	5.29	
13	6.17	4.84	7.08	6.30	6.25	6.08	5.81	4.69	5.80	4.81
14	5.50	6.20	5.79	6.28		5.76	4.39	4.98	4.41	4.61
15	5.33	5.96	5.28	5.18	5.00			6.21	6.23	5.89
16	4.72	4.83	5.91	5.64	5.93	5.49		5.48	4.53	5.45
17	5.08	5.55	4.77	5.51	5.97	5.46	5.30	4.82	6.55	5.36
18	7.04	6.48	7.53	5.82		5.62	5.68	4.50	4.71	6.26
19	4.99	4.40	5.05	6.45		5.22	6.80	5.36	7.26	6.44
20	4.41	5.42	4.53	5.37	5.03	4.55	5.08	4.23	6.30	5.03
21		4.16			4.53	4.12		5.79	5.75	4.97
22	5.70	5.20		5.60		6.16	6.14	5.74	6.04	6.94
23		4.77	5.27	5.44	4.84	5.63		4.88	5.41	4.48
24	5.60	6.23	5.39	5.90	5.38		5.21	4.48	5.96	5.48
25	5.68	7.09		6.42	6.59	6.14	5.76	6.81	6.34	4.47
26	5.16		6.81	6.34		5.77		6.04		5.08
27	5.62	5.84	5.28	5.17	6.19	5.80	7.22	6.05	6.43	5.88
28	6.17	5.05	4.47	5.68		6.16	6.84	6.59		
29	5.18	5.98	5.77	6.50		5.53	5.03	4.80	4.99	5.96
30	4.41		5.84	6.86	5.09	5.53	5.68	4.96		4.79
31	4.27	6.77		4.86	5.97	5.79	6.29	6.08	6.14	4.59
32	5.08	5.46	6.43	7.87	5.12	5.83	6.26	5.26	6.21	5.54
33	6.85	4.14	4.37	5.09	6.15	4.54	4.57	6.22	4.78	4.52
34	4.83	5.57	7.08	5.88	5.37	4.76	7.27	5.08	5.90	4.75
35	6.28	5.59	7.27	6.83	5.25	7.24		6.94	6.80	6.04
36		4.53		5.14	7.43	6.36	7.94	6.35	6.89	5.64
37	5.92	6.10	4.92	5.42	6.98		7.52	6.13	5.33	6.54
38	5.69	4.72	6.59	7.73		5.24	5.88	5.31	6.19	5.58
39		5.26	6.70	6.31	6.12	5.34	4.80	4.80	6.35	5.75
40	5.50	5.68	6.48	5.63	4.76		4.64	5.45	5.97	5.47
41	5.23	5.51	5.15	7.72	6.71	6.38	4.52	5.56	4.43	5.39
42	4.51	4.64	5.70		4.99	5.41	5.14	5.43	4.69	6.33
43	4.74	6.48	5.30	7.51	5.67	5.79	5.39	6.10	5.43	5.95
44	6.17	4.82	4.93	7.01	4.63	6.60	4.40	5.11	5.15	7.70
45	4.74	5.26	4.98	4.69	6.57	4.76	8.09	6.95	5.13	5.03
46	5.25	6.13	5.87	4.93	5.84	6.44	5.31	5.55	4.89	4.58
47	4.94	5.97	5.40			7.22	5.61			5.49
48	7.14	4.59	5.46	5.51	5.58	5.22	6.24	6.34	6.33	4.80
49	5.67	5.24	7.23	5.59	5.83	5.09	5.20	5.51	7.52	5.78
50	4.73	6.11	5.71	5.90		7.24	5.56	6.09	4.55	4.99
51	5.49	5.84	6.04	5.27		7.47		5.58	5.69	5.78
52	7.38	5.16	5.15	5.81	6.12	5.58	7.29	5.38	5.11	4.82
53	4.68	5.40	6.93			7.29	5.56	4.95	5.68	5.49
54	5.78	6.26		6.34	5.65		5.23	7.16	4.84	6.42
55	4.87	4.27	5.82	5.76	5.34	5.06	7.36	6.72	5.63	5.05
56	4.82	5.04	4.97	7.79	5.87	7.31	6.46	5.49	6.85	7.78
57	6.44	5.83	7.02	7.26	6.10	5.53	6.74	5.62	5.42	
58	5.87	6.52	4.98	6.43	5.42	6.44	5.68	5.67	5.61	4.78
59	5.85	4.87	6.11	5.22	4.27	5.71	5.92	4.68	6.39	5.15
60	4.55	5.22	6.08	6.00	7.20	4.90	5.84	6.08	4.80	6.78
61	5.50	6.49	5.72	7.45	4.45	7.17	6.25	5.92		6.48
62	6.49		5.55	6.42	6.60	5.92	6.07	7.16	4.55	6.41
63	5.30	6.63	7.38	5.47	5.79	7.42	6.32	6.51	5.47	6.57
64	6.23	6.79	5.47	6.73	5.41	7.77	5.20	5.25	7.21	6.86
65	6.50	7.92	6.71	5.23	5.57	5.00	5.40	5.56	4.78	

**1997 Cannelton Clam Biomonitoring Study
End-of-Test Whole-Animal Wet-Weights (g) by Station**

66	6.08	5.18	4.32	7.62		7.61	4.94	7.46	5.30		
67	6.43	5.87	4.84	7.88		6.16	5.30	5.47	4.93	6.28	
68	5.94	6.76	6.47	6.13		6.10	5.78	5.70	4.88	6.33	
69	6.37	5.39	5.99	6.55	7.76	4.56		6.81	5.75	4.91	
70	6.13	5.70	5.84		6.24	5.82	6.31	6.09	6.02	6.04	
71	6.05	5.99	5.41	4.80	4.96	7.33	5.39	6.94	5.39	4.69	
72	7.72	5.54	6.34	5.44	5.84	4.54			4.68	5.35	
73	6.79	8.05	7.38	6.33	4.93	5.11	5.56	4.93	7.93	5.34	
74	4.96	4.67	6.05	5.08	4.69	6.62	7.75	5.92	5.98	6.51	
75	6.80			7.00		5.20	6.36	5.76	6.86	5.87	
Rep 4-	1	4.96	7.54		6.56	6.13	5.13	5.70	5.67	5.15	4.86
	2	4.60	5.11	4.57	5.01	5.65	5.03	4.62	5.32	4.55	6.46
	3	6.69		5.34	5.69	5.69	5.18	4.69	4.15	4.51	5.84
	4	4.81	6.00	4.47		4.56	4.70	4.86		5.64	4.90
	5	6.46	5.20	5.19	6.28	5.34	5.84	4.15	5.14	5.95	4.88
	6	6.03	5.23	5.88	4.96	5.48	5.10	6.40	6.34	5.01	4.76
	7	5.26		4.49	4.82	6.25	5.17	5.53	6.23	6.64	5.41
	8	4.52	5.35	6.13	4.15	5.67	6.38	5.76	4.39	5.48	6.36
	9	5.78	6.53	5.63	4.98	4.99	5.35	7.76	5.65	6.19	4.40
	10	7.60	5.93	4.56	5.16		5.44	5.01		4.33	5.65
	11	4.91	4.72	5.40	5.39	6.17		5.63	5.39	4.90	4.82
	12	6.01	6.04	6.47	5.50		4.75	4.88	4.85	4.31	6.08
	13	5.09	5.55		4.35	4.98	5.43	6.09	5.68	7.10	5.54
	14	5.61	5.04	5.95	5.04	5.87	4.94	5.28	4.69	5.00	4.35
	15	5.94	4.52	4.59	5.57	4.63	5.63	6.69	4.63	5.61	5.25
	16	4.33	4.99	7.66	4.77	4.03	5.68	5.26	4.54	4.39	4.86
	17	5.73	6.07	7.55	4.74	4.33	5.83	5.30	5.14	6.25	4.83
	18	5.66	5.03	5.00		4.57	5.83	6.63	5.79	5.08	6.57
	19	5.53	4.56	6.12	5.56	5.12	4.55	5.71	4.13	6.18	6.09
	20	5.09	5.01	5.60	4.87	6.35	4.94	4.80	4.18	4.44	5.90
	21	5.23	5.82	5.54		6.75	6.27	4.43	4.46	6.18	5.30
	22	5.72	5.03	6.56	6.09		5.93	5.09	4.81	5.24	4.54
	23	6.23	5.35	5.99	6.58		6.46	4.79	5.51	4.77	4.43
	24	4.86	4.95	5.11	5.29	5.58	4.30	5.98	5.12		5.10
	25		5.78	5.68	6.35		5.18	5.74	4.65	4.96	7.78
	26	6.58	6.83	5.45	5.78	5.74	5.19	5.20	5.70	5.24	
	27	5.03	5.92	5.13	5.43	5.84	5.41	5.97	5.66	4.98	7.35
	28	4.21	6.64	4.58		4.27	5.07	5.50	5.09		
	29	4.95	5.95	6.72	4.78	7.05	4.61	5.91	6.21	6.52	
	30	4.27	4.96	6.87	5.98	5.20	5.91	4.77	5.80	6.26	6.62
	31	5.84		5.00	5.03	5.22	5.87	7.27	6.06	5.61	
	32	5.97	5.78	5.69	6.53	6.93	4.47	5.46	5.37	4.98	4.95
	33	6.64	5.50	5.35	6.55	5.40	7.04	7.47	5.19	5.59	5.30
	34		4.73	6.43	6.04	4.10	5.04	5.66	4.39	5.41	5.31
	35	5.36	6.01	4.85	5.74		4.40	4.97	6.48	5.99	5.17
	36	5.13	5.99	4.33	6.08		5.62	5.44		5.24	
	37	5.64	5.07	4.86	5.55	5.78	4.34	5.97	4.80	4.83	6.15
	38	5.63	6.53	6.80		5.48	6.70	8.02	6.72	7.12	6.02
	39	4.94	4.64	5.31	5.17	6.52	6.63	4.68	5.16	7.16	5.55
	40	5.17	4.40	6.74			6.41	5.47	5.43		
	41	5.29	4.03	4.91	6.06		5.37	6.17	6.77	5.04	5.95
	42	4.51	4.51		5.47	5.06	4.89	4.33	6.05	4.88	7.44
	43	5.89	7.10	7.90	6.83	5.64	6.07	5.28	5.17	5.73	6.01
	44	5.52	6.79	5.90		5.81	5.18	6.26	5.16	5.89	4.56
	45	5.42	5.48	5.91	7.22	4.32	6.03	6.03	6.65	5.06	4.93
	46	4.37	5.19	4.32	5.02	4.63	5.29	4.66	5.99	5.21	4.83

1997 Cannelton Clam Biomonitoring Study
End-of-Test Whole-Animal Wet-Weights (g) by Station

47		5.24	5.33	5.07		4.89	5.38	4.91	5.07	6.27
48		6.19	5.98	5.01	5.80	6.37	6.79	4.75	6.15	
49	4.81	6.94	4.26	6.92		6.95	5.15	5.52		5.39
50	4.97	4.78	7.02	5.61	5.34	4.91		4.93	5.51	6.36
51	6.11		5.42	6.94	6.47	6.51	6.09		6.55	7.57
52	6.40	4.44	4.73	4.66	6.16	4.93	4.22	7.21	7.37	6.17
53	5.29		6.17	5.54	6.41	6.39	5.41		5.54	5.17
54	5.10		5.07		6.16	4.71	6.19	4.78	4.87	4.71
55	4.42	5.46	5.14	6.61	4.36	7.30	6.06	5.63	6.01	5.35
56	4.59	5.80	5.46	8.06	7.78		4.89	5.94	5.98	7.28
57	5.62	4.72	4.64	5.25	5.13	6.23	5.11	6.61	6.74	6.46
58	6.04	5.08	6.16			6.21	5.06	4.64	5.83	5.85
59	5.35	6.49	5.25	5.18	4.75	6.54	4.33	4.80	4.58	5.67
60	5.89	6.49	5.19	6.43	4.77	6.62	6.75	4.62	5.00	6.22
61	7.18	5.89	7.59	6.90	6.05	7.40	4.68	5.62	4.59	6.05
62	6.84	5.81	5.98	4.71	4.65	6.45	6.68		5.57	5.66
63	6.74	4.68	7.04		6.17	4.72	6.25	5.50	4.79	7.29
64	5.61	5.43	7.21	5.98	5.84	5.14	6.38	7.16		7.70
65	7.03	6.01		5.79	7.09	6.01	5.84	4.74	4.97	5.21
66		5.04	6.65	7.40	5.15	5.82	6.53	5.42	5.18	7.08
67	7.40	5.70	5.33	5.66	4.93	5.19		4.88	6.97	5.48
68	6.64	4.75	8.06	5.28	6.00	6.94	5.79	5.84	5.88	5.36
69	4.90	4.48		6.02		5.26	6.30	4.16	7.22	5.11
70	5.88	5.26	5.66	5.31	6.59	5.54	5.55	6.83	5.92	6.60
71	4.70	4.80	4.49	5.74	4.97	4.62	6.12	5.31	5.40	5.54
72	4.82		5.67		5.79		5.63	5.25	5.95	5.73
73	6.52	6.14	5.60	6.80	5.78	4.78	6.06	5.17	6.92	
74	5.89	7.84	5.46	4.61		4.95	6.69	5.99	7.28	6.41
75	6.94	6.92	4.88	5.27	5.92	5.32	6.64	5.18		5.75

1997 Cannelton Clam Biomonitoring Study Change in Whole-Animal Wet-Weight (g) by Station

mean	0.04	0.11	0.18	0.14	0.08	0.22	0.19	0.15	0.21	0.15
min	-0.39	-0.6	-0.25	-0.45	-0.55	-0.18	-0.21	-0.63	-0.58	-0.15
max	0.31	0.36	0.57	0.78	0.39	0.56	0.55	0.7	0.58	0.46
stdev	0.09	0.11	0.12	0.12	0.11	0.12	0.12	0.13	0.11	0.09
N	277	280	273	270	261	284	275	284	280	277

Cage #s:	13,22,25,43	5,15,24,35	2,11,30,37	3,17,23,34	4,18,27,42	14,19,26,41	1,9,20,38	16,28,33,44	8,10,21,39	6,12,31,40
	<u>Sta 1</u>	<u>Sta 2</u>	<u>Sta 3</u>	<u>Sta 4</u>	<u>Sta 5</u>	<u>Sta 6</u>	<u>Sta 7</u>	<u>Sta 8</u>	<u>Sta 9</u>	<u>Sta 10</u>
Rep 1 - 1	0.01	0.16		0.11	0.16	0.23	0.06	0.18	0.10	0.14
2	-0.02	0.11	0.23	0.14	0.17	0.21	0.32	0.29	0.32	0.19
3	0.02	0.11	0.08	0.26	0.09	0.31	0.10	0.17	0.31	0.18
4	-0.04	0.25	0.17	0.08	0.14	0.17	0.14	0.25	0.33	0.17
5	-0.02	0.20	0.10	0.09	0.00	0.07	0.18	0.02	0.30	0.17
6	0.02	0.25	0.24	0.16	0.04		0.33		-0.58	0.09
7	0.03		0.33	0.27	0.16	0.16		0.11	0.03	0.15
8	0.08	0.19	0.31	0.11	0.12	0.20	0.17	0.70	0.32	0.16
9	0.02	0.26	0.11	0.15	0.11	0.27	0.34	0.12	0.21	0.09
10	0.01	0.25	0.03	0.30	0.17	0.11	0.08	0.06	0.53	0.27
11	0.14	0.10	0.30	0.09	0.23	0.45	0.16	-0.58	0.08	0.22
12	0.03	0.04	0.12	0.31	0.08	0.47	0.22	0.14	0.20	0.25
13	-0.02	0.11	0.32	0.03	-0.01		0.03	0.37		0.46
14	0.13	0.31	0.17	0.25	0.08	0.33	-0.12	0.20	0.23	0.01
15	0.02		0.28	0.10	0.04	0.24	0.19	0.32	0.38	0.12
16		0.27	0.02	0.05	0.10	0.18	0.17	0.12	0.30	0.09
17		0.08	0.21	0.15	0.08	0.27	0.05	0.14	0.06	0.18
18	0.06	0.26	0.24	0.44	0.14	0.15	0.22	0.35	0.19	0.33
19	0.00		0.20	0.09	0.03	0.19	0.03	0.24	0.21	0.05
20	-0.12	0.18	0.21	0.44	0.01	0.25	0.15	0.10	0.23	0.20
21	0.11	0.19	0.22	0.16	0.13	0.25	-0.01	0.21	0.23	0.19
22	0.06		0.25	0.19	0.06			0.11	0.16	0.06
23	-0.01	0.23	0.11	0.15	0.24	0.37	0.12	0.10	0.40	0.23
24	-0.01	-0.60	0.15	0.16	0.26	0.17	0.15	0.17	0.22	0.23
25	0.04	0.20	0.16	0.06	0.16	0.09	-0.06	0.38		0.10
26	0.05	0.13	0.20	0.11	0.13	0.36	0.24	0.16	0.15	0.14
27	0.09	0.14	0.34	0.28	0.19	0.13		0.16	0.32	0.22
28	0.04	0.10	0.04	0.38	0.12		0.29	0.08	0.18	0.25
29	-0.02	0.08	0.30	0.11		0.07		0.10	0.23	0.25
30		0.09	-0.20	-0.13	0.07	0.26	0.28	0.17	0.32	0.10
31	-0.01	0.18	-0.05	0.14	0.06	0.12	0.18	0.15	0.10	0.07
32	0.01	0.12	0.02	0.36	0.12	0.13	0.30	0.28	0.16	0.15
33	0.20	-0.10		0.10	0.21	0.24	0.32	0.35	0.04	0.13
34	0.07	0.27	0.41	0.19		0.19	0.38	0.13	0.17	0.27
35	0.12	0.09	0.14	0.18	0.07	0.17	0.32	0.17	0.26	0.17
36	-0.14	0.15	0.38	0.08	0.13	0.51	0.19	0.11	0.21	0.04
37	0.27	0.12	0.27	0.10	0.11	0.31	0.34	0.13	0.44	0.25
38	-0.01	0.31	0.15	0.31	0.03	0.26	0.22	0.37	0.30	0.14
39	0.03	0.12	0.14		-0.04	0.12	0.18	0.14	-0.03	-0.04
40	0.03	-0.06	0.10	-0.29	0.06	0.31		0.26	0.19	0.19
41	0.08	0.27	0.20	0.05	0.13	0.51	0.19	0.08	0.34	-0.05
42	0.02	0.15	0.10	0.20	0.11	0.26	-0.18	0.16	0.25	0.08
43		0.10	0.23	0.40	0.31	0.26	0.27		0.17	0.13
44	0.13	0.21	0.37	0.29	0.21	0.26	0.19	0.09	0.43	0.17
45	0.16		0.09	0.17	0.19	0.19	0.27	0.31	0.17	0.19
46	-0.02	0.21	0.06	0.23	0.19	0.17	0.17	0.24	0.15	0.17

1997 Cannelton Clam Biomonitoring Study
Change in Whole-Animal Wet-Weight (g) by Station

47	0.10	0.07		0.14	0.10	0.41	0.17	0.14	0.00	
48	-0.02	0.23	0.17	0.22	0.06	-0.02	0.20	0.18	0.13	0.25
49		0.09	0.24	0.11	0.04	-0.06	0.17	-0.02	0.35	0.11
50		0.16	0.25	0.16	-0.06	0.15	0.21	0.19	0.18	
51	0.02	0.23	0.18	0.30		0.36	0.24	0.10	0.13	
52	0.12	0.12	0.15	0.15	0.01	0.05	0.25	0.36	0.20	0.11
53		0.01		0.16	0.09	0.08	0.11	-0.03	0.18	0.12
54		0.07	0.18	0.13	0.13	0.13	0.26	0.23	0.27	0.06
55	0.05	0.21	0.32	0.34	0.13	0.16	0.30	0.11	0.43	0.34
56	0.04	0.12	0.22	0.25	0.19	0.30	0.21	0.34	0.32	0.21
57	0.11	0.18	0.30	0.11	0.09	0.46	0.22	0.20	0.14	0.21
58	-0.02	0.11	0.17	0.08	0.17	0.02		0.15	0.17	0.25
59	-0.01	0.23	0.25		0.23	0.33	0.13	0.14	0.32	0.18
60	0.04	0.14	0.08	0.08	0.18		0.00		0.26	0.29
61		0.31	0.16	0.16	0.17	0.46	0.20	0.29	0.24	0.34
62	0.09	0.16	0.08	0.17	0.11	0.24	0.08	0.24	0.28	0.17
63	0.10	0.12	0.06	0.36	0.11	0.39	0.32	0.06	0.27	0.16
64	-0.01	0.17	0.04	0.01	0.21	0.30	-0.08	0.23	0.11	0.25
65	0.11	0.14	0.11	0.14	-0.04	0.23	0.17	0.31		0.21
66	0.16	0.01	0.15	0.25	0.22	0.25	0.31	0.16	0.22	0.08
67	0.06	0.29	-0.09	0.26	0.15	0.31	0.06		0.28	0.19
68		0.20	0.20		0.07	0.53	0.27	0.27	0.26	0.44
69	-0.03	0.23	0.23	0.10	0.14	0.34	0.18	0.10		0.16
70		0.12	0.23	0.05	0.14	0.21	0.12	0.13	0.17	0.23
71	-0.02	0.30	0.18	0.27	0.24	0.33		0.20	0.37	0.28
72	-0.18	0.23	0.18	0.23	0.12	0.30	0.37	0.46	0.17	0.32
73	0.05	0.15	0.28	0.08	0.24	0.33	0.28	0.15	0.34	0.14
74	0.04	0.21	0.01	0.34	0.04	0.25	0.27	0.13	0.24	0.27
75	-0.09	0.13	0.11	0.26	0.11	0.29	0.14	0.16	0.54	0.28
Rep 2 - 1	0.15	0.23	0.13	0.13		0.29	0.19	0.31	0.05	0.11
2	0.16	-0.01	0.12	0.18	0.07	0.30	0.06	0.13	0.19	
3	0.00	-0.01	0.15	0.00	0.18	0.04	0.15	0.11		0.26
4	0.10	0.11	0.35	0.16	0.19	0.19	0.16	0.02	0.05	0.15
5	0.00	-0.11	0.06		0.03	0.23	0.05	0.07	0.16	0.06
6	0.20	0.13	0.14		0.10	0.20	0.04	0.04	0.17	0.08
7	-0.06	0.16	0.16		0.15	0.38	0.22	0.03	0.28	0.08
8	0.16	0.06	0.32	0.13	0.19	0.19	0.25	0.21	0.29	0.19
9	0.16	0.04	0.14	0.10	0.24	0.29	0.22	0.18	0.39	0.29
10	0.15	0.18	0.26	0.24	0.12	0.27	0.29		0.19	0.16
11	0.02	0.20	0.15		0.05	0.18	0.19	0.36	0.33	0.15
12	0.02	0.15		0.07	0.22	0.26	0.23	0.29	0.20	0.17
13	0.03	0.09	0.36	0.01		0.16	0.05	0.40	0.18	0.17
14	0.11	0.18	0.34	0.19	0.13	0.19	0.51	0.28	0.12	0.17
15	0.15	0.12		0.13	0.16	0.17	0.24	0.19	0.27	0.21
16	0.00	0.15	0.28	0.08	0.08	0.24	0.30	0.27	0.06	0.08
17	0.05	0.21	0.35	0.02	0.09	0.36	0.35	0.29	0.23	0.25
18		0.13	0.46	0.15	0.39	0.31	0.09	0.33	0.31	0.14
19	0.01	0.01		0.07		0.16	0.17		0.16	0.10
20	-0.12	0.17		0.11	0.09	0.18	0.19	0.09	0.26	0.14
21	0.03	0.13	0.48	0.20	0.24	0.16		0.29	0.23	0.14
22	0.01	0.27	0.09	0.30	0.07	0.23		0.15	0.42	0.22
23	0.16	0.21	0.27	0.23	0.15	0.13	0.25	0.38	0.14	0.16
24	0.02	0.05	0.35	0.17	0.10	0.19	0.43	-0.10		0.10
25	0.04	0.22	0.31	0.12	0.32	0.12	0.19	0.37	0.30	0.11
26	0.10	-0.04	0.18	0.09	0.05	0.18	0.11	0.01	0.24	-0.15
27	0.25	-0.17	-0.02		-0.23	0.17	0.25	0.27	0.18	0.17

**1997 Cannelton Clam Biomonitoring Study
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28	0.17	0.12	0.08	0.04	0.06	0.11	0.07		0.06	0.12
29	0.28	0.08	0.17	0.06	0.12	0.27	0.25	0.15	0.30	0.21
30	0.05	-0.03	-0.20	0.03	0.14	0.21	0.24	0.09		-0.06
31	0.26	0.03	-0.15	0.19	0.06	-0.04	0.09	0.13	0.21	-0.05
32		0.08	0.19	0.14		0.11	0.22	0.07	0.13	0.14
33	0.26	0.17	0.12	0.12	0.20	0.12	0.22	0.08	0.21	0.11
34	0.09	0.08	0.31	0.00	0.24	0.15	0.28	0.06	0.21	0.13
35	-0.01	-0.27	0.06	0.06	0.18	0.15	0.13	0.06	0.34	0.14
36	0.08	0.03	0.13		0.23	0.15	0.19	-0.07	0.22	0.12
37	-0.03		0.17	0.08	0.34	0.31	0.32	0.37	0.21	0.01
38	0.06	0.12	0.24	0.10	0.03		0.12	0.26	0.26	0.27
39	0.02	0.13	0.04	0.10	0.09	0.12	0.02	0.33	0.27	
40	0.07	0.08	0.18	0.09	0.02	0.14	0.52	0.06	0.15	0.27
41	0.09	0.08	0.39	0.22	0.22	0.40	0.14	-0.01	0.30	0.12
42	0.05	0.10	0.33	0.16	0.17	0.50	0.14	0.24	0.22	0.10
43	0.02	0.12			0.30	0.17		0.19	0.08	
44	0.00		0.57	0.13	0.22	0.15	0.32	0.14	0.32	0.19
45	0.11	0.04	0.18	-0.08	0.02	0.23	0.11	0.03	0.30	0.19
46		0.11	0.15	0.14	0.13	0.25	0.08	0.21	0.13	0.20
47	0.12		0.35	0.02	0.25	0.12	0.17	0.21	0.25	0.09
48	0.15	0.21	0.27	0.02	-0.07	0.19	0.07	0.33	0.07	0.07
49	0.07	0.24	0.12	0.01	0.04	0.20	0.16	0.22	0.23	0.13
50	0.06	0.08		0.06	0.09	0.32	0.19	0.10	-0.07	0.10
51	0.13	0.09	0.16		0.24	0.32	0.16	0.11	0.21	0.16
52	0.06	0.09	0.29	0.13	0.11	0.32	0.22	0.00	0.09	0.13
53	-0.01	0.08		-0.02	-0.07	0.19	0.20	0.19	0.18	0.05
54	0.02	-0.11	0.23	0.05	0.09	0.14		0.06	0.10	0.09
55	0.00	0.05	0.40	-0.05	0.13	0.06	0.20		0.15	-0.06
56	0.00	0.06	0.29	0.15			0.46	0.20	0.21	0.22
57	-0.06	0.02	-0.03		0.10	0.11	0.28	0.13	0.21	0.22
58	0.01	-0.04	0.09	0.06	0.01	0.28	0.12	-0.09	0.28	
59	0.07		0.22	0.27	0.03	0.17		0.27	0.16	0.15
60	0.03	0.02	0.23	0.20	0.03	0.30	0.55	0.14	0.19	0.09
61	-0.08	0.14	0.34	0.10	0.03	0.19	0.16	0.18	0.18	
62	0.12	0.08	0.21	0.37	0.21	0.12	0.29	-0.10	0.18	
63	-0.07	-0.24	0.38	0.12	-0.18	0.34	0.18	0.23		0.14
64	0.02	0.08	0.01	0.11	0.05	0.38	0.25	0.22	0.33	
65	0.03	0.13	0.30	0.12	0.02	0.29	0.27	0.00	0.33	0.20
66	0.08	0.24	0.08	0.14	0.12	0.18	0.49	0.19	0.00	0.05
67	-0.01	0.11	0.44	0.14	0.13	0.14	0.20	0.14	0.09	0.15
68	0.10	0.20	0.20		0.10	0.09		-0.02	0.15	0.15
69	-0.02	0.04	0.21	-0.14	0.13	0.13	0.15	0.13	0.14	0.11
70	0.03	0.08		0.15	-0.26	0.03	0.16	0.07	0.10	0.16
71	0.04	0.19		0.09	0.12	0.08	0.22	0.14	0.26	0.22
72	0.23	0.10	0.17	0.06	0.15	0.27	0.18	0.08	0.20	0.08
73	-0.09	0.11	0.21	0.11	0.12	0.16	0.21	0.11	0.22	0.17
74	0.15	0.14	0.10	0.09	0.09	0.21	0.25	0.07	0.04	0.13
75	0.15	0.20	0.32	0.07	-0.08	0.38	0.17	0.02	0.21	0.07
Rep 3 - 1	-0.01	0.07		0.25	-0.38	0.04		-0.04	0.12	0.00
2	-0.20	0.11	0.13	0.39	-0.01	0.13	0.29	0.14	0.23	0.08
3	0.07	0.02	0.10	0.17		0.39	0.32	-0.63	0.07	0.12
4	0.06	0.10	0.09	0.21	0.07	0.41	0.14	0.21		-0.01
5	0.03	0.01	0.23		0.06	0.38	0.13	0.18	0.30	0.11
6	0.01	0.13	0.21	0.28	0.13	0.24	0.07	0.43	0.36	0.19
7	-0.05	-0.15	0.05	0.05	-0.02	0.15	0.21	0.23	0.31	0.07
8	0.12	0.15	0.18	0.18	0.09	0.22	0.14	0.13	0.58	0.17

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Change in Whole-Animal Wet-Weight (g) by Station

9	0.08	0.08	0.20	0.15	0.08	0.24	0.23	0.18	0.10	
10	0.07	0.29	0.24	0.27	0.15	0.26	0.20	0.26	0.20	0.14
11	0.01	0.19	0.34	0.18	0.16	0.28	0.18	0.17	0.45	0.15
12	-0.01	0.08		0.21	0.00	0.27	0.29	0.19	0.21	
13	0.08	0.09	0.17	0.29	0.05	0.32	0.08	0.28	0.28	0.05
14	0.11	0.17	0.15	0.15		0.25	0.11	0.14	0.36	0.27
15	0.02	0.25	0.31	-0.02	-0.03			0.06	0.25	0.11
16	0.18	0.06	0.12	-0.03	-0.09	0.23		0.05	0.16	0.08
17	0.06	0.17	0.34	0.08	-0.29	0.32	0.17	0.11	0.24	0.20
18	0.11	0.05	0.05	0.17		0.29	0.20	0.05	0.07	0.19
19	0.01	0.26	-0.03	0.23		0.30	0.05	0.17	0.21	0.08
20	0.08	0.26	0.08	0.18	0.00	0.26	0.29	0.12	0.22	0.17
21		0.12			-0.05	-0.11		0.12	0.17	0.13
22	0.05	-0.03		0.23		-0.03	0.08	0.04	0.22	0.16
23		0.34	0.24	0.15	0.02	0.56		0.07	0.19	0.16
24	0.23	0.36	0.38	0.15	0.04		0.17	0.00	0.01	0.08
25	0.06	0.22		0.16	-0.27	0.25	-0.01	0.16	0.25	0.16
26	0.10		0.21	0.11		0.06		0.15		0.10
27	0.08	0.17	0.19	0.29	-0.03	0.28	0.43	0.18	0.36	0.08
28	-0.05	0.07	0.19	0.20		0.15	-0.11	0.20		
29	0.13	0.12	0.27	0.12		0.24	0.40	0.20	0.39	0.16
30	-0.13		0.10	0.29	0.02	0.20	0.21	0.10		0.12
31	-0.02	0.06		0.21	-0.01	0.21	0.21	0.26	0.06	0.26
32	0.07	0.05	0.14	0.18	-0.05	0.26	0.02	0.11	0.17	0.09
33	0.09	0.07	0.32	0.04	0.04	0.34	0.26	0.07	0.39	0.12
34	0.04	0.14	0.19	0.10	-0.02	0.06	0.32	0.27	0.27	-0.04
35	-0.04	0.12	0.15	0.22	-0.01	0.23		0.21	0.30	0.08
36		0.09		0.18	0.08	0.26	0.12	0.18	0.34	0.23
37	0.13	0.27	0.16	0.28	0.09		0.28	0.17	0.38	0.25
38	0.07	0.19	0.16	0.26		0.14	0.23	0.13	-0.09	0.12
39		0.17	0.12	0.24	0.28	0.48	0.10	0.14	0.12	0.15
40	0.06	0.00	0.35	0.13	-0.05		0.40	0.11	0.12	0.26
41	0.04	0.19	0.29	0.13	-0.02	0.15	0.24	0.20	0.17	0.17
42	0.14	0.25	0.07		-0.04	0.45	0.12	0.12	0.23	0.15
43	0.05	0.17	0.25	0.15	-0.09	0.17	0.05	0.12	0.15	0.05
44	0.00	0.08	0.06	0.13	-0.14	0.24	0.15	0.06	0.08	0.06
45	0.02	0.11	0.38	0.25	0.15	0.32	0.18	0.28	0.04	0.14
46	0.25	0.06	0.13	0.27	0.00	0.40	0.25	0.24	0.13	0.10
47	-0.18	0.23	0.20			0.24	-0.02			0.06
48	-0.04	0.20	0.20	0.24	0.09	0.37	0.11	0.15	0.18	0.15
49	0.06	0.21	0.18	0.18	0.00	0.31	0.03	0.15	0.11	0.15
50	0.03	0.08	0.20	0.18		0.16	0.11	0.17	0.02	0.10
51	-0.06	0.06	0.08	0.09		0.09		0.32	0.23	0.10
52	-0.07	0.06	0.16	0.10	0.14	0.16	0.15	0.15	0.20	0.11
53	0.04	0.07	0.23			0.20	0.05	0.24	0.12	0.14
54	0.07	0.10		0.18	-0.02		0.18	0.25	0.16	0.19
55	0.03	0.17	0.03	0.06	0.20	0.29	0.17	0.08	0.16	0.17
56	0.09	0.36	0.33	0.14	0.23	0.38	0.15	0.11	0.16	0.16
57	0.22	0.05	0.15	-0.02	0.20	0.20	0.16	0.09	0.30	
58	0.04	0.04	0.37	0.13	0.08	0.47	0.07	0.11	0.03	0.22
59	0.15	0.22	0.13	0.07	0.01	0.15	0.11	0.22	0.20	0.06
60	0.04	0.05	0.12	-0.45	-0.03	0.14	0.21	-0.06	0.19	0.17
61	-0.17	0.13	0.06	0.06	-0.02	0.05	0.18	0.11		0.14
62	0.10		0.06	0.12	0.10	0.15	0.26	0.21	0.27	0.27
63	0.05	0.12	0.30	0.18	-0.16	0.19	0.15	0.22	0.19	0.04
64	0.31	0.09	0.20	-0.01	-0.15	0.26	0.22	-0.02	0.28	0.21

**1997 Cannelton Clam Biomonitoring Study
Change in Whole-Animal Wet-Weight (g) by Station**

65	-0.05	-0.01	0.20	0.14	-0.05	0.11	0.27	0.14	0.26	
66	0.01	-0.01	0.22	0.17			0.30	0.20	0.31	0.30
67	-0.08	-0.07	-0.25	0.08		0.15	0.12	-0.03	0.13	0.05
68	-0.15	0.08	0.14	0.03		0.24	0.06	0.12	0.13	0.13
69	-0.14	0.15	0.15	0.07	0.07	0.20		0.31	0.18	0.19
70	-0.33	0.12	0.01		0.01	0.16	0.29	0.14	0.15	0.24
71	0.14	0.15	0.10	0.26	0.05	0.21	0.28	0.18	0.31	0.19
72	0.02	0.24	0.15	-0.04	-0.06	0.16			0.14	0.23
73	-0.02	0.13	0.10	0.09	0.10	0.37	0.05	0.11	0.25	0.10
74	0.06	0.14	0.01	0.10	0.02	0.26	0.17	0.18	0.10	0.06
75	-0.05			0.18		0.11	0.28	0.06	0.19	0.04
Rep 4 - 1	0.08	-0.12		0.09	-0.18	0.24	0.05	0.07	0.19	-0.08
2	0.02	0.21	0.23	0.13	0.22	0.21	0.26	0.15	0.25	0.30
3	0.00		0.15	0.78	-0.03	0.35	0.22	0.13	0.37	0.18
4	0.07	0.12	0.14		0.12	0.31	0.26		0.36	-0.04
5	-0.06	0.22	0.42	-0.08	0.17	0.32	0.07	0.16	0.15	0.06
6	-0.22	0.14	0.18	0.10	0.19	0.44	0.17	0.01	0.18	0.33
7	-0.03		0.16	0.10	0.00	0.29	0.11	0.15	0.17	0.11
8	0.13	0.09	0.37	0.13	0.05	0.38	0.16	0.36	0.25	0.13
9	0.07	-0.03	0.43	-0.02	0.18	0.02	0.12	0.28	0.13	0.12
10	0.01	0.00	0.25	0.14		0.25	0.34		0.20	0.21
11	0.11	0.17	0.25	0.15	-0.01		0.21	0.30	0.18	0.29
12	-0.04	0.10	0.27	0.40		0.27	0.38	0.09	0.23	0.09
13	0.00	0.19		0.28	-0.55	0.35	0.04	0.13	0.15	0.05
14	0.03	0.31	0.20	0.43	0.20	0.41	0.32	0.38	0.18	0.21
15	-0.07	0.03	0.30	0.36	0.08	0.41	0.25	0.12	0.18	0.11
16	0.04	0.12	0.21	0.20	-0.10	0.23	0.23	0.23	0.19	0.14
17	0.02	0.12	0.15	0.23	0.06	0.20	0.30	0.10	0.27	0.21
18	0.11	0.07	0.27		0.05	0.17	0.16	0.25	0.31	0.02
19	0.04	0.15	0.14	0.14	0.11	0.25	0.08	0.11	0.23	0.08
20	-0.01	0.04	0.19	0.10	0.10	0.15	0.49	0.06	0.13	0.12
21	0.16	-0.05	0.33		0.04	0.41	0.03	0.12	0.02	0.01
22	0.02	0.25	0.18	0.26		0.32	0.18	0.24	0.32	0.08
23	-0.18	0.02	0.08	0.17		0.16	0.40	0.00	0.15	0.09
24	0.21	0.02	0.27	0.09	0.12	0.22	0.44	0.24		0.04
25		0.11	0.22	-0.04		0.37	-0.21	0.04	0.24	0.08
26	0.12	0.11	-0.07	0.05	0.12	0.38	0.20	0.02	0.09	
27	0.02	0.20	0.17	0.14	0.08	0.17	0.01	0.14	0.15	0.07
28	0.03	0.10	-0.08		0.06	0.03	0.25	0.01		
29	-0.03	0.22	0.05	0.38	0.00	-0.03	0.27	0.13	0.10	
30	0.07	0.02	0.11	0.12	0.09	0.29	0.10	0.26	0.17	0.06
31	-0.07		0.20	0.23	0.03	0.12	0.46	0.14	0.12	
32	0.02	-0.01	0.15	0.12	0.14	0.12	0.13	0.13	0.22	0.19
33	0.04	0.07	0.12	0.01	0.07	0.10	0.19	0.13	0.12	0.09
34		0.10	0.06	0.17	-0.10	0.11	0.17	0.08	0.27	0.31
35	0.07	0.12	0.14	0.11		0.29	0.35	0.10	0.36	-0.01
36	0.15	0.04	0.11	0.12		0.31	0.31		0.32	
37	0.13	0.10	0.40	0.34	0.11	0.17	0.30	0.25	0.31	0.24
38	0.05	0.08	0.25		0.11	0.25	0.18	0.42	0.24	0.14
39	0.11	0.17	0.04	0.14	0.11	0.12	0.15	0.26	0.35	0.12
40	-0.03	0.08	0.13			0.11	0.27	0.16		
41	-0.01	-0.02	0.28	0.16		-0.09	0.49	0.12	0.44	0.11
42	0.11	0.25		-0.40	-0.01	0.19	0.01	0.16	0.32	0.22
43	0.03	0.17	0.17	0.04	-0.01	0.13	0.28	0.12	0.34	0.13
44	0.11	-0.39	0.00		0.05	0.48	0.28	0.18	0.30	0.09
45	0.13	0.22	0.09	0.18	0.10	0.44	0.34	0.37	0.28	0.27

1997 Cannelton Clam Biomonitoring Study
Change in Whole-Animal Wet-Weight (g) by Station

46	0.03	0.22	0.17	0.25	-0.01	0.17	0.10	0.14	0.19	0.20
47		-0.23	0.22	0.09		0.30	0.21	0.30	0.24	0.08
48		0.23	0.20	0.18	-0.03	0.15	0.22	0.22	0.21	
49	0.06	0.12	-0.01	0.08		0.35	0.23	0.24		0.26
50	0.13	0.14	0.28	0.08	0.10	0.19		0.22	0.08	0.45
51	0.02		0.15	0.06	0.14	0.05	0.04		0.22	0.14
52	0.04	0.13	0.16	0.09	0.12	0.03	0.18	0.05	0.24	0.09
53	-0.06		0.12	0.09	0.02	0.15	0.12		0.15	0.15
54	0.11		0.19		0.08	0.31	0.14	0.28	0.34	0.23
55	0.00	0.16	0.11	-0.01	-0.01	0.17	0.06	0.11	0.24	0.08
56	0.04	0.09	0.22	0.11	0.14		0.29	0.06	0.35	0.21
57	0.10	0.12	-0.10	0.27	0.05	0.20	0.17	0.20	0.19	0.03
58	0.11	0.03	0.16			0.16	0.25	0.16	0.16	0.04
59	0.15	0.12	0.24	0.16	0.01	-0.01	0.08	0.11	0.29	0.04
60	0.11	-0.01	0.09	0.03	0.10	0.26	0.15	0.01	0.12	0.12
61	0.10	-0.01	0.03	0.05	0.02	0.27	0.12	0.13	0.16	0.21
62	-0.07	0.01	0.09	0.04	0.05	-0.05	0.17		0.24	0.18
63	-0.18	0.10	0.08		0.06	0.23	0.19	0.04	0.35	0.15
64	-0.39	0.03	0.04	0.09	-0.14	0.11	0.12	-0.04		0.07
65	-0.06	0.13		0.00	-0.04	0.41	0.10	0.03	0.40	0.14
66		-0.08	0.06	0.13	0.09	-0.08	0.11	0.00	0.22	0.19
67	-0.04	0.12	-0.02	0.02	-0.01	0.02		-0.13	0.08	-0.03
68	-0.06	0.12	0.14	0.04	0.03	-0.18	-0.03	0.01	0.23	0.10
69	0.03	0.10		0.13		0.02	0.25	0.01	0.17	0.04
70	0.01	0.11	0.09	0.05	0.03	0.06	0.19	0.15	0.26	0.10
71	0.02	0.17	0.13	0.04	0.13	0.11	0.23	0.03	0.29	0.13
72	0.10		0.11		0.05		0.31	-0.08	0.27	0.30
73	-0.01	0.11	0.00	0.22	-0.17	0.25	0.12	0.05	0.31	
74	-0.07	0.03	0.17	0.12		0.24	0.24	-0.04	0.42	0.16
75	-0.01	0.09	0.01	-0.01	0.07	0.14	0.04	0.00		0.10

**1997 Cannelton Clam Biomonitoring Study
Whole-Animal Wet-Weight Growth Rates (mg/wk) by Station**

mean	5.16	14.49	22.49	17.92	9.57	28.04	24.26	19.25	27.24	18.56
min	-49.62	-76.34	-31.81	-57.25	-69.97	-22.90	-26.72	-80.15	-73.79	-19.08
max	39.44	45.80	72.52	99.24	49.62	71.25	69.97	89.06	73.79	58.52
stdev	11.80	14.17	15.31	15.49	14.63	15.56	14.77	16.40	14.51	11.18
N	277	280	273	270	261	284	275	284	280	277

Cage #s:	13,22,25,43	5,15,24,35	2,11,30,37	3,17,23,34	4,18,27,42	14,19,26,41	1,9,20,38	16,28,33,44	8,10,21,39	6,12,31,40
	<u>Sta 1</u>	<u>Sta 2</u>	<u>Sta 3</u>	<u>Sta 4</u>	<u>Sta 5</u>	<u>Sta 6</u>	<u>Sta 7</u>	<u>Sta 8</u>	<u>Sta 9</u>	<u>Sta 10</u>
Rep 1 - 1	1.27	20.36		13.99	20.36	29.26	7.63	22.90	12.72	17.81
2	-2.54	13.99	29.26	17.81	21.63	26.72	40.71	36.90	40.71	24.17
3	2.54	13.99	10.18	33.08	11.45	39.44	12.72	21.63	39.44	22.90
4	-5.09	31.81	21.63	10.18	17.81	21.63	17.81	31.81	41.98	21.63
5	-2.54	25.45	12.72	11.45	0.00	8.91	22.90	2.54	38.17	21.63
6	2.54	31.81	30.53	20.36	5.09		41.98		-73.79	11.45
7	3.82		41.98	34.35	20.36	20.36		13.99	3.82	19.08
8	10.18	24.17	39.44	13.99	15.27	25.45	21.63	89.06	40.71	20.36
9	2.54	33.08	13.99	19.08	13.99	34.35	43.26	15.27	26.72	11.45
10	1.27	31.81	3.82	38.17	21.63	13.99	10.18	7.63	67.43	34.35
11	17.81	12.72	38.17	11.45	29.26	57.25	20.36	-73.79	10.18	27.99
12	3.82	5.09	15.27	39.44	10.18	59.80	27.99	17.81	25.45	31.81
13	-2.54	13.99	40.71	3.82	-1.27		3.82	47.07		58.52
14	16.54	39.44	21.63	31.81	10.18	41.98	-15.27	25.45	29.26	1.27
15	2.54		35.62	12.72	5.09	30.53	24.17	40.71	48.35	15.27
16		34.35	2.54	6.36	12.72	22.90	21.63	15.27	38.17	11.45
17		10.18	26.72	19.08	10.18	34.35	6.36	17.81	7.63	22.90
18	7.63	33.08	30.53	55.98	17.81	19.08	27.99	44.53	24.17	41.98
19	0.00		25.45	11.45	3.82	24.17	3.82	30.53	26.72	6.36
20	-15.27	22.90	26.72	55.98	1.27	31.81	19.08	12.72	29.26	25.45
21	13.99	24.17	27.99	20.36	16.54	31.81	-1.27	26.72	29.26	24.17
22	7.63		31.81	24.17	7.63			13.99	20.36	7.63
23	-1.27	29.26	13.99	19.08	30.53	47.07	15.27	12.72	50.89	29.26
24	-1.27	-76.34	19.08	20.36	33.08	21.63	19.08	21.63	27.99	29.26
25	5.09	25.45	20.36	7.63	20.36	11.45	-7.63	48.35		12.72
26	6.36	16.54	25.45	13.99	16.54	45.80	30.53	20.36	19.08	17.81
27	11.45	17.81	43.26	35.62	24.17	16.54		20.36	40.71	27.99
28	5.09	12.72	5.09	48.35	15.27		36.90	10.18	22.90	31.81
29	-2.54	10.18	38.17	13.99		8.91		12.72	29.26	31.81
30		11.45	-25.45	-16.54	8.91	33.08	35.62	21.63	40.71	12.72
31	-1.27	22.90	-6.36	17.81	7.63	15.27	22.90	19.08	12.72	8.91
32	1.27	15.27	2.54	45.80	15.27	16.54	38.17	35.62	20.36	19.08
33	25.45	-12.72		12.72	26.72	30.53	40.71	44.53	5.09	16.54
34	8.91	34.35	52.16	24.17		24.17	48.35	16.54	21.63	34.35
35	15.27	11.45	17.81	22.90	8.91	21.63	40.71	21.63	33.08	21.63
36	-17.81	19.08	48.35	10.18	16.54	64.89	24.17	13.99	26.72	5.09
37	34.35	15.27	34.35	12.72	13.99	39.44	43.26	16.54	55.98	31.81
38	-1.27	39.44	19.08	39.44	3.82	33.08	27.99	47.07	38.17	17.81
39	3.82	15.27	17.81		-5.09	15.27	22.90	17.81	-3.82	-5.09
40	3.82	-7.63	12.72	-36.90	7.63	39.44		33.08	24.17	24.17
41	10.18	34.35	25.45	6.36	16.54	64.89	24.17	10.18	43.26	-6.36
42	2.54	19.08	12.72	25.45	13.99	33.08	-22.90	20.36	31.81	10.18
43		12.72	29.26	50.89	39.44	33.08	34.35		21.63	16.54
44	16.54	26.72	47.07	36.90	26.72	33.08	24.17	11.45	54.71	21.63
45	20.36		11.45	21.63	24.17	24.17	34.35	39.44	21.63	24.17
46	-2.54	26.72	7.63	29.26	24.17	21.63	21.63	30.53	19.08	21.63
47	12.72	8.91		17.81	12.72	52.16	21.63	17.81	0.00	

**1997 Cannelton Clam Biomonitoring Study
Whole-Animal Wet-Weight Growth Rates (mg/wk) by Station**

48	-2.54	29.26	21.63	27.99	7.63	-2.54	25.45	22.90	16.54	31.81
49		11.45	30.53	13.99	5.09	-7.63	21.63	-2.54	44.53	13.99
50		20.36	31.81	20.36	-7.63	19.08	26.72	24.17	22.90	
51	2.54	29.26	22.90	38.17		45.80	30.53	12.72	16.54	
52	15.27	15.27	19.08	19.08	1.27	6.36	31.81	45.80	25.45	13.99
53		1.27		20.36	11.45	10.18	13.99	-3.82	22.90	15.27
54		8.91	22.90	16.54	16.54	16.54	33.08	29.26	34.35	7.63
55	6.36	26.72	40.71	43.26	16.54	20.36	38.17	13.99	54.71	43.26
56	5.09	15.27	27.99	31.81	24.17	38.17	26.72	43.26	40.71	26.72
57	13.99	22.90	38.17	13.99	11.45	58.52	27.99	25.45	17.81	26.72
58	-2.54	13.99	21.63	10.18	21.63	2.54		19.08	21.63	31.81
59	-1.27	29.26	31.81		29.26	41.98	16.54	17.81	40.71	22.90
60	5.09	17.81	10.18	10.18	22.90		0.00		33.08	36.90
61		39.44	20.36	20.36	21.63	58.52	25.45	36.90	30.53	43.26
62	11.45	20.36	10.18	21.63	13.99	30.53	10.18	30.53	35.62	21.63
63	12.72	15.27	7.63	45.80	13.99	49.62	40.71	7.63	34.35	20.36
64	-1.27	21.63	5.09	1.27	26.72	38.17	-10.18	29.26	13.99	31.81
65	13.99	17.81	13.99	17.81	-5.09	29.26	21.63	39.44		26.72
66	20.36	1.27	19.08	31.81	27.99	31.81	39.44	20.36	27.99	10.18
67	7.63	36.90	-11.45	33.08	19.08	39.44	7.63		35.62	24.17
68		25.45	25.45		8.91	67.43	34.35	34.35	33.08	55.98
69	-3.82	29.26	29.26	12.72	17.81	43.26	22.90	12.72		20.36
70		15.27	29.26	6.36	17.81	26.72	15.27	16.54	21.63	29.26
71	-2.54	38.17	22.90	34.35	30.53	41.98		25.45	47.07	35.62
72	-22.90	29.26	22.90	29.26	15.27	38.17	47.07	58.52	21.63	40.71
73	6.36	19.08	35.62	10.18	30.53	41.98	35.62	19.08	43.26	17.81
74	5.09	26.72	1.27	43.26	5.09	31.81	34.35	16.54	30.53	34.35
75	-11.45	16.54	13.99	33.08	13.99	36.90	17.81	20.36	68.70	35.62
Rep 2 - 1	19.08	29.26	16.54	16.54		36.90	24.17	39.44	6.36	13.99
2	20.36	-1.27	15.27	22.90	8.91	38.17	7.63	16.54	24.17	
3	0.00	-1.27	19.08	0.00	22.90	5.09	19.08	13.99		33.08
4	12.72	13.99	44.53	20.36	24.17	24.17	20.36	2.54	6.36	19.08
5	0.00	-13.99	7.63		3.82	29.26	6.36	8.91	20.36	7.63
6	25.45	16.54	17.81		12.72	25.45	5.09	5.09	21.63	10.18
7	-7.63	20.36	20.36		19.08	48.35	27.99	3.82	35.62	10.18
8	20.36	7.63	40.71	16.54	24.17	24.17	31.81	26.72	36.90	24.17
9	20.36	5.09	17.81	12.72	30.53	36.90	27.99	22.90	49.62	36.90
10	19.08	22.90	33.08	30.53	15.27	34.35	36.90		24.17	20.36
11	2.54	25.45	19.08		6.36	22.90	24.17	45.80	41.98	19.08
12	2.54	19.08		8.91	27.99	33.08	29.26	36.90	25.45	21.63
13	3.82	11.45	45.80	1.27		20.36	6.36	50.89	22.90	21.63
14	13.99	22.90	43.26	24.17	16.54	24.17	64.89	35.62	15.27	21.63
15	19.08	15.27		16.54	20.36	21.63	30.53	24.17	34.35	26.72
16	0.00	19.08	35.62	10.18	10.18	30.53	38.17	34.35	7.63	10.18
17	6.36	26.72	44.53	2.54	11.45	45.80	44.53	36.90	29.26	31.81
18		16.54	58.52	19.08	49.62	39.44	11.45	41.98	39.44	17.81
19	1.27	1.27		8.91		20.36	21.63		20.36	12.72
20	-15.27	21.63		13.99	11.45	22.90	24.17	11.45	33.08	17.81
21	3.82	16.54	61.07	25.45	30.53	20.36		36.90	29.26	17.81
22	1.27	34.35	11.45	38.17	8.91	29.26		19.08	53.44	27.99
23	20.36	26.72	34.35	29.26	19.08	16.54	31.81	48.35	17.81	20.36
24	2.54	6.36	44.53	21.63	12.72	24.17	54.71	-12.72		12.72
25	5.09	27.99	39.44	15.27	40.71	15.27	24.17	47.07	38.17	13.99
26	12.72	-5.09	22.90	11.45	6.36	22.90	13.99	1.27	30.53	-19.08
27	31.81	-21.63	-2.54		-29.26	21.63	31.81	34.35	22.90	21.63
28	21.63	15.27	10.18	5.09	7.63	13.99	8.91		7.63	15.27

**1997 Cannelton Clam Biomonitoring Study
Whole-Animal Wet-Weight Growth Rates (mg/wk) by Station**

29	35.62	10.18	21.63	7.63	15.27	34.35	31.81	19.08	38.17	26.72
30	6.36	-3.82	-25.45	3.82	17.81	26.72	30.53	11.45		-7.63
31	33.08	3.82	-19.08	24.17	7.63	-5.09	11.45	16.54	26.72	-6.36
32		10.18	24.17	17.81		13.99	27.99	8.91	16.54	17.81
33	33.08	21.63	15.27	15.27	25.45	15.27	27.99	10.18	26.72	13.99
34	11.45	10.18	39.44	0.00	30.53	19.08	35.62	7.63	26.72	16.54
35	-1.27	-34.35	7.63	7.63	22.90	19.08	16.54	7.63	43.26	17.81
36	10.18	3.82	16.54		29.26	19.08	24.17	-8.91	27.99	15.27
37	-3.82		21.63	10.18	43.26	39.44	40.71	47.07	26.72	1.27
38	7.63	15.27	30.53	12.72	3.82		15.27	33.08	33.08	34.35
39	2.54	16.54	5.09	12.72	11.45	15.27	2.54	41.98	34.35	
40	8.91	10.18	22.90	11.45	2.54	17.81	66.16	7.63	19.08	34.35
41	11.45	10.18	49.62	27.99	27.99	50.89	17.81	-1.27	38.17	15.27
42	6.36	12.72	41.98	20.36	21.63	63.61	17.81	30.53	27.99	12.72
43	2.54	15.27			38.17	21.63		24.17	10.18	
44	0.00		72.52	16.54	27.99	19.08	40.71	17.81	40.71	24.17
45	13.99	5.09	22.90	-10.18	2.54	29.26	13.99	3.82	38.17	24.17
46		13.99	19.08	17.81	16.54	31.81	10.18	26.72	16.54	25.45
47	15.27		44.53	2.54	31.81	15.27	21.63	26.72	31.81	11.45
48	19.08	26.72	34.35	2.54	-8.91	24.17	8.91	41.98	8.91	8.91
49	8.91	30.53	15.27	1.27	5.09	25.45	20.36	27.99	29.26	16.54
50	7.63	10.18		7.63	11.45	40.71	24.17	12.72	-8.91	12.72
51	16.54	11.45	20.36		30.53	40.71	20.36	13.99	26.72	20.36
52	7.63	11.45	36.90	16.54	13.99	40.71	27.99	0.00	11.45	16.54
53	-1.27	10.18		-2.54	-8.91	24.17	25.45	24.17	22.90	6.36
54	2.54	-13.99	29.26	6.36	11.45	17.81		7.63	12.72	11.45
55	0.00	6.36	50.89	-6.36	16.54	7.63	25.45		19.08	-7.63
56	0.00	7.63	36.90	19.08			58.52	25.45	26.72	27.99
57	-7.63	2.54	-3.82		12.72	13.99	35.62	16.54	26.72	27.99
58	1.27	-5.09	11.45	7.63	1.27	35.62	15.27	-11.45	35.62	
59	8.91		27.99	34.35	3.82	21.63		34.35	20.36	19.08
60	3.82	2.54	29.26	25.45	3.82	38.17	69.97	17.81	24.17	11.45
61	-10.18	17.81	43.26	12.72	3.82	24.17	20.36	22.90	22.90	
62	15.27	10.18	26.72	47.07	26.72	15.27	36.90	-12.72	22.90	
63	-8.91	-30.53	48.35	15.27	-22.90	43.26	22.90	29.26		17.81
64	2.54	10.18	1.27	13.99	6.36	48.35	31.81	27.99	41.98	
65	3.82	16.54	38.17	15.27	2.54	36.90	34.35	0.00	41.98	25.45
66	10.18	30.53	10.18	17.81	15.27	22.90	62.34	24.17	0.00	6.36
67	-1.27	13.99	55.98	17.81	16.54	17.81	25.45	17.81	11.45	19.08
68	12.72	25.45	25.45		12.72	11.45		-2.54	19.08	19.08
69	-2.54	5.09	26.72	-17.81	16.54	16.54	19.08	16.54	17.81	13.99
70	3.82	10.18		19.08	-33.08	3.82	20.36	8.91	12.72	20.36
71	5.09	24.17		11.45	15.27	10.18	27.99	17.81	33.08	27.99
72	29.26	12.72	21.63	7.63	19.08	34.35	22.90	10.18	25.45	10.18
73	-11.45	13.99	26.72	13.99	15.27	20.36	26.72	13.99	27.99	21.63
74	19.08	17.81	12.72	11.45	11.45	26.72	31.81	8.91	5.09	16.54
75	19.08	25.45	40.71	8.91	-10.18	48.35	21.63	2.54	26.72	8.91
Rep 3	-	-1.27	8.91	31.81	-48.35	5.09		-5.09	15.27	0.00
1										
2	-25.45	13.99	16.54	49.62	-1.27	16.54	36.90	17.81	29.26	10.18
3	8.91	2.54	12.72	21.63		49.62	40.71	-80.15	8.91	15.27
4	7.63	12.72	11.45	26.72	8.91	52.16	17.81	26.72		-1.27
5	3.82	1.27	29.26		7.63	48.35	16.54	22.90	38.17	13.99
6	1.27	16.54	26.72	35.62	16.54	30.53	8.91	54.71	45.80	24.17
7	-6.36	-19.08	6.36	6.36	-2.54	19.08	26.72	29.26	39.44	8.91
8	15.27	19.08	22.90	22.90	11.45	27.99	17.81	16.54	73.79	21.63

**1997 Cannelton Clam Biomonitoring Study
Whole-Animal Wet-Weight Growth Rates (mg/wk) by Station**

9	10.18	10.18	25.45	19.08	10.18	30.53	29.26	22.90	12.72	
10	8.91	36.90	30.53	34.35	19.08	33.08	25.45	33.08	25.45	17.81
11	1.27	24.17	43.26	22.90	20.36	35.62	22.90	21.63	57.25	19.08
12	-1.27	10.18		26.72	0.00	34.35	36.90	24.17	26.72	
13	10.18	11.45	21.63	36.90	6.36	40.71	10.18	35.62	35.62	6.36
14	13.99	21.63	19.08	19.08		31.81	13.99	17.81	45.80	34.35
15	2.54	31.81	39.44	-2.54	-3.82			7.63	31.81	13.99
16	22.90	7.63	15.27	-3.82	-11.45	29.26		6.36	20.36	10.18
17	7.63	21.63	43.26	10.18	-36.90	40.71	21.63	13.99	30.53	25.45
18	13.99	6.36	6.36	21.63		36.90	25.45	6.36	8.91	24.17
19	1.27	33.08	-3.82	29.26		38.17	6.36	21.63	26.72	10.18
20	10.18	33.08	10.18	22.90	0.00	33.08	36.90	15.27	27.99	21.63
21		15.27			-6.36	-13.99		15.27	21.63	16.54
22	6.36	-3.82		29.26		-3.82	10.18	5.09	27.99	20.36
23		43.26	30.53	19.08	2.54	71.25		8.91	24.17	20.36
24	29.26	45.80	48.35	19.08	5.09		21.63	0.00	1.27	10.18
25	7.63	27.99		20.36	-34.35	31.81	-1.27	20.36	31.81	20.36
26	12.72		26.72	13.99		7.63		19.08		12.72
27	10.18	21.63	24.17	36.90	-3.82	35.62	54.71	22.90	45.80	10.18
28	-6.36	8.91	24.17	25.45		19.08	-13.99	25.45		
29	16.54	15.27	34.35	15.27		30.53	50.89	25.45	49.62	20.36
30	-16.54		12.72	36.90	2.54	25.45	26.72	12.72		15.27
31	-2.54	7.63		26.72	-1.27	26.72	26.72	33.08	7.63	33.08
32	8.91	6.36	17.81	22.90	-6.36	33.08	2.54	13.99	21.63	11.45
33	11.45	8.91	40.71	5.09	5.09	43.26	33.08	8.91	49.62	15.27
34	5.09	17.81	24.17	12.72	-2.54	7.63	40.71	34.35	34.35	-5.09
35	-5.09	15.27	19.08	27.99	-1.27	29.26		26.72	38.17	10.18
36		11.45		22.90	10.18	33.08	15.27	22.90	43.26	29.26
37	16.54	34.35	20.36	35.62	11.45		35.62	21.63	48.35	31.81
38	8.91	24.17	20.36	33.08		17.81	29.26	16.54	-11.45	15.27
39		21.63	15.27	30.53	35.62	61.07	12.72	17.81	15.27	19.08
40	7.63	0.00	44.53	16.54	-6.36		50.89	13.99	15.27	33.08
41	5.09	24.17	36.90	16.54	-2.54	19.08	30.53	25.45	21.63	21.63
42	17.81	31.81	8.91		-5.09	57.25	15.27	15.27	29.26	19.08
43	6.36	21.63	31.81	19.08	-11.45	21.63	6.36	15.27	19.08	6.36
44	0.00	10.18	7.63	16.54	-17.81	30.53	19.08	7.63	10.18	7.63
45	2.54	13.99	48.35	31.81	19.08	40.71	22.90	35.62	5.09	17.81
46	31.81	7.63	16.54	34.35	0.00	50.89	31.81	30.53	16.54	12.72
47	-22.90	29.26	25.45			30.53	-2.54			7.63
48	-5.09	25.45	25.45	30.53	11.45	47.07	13.99	19.08	22.90	19.08
49	7.63	26.72	22.90	22.90	0.00	39.44	3.82	19.08	13.99	19.08
50	3.82	10.18	25.45	22.90		20.36	13.99	21.63	2.54	12.72
51	-7.63	7.63	10.18	11.45		11.45		40.71	29.26	12.72
52	-8.91	7.63	20.36	12.72	17.81	20.36	19.08	19.08	25.45	13.99
53	5.09	8.91	29.26			25.45	6.36	30.53	15.27	17.81
54	8.91	12.72		22.90	-2.54		22.90	31.81	20.36	24.17
55	3.82	21.63	3.82	7.63	25.45	36.90	21.63	10.18	20.36	21.63
56	11.45	45.80	41.98	17.81	29.26	48.35	19.08	13.99	20.36	20.36
57	27.99	6.36	19.08	-2.54	25.45	25.45	20.36	11.45	38.17	
58	5.09	5.09	47.07	16.54	10.18	59.80	8.91	13.99	3.82	27.99
59	19.08	27.99	16.54	8.91	1.27	19.08	13.99	27.99	25.45	7.63
60	5.09	6.36	15.27	-57.25	-3.82	17.81	26.72	-7.63	24.17	21.63
61	-21.63	16.54	7.63	7.63	-2.54	6.36	22.90	13.99		17.81
62	12.72		7.63	15.27	12.72	19.08	33.08	26.72	34.35	34.35
63	6.36	15.27	38.17	22.90	-20.36	24.17	19.08	27.99	24.17	5.09
64	39.44	11.45	25.45	-1.27	-19.08	33.08	27.99	-2.54	35.62	26.72

**1997 Cannelton Clam Biomonitoring Study
Whole-Animal Wet-Weight Growth Rates (mg/wk) by Station**

65	-6.36	-1.27	25.45	17.81	-6.36	13.99	34.35	17.81	33.08	
66	1.27	-1.27	27.99	21.63			38.17	25.45	39.44	38.17
67	-10.18	-8.91	-31.81	10.18		19.08	15.27	-3.82	16.54	6.36
68	-19.08	10.18	17.81	3.82		30.53	7.63	15.27	16.54	16.54
69	-17.81	19.08	19.08	8.91	8.91	25.45		39.44	22.90	24.17
70	-41.98	15.27	1.27		1.27	20.36	36.90	17.81	19.08	30.53
71	17.81	19.08	12.72	33.08	6.36	26.72	35.62	22.90	39.44	24.17
72	2.54	30.53	19.08	-5.09	-7.63	20.36			17.81	29.26
73	-2.54	16.54	12.72	11.45	12.72	47.07	6.36	13.99	31.81	12.72
74	7.63	17.81	1.27	12.72	2.54	33.08	21.63	22.90	12.72	7.63
75	-6.36			22.90		13.99	35.62	7.63	24.17	5.09
Rep 4 - 1	10.18	-15.27		11.45	-22.90	30.53	6.36	8.91	24.17	-10.18
2	2.54	26.72	29.26	16.54	27.99	26.72	33.08	19.08	31.81	38.17
3	0.00		19.08	99.24	-3.82	44.53	27.99	16.54	47.07	22.90
4	8.91	15.27	17.81		15.27	39.44	33.08		45.80	-5.09
5	-7.63	27.99	53.44	-10.18	21.63	40.71	8.91	20.36	19.08	7.63
6	-27.99	17.81	22.90	12.72	24.17	55.98	21.63	1.27	22.90	41.98
7	-3.82		20.36	12.72	0.00	36.90	13.99	19.08	21.63	13.99
8	16.54	11.45	47.07	16.54	6.36	48.35	20.36	45.80	31.81	16.54
9	8.91	-3.82	54.71	-2.54	22.90	2.54	15.27	35.62	16.54	15.27
10	1.27	0.00	31.81	17.81		31.81	43.26		25.45	26.72
11	13.99	21.63	31.81	19.08	-1.27		26.72	38.17	22.90	36.90
12	-5.09	12.72	34.35	50.89		34.35	48.35	11.45	29.26	11.45
13	0.00	24.17		35.62	-69.97	44.53	5.09	16.54	19.08	6.36
14	3.82	39.44	25.45	54.71	25.45	52.16	40.71	48.35	22.90	26.72
15	-8.91	3.82	38.17	45.80	10.18	52.16	31.81	15.27	22.90	13.99
16	5.09	15.27	26.72	25.45	-12.72	29.26	29.26	29.26	24.17	17.81
17	2.54	15.27	19.08	29.26	7.63	25.45	38.17	12.72	34.35	26.72
18	13.99	8.91	34.35		6.36	21.63	20.36	31.81	39.44	2.54
19	5.09	19.08	17.81	17.81	13.99	31.81	10.18	13.99	29.26	10.18
20	-1.27	5.09	24.17	12.72	12.72	19.08	62.34	7.63	16.54	15.27
21	20.36	-6.36	41.98		5.09	52.16	3.82	15.27	2.54	1.27
22	2.54	31.81	22.90	33.08		40.71	22.90	30.53	40.71	10.18
23	-22.90	2.54	10.18	21.63		20.36	50.89	0.00	19.08	11.45
24	26.72	2.54	34.35	11.45	15.27	27.99	55.98	30.53		5.09
25		13.99	27.99	-5.09		47.07	-26.72	5.09	30.53	10.18
26	15.27	13.99	-8.91	6.36	15.27	48.35	25.45	2.54	11.45	
27	2.54	25.45	21.63	17.81	10.18	21.63	1.27	17.81	19.08	8.91
28	3.82	12.72	-10.18		7.63	3.82	31.81	1.27		
29	-3.82	27.99	6.36	48.35	0.00	-3.82	34.35	16.54	12.72	
30	8.91	2.54	13.99	15.27	11.45	36.90	12.72	33.08	21.63	7.63
31	-8.91		25.45	29.26	3.82	15.27	58.52	17.81	15.27	
32	2.54	-1.27	19.08	15.27	17.81	15.27	16.54	16.54	27.99	24.17
33	5.09	8.91	15.27	1.27	8.91	12.72	24.17	16.54	15.27	11.45
34		12.72	7.63	21.63	-12.72	13.99	21.63	10.18	34.35	39.44
35	8.91	15.27	17.81	13.99		36.90	44.53	12.72	45.80	-1.27
36	19.08	5.09	13.99	15.27		39.44	39.44		40.71	
37	16.54	12.72	50.89	43.26	13.99	21.63	38.17	31.81	39.44	30.53
38	6.36	10.18	31.81		13.99	31.81	22.90	53.44	30.53	17.81
39	13.99	21.63	5.09	17.81	13.99	15.27	19.08	33.08	44.53	15.27
40	-3.82	10.18	16.54			13.99	34.35	20.36		
41	-1.27	-2.54	35.62	20.36		-11.45	62.34	15.27	55.98	13.99
42	13.99	31.81		-50.89	-1.27	24.17	1.27	20.36	40.71	27.99
43	3.82	21.63	21.63	5.09	-1.27	16.54	35.62	15.27	43.26	16.54
44	13.99	-49.62	0.00		6.36	61.07	35.62	22.90	38.17	11.45
45	16.54	27.99	11.45	22.90	12.72	55.98	43.26	47.07	35.62	34.35

**1997 Cannelton Clam Biomonitoring Study
Whole-Animal Wet-Weight Growth Rates (mg/wk) by Station**

46	3.82	27.99	21.63	31.81	-1.27	21.63	12.72	17.81	24.17	25.45
47		-29.26	27.99	11.45		38.17	26.72	38.17	30.53	10.18
48		29.26	25.45	22.90	-3.82	19.08	27.99	27.99	26.72	
49	7.63	15.27	-1.27	10.18		44.53	29.26	30.53		33.08
50	16.54	17.81	35.62	10.18	12.72	24.17		27.99	10.18	57.25
51	2.54		19.08	7.63	17.81	6.36	5.09		27.99	17.81
52	5.09	16.54	20.36	11.45	15.27	3.82	22.90	6.36	30.53	11.45
53	-7.63		15.27	11.45	2.54	19.08	15.27		19.08	19.08
54	13.99		24.17		10.18	39.44	17.81	35.62	43.26	29.26
55	0.00	20.36	13.99	-1.27	-1.27	21.63	7.63	13.99	30.53	10.18
56	5.09	11.45	27.99	13.99	17.81		36.90	7.63	44.53	26.72
57	12.72	15.27	-12.72	34.35	6.36	25.45	21.63	25.45	24.17	3.82
58	13.99	3.82	20.36			20.36	31.81	20.36	20.36	5.09
59	19.08	15.27	30.53	20.36	1.27	-1.27	10.18	13.99	36.90	5.09
60	13.99	-1.27	11.45	3.82	12.72	33.08	19.08	1.27	15.27	15.27
61	12.72	-1.27	3.82	6.36	2.54	34.35	15.27	16.54	20.36	26.72
62	-8.91	1.27	11.45	5.09	6.36	-6.36	21.63		30.53	22.90
63	-22.90	12.72	10.18		7.63	29.26	24.17	5.09	44.53	19.08
64	-49.62	3.82	5.09	11.45	-17.81	13.99	15.27	-5.09		8.91
65	-7.63	16.54		0.00	-5.09	52.16	12.72	3.82	50.89	17.81
66		-10.18	7.63	16.54	11.45	-10.18	13.99	0.00	27.99	24.17
67	-5.09	15.27	-2.54	2.54	-1.27	2.54		-16.54	10.18	-3.82
68	-7.63	15.27	17.81	5.09	3.82	-22.90	-3.82	1.27	29.26	12.72
69	3.82	12.72		16.54		2.54	31.81	1.27	21.63	5.09
70	1.27	13.99	11.45	6.36	3.82	7.63	24.17	19.08	33.08	12.72
71	2.54	21.63	16.54	5.09	16.54	13.99	29.26	3.82	36.90	16.54
72	12.72		13.99		6.36		39.44	-10.18	34.35	38.17
73	-1.27	13.99	0.00	27.99	-21.63	31.81	15.27	6.36	39.44	
74	-8.91	3.82	21.63	15.27		30.53	30.53	-5.09	53.44	20.36
75	-1.27	11.45	1.27	-1.27	8.91	17.81	5.09	0.00		12.72

1997 Cannelton Clam Biomonitoring Study End-of-Test Tissue Weights (g-wet) by Station

mean	0.74	0.84	0.92	0.87	0.81	0.90	0.88	0.89	0.88	0.83	0.66
min	0.34	0.39	0.5	0.47	0.42	0.42	0.41	0.45	0.42	0.42	0.32
max	1.18	1.28	1.39	1.3	1.27	1.63	1.41	1.71	1.25	1.33	1.09
stdev	0.14	0.14	0.16	0.15	0.13	0.16	0.17	0.15	0.15	0.14	0.14
N	277	284	274	270	261	284	275	285	280	277	300

Cage #'s: 13,22,25,43 5,15,24, 35 2,11,30,37 3,17,23,34 4,18,27,42 14,19,26,41 1,9,20,38 16,28,33,44 8,10,21,39 6,12,31,40 7,29,32,36

	<u>Sta 1</u>	<u>Sta 2</u>	<u>Sta 3</u>	<u>Sta 4</u>	<u>Sta 5</u>	<u>Sta 6</u>	<u>Sta 7</u>	<u>Sta 8</u>	<u>Sta 9</u>	<u>Sta 10</u>	<u>Initial (To)</u>	
Rep 1	-	0.61	0.86		0.98	1.07	0.96	0.95	0.79	0.87	0.95	0.67
1												
2	0.81	0.81	0.73	0.94	1.05	0.83	0.68	0.93	0.83	0.73	0.53	
3	0.70	0.94	0.83	0.88	0.82	0.57	0.93	1.03	1.02	0.87	0.71	
4	0.80	0.74	1.16	1.06	0.84	0.96	0.74	0.72	0.81	0.78	0.59	
5	0.72	0.60	0.93	1.03	0.73	0.68	0.57	0.80	0.81	0.72	0.58	
6	0.62	0.81	0.81	0.77	0.80		0.65		0.42	1.05	0.78	
7	0.90		1.00	0.82	0.85	1.00		0.73	0.61	0.73	0.59	
8	1.02	0.78	0.72	0.87	0.69	0.86	0.71	1.02	0.88	0.85	0.60	
9	0.61	0.59	1.00	0.67	0.69	0.80	0.78	0.93	0.86	0.72	0.80	
10	0.73	1.02	0.61	0.61	0.79	0.76	0.76	1.02	1.08	0.71	0.67	
11	0.64	0.82	0.84	0.76	0.85	0.85	0.90	0.86	0.83	0.96	0.62	
12	0.71	0.52	0.74	0.74	0.68	0.77	1.36	1.15	0.79	0.65	0.58	
13	0.55	0.88	0.69	0.83	0.57		0.63	0.88		0.70	0.50	
14	0.50	0.82	0.98	0.80	0.69	0.90	0.65	0.94	0.91	0.42	0.50	
15	0.85		0.76	0.86	0.67	0.76	0.85	0.80	0.96	0.85	0.57	
16		0.71	1.10	0.92	1.01	0.64	0.86	0.79	0.88	0.75	0.74	
17		0.86	0.73	0.92	0.68	1.63	0.92	0.98	0.75	0.85	0.54	
18	0.74	0.78	0.68	0.73	0.77	0.75	0.73	0.89	0.84	0.83	0.41	
19	0.77		1.16	1.17	1.00	0.99	1.04	1.10	1.03	0.90	0.79	
20	0.34	0.74	0.77	0.81	0.51	0.84	0.78	0.87	0.86	0.71	0.56	
21	0.71	0.95	0.89	1.15	0.83	0.81	0.88	0.95	0.86	0.84	0.53	
22	0.69		0.96	0.91	0.84			0.82	0.94	0.54	0.63	
23	0.83	0.87	0.97	0.83	0.80	0.93	1.05	1.03	0.89	0.95	0.61	
24	0.71	0.96	0.82	0.94	0.72	0.84	0.83	0.85	1.07	0.63	0.62	
25	0.66	1.13	1.04	0.87	0.99	0.82	0.61	0.80		0.67	0.63	
26	0.89	0.83	1.24	0.90	0.92	0.91	1.10	0.79	0.81	0.79	0.60	
27	0.90	0.77	0.92	0.83	0.97	1.04		0.87	1.02	0.90	0.68	
28	0.85	0.93	1.11	1.30	1.01		1.23	1.22	0.93	0.91	0.77	
29	0.58	0.82	0.92	0.85		0.74		0.75	0.87	0.88	0.62	
30		1.19	0.60	1.07	0.81	0.79	0.90	1.14	0.77	0.92	0.88	
31	0.56	0.79	0.79	0.95	0.91	0.77	0.99	0.75	0.76	0.83	0.65	
32	0.50	0.65	0.78	0.70	0.72	0.77	0.99	0.87	0.83	0.69	0.62	
33	0.63	1.13		0.84	0.64	0.79	0.63	0.74	0.81	0.82	0.65	
34	0.75	0.56	0.76	0.73		0.79	0.80	0.88	0.59	0.58	0.54	
35	0.61	0.92	0.93	0.65	0.73	1.11	0.83	0.78	1.16	1.09	0.62	
36	0.57	0.84	1.10	0.83	1.01	1.17	1.26	0.83	0.96	0.75	0.76	
37	0.67	0.85	0.72	1.03	0.64	0.79	1.04	0.94	0.77	0.74	1.01	
38	0.64	0.67	1.13	0.89	0.78	0.88	1.02	0.90	0.85	0.76	0.55	
39	0.51	0.89	0.97		0.88	1.06	1.07	0.91	0.85	1.14	0.67	
40	0.67	0.72	1.11	0.47	0.93	1.01		1.00	0.90	0.99	0.48	
41	0.84	0.80	1.12	0.92	0.69	0.94	1.08	1.10	0.69	0.81	0.61	
42	0.73	0.95	0.87	1.18	0.88	1.04	0.59	0.88	0.96	0.71	0.83	
43		0.97	0.90	0.87	0.78	0.73	0.88		1.03	0.77	0.65	
44	0.64	0.68	0.92	0.71	0.73	0.95	0.88	0.71	0.98	0.91	0.84	
45	0.66		0.88	1.03	1.01	1.26	1.11	0.83	0.94	0.97	0.86	
46	0.87	0.85	0.93	0.92	0.54	0.84	1.19	0.89	0.75	0.73	0.57	

**1997 Cannelton Clam Biomonitoring Study
End-of-Test Tissue Weights (g-wet) by Station**

47	0.71	0.80		0.72	0.87	0.81	0.92	1.19	1.08		0.59	
48	0.69	0.78	0.93	0.74	0.85	0.94	0.88	0.70	1.16	0.61	1.07	
49		0.84	0.85	1.03	0.94	0.67	0.95	0.88	0.96	0.94	0.71	
50		0.91	0.79	0.79	0.69	1.03	0.77	0.99	1.03		0.41	
51	0.48	0.94	0.94	0.97		0.99	1.04	1.09	0.81		0.68	
52	0.85	0.86	0.71	0.77	0.91	1.06	0.74	0.99	1.00	0.72	0.94	
53		0.41		0.91	0.74	0.88	0.91	0.78	0.93	0.90	0.51	
54		0.88	0.89	0.93	0.83	0.84	0.91	0.87	1.19	0.83	0.95	
55	0.45	0.82	1.11	0.79	0.81	1.15	0.76	1.00	1.00	0.75	0.64	
56	0.66	0.85	0.74	0.71	0.87	0.97	0.86	0.83	0.78	0.75	0.75	
57	0.61	0.93	0.83	0.88	0.95	1.31	1.11	0.95	0.65	0.83	0.67	
58	0.76	0.75	0.65	0.92	0.93	0.92		1.09	1.13	0.73	0.71	
59	0.85	1.09	0.84		0.95	1.24	0.73	1.04	0.92	0.77	0.83	
60	0.77	0.81	1.08	0.73	0.86		0.87		1.07	0.80	0.60	
61		0.87	0.82	0.74	0.74	1.16	0.78	0.68	1.20	0.91	0.69	
62	0.81	0.97	0.84	0.84	0.88	1.15	1.18	0.80	1.00	0.93	0.85	
63	0.89	1.07	0.94	0.98	1.01	0.99	1.11	1.00	1.06	0.90	0.65	
64	0.85	0.93	0.86	0.81	0.84	1.02	0.62	0.99	1.00	0.90	0.90	
65	0.96	1.12	0.67	0.90	0.61	0.75	1.08	0.98		0.88	0.68	
66	0.63	0.75	0.60	0.67	0.72	0.95	0.77	0.93	0.90	0.79	0.79	
67	0.77	1.00	0.90	1.00	0.92	1.06	0.73		0.78	0.84	0.76	
68		1.28	1.21		1.04	0.87	1.28	0.96	1.07	1.33	0.74	
69	0.64	0.83	1.03	0.70	0.76	1.06	0.96	1.07		0.97	0.61	
70		0.97	0.98	1.12	1.01	0.85	1.04	0.99	0.93	0.83	0.93	
71	0.56	0.76	0.78	0.76	0.81	1.09		0.77	0.76	0.57	0.84	
72	0.80	1.24	1.04	1.01	0.91	0.97	0.80	0.69	0.92	0.86	0.74	
73	0.68	0.81	1.03	0.97	1.00	0.95	0.93	0.90	1.03	1.16	0.73	
74	0.64	0.79	0.70	0.83	0.42	0.94	0.94	1.03	1.01	1.15	0.66	
75	0.72	0.99	0.96	1.05	0.86	1.03	0.83	1.08	1.09	1.12	0.71	
Rep 1	2	0.61	0.69	0.94	0.66		1.03	0.97	0.62	1.10	0.74	0.64
	2	0.78	1.13	0.90	0.98	0.79	0.77	0.82	0.84	1.01		0.50
	3	1.01	0.78	0.95	0.64	1.01	0.71	0.80	0.71		0.71	0.63
	4	0.65	0.91	0.98	0.67	0.72	1.09	0.59	1.16	0.53	0.88	0.59
	5	0.85	1.05	0.91		0.90	0.81	0.83	0.99	0.87	0.97	0.54
	6	0.69	0.81	0.89		0.84	0.82	0.73	0.54	0.76	0.64	0.61
	7	0.51	0.91	1.16		1.03	0.81	1.07	1.09	0.90	0.70	0.54
	8	0.71	0.76	0.97	0.94	0.81	0.99	1.00	0.73	0.92	0.74	0.57
	9	0.67	0.97	0.98	0.69	0.85	0.87	1.02	0.67	0.86	0.71	0.57
	10	0.58	1.02	1.23	0.82	0.83	1.09	1.05		0.96	0.87	0.51
	11	0.76	0.98	0.99		0.73	0.89	0.70	0.72	0.81	0.93	0.61
	12	0.66	0.73		0.62	0.95	1.10	0.70	1.16	0.74	0.66	0.59
	13	0.69	0.96	0.88	1.11		0.84	0.82	0.89	1.00	0.68	0.62
	14	0.54	0.81	0.79	0.66	0.86	1.19	0.73	0.65	0.77	0.89	0.72
	15	0.65	0.74		0.95	0.77	0.77	1.28	0.93	0.82	0.63	0.58
	16	0.71	0.78	0.88	0.78	1.04	1.03	0.66	0.89	0.55	0.68	0.57
	17	0.76	0.89	0.73	0.68	0.64	0.87	0.68	0.69	0.67	0.72	0.58
	18		0.67	0.73	0.79	0.69	0.70	0.59	0.84	0.71	0.66	0.66
	19	0.65	0.85		0.94		1.13	1.15		1.09	1.05	0.59
	20	0.71	0.89		0.88	0.70	0.91	0.71	0.76	0.77	0.88	0.64
	21	0.70	0.94	0.97	0.70	0.65	1.03		0.89	1.03	0.64	0.63
	22	0.84	0.68	0.86	0.93	0.63	0.97		0.76	0.80	0.70	0.82
	23	0.71	0.68	0.76	0.82	0.70	0.62	1.06	0.87	0.83	0.96	0.70
	24	0.90	1.05	0.99	0.76	0.77	0.86	0.98	0.77		0.86	0.68
	25	0.84	0.96	0.87	0.74	0.82	0.68	0.89	0.72	0.76	0.88	0.80
	26	0.87	0.92	1.27	1.13	0.90	0.86	0.70	0.80	0.89	0.80	0.92

**1997 Cannelton Clam Biomonitoring Study
End-of-Test Tissue Weights (g-wet) by Station**

27	0.93	0.89	0.96		0.60	1.16	0.97	0.82	0.90	0.91	0.64	
28	1.12	0.91	1.06	0.82	0.86	0.97	0.88		0.67	0.80	0.62	
29	0.78	0.74	0.83	0.60	0.55	0.70	0.74	1.15	0.81	0.74	0.50	
30	0.82	0.72	1.03	0.64	1.05	1.15	0.97	0.76		0.83	0.61	
31	0.93	0.76	0.82	0.97	0.79	0.85	1.07	1.00	0.78	0.50	0.48	
32		0.83	0.78	0.68		1.12	0.96	0.91	0.62	0.67	0.81	
33	0.55	0.53	0.84	0.71	0.91	0.96	0.87	0.73	1.03	0.87	0.50	
34	0.71	0.84	0.92	0.83	0.78	1.03	0.74	0.96	0.67	0.96	0.67	
35	0.79	0.63	0.92	0.80	1.19	1.02	0.78	0.84	0.99	0.98	0.79	
36	0.61	0.91	0.92		0.84	0.98	0.90	0.53	1.25	0.97	0.61	
37	0.83		1.02	1.12	0.90	0.88	0.89	0.85	0.80	0.69	0.68	
38	0.84	0.67	1.19	0.85	0.74		0.83	1.14	0.92	0.61	0.51	
39	0.77	0.87	0.95	0.87	0.81	0.83	0.41	1.10	0.91		1.09	
40	0.73	1.01	1.03	0.96	0.76	1.06	1.23	0.82	1.06	0.91	0.70	
41	0.59	0.87	0.78	0.92	0.66	0.89	0.97	0.66	0.80	1.12	0.87	
42	0.71	0.97	1.04	0.78	0.94	1.03	1.09	0.82	0.70	0.75	0.55	
43	0.84	1.02			0.89	0.93		0.96	0.75		0.67	
44	0.70		0.92	0.93	0.88	0.79	0.86	0.72	0.88	0.84	0.64	
45	0.72	0.73	0.89	0.83	0.75	1.10	0.74	0.47	0.91	0.84	0.61	
46		0.85	0.92	0.68	0.82	1.00	0.72	0.80	0.73	0.66	0.64	
47	0.74		0.67	0.75	0.82	0.99	1.09	1.13	0.58	0.64	0.53	
48	0.85	0.70	0.75	0.86	0.74	0.92	0.91	1.28	0.97	0.76	0.47	
49	1.00	0.91	0.89	0.75	0.87	0.93	0.62	1.02	0.92	0.79	0.62	
50	0.69	0.85		0.93	0.81	1.02	0.70	0.67	0.79	0.88	0.62	
51	0.74	0.82	1.01		0.76	1.10	0.89	1.04	0.88	0.94	0.65	
52	0.70	0.62	1.11	0.90	0.62	0.90	1.13	0.90	1.05	0.91	0.62	
53	0.73	0.71		0.93	0.83	1.10	1.13	1.00	1.10	0.84	0.54	
54	0.67	0.99	1.10	1.01	0.97	0.81		0.77	1.13	0.69	0.58	
55	1.02	0.92	0.86	0.80	0.87	0.64	0.83		0.95	0.99	0.68	
56	0.89	0.78	0.82	0.80			0.87	0.83	0.79	0.75	0.94	
57	0.95	1.06	0.70		0.97	0.96	1.02	1.03	0.85	0.80	0.92	
58	0.92	0.58	1.00	0.83	0.69	0.80	1.13	0.82	0.96		0.95	
59	1.02		0.98	0.65	0.68	0.99		0.85	0.71	0.76	0.57	
60	0.67	0.86	1.28	1.05	0.69	0.91	1.32	0.91	0.90	1.09	1.06	
61	0.79	0.92	1.08	0.78	0.80	1.02	0.98	1.00	0.96		0.45	
62	0.67	0.77	0.89	0.82	0.81	0.84	1.41	0.98	0.83		0.71	
63	0.57	0.95	1.04	1.01	0.74	1.14	1.16	0.90		0.79	0.55	
64	0.80	0.86	1.00	0.97	0.61	1.17	1.11	1.04	0.86		0.82	
65	0.58	1.09	0.97	1.10	0.78	0.79	0.98	1.01	0.79	0.88	0.61	
66	0.68	0.75	0.92	1.01	0.74	0.86	0.85	0.91	1.03	0.71	0.74	
67	0.65	0.85	0.87	0.93	0.81	0.92	1.06	1.02	0.97	0.97	0.71	
68	0.60	0.83	1.32		0.97	0.74		0.83	1.13	0.75	0.65	
69	0.96	0.69	1.10	0.74	0.92	0.86	1.03	0.81	1.21	0.92	0.87	
70	0.84	0.99		0.92	0.94	0.93	0.99	1.14	0.77	0.91	0.71	
71	0.68	0.79		0.91	0.84	0.77	0.92	1.10	0.68	0.65	0.81	
72	0.94	0.85	1.23	0.78	0.79	0.79	0.77	1.12	0.84	0.87	0.80	
73	0.83	0.93	0.95	1.09	0.89	1.09	1.09	1.08	0.79	0.70	0.68	
74	1.18	0.84	1.03	0.93	0.92	1.03	0.91	0.99	0.71	0.99	0.84	
75	0.79	1.12	1.09	0.89	0.63	1.04	0.98	0.95	0.86	0.74	0.74	
Rep 1	3	0.61	0.80		0.93	0.80	0.96		0.81	0.70	0.95	0.67
	2	0.55	0.89	0.75	0.90	0.93	0.75	0.71	0.94	0.82	0.66	0.50
	3	0.65	0.69	0.80	1.01		0.67	0.74	1.15	1.03	0.81	0.58
	4	0.59	0.79	0.70	0.88		0.62	0.86	0.86	0.78	0.89	0.61
	5	0.57	0.64	0.89		0.78	0.79	0.73	0.75	0.86	0.88	1.08
	6	0.59	0.80	0.96	0.57	0.84	0.62	0.93	0.79	0.72	0.73	0.50

**1997 Cannelton Clam Biomonitoring Study
End-of-Test Tissue Weights (g-wet) by Station**

7	0.67	0.74	0.81	0.67	0.70	1.00	0.87	1.02	0.98	0.79	0.79
8	0.62	0.77	1.08	1.10	0.59	0.75	0.96	1.02	0.83	0.86	0.88
9	0.66	0.68	1.03	0.89	0.83	0.76	0.82	0.79	0.59		0.52
10	0.90	0.95	0.82	0.96	0.80	0.86	0.94	0.77	0.83	0.73	0.53
11	0.73	0.66	1.14	0.79	0.71	1.23	1.03	0.77	0.87	0.68	0.56
12	0.52	0.80		1.06	0.96	0.91	0.72	0.93	0.75		0.70
13	0.74	0.75	1.05	1.07	0.97	0.80	0.70	0.81	1.01	0.64	0.60
14	0.78	0.89	0.88	0.94		0.91	0.67	0.73	0.93	0.75	0.52
15	0.76	0.99	0.89	0.66	0.73			1.00	0.74	0.77	0.66
16	0.64	0.70	1.11	0.79	0.61	0.75		0.79	0.73	0.87	0.44
17	0.64	0.94	0.74	0.77	0.71	0.72	0.76	0.84	1.03	0.73	0.61
18	0.95	0.99	0.92	0.91		0.66	0.83	0.77	0.74	0.79	0.45
19	0.58	0.66	0.71	1.07		0.83	0.93	0.92	1.23	0.99	0.55
20	0.62	0.78	0.75	0.93	0.75	0.68	0.69	0.74	1.01	0.81	0.73
21		0.60			0.72	0.56		0.87	0.87	0.78	0.80
22	0.65	0.80		0.80		0.90	1.04	0.84	0.97	0.90	0.69
23		0.68	0.77	0.85	0.69	0.75		0.70	0.90	0.68	0.68
24	0.66	0.94	0.81	0.82	0.75		0.70	0.82	0.92	0.85	0.67
25	0.60	1.12		0.86	0.90	0.85	0.80	1.00	1.02	0.65	0.49
26	0.70		1.08	1.11		0.95		0.97		0.79	0.83
27	0.72	0.79	0.97	0.72	0.89	0.87	1.04	1.04	0.93	0.76	0.32
28	0.75	0.61	0.69	1.05		0.95	0.58	1.04			0.53
29	0.66	0.90	1.00	1.05		0.75	0.74	0.73	0.77	0.80	0.73
30	0.43		0.94	0.83	0.77	0.79	0.88	0.92		0.73	0.40
31	0.89	0.90		0.79	0.82	0.86	0.93	0.92	0.85	0.71	0.68
32	0.44	0.89	1.04	1.04	0.66	0.94	0.91	1.08	0.92	0.81	0.65
33	0.66	0.64	0.76	0.84	0.94	0.73	0.67	1.01	0.70	0.65	0.52
34	0.52	0.87	1.39	0.94	0.71	0.67	1.10	0.79	0.93	0.79	0.53
35	0.77	0.95	1.28	0.99	0.76	1.14		1.08	1.04	0.97	0.45
36		0.70		0.87	1.27	1.01	1.19	0.98	0.99	0.93	0.71
37	0.79	0.93	0.93	0.84	1.10		1.13	1.13	0.80	1.05	0.59
38	0.74	0.70	1.11	1.23		0.82	0.93	0.91	0.88	0.96	0.63
39		0.87	1.12	1.00	1.02	0.93	0.77	0.81	0.96	0.90	0.77
40	0.68	0.90	1.00	0.74	0.73		0.75	0.93	0.96	0.79	0.67
41	0.63	0.81	0.93	1.29	0.99	0.90	0.67	0.72	0.61	0.75	0.68
42	0.57	0.76	0.91		0.78	0.90	0.71	0.78	0.64	0.93	0.73
43	0.80	1.04	0.87	1.07	0.72	0.94	0.83	1.16	0.79	0.86	0.71
44	0.65	0.71	0.82	0.93	0.66	1.09	0.67	0.85	0.74	1.16	0.61
45	0.79	0.75	0.75	0.63	0.79	0.72	1.15	1.08	0.76	0.78	0.86
46	0.63	0.69	0.89	0.84	0.77	0.80	0.76	0.86	0.80	0.65	0.55
47	0.57	0.80	0.86			1.15	0.76			0.76	0.54
48	0.88	0.68	0.96	0.89	0.70	0.80	0.79	1.02	1.03	0.81	0.62
49	0.64	0.76	1.29	0.89	0.81	0.77	0.84	0.83	1.13	0.87	0.65
50	0.60	0.86	0.93	0.88		1.07	0.89	0.99	0.75	0.81	0.60
51	0.82	0.97	0.93	0.73		1.03		0.88	0.94	0.82	0.91
52	0.97	0.72	0.84	0.87	0.78	0.84	1.06	0.88	0.85	0.85	0.60
53	0.67	1.00	0.98			1.10	0.94	0.75	1.04	0.82	0.77
54	0.83	1.06		1.13	0.68		0.83	0.90	0.72	0.93	0.58
55	0.74	0.65	0.97	0.74	0.80	0.68	1.05	1.00	1.00	0.75	0.84
56	0.79	0.76	0.80	1.17	0.88	0.96	1.06	0.81	1.23	1.11	0.59
57	0.90	0.90	1.22	1.05	0.84	0.99	1.07	0.96	0.95		0.77
58	0.66	1.00	0.76	0.98	0.86	0.96	0.75	0.66	0.68	0.69	0.70
59	0.81	0.77	1.10	0.83	0.62	0.88	0.92	0.72	1.10	0.71	0.54
60	0.87	0.81	0.99	0.81	0.92	0.78	0.89	1.04	0.70	0.94	0.79
61	0.72	0.92	0.91	1.20	0.59	1.14	0.84	0.70		1.02	0.86
62	0.60		0.96	0.94	0.96	0.99	0.97	1.01	0.62	1.00	0.87

**1997 Cannelton Clam Biomonitoring Study
End-of-Test Tissue Weights (g-wet) by Station**

	63	0.77	0.90	0.97	0.92	0.70	1.10	0.89	1.08	0.87	1.02	0.78
	64	0.85	0.91	0.86	0.58	0.86	1.29	0.73	0.50	1.09	0.96	0.63
	65	0.85	1.05	0.81	0.80	0.80	0.82	0.78	0.91	0.77		0.75
	66	0.87	0.85	0.64	1.00			1.23	0.80	1.14	0.66	0.77
	67	0.84	0.86	0.52	1.28		1.09	0.73	0.95	0.84	0.91	1.08
	68	0.77	0.85	1.04	0.87		0.87	0.78	0.91	0.81	0.83	0.70
	69	0.81	0.79	0.96	0.97	1.03	0.74		1.04	0.91	0.69	0.54
	70	0.81	0.78	0.89		0.92	0.85	0.93	1.04	0.97	0.91	0.51
	71	0.89	0.96	0.87	0.69	0.78	1.13	0.87	0.89	0.81	0.63	0.90
	72	1.04	0.82	1.05	0.64	0.56	0.74			0.78	0.81	0.56
	73	0.60	1.05	1.21	1.06	0.70	0.83	0.80	0.89	1.20	0.74	1.08
	74	0.65	0.76	0.91	0.71	0.68	1.13	0.79	0.97	0.88	0.95	0.66
	75	1.11			1.08		1.11	0.89	1.01	1.15	1.03	0.81
Rep	4-	0.54	1.03		0.81	0.85	0.77	0.70	1.03	0.82	0.47	0.63
1												
	2	0.64	0.77	0.74	0.75	0.75	0.79	0.64	0.84	0.74	1.01	0.51
	3	0.87	0.82	0.97	0.82	0.72	0.79	0.72	0.75	0.69	1.00	0.72
	4	0.69	0.87	0.70		0.63	0.71	0.76		0.84	0.45	0.62
	5	0.96	0.73	0.91	0.85	0.73	0.84	0.67	0.84	0.96	0.86	0.54
	6	0.84	0.74	0.99	0.78	0.82	0.85	0.92	1.02	0.73	0.81	0.73
	7	0.58	1.21	0.84	0.92	0.66	0.87	0.89	1.05	1.04	0.83	0.49
	8	0.51	0.78	1.07	0.62	0.98	1.08	0.87	0.75	0.90	0.98	0.61
	9	0.83	1.04	0.97	0.80	0.74	0.75	0.86	0.94	0.98	0.70	0.47
	10	1.01	0.68	0.82	0.74		0.97	0.84		0.71	0.92	0.64
	11	0.66	0.61	0.88	0.80	1.01		0.94	0.81	0.83	0.68	0.41
	12	0.94	1.06	1.10	0.87		0.73	0.78	0.83	0.73	0.93	0.60
	13	0.72	0.66		0.68	0.94	0.83	0.90	0.99	1.19	0.81	0.55
	14	0.75	0.89	0.90	0.78	0.83	0.73	0.78	0.78	0.70	0.66	0.76
	15	0.74	0.71	0.72	0.91	0.64	0.80	1.05	0.72	0.94	0.82	0.86
	16	0.64	0.83	1.09	0.58	0.84	0.86	0.79	0.73	0.82	0.73	0.71
	17	0.75	0.94	1.26	0.81	0.57	1.03	0.81	0.77	0.94	0.75	0.55
	18	0.76	0.89	0.77		0.66	0.91	1.06	0.97	0.67	0.67	0.70
	19	0.90	0.72	0.97	0.75	0.75	0.76	0.78	0.69	1.03	0.88	0.41
	20	0.72	0.72	1.02	0.77	0.91	0.71	0.70	0.68	0.53	0.88	0.71
	21	0.70	0.81	0.89		0.74	0.91	0.69	0.64	0.90	0.75	0.90
	22	0.72	0.86	1.16	0.93		0.92	0.87	0.69	0.84	0.72	0.50
	23	0.77	0.83	1.06	1.04		1.06	0.79	0.99	0.70	0.75	0.73
	24	0.70	0.72	0.87	0.83	0.80	0.78	0.89	0.95		0.81	0.58
	25		0.86	1.04	0.90		0.77	0.80	0.79	0.70	1.14	0.52
	26	0.85	0.99	0.69	0.80	0.99	0.76	0.97	0.77	0.83		0.54
	27	0.67	0.99	0.71	0.79	0.76	1.04	0.64	0.85	0.76	1.10	0.77
	28	0.61	0.92	0.50		0.62	0.42	0.79	0.66			0.56
	29	0.69	0.70	1.08	0.61	0.96	0.80	0.84	0.94	0.91		0.57
	30	0.69	0.80	0.92	0.99	0.70	1.00	0.67	0.91	1.02	1.03	0.78
	31	0.71		0.66	0.80	0.66	0.89	0.96	1.09	0.88		0.52
	32	0.75	0.66	0.96	1.13	0.98	0.69	0.80	0.89	0.78	0.71	0.78
	33	0.93	0.85	0.83	0.84	0.78	1.04	1.11	0.93	0.82	0.93	0.63
	34		0.80	0.95	1.01	0.64	0.83	0.83	0.67	0.89	0.83	0.84
	35	0.70	0.92	0.69	0.90		0.69	0.78	1.29	0.76	0.87	0.56
	36	0.79	0.91	0.76	0.82		0.88	1.02		0.73		0.41
	37	0.88	0.70	0.81	0.74	0.78	0.74	0.98	0.85	0.80	0.94	0.63
	38	0.89	1.10	1.13		0.88	1.04	1.14	1.30	1.12	0.83	0.67
	39	0.75	0.71	0.88	0.89	0.85	0.83	0.80	0.86	1.10	0.88	0.56
	40	0.87	0.69	1.09			1.17	0.75	0.80			0.52
	41	0.88	0.39	0.70	0.75		0.78	0.84	1.04	0.72	0.89	0.62
	42	0.69	0.61		0.73	0.62	0.78	0.67	0.89	0.68	1.05	0.61

**1997 Cannelton Clam Biomonitoring Study
End-of-Test Tissue Weights (g-wet) by Station**

43	0.76	1.04	1.32	1.19	0.76	0.88	0.82	0.86	0.78	0.99	0.68
44	0.82	0.48	0.83		0.97	0.83	1.07	0.97	0.82	0.70	0.40
45	0.78	0.76	1.05	1.14	0.57	0.93	0.94	1.02	0.74	0.79	0.66
46	0.61	0.89	0.76	0.74	0.70	0.95	0.72	0.98	0.76	0.85	0.52
47		0.83	0.76	0.73		0.84	0.74	0.84	0.79	0.84	0.72
48		1.03	1.00	0.61	0.78	1.08	1.22	0.81	0.96		0.74
49	0.66	1.09	0.78	0.85		1.08	0.78	0.88		0.85	0.65
50	0.62	0.81	1.21	0.74	0.83	0.81		0.74	0.81	0.99	0.71
51	0.79		0.78	0.96	0.97	0.94	0.94		0.96	1.29	0.65
52	0.95	0.81	0.81	0.77	0.84	0.74	0.57	0.74	1.10	1.05	0.56
53	0.74	0.66	0.91	0.86	0.83	0.89	0.65		0.92	0.85	0.70
54	0.73	1.08	0.82		0.72	0.68	0.91	0.73	0.77	0.79	0.68
55	0.60	0.83	0.90	0.87	0.61	1.15	0.80	0.96	0.83	0.77	0.61
56	0.58	0.99	0.89	1.18	1.18		0.83	0.82	0.84	1.08	0.65
57	0.75	0.71	0.60	0.66	0.70	0.89	0.76	0.88	1.00	0.94	0.65
58	0.90	0.72	1.12			0.98	0.75	0.66	0.87	0.87	0.64
59	0.69	1.03	0.88	0.75	0.71	0.53	0.68	0.78	0.71	0.90	0.95
60	0.66	0.97	0.91	0.87	0.74	0.90	1.04	0.82	0.86	0.87	0.56
61	0.92	0.93	1.26	0.98	0.94	1.07	0.80	0.99	0.72	0.81	0.39
62	1.02	1.06	0.99	0.75	0.68	1.01	1.15	0.92	0.90	0.92	0.67
63	0.66	0.75	1.05		1.01	0.70	1.01	0.90	0.76	1.13	0.71
64	0.88	0.73	1.23	0.95	0.69	0.77	1.07	1.01		1.17	1.06
65	0.98	0.87	1.13	0.83	0.95	0.79	1.02	1.71	0.70	0.88	0.88
66		0.72	0.91	1.21	0.76	0.83	1.04	0.86	0.88	0.87	0.73
67	1.11	0.74	0.80	0.84	0.64	0.69		0.45	0.95	0.79	0.89
68	0.53	0.70	1.22	0.90	0.89	0.88	0.55	0.83	0.97	0.91	0.77
69	0.70	0.69		0.94		0.88	1.05	0.66	0.98	0.78	0.58
70	0.87	0.80	0.80	0.83	0.88	0.83	1.00	0.99	0.77	0.93	0.51
71	0.66	0.72	0.67	0.94	0.69	0.65	1.06	0.99	0.81	0.90	0.53
72	0.69		0.95		0.81		0.81	0.79	0.92	0.74	0.78
73	0.95	0.84	0.84	1.07	0.86	0.82	0.94	0.77	1.02		0.61
74	0.81	1.08	0.82	0.72		0.75	0.98	0.92	1.11	1.01	0.72
75	0.82	1.07	0.71	0.87	0.84	0.86	1.02	0.78		0.94	0.69

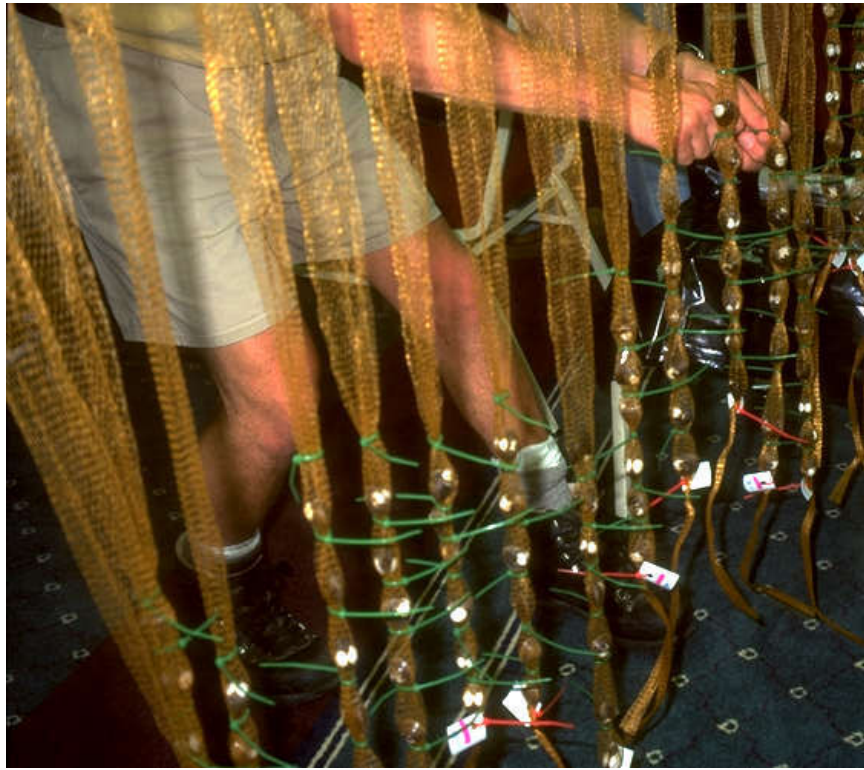
APPENDIX F
PHOTOGRAPHS OF SAMPLING EVENTS AND ACTIVITIES



1. Sorting clams by size prior to distributing among mesh bags



2. Weighing individual clams



3. Distributing clams to mesh tubes. Plastic cable ties used to maintain order and create "compartments" in mesh tubes



4. Attaching filled mesh tubes to PVC cages prior to deployment in Tannery Bay



5. PVC cages containing clams prior to deployment



6. Attaching predator mesh



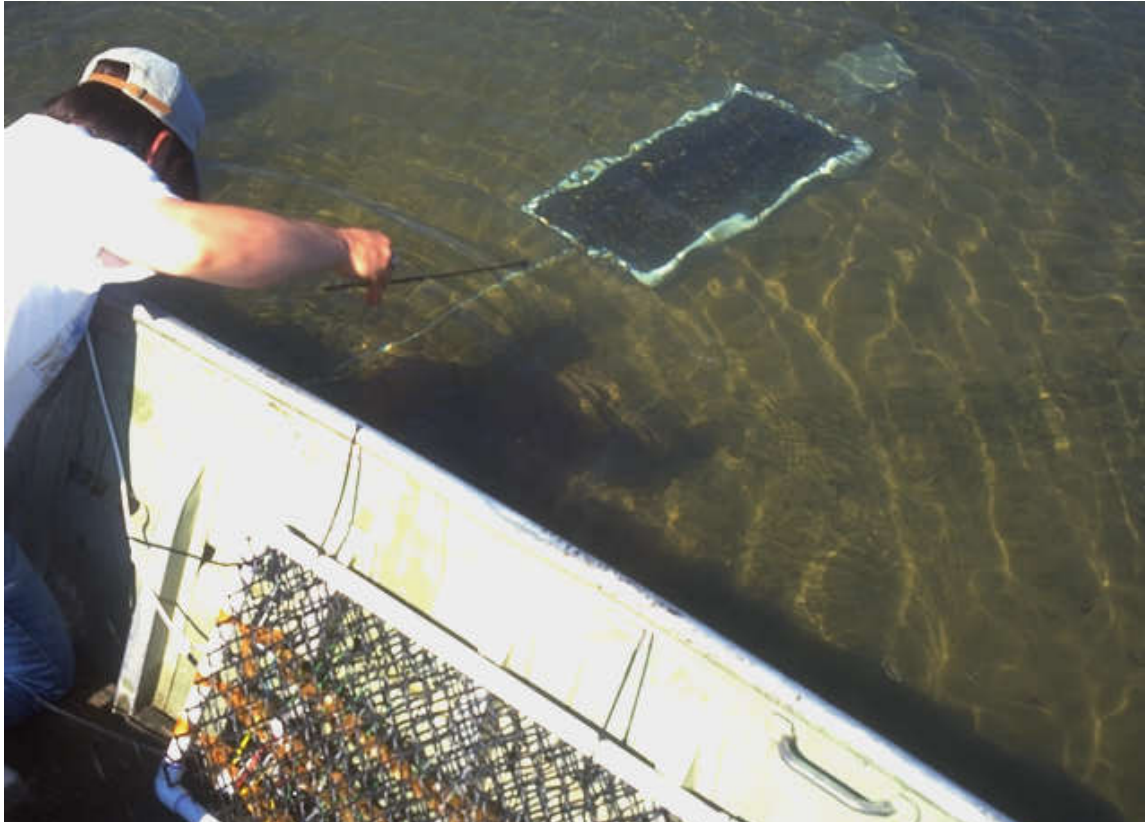
7. Deploying a clams at the holding site



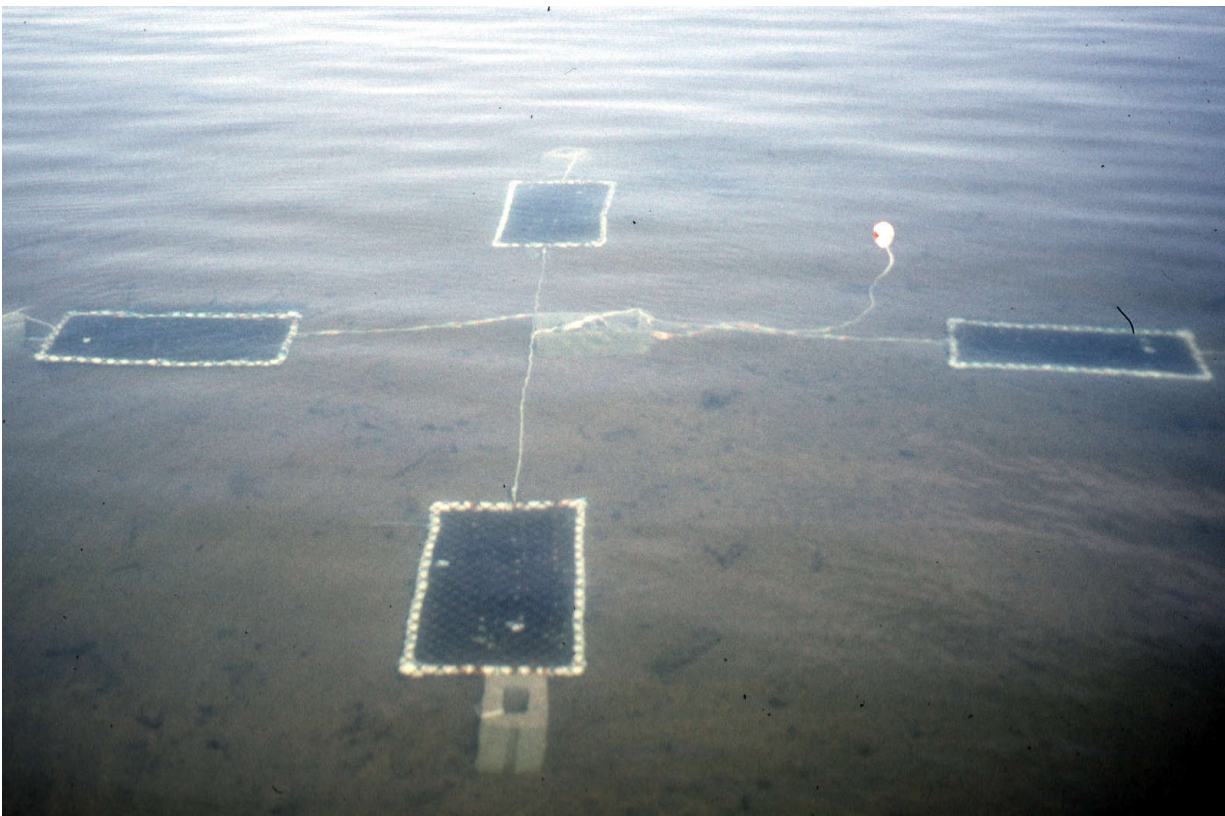
8. Retrieving clams at the holding site



9. Preparing cages for deployment. For each station, caged clams, surrounded with predator-protection mesh, are tethered together and attached to a cement block



10. Deploying caged clams in Tannery Bay



11. Completed deployment of 4 cages and cement weight



12. Removing soft tissues from clams for chemical analyses



13. Compartmentalized tray used to maintain order of clams during the tissue removal process



14. Weighing soft tissues from individual clams prior to preparing composites for chemical analysis



15. Aerial shot of Tannery Bay