NOAA Technical Memorandum NOS ORCA 136

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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Hazardous Materials Response and Assessment Division
National Ocean Service
National Oceanic and Atmospheric Administration
7600 Sand Point Way NE
Seattle, Washington 98115-0070

and

EVS Consultants, Inc.
200 West Mercer Street, Suite 403
Seattle, Washington 98119

September 1998

Seattle, Washington

Hazardous Materials Response and Assessment Division
Office of Ocean Resources Conservation and Assessment
National Ocean Service
National Oceanic and Atmospheric Administration
U.S. Department of Commerce
Silver Spring, Maryland

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Cannelton Industries Site
Sault Ste. Marie, Michigan
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Prepared for

U.S. Environmental Protection Agency, Region V
77 West Jackson Boulevard
Chicago, Illinois 60604

Prepared by

Hazardous Materials Response and Assessment Division
National Oceanic and Atmospheric Administration
7600 Sand Point Way NE
Seattle, Washington 98115-0070

and

EVS Consultants, Inc.
200 West Mercer Street, Suite 403
Seattle, Washington 98119

EVS Project No. 2/575-38

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1.0 Introduction

The purpose of this document is to present the results of the baseline clam monitoring study conducted for the Cannelton Industries, Inc. site, situated adjacent to the St. Mary's River, Sault Ste. Marie, Michigan. This baseline is being conducted as an initial phase of long-term monitoring to verify the effectiveness of the selected remedy for this site. There is concern that indigenous and migrating species utilizing the site may be subject to adverse impacts from waste materials at the site (Cannelton Ind. 1995a). Metals contamination in Tannery Bay is largely present in tannery waste and organic soils, which have the capacity to immobilize metals and limit their bioavailability.

Previous analyses indicated that contaminated soils, wastes, and sediments have low potential for leaching (Cannelton Ind. 1995a). The results of these studies also suggest that there is minimal leaching and movement of contaminants from site soils into groundwater and surface water. Sediment toxicity and bioaccumulation studies performed during pre-design investigations indicated that contaminated soil and sediment which would remain unremediated do not pose an unacceptable risk to aquatic and terrestrial organisms. However, some results of these studies were inconclusive. The Pre-Design studies suggest that the high organic load in Tannery Bay sediments is reducing the availability of metals for accumulation by aquatic organisms (Cannelton Ind. 1995a). Analysis of aerial photos indicates that sedimentation is occurring in the western portion of Tannery Bay and may be providing a natural cap for contaminated sediments.

The Amended ROD (U.S. EPA 1996) requires that a monitoring program for Tannery Bay include evaluation of the bioavailability of site contaminants to ensure the protectiveness of the remedy for aquatic organisms and wildlife. In response to the U.S. EPA's request, NOAA designed a biological monitoring program using caged clams and conducted the baseline sampling. This report details the methods and results for the baseline study, and provides recommendations for future years' monitoring.

1.1 Background

The Cannelton Industries, Inc. site, the location of a former tannery, covers 23 hectares (ha) (75 acres) along St. Mary's River in Sault Ste. Marie, Michigan (Figure 1). Most of the shore areas are wetlands, with wetland vegetation, soils, and hydrology. Wetland forest species and emergent cattail marshes are the primary vegetation types present. From 1900 to 1958, tannery and animal-hide processing operations were conducted at the site. Waste products from these operations were routinely discharged to shoreline areas via three facility

drainage systems. Trace elements (chromium, mercury, lead, cadmium, and arsenic), cyanide, calcium carbonate, sulfide, brine, organic solvents, formic acid, carbolic acid, formaldehyde, ammonia, and alcohols were the primary contaminants associated with the waste products (WW Engineering 1991). In 1955 the site became the property of the Fiborn Limestone Company, a subsidiary of Algoma Steel Corporation. A fire damaged the buildings in 1958, which were subsequently torn down and removed. The facility has remained unused and vacant since then. In 1964 the property was transferred to Cannelton Industries, another Algoma subsidiary.

In 1978, the Michigan Department of Natural Resources determined that soils, groundwater, and river sediment from the site were contaminated with heavy metals, primarily chromium and mercury (U.S. EPA 1994). The site was listed as a National Priorities List (NPL) site in 1990 (U.S. EPA 1994). Supplemental investigations confirmed that surface sediments in Tannery Bay contained elevated concentrations of chromium and mercury (Kracko 1992). Maximum concentrations of chromium and mercury reported in that study were 40,000 and 2.29 mg/kg dry weight, respectively. Laboratory tests conducted with sediments collected from St. Mary's River and Tannery Bay suggested potential toxicity. However, the responses of test organisms were associated, not clearly correlated, with site contaminant concentrations. The small size of the data set limits definitive conclusions. Laboratory tests were conducted with the midge *(Chironomus riparius),* amphipods *(Hyalella azteca),* and green *algae (Selenastrum capricornutum).* The results of the *Chironomus* bioassays indicated that sediments were not acutely toxic; there were no statistically significant differences in mortality between sample locations and the reference location or the laboratory control. The weight of *C. riparius* was moderately correlated (r^2=0.63) with chromium concentration. The results of the *Hyalella* test were mixed. Mortality was observed in all sediment samples, including sediment from the upstream reference location, and ranged from 45% to 100%. There was no correlation between observed mortality and chromium concentrations, nor between any other metal concentration or physical parameter measured.

As mandated in the signed 1992 ROD for the Cannelton Industries site, a study was initiated in 1994 to determine the extent of contamination in river sediments and the bioaccumulation of chromium and mercury in aquatic biota. Sediments in Tannery Bay were found to be contaminated with chromium and mercury at maximum concentrations of 30,000 and 1.7 mg/kg wet weight, respectively (U.S. EPA/ERT 1995). Fish and crayfish were also collected from Tannery Bay during that study; tissues were analyzed for metals and percent moisture. Maximum concentrations of chromium in minnows and crayfish collected from Hairball Beach were 7.6 and 29 mg/kg wet weight, respectively. Maximum concentrations of mercury in the same species were 0.03 and 0.08 mg/kg wet weight, respectively. Based on the results of aquatic studies, the U.S. EPA has concluded that, although there are potential ecological risks due to mercury

exposure at the site, there is no incremental increase in mercury risk associated with the site (Jones 1996). This decision was based on the absence of any demonstrated difference in mercury body burden between the reference and any other sampling locations, or between sampling locations. The mercury risk conclusion was consistent with the system-wide problem of mercury in St. Mary's River.

1.2 Program Objectives

The purpose of the biomonitoring program is to document whether the selected remedy for the site is effective at reducing concentrations of bioavailable trace elements in Tannery Bay. The specific objectives of the biomonitoring program are to determine 1) whether chromium, total mercury, methylmercury, lead, cadmium, and arsenic in Tannery Bay sediments are available to biota residing in and/or using the Bay, and 2) whether exposure to bioavailable concentrations of metals may adversely affect local biota.

The objective of this study is to provide baseline data for the biomonitoring program. To assess availability, uptake of these trace elements was measured in tissues of caged clams, *Corbicula fluminea,* transplanted to Tannery Bay and reference areas. Changes in bioavailability over time will be determined by comparing tissue residue levels measured in future years with the values measured in the present baseline study. Survival and changes in clam whole-animal weights and end-of-test tissue weights were evaluated as indicators of potentially adverse effects. This study is not designed to assess all acute and chronic aquatic toxicity endpoints. Therefore, lack of effects demonstrated by this study does not preclude the potential for reproductive or other physiological effects. Measurements made during 1997 will provide a baseline for subsequent monitoring years. Impacts of contamination to the ecological food chain will be assessed in subsequent sampling events following remediation.

The long-term biomonitoring program will generate biological and chemical data to meet the program objectives. This biomonitoring program has three components: 1) evaluation of clams transplanted to the study area for uptake of trace elements and growth effects, 2) analysis of sediments for concentrations of metals and selected physicochemical parameters, and 3) analysis of surface water for chlorophyll-*a* and selected physicochemical parameters. Evaluation of these synoptic data can be used to evaluate changes in chemical bioavailability and potential effects on local biota.

2.0 Study Design and Methods

This section describes the methods used in the baseline biomonitoring study with caged clams. The bioavailability of chemicals was assessed by measuring accumulation in clam tissues after a fixed exposure period. Effects from exposure to site-specific conditions were assessed by comparing survival and changes in growth among stations. The methods used to collect and analyze the surface-water and sediment samples are being prepared by Cannelton as a separate report. The appendices contain all data obtained during the baseline monitoring study, as well as the statistical processes used to analyze this data, and procedures for elements of this study that are not readily available in the open literature.

2.1 Site Description, Sampling, and Reference Stations

The Cannelton Industries site is located on the south bank of St. Mary's River in Sault Ste. Marie, Chippewa County, Upper Peninsula, Michigan (Figure 1). The site is bounded to the north by St. Mary's River and Tannery Bay, to the south by 4th Avenue and the Soo Railway, to the west by 18th Street, and to the east by open land. Tannery Bay and St. Mary's River were general waste dumping areas and tannery waste discharge areas during facility operations (U.S. EPA/ERT 1995). Aerial photographs indicate that some of the tannery waste deposited on the St. Mary's River shoreline has eroded over time. Both this eroded material and material dumped into the river during the plant's operation were likely carried downstream by the river and deposited both along the shoreline of Tannery Point and in the low-energy water found downstream in Tannery Bay (WW Engineering 1991).

Tannery Bay was selected as the primary area of investigation for this biomonitoring program because sediments from this area historically have the highest concentrations of trace elements associated with tannery wastes. Eight stations in Tannery Bay were monitored during this baseline monitoring study (Figure 1). The distribution of stations in Tannery Bay was designed to allow a thorough evaluation of chemical bioavailability. Some of these stations represent areas previously identified as ìhot spotsî of chromium and/or mercury contamination.

Reference areas have a key role in evaluating field bioassays. Reference areas should be similar to the treatment sites, with no source of contamination, and reflect conditions that exist at the treatment sites. Because of the difficulty in identifying one representative reference site, more than one reference station is used. In this approach, the reference locations are not viewed as a single station or point, but as the average of all the individual reference samples. Because of widespread contamination in Tannery Bay and in St. Mary's River in the vicinity of the tannery site, it was deemed necessary to situate reference stations in other

embayments of the river. Potential reference sites along the open shore areas of St. Mary's River to the west of the Cannelton facility–including Seymour Creek, Izaak Walton Bay, and Waiska Bay–were surveyed and evaluated for their suitability as reference areas. One reference station (Reference Station 1) was established in Waiska Bay to represent highly vegetated, shallow habitats. A second reference station (Reference Station 2) was established in St. Mary's River near the mouth of Seymour Creek to represent sandy, shallow habitats with minimal vegetation. St. Mary's River is a highly dynamic system, with very few low-energy areas similar to Tannery Bay making it difficult to identify areas appropriate for use as reference.

In addition to the two reference areas, a holding site was identified and used for short-term holding of clams and as a source of clean water from St. Mary's River. The holding site was located nearshore in St. Mary's river upstream of the old Oriole Boulevard boat ramp (Figure 1).

2.2 Species Selection

A non-resident freshwater clam, *Corbicula fluminea,* was selected for this monitoring program because they are routinely used in environmental assessment programs and have been used extensively to assess metals and organic chemical contamination (Belanger et al. 1987; Colombo et al. 1995; Doherty 1990; Elder and Mattraw 1984; Farris et al. 1988; Foe and Knight 1987; Leland and Scudder 1990; Luoma et al. 1990; Mac et al. 1984; Tatem 1986). *Corbicula fluminea* exhibit a high tolerance for the effects resulting from exposure to toxic substances. They accumulate and concentrate trace elements and metals to concentrations that are orders of magnitude greater than concentrations found in surface waters without demonstrating high rates of mortality. If the transplanted species shows accumulation of chemicals, then exposure and effects in resident species, including predator species, may also be of concern.

Corbicula live in the sediments but are filter feeders – they feed primarily on suspended seston (i.e., phytoplankton, bacteria, and fine detritus) by filtering suspended material from water as it passes over the gills. *Corbicula* filter particles from 1.5 to 10 microns (μ) in size and can efficiently filter particles smaller than 1.0 μ. Although *Corbicula* inhabit, and remove detrital particles from the sediments, they do not ingest sediment directly (D. Cherry, pers. commun. 1998). Researchers conducting extensive studies on *Corbicula* over the past 20 years have examined numerous clams and found none to contain sediment in their gut. Denser, larger particles are bound in mucus and carried by a ciliated ventral groove to the tip of the palp for release onto the mantle as pseudofeces; pseudofeces are carried by mantle cilia and expelled through the inhalant siphon. Particle sorting appears to be a function of particle size and density (McMahon 1991). This feeding strategy makes *Corbicula* a good biomonitoring organism: they are actively exposed to the sediment/surface-water interface where chemical activity and chemical exchange between the water and sediments are high due to continuously changing physical/chemical conditions (D. Cherry, pers. commun. 1998).

2.3 Clam Collection, Sorting, Distribution, and Deployment

Clams *(Corbicula fluminea)* were collected by hand from runs and riffles in Saline River, Arkansas on July 8, 1997 by Dr. J. L. Farris, Arkansas State University. All clams were collected from areas presumed free of chemical contamination, disease, and pest species (e.g., Zebra mussels). At the collection site, clams were sorted by size (>1 cm, <3 cm shell length) and checked for condition (i.e., damaged shells). Clams outside the desired size range or in poor condition were rejected. Clams were held in a laboratory flow-through system without sediment for 4 days for acclimation to temperature, dissolved oxygen, and pH conditions characteristic of the deployment sites. The clams were not fed during the acclimation period to encourage elimination of all material from the gut. After acclimation, approximately 5000 clams were placed in ice chests containing cool, moist packing material (not wet) and sent via air freight to Sault Ste. Marie, Michigan. Total shipment time was approximately 15 hours. Within 6 hours of delivery in Sault Ste. Marie on July 15, 1997, the clams were removed from their packing and inspected for overall condition. The clams appeared to be in excellent health, with less than 1% mortality.

Whole-animal wet weight, measured to the nearest 0.01 g, was the criterion used to select clams for this baseline monitoring study. The clams were removed from their packing material and placed into tubs containing fresh water from the holding site. All clams were processed and treated according to the draft guidelines submitted to ASTM for review (Appendix A). A rough sort was conducted to separate clams into small, medium, large, and extra large size-classes. Based on the distribution of sizes, the number within each size category, and the amount of tissue required for chemical analyses, only clams >4.0 and <8.0 g whole-animal wet weight were selected for use in this study. Following the rough sort, the clams were distributed to the mesh tubes as described below. The pre-sorted clams were maintained in the holding tubs until needed for distribution. Their normal temperature range was maintained during all phases of the setup activities by placing bags of ice in the tubs of fresh river water. Detailed attention was given to the care and handling of clams throughout the setup process to minimize stress to the animals and to ensure that all test animals were of high quality.

Just before the final measurement and distribution processes, small batches of clams were removed from the holding tubs and placed into smaller bowls filled with cool, fresh water. The clams were kept in water before being measured to ensure the internal cavity between the shells was completely filled with water, eliminating potential errors in whole-animal wet weights associated with air bubbles. Only live animals that were completely submerged and fully closed, or those that closed immediately upon light physical stimulation, were used. Closed clams that appeared to be ìfloatingî or ìbuoyantî were not used because this is a sign of air bubbles between the shells.

The measurement process involved obtaining and recording the whole-animal wet weight for each clam, measured to the nearest 0.01†g with an electronic balance. After the weight measurements, each clam was placed into a pre-labeled mesh tube ~10.2 cm (4 inches) in diameter and 2.1 m (7 ft) long; 0.6-cm (0.25-inch) mesh size. Nylon cable ties were used to separate individual clams within the tube. Each tube contained 25 clams. After all clams were distributed to the mesh tubes, they were placed in an ice chest and transported to the holding area for overnight deployment. To minimize predation, the mesh tubes containing clams were placed inside an envelope made of heavy-duty plastic screen. The clams were held at this location for approximately 14 hours before deployment in Tannery Bay beginning on July 16, 1997.

Four cages, each containing 75 clams, were deployed at ten stations: eight Tannery Bay and two reference stations. Station 11 was used to represent the clams to be used for beginning-of-test weight measurements and chemical analysis of tissues. Prior to deployment in Tannery Bay and at the reference stations, the mesh tubes containing clams were affixed to cages ~0.5 m wide by 1 m high constructed of 2.5-cm diameter polyvinyl chloride (PVC) pipe material. Each cage contained 75 clams, and 4 cages were prepared for each station for a total of 300 clams per station. Large nylon cable ties were used to secure the mesh bags to the PVC cage. One continuously recording temperature-monitoring device was attached to one clam cage for each station and set to collect temperature data at 12-min intervals over the deployment period. The cages were then wrapped with the heavy-duty plastic screen (~2.5-cm mesh size) to discourage predators. The completed cages were then placed back into the water at the holding area until deployment.

Before deployment, a random-numbers table was used to assign cages to stations. The cages, numbered from 1 to 44, were assigned station numbers by using the first 2 digits of the 5-digit random numbers. If the 2-digit number was between 01 and 11, it was used as the station number for Cage 1. The next 2-digit number between 01 and 11 was identified and used as the station number for Cage 2. This process was continued until all cages were assigned a station number from 1 through 11, with four occurrences of each station number.

The data were normally distributed; an Analysis of Variance test (ANOVA) was used to confirm statistically similar size distribution of clams among cages and stations (P=0.05). At the beginning of the test, the mean clam weight was statistically similar among all 44 cages. The data were pooled by station and analyzed for similar size distribution; there was no statistical difference in mean clam size among any of the 11 stations at the beginning of the test. Results of the statistical analyses are summarized below; complete details are provided in Appendix D.

ANOVA Results
H_0 = No significant differences in whole-animal wet weight among cages.

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between groups	32.243	42	0.7677	1.093392	0.314455	1.387843
Within groups	2234.168	3182	0.702127			
Total	2266.411	3224				

ANOVA Results
H_0 = No significant differences in whole-animal wet weight among stations.

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between groups	5.851184	10	0.585118	0.831173	0.598455	1.833573
Within groups	2315.347	3289	0.703967			
Total	2321.199	3299				

SS–sums of squares; df–degrees of freedom; MS–mean square; F–F statistic = group MS/ error MS; P-value–probability value; F crit–critical value for determining significance of F statistic.

Cages were deployed at Stations 1, 3, 4, 5, 6, and 8 on July 16, 1997. The remaining cages for Stations 2, 7, 9 and 10 were held overnight at the holding area until deployment the following day. Four cages of clams were deployed at each station and placed about 2 m apart around the center of the station (Figure 2). A cement block was positioned in the center of the deployment station. The cages were secured to the block with nylon rope and situated ~2 m from the block. Smaller cement blocks were used as weights to hold each cage in position. Surface markers were used to identify the deployment locations. Cages for Station 8 and Reference Station 2, areas likely encountered by boaters, were labeled with a warning tag to discourage vandalism or removal by trespassers. Stations were positioned using a Trimble ProXL and ProBeacon differential GPS. Latitude and longitude coordinates for the stations are provided in Table 1. The survey locations are accurate to approximately ±2 m.

The water depth at each station was taken during deployment using a stick and metal tape measure. Depths ranged from 0.5 m (1.6 ft) to 1.4 m (4.5 ft) (Table 1). Because of the concern that some areas of Tannery Bay or Saint Mary's River would be exposed to air during a seiche, two pressure transducers (InSitu, Inc., PDX-260) were installed on July 18, 1997, one at the ìnorthernî end of the bay and one at the ìsouthernî end (Figure 1). The purpose of these transducers was to record water-level changes over the course of the biomonitoring study.

The transducers were removed on September 10, 1997. Figure 3 illustrates the water-level fluctuations during the study. The water levels ranged from –0.2 to 0.4 m (–0.47 to 0.97 ft) relative to the initial baseline measurement (Table 1). Comparing the initial water depths with the changes in depth shown in Figure 3 shows that the clams remained submerged throughout the entire study.

2.4 Beginning-of-Test Tissue Preparation

An additional 300 clams (i.e., 4 cages of 75 clams each) were used for initial tissue-weight determinations and chemical analyses to obtain background concentrations of contaminants. For tissue chemistry analysis, tissues from 75 individual clams in each cage are combined to form a replicate; therefore, each cage is considered an analytical replicate. All equipment (i.e., shucking knives and the aluminum foil covering the cutting boards) used during tissue extraction was thoroughly cleaned before processing a new batch (i.e., replicate) according to the following process: Wash with Liquinox, rinse with hot tapwater, rinse with deionized water. Prior to tissue removal, all staff thoroughly washed their hands with Liquinox. Gloves were not worn during the shucking process to reduce the potential for injury from slippery hands and handling wet clams. The shucking process began by notching the clam shell with a sturdy knife to allow penetration of a thin-bladed knife. A thin-bladed stainless steel knife was inserted into the notch and used to slice the clams in half. After the shells were spread apart, the thin-bladed knife was used to remove the soft tissues. The severed tissue was held in such a position that the excess liquid was allowed to drain. The soft tissues were kept on the shell during extraction and after complete separation. The shell was used as a ìholding dishî until tissue weights were made. A weigh pan was made from decontaminated aluminum foil. The soft tissues were placed on the weigh pan using the original shucking knife.

When all tissues of a ìreplicateî were weighed, the tissues were transferred from the weigh pan to certified clean sample jars provided by Brooks Rand, the analytical laboratory. Each sample jar was tightly capped, affixed with a prepared label, and placed in the freezer. The aluminum-foil weigh boat and cutting-board cover were discarded after all tissues of a given replicate were shucked and weighed. All shucking equipment was decontaminated before proceeding to the next sample.

The average whole-animal wet weights by cage for these 300 clams were statistically similar to each of the other cages prepared for deployment at the Tannery Bay stations. Actual whole-animal wet weights and tissue weight data for the 300 clams used to define initial weights for all clams are provided in Appendix E. The average tissue weight of 0.66 g was used as an initial estimate for all field-deployed clams.

2.5 End-of-Test Measurements and Tissue Preparation

All clam cages were successfully found and retrieved after the 55-day exposure period. Clams at Stations 1, 3, 4, 5, 6, and 8 were retrieved on September 9, 1997; clams at Stations 2, 7, 9 and 10 were retrieved the following day. After removal from the field stations, the caged clams were transported to Station 2 (the shallow-water reference site) for an overnight depuration period to purge their guts. To facilitate deployment logistics, the cages retrieved on September 9 were altered by combining all clam tubes for a given station onto one PVC frame. A fewer number of cages were retrieved on September 10th so that all station clams were not combined onto one cage for overnight depuration; clams remained attached to their original cages. For both days, the cages were deployed in a horizontal configuration on top of the cinder blocks used for tethering at each site. Several cinder blocks were used to ensure a stable configuration. This configuration prevented the clams from coming in direct contact with the sediments at the depuration site. Before retrieving the cages the following morning, they were visually inspected to ensure that they had not shifted via river current or vandalism during the night. Prior to making the end-of-test measurements, the clams were assessed for overall condition, and the number of dead and/or missing animals was recorded for each station. Clams that were gaping or did not close upon light physical stimulation were considered dead.

The end-of-test measurements involved whole-animal wet weights and soft-tissue weights for each live individual. The clams were processed one cage at a time. The clams were removed from the mesh tubes and placed, in sequence starting with the first clam in Bag-1, into compartmentalized holding trays. If a dead clam was encountered, the empty shells were placed into the compartmentalized holding tray as a marker. These holding trays were then placed into tubs containing river water to eliminate air bubbles between the clam shells. Starting with the first clam, the clam was taken from the holding tray, blotted dry, and the whole-animal wet-weight measurements were made using an electronic balance. The weighed clam was then put into a second compartmentalized tray to maintain proper sequence. The weight data were recorded manually onto laboratory data sheets and electronically to a computer file. The process was repeated until all individuals of a given cage were measured.

The clam tissues were processed after all whole-animal wet-weight measurements were made. The tissue extraction process was the same for the beginning-of-test clams (see Section 2.3). Tissues from all live clams (~75 individuals) found within each cage were pooled, creating a replicate sample for chemical analysis. When all tissues of a ìreplicateî were weighed, the tissues were transferred from the weigh pan into certified cleaned sample jars, as provided by Brooks Rand, Ltd. Immediately after compositing, the clam tissue samples were placed into a freezer. The frozen tissue samples were packed, cooled with blue ice to 0°C, and hand delivered to Brooks Rand, Ltd., of Seattle, Washington for homogenization, lipid analysis, percent water determination,

and chemical analysis of chromium, total and methylmercury, lead, cadmium, and arsenic.

2.6 Chemical Analyses

All tissue samples were received, stored, prepared, and analyzed according to Brooks Rand, Ltd., Standard Operating Procedures (Appendix C). Upon receipt, the tissue samples were assigned an internal tracking number. The tissue samples were preserved by freezing and stored in a Brooks Rand freezer until further processing.

For each chemical replicate, all tissues comprising that replicate were homogenized using stainless-steel homogenization equipment. All equipment was cleaned with Alconox and thoroughly rinsed with deionized water. One homogenization blank was collected for each homogenization batch. Blanks were collected between samples after equipment had undergone the normal cleaning procedure. All samples were homogenized prior to weighing aliquots for the various analytical parameters.

Methylmercury analyses were conducted in accordance with Brooks Rand Standard Operating Procedure (SOP) BR-0011. Before analysis, the tissue samples were digested in 25% KOH in methanol (w/v) in Teflon vials for 4 hr at 65°C. Samples were then analyzed by aqueous phase ethylation, Tenax trap collection, gas chromatograph (GC) separation, isothermal decomposition, and cold vapor atomic fluorescence spectrophotometry (CVAFS).

Total mercury analyses were conducted in accordance with SOP BR-0002. Before analysis, all tissue samples were digested with a 70:30 HNO_3:H_2SO_4 acid mixture and allowed to reflux for at least 3 hr. Samples were then brought to volume with deionized water and further oxidized with the addition of BrCl. Samples were analyzed by $SnCl_2$ reduction, gold amalgamation, and CVAFS detection.

Tissue samples to be analyzed for arsenic, cadmium, chromium, and lead were digested in accordance with EPA Method 200.3. No problems were encountered and no unusual observations were made during these analyses. Analyses for total lead, chromium, total cadmium, and total arsenic were performed in accordance with EPA Method 200.9. Samples were analyzed by stabilized temperature platform–graphite furnace atomic absorption (STP-GFAA) detection.

Dry-weight determinations (SOP BR-1501) were made by weighing out tissues on pre-weighed weigh boats and placing them in a drying oven (105°C). After 16 to 24 hr, the samples were removed and reweighed. One duplicate dry weight was measured for each batch of samples.

Percent lipid determinations were made by the Bligh and Dyer method. Weighed tissue-sample aliquots were placed in a glass tissue grinder with chloroform and methanol and ground for at least 2 min. More chloroform was added and the sample ground for 30 sec. Deionized water was added and the sample was ground again for approximately 30 sec. In the resulting biphase system, the chloroform layer contains the lipids and the methanol-water layer the non-lipids. A purified lipid extract is obtained when the chloroform layer is isolated. Samples were then allowed to dry at 55°C for at least 30 min. After drying, total lipids were determined by weight and converted to percent lipids based on the original aliquot weight, according to the following equation:

$$\text{Total lipid} = \frac{(\text{weight of lipid in aliquot}) * (\text{volume of chloroform layer})}{\text{Volume of aliquot}} .$$

For each chemical, the content (µg) in clam tissues was calculated on a per-replicate basis using the average whole-animal dry-weight value for that replicate and the chemical concentration data for that replicate. The content is reported in units of µg because this eliminates the need for many decimal places in the presentation. This process provided four content values per station for statistical comparison. Tissue content was calculated according to the following equation:

$$\text{Content (µg)} = [\text{concentration (mg/kg dry)}] * [\text{EOT tissue weight (g dry)}] * 1\ \text{kg}/1000\ \text{g} * 1000\ \text{µg}/1\ \text{mg} .$$

The content information was used to determine whether growing clams actually accumulated chemicals of concern, since the overall concentrations may actually decrease in fast-growing individuals due to growth dilution. Salazar & Salazar (1995) and Riisgård & Hansen (1990) have shown that faster-growing, smaller bivalves take up more contaminants, even though tissue concentrations decrease. Therefore, content provides data on net uptake or depuration and was used in this study to determine whether clams transplanted in St. Mary's River for 55 days contained more of a specific trace element than at the onset of the study.

2.7 Data Quality and Status Summary

2.7.1 Tissue Chemistry Data

All chemical data for this project were subjected to a quality assurance/quality control (QA/QC) review. Results of the laboratory QC measurements are provided in Appendix B. The data for the chemical analyses were also evaluated using the criteria described in the *ìFunctional Guidelines for Evaluating Inorganics Analysesî* in conjunction with laboratory-established quality control limits and the data-quality objectives specified in the *ìQuality Assurance Project Plan for Development and Implementation of Bivalve Monitoring Studyî* prepared for U.S. EPA Region V by NOAA/EVS Consultants (1997). In addition to checking the data against the project-specific data quality objectives (Table 2), the data were evaluated as listed below.

Holding Times ¾ The holding times for arsenic, cadmium, chromium, and lead are 6 months for unfrozen or 2 years for frozen samples. The holding times for mercury and methylmercury are 28 days for unfrozen and 1 year for frozen samples.

Initial calibrations and continuing calibration verifications ¾ The initial calibration must be established before each analysis period and have a regression factor of 0.995 or better. The continuing calibrations must be analyzed after every 10 samples and be within 25% of the absolute value.

Blanks ¾ A preparation blank must be digested and analyzed with each sample batch. In addition, a continuing calibration-verification blank must be analyzed after each continuing calibration verification. Analytes present in blanks must not be greater than 5 times the method reporting limit.

Laboratory control sample or certified reference material ¾ A laboratory control sample or certified reference material must be analyzed with each sample batch. The value must be within the project specific limit for accuracy.

Duplicate sample analyses ¾ A duplicate sample analysis must be analyzed with each sample batch. The relative percent difference determined from the two analyses must be within the project specific limit for precision.

Matrix spike analyses ¾ A matrix spike analysis must be performed with each sample batch. The percent recovery must be within the project specific limit for accuracy.

Sample result verification¾ At least 10% of the sample results should be verified for calculation and/or transcription errors. In addition, 100% of the quality-control sample results (relative percent differences and percent recovery) should be verified for calculation and/or transcription errors.

Overall assessment¾ Sample results should be assessed for overall use.

2.7.2 Clam Growth Data

The QA/QC procedures for the clam growth measurements stated that 5% of the clams would be remeasured for shell length and whole-animal wet weight. These procedures further stated that this QA/QC check would be conducted only if sufficient time was available, without jeopardizing the other components of the study. The formal QA/QC check was completed during both the initial and end-of-test field components of this study.

2.8 Data Analysis

The bioavailability and uptake of trace elements were assessed using the tissue concentration and content measurements. Whole-animal wet weights and tissue weights were used to calibrate, or normalize, the tissue chemistry data by determining whether growth dilution or ìshrinkage-enhancementî had occurred. Effects were assessed using survival, changes in whole-animal wet weights, and tissue weight measurements. Survival was used as a general indicator of conditions at the stations. Low survival would suggest physicochemical conditions at the station are degraded, but it would be impossible to determine which parameter is responsible for the observed mortality.

For bioaccumulation, each composited sample (e.g., tissues from all surviving clams from one cage) is considered a replicate. Four composites were prepared for each station; therefore, the level of replication for the bioaccumulation data is four. For whole-animal wet weight and end-of-test tissue weight, each individual clam is considered a replicate. Therefore, for these measurements, the maximum possible level of replication at each station is 300, if all clams survived. For this monitoring study, the maximum survival was 284 clams, which occurred at Station 8. Descriptive summary statistics (e.g., mean and standard deviation) were calculated for all bioaccumulation and clam growth data collected during this baseline monitoring study.

For the reference stations, all data for both reference stations were pooled and analyzed as a single unit for comparisons against the Tannery Bay stations. The pooled results are referred to as the average of the Reference Stations.

2.8.1 Survival, Tissue Chemistry, and Clam Growth Metrics

Statistical analyses were performed on bioaccumulation (i.e., concentration and content), survival, whole-animal weight, and tissue weight data from the *in situ* clam study. Two general hypotheses were tested:

1. Contaminants in Tannery Bay sediments and surface waters are bioavailable to aquatic receptors in Tannery Bay

2. Accumulation of bioavailable metals may adversely affect aquatic receptors in Tannery Bay as assessed by changes in whole-animal wet weights and tissue weights in clams

These general hypotheses were tested by statistical analyses of contaminant accumulation and growth in caged clams exposed to ambient Tannery Bay conditions. The following specific hypotheses were tested:

- There is no difference in mean response between Tannery Bay stations and reference stations.

- There is no difference in mean response among Tannery Bay stations.

- There is no difference in mean response between beginning and end of test.

The specific hypotheses were tested using a one-way Analysis of Variance (ANOVA). If the hypotheses were rejected, indicating that significant differences among all stations were detected, pairwise contrasts were performed to determine which stations differed from the reference stations. The Student Newman-Keuls test was used to test for differences among Tannery Bay stations. All tests were conducted at P=0.05.

Before proceeding with the ANOVA, the bioaccumulation, whole-animal weight, and tissue weight data were evaluated to ensure that they met the assumptions of the statistical tests (i.e., approximate normality and homogeneity of variances for the ANOVA, Bonferroni multiple contrasts, and Dunnett's multiple contrasts). This evaluation was performed using normal probability plots and a plot of the variance on a station-by-station basis (Appendix D). Data that violated the assumptions of the statistical tests were transformed before parametric analysis. The normal probability plots were used to guide the transformation process. Data that had a log distribution were log transformed; data that did not conform to a normal distribution were transformed using the rank-it process.

Survival¾ Survival rates for the *in situ* study were based on the number of live clams found at the end of the test relative to the total number of individuals (both dead and alive) found at the end of the test. Clams were considered ìmissingî if there was an empty space between 2 nylon cable ties, although only 3 clams were found to be missing out of the 3000 clams deployed in the study. Survival rates among stations were compared using a chi-squared contingency analysis (P=0.05). A chi-square test compares the observed and expected frequencies of animals alive or dead at the end of the test, with the null hypothesis stating that the probability of survival is the same at all stations. If rejected, the contingency table was partitioned to compare each station with a mean survival less than the mean of the reference stations with expected values to determine where differences occurred. ëExpected' frequencies were based on the mean of the percent survival for Reference Stations 1 and 2.

Pairwise multiple comparisons between survival values at all sites were performed using Simes method for binomial data (Piegorsch & Bailer 1997). The procedure is directly analogous to multiple comparisons between population means using normal statistics. The Simes procedure includes a necessary adjustment for using binomial data while maintaining some control over experiment-wise error. The null hypothesis (of no difference in survival) is rejected if the test statistic is greater than the Simes-corrected critical P-value, which takes into account the results from the other comparisons.

Tissue Chemistry —The bioaccumulation potential at Tannery Bay stations was considered to be the component of primary interest for this study. For this reason, the statistical design chosen for analysis of the bioaccumulation data was one which considered the Type I pair-wise and Type II experiment-wise error rates at each station. Using standard values for the pair-wise comparisons, the station-specific rates were set at 5% for false positives (Type I errors, a=0.05) and 20% for false negatives (Type II errors, a=0.2). An *a priori* power analysis using data on the variability among replicates for similar species and similar compounds indicated that three replicates were sufficient to detect as low as a 50% increase over reference tissue concentrations, for the one-tail t-test using the specified error rates. As a precaution against possible increased variability in the chemistry data, a forth replicate has been added to improve the confidence with which a 50% difference can be detected. These power results were used to approximate the power of the planned multiple contrasts.

For tissue chemistry data, the concentrations of chromium, lead, and mercury across all stations failed to fit a normal distribution. However, each of these trace elements came within reasonable bounds of a normal distribution when log-transformed. Cadmium, chromium, lead, and mercury were not normal after calculated as content. The first three were corrected through log-transformation, though mercury required rank-it transformation to correct for one data point which lay significantly outside of the bounds of the normal distribution.

Bonferroni's multiple contrasts test was used for the post hoc comparisons for the tissue chemistry data because of its ability to account for the number of means being tested against the two references. Because two reference stations were used in this study, the hypothesis comparing each Tannery Bay station to ìreferenceî is represented by the following equation:

$$\mu_{site1} = 1/2(\mu_{ref1} + \mu_{ref2}) .$$

The pair-wise error rate was set at 0.05 as an upper boundary.

Clam Growth Metrics ¾ Among the clam measurement data, tissue weights were normally distributed, end-of-test whole-animal wet weight required log-transformation, and growth rates based on weight needed to be transformed using rank-its to comply with statistical assumptions for the ANOVA.

Dunnett's multiple comparisons tests were used for the post hoc comparisons for the clam growth data. The Dunnett's test was used for these data rather than the Bonferroni test because of the high level of replication (i.e., n=284) available for each growth metric and the extreme robustness of the Dunnett's test.

2.8.2 Temperature

Water temperatures were taken at 8 study sites and 2 reference stations in 12-min intervals over a period of approximately 55 days (7/17/97–9/9/97). Temperature data were downloaded from the logging devices using the instruments' data recovery software. The start and end of the temperature series at some sites were dropped so that all series would be of equal length and covered the same time period. Minimum, maximum, and mean temperatures were calculated for each station. Temperature profiles were generated for each station and used to identify overall temperature trends. Temperature differences among reference and treatment stations were investigated using statistical approaches to test two primary hypotheses:

1. There is no difference in mean temperature across stations, and
2. There is no difference in the range of temperatures across stations.

Before testing for differences in mean temperatures across stations, it was necessary to test for autocorrelations, a measure of the dependence between

observations of the same series. The temperature series for all stations showed very strong trend and cyclical autocorrelations, requiring a non-standard analysis of mean differences. To reduce variability and autocorrelation, each series was reduced to daily mean temperatures, then a pair-wise station analysis was performed on the differences between the daily means at each site. This analysis requires the assumption that the trend in the daily averages is similar across stations. These series of mean differences were then regularly subsampled at a frequency determined by the autocorrelation function. For example, if the series of differences in daily means was autocorrelated to lag 6, an essentially independent set of observations was generated by choosing every 7th time point. The extent of the autocorrelation varies in the mean difference series; therefore, to achieve equal sample sizes across sites the maximum significant autocorrelation was used to subsample all sites. The observed pattern of differences in daily mean temperatures can be used to determine whether one station was consistently warmer than another; if the differences were not distinguishable from zero, then the two stations are said to have similar daily mean temperatures. The data were reduced to 16 sets of independent observations describing pair-wise differences in temperature between two reference sites and eight study sites. These 16 sets were tested for differences from zero using one-sample *t*-tests, with two-tailed alpha levels of 0.05.

To assess the effects of temperature conditions on clam growth, temperature ranges over 1-week periods were evaluated. First, the minimum weekly temperature was subtracted from the maximum weekly temperature at each station, resulting in eight observations of temperature range per station. These series were not significantly autocorrelated, and the variances were approximately equal across stations. Normality was assessed by plotting a histogram and quantile plot for residuals from an initial ANOVA fit. There was one large outlier (Reference Station 2, 7/17/97 6:48) which may have too large an influence on the results. With this outlier removed and the ranges recalculated, the data were approximately log-normal. A one-way ANOVA was performed to test for differences between the log-transformed ranges.

3.0 Results

The *in situ* bioaccumulation study with caged clams was completed as proposed. Clams were deployed on July 16 and 17, 1997 and retrieved 55 days (7.85 weeks) later from all field stations on September 9 and 10, 1997. All cages were in excellent condition upon retrieval. There were no signs of predation or vandalism. In general, the clams were in very good condition. A few individuals had broken or eroded shells.

Appendix B contains detailed data reports for tissue chemistry; Appendix C contains the laboratory operating procedures: Appendix D contains tissue chemistry and growth statistical analyses; Appendix E contains the data reports for clam whole-animal wet weight, growth rates, and tissue weights. Appendix F contains a series of photographs depicting the sampling events and activities.

3.1 Data Quality Review

All data collected as part of the baseline clam monitoring study were subjected to data quality review to ensure that the data met the project quality objectives and were suitable for analysis and interpretation. The data-quality parameters used to assess the acceptability of the data were precision, accuracy, representativeness, comparability, and completeness.

3.1.1 Tissue Chemistry Data

The chemistry data package received from Brooks Rand consisted of 40 tissue samples and three filter blank samples. All data were acceptable as reported and were considered usable. Data qualified *J* were considered usable as estimates. A summary of the data review is provided in this section. All data-quality objectives for this project (Table 2) were met with the exceptions discussed below. Chemicals reported as undetected were included in statistical calculations using a value of one-half of the reported detection limit.

Arsenic, Chromium, Cadmium, Lead ¾ A method blank was digested with each batch of samples submitted for metals. In addition, continuing calibration blanks were analyzed for every 10 samples. No target analytes were detected with the exception of chromium. Low levels of chromium were detected in two preparation blanks (0.62 µg Cr/L each) and two continuing calibration blanks (0.47 µg Cr/L each). The levels detected in the blanks were less than 5 times the target detection limit. Since the values detected in the associated samples were greater than 5 times the amount detected in the blanks, the results for chromium were not affected. A matrix spike and a certified reference material were analyzed with each batch, and all results were within the specified control limits. A sample duplicate was analyzed with each batch and the results met the established control limit.

Mercury, Methylmercury ¾ A method blank was digested with each batch of samples submitted for total mercury and methylmercury. In addition, continuing calibration blanks were analyzed for every 10 samples. No target analytes were detected in any of the blanks. A matrix spike and a certified reference material were analyzed with each batch, and all results were within the specified control limits. A sample duplicate was analyzed with each batch and the results met the established control limit.

3.1.2 Growth Data

All clam whole-animal wet-weight, tissue-weight, and growth-rate data are considered usable for the purpose of this report. The remeasurement process indicated that field staff were consistent in the measurement technique and that the error associated with those measurements was well within the 5% deviation as described in the Field Sampling Plan. No data were considered outliers; therefore, none were excluded from the data set.

Growth rates (mg/wk) were calculated as:

$$(\text{Measurement}_{\text{final}} - \text{Measurement}_{\text{initial}})/7.85.$$

Growth rates were calculated for individuals using the beginning- and end-of-test whole-animal wet-weight data. In some cases, negative values appear for growth rates. A loss in whole body weight can be attributed to adverse conditions or measurement error.

3.2 Survival

Survival was moderately high, ranging from 77% to 97% for all cages (Figure 4; Table 3). Average survival by station ranged from 87% to 95%. The survival data were analyzed for differences among stations using a contingency table. Station 5, with a significantly lower percentage of animals surviving, was the only treatment station that differed significantly from the average of the reference clams (Table 3). Survival of individual cages at Station 5 ranged from 77% to 96%, a difference of 19% among cages. Survival at other stations varied only 6% on average among the four cages. Results of the within-Tannery Bay comparisons using the Simes procedure indicated that Stations 5 and 8 were the only two bay stations which differed significantly from each other in percent survival.

3.3 Tissue ChemistryóConcentration and Content

The concentrations of all trace elements measured in clam tissues are expressed as dry weight. The results presented for each station represent the average of the four replicated samples for that station. For each trace element, the concentration results (Table 4) and the content results (Table 5) are presented**.** The end-of-test tissue chemistry results were statistically analyzed as follows: a) Tannery Bay stations (for each station, n=4) were compared with the 2 reference stations (n=8); b) Tannery Bay stations were compared against each other, and c) all stations (n=4 for each) were compared against the initial tissue chemistry measurements made on the 4 composited samples from the 300 T_0 clams. The results of statistical comparisons on tissue concentration are provided in Table 6; results for statistical comparisons on tissue content are provided in Table 7.

3.3.1 Arsenic

Clams at all stations, including the references, contained lower concentrations of arsenic at the end of the test than the average initial concentration of 6.25 mg/kg (Figure 5a; Tables 4, 6). Clams from Stations 4, 7, and 9 contained significantly less arsenic in their tissues than the T_0 clams. Average arsenic concentrations by station ranged from 5.04 to 5.92 mg/kg dry weight. The lowest mean concentration was detected in clams at Station 9 and the highest concentration was found in clams at Station 8. No significant differences (P=0.05) were detected between arsenic concentrations measured in any of the treatment station clams and the reference station clams. Similarly, no significant differences in arsenic concentration were detected among Tannery Bay stations when compared with one another (Table 6).

Arsenic content ranged from 0.62 µg in clams at Station 1 to 0.82 µg in clams at Station 8. The end-of-test arsenic content was significantly higher in clams at Stations 3, 6, and 8 than the initial arsenic content of 0.63 µg (Figure 5b; Table 5). Clams from these stations, as well as Station 7, also had significantly higher arsenic contents than the 0.65 µg average of clams at the reference stations (Table 7). Clams at Stations 4, 5, 9, and 10, while not statistically significant, had higher arsenic contents than the average of the reference clams. Results of the within-Tannery Bay comparison (Table 7) indicated the following statistical differences in end-of-test arsenic contents:

Station 8 □ Station 4, 5, 10.

3.3.2 Cadmium

Cadmium concentrations in end-of-test clams ranged from 2.23 to 3.40 mg/kg dry weight (Figure 6a, Table 4). None of these concentrations were significantly different from the average concentration of 3.06 mg/kg dry weight measured in T_0 clams (Table 6). At the end of the deployment, clams at Station 8 had a cadmium concentration of 3.40 mg/kg dry weight, which was significantly higher than the average concentration of the reference clams (Table 6). Although the cadmium concentration in clams at Stations 5, 6, and 10 were slightly higher than the average of the reference stations, the increase was not statistically significant. The results of the within-Tannery Bay comparison indicated cadmium concentrations in clams at Station 8 (3.40 mg/kg dry weight) were significantly higher than for clams at Station 4 (2.26 mg/kg dry weight). Among the Tannery Bay stations, only clams at Stations 4 and 8 differed from each other in cadmium concentration (Table 6).

Cadmium content ranged from 0.25 µg at Station 1 to 0.47 µg at Station 8 (Table 5). At the end of the study, clams at Station 8 contained significantly more cadmium than the initial content of T_0 clams (Figure 6b; Table 5) and significantly more cadmium per individual than the average of the reference

stations (Table 7). Results of the within-Tannery Bay comparison indicated cadmium content for clams at Station 8 was significantly different from clams at Stations 4, 5, 6, 9, and 10 (Table 7).

3.3.3 Total Chromium

All Tannery Bay clams accumulated chromium during the deployment period when compared with the initial concentration of 2.74 mg/kg dry weight (Figure 7a; Table 4). At the end of the study, clams at the reference stations had an average chromium concentration of 7.04 mg/kg dry weight. This average concentration was significantly lower than that measured in clams from Stations 4, 5, 6, 7, and 8 in Tannery Bay (Table 6). The highest chromium concentrations were measured in clams from Station 5 (70.23 mg/kg dry weight) and Station 8 (49.90 mg/kg dry weight); the lowest concentration measured in Tannery Bay clams was 9.47 mg/kg dry weight (Station 10). Results of the within-Tannery Bay comparison (Table 6) indicated that clams at Stations 5 and 8 had similar chromium concentrations, but these were significantly higher than concentrations measured in other Tannery Bay stations.

Historical concentrations of chromium in sediments indicate that the highest concentrations of chromium on the site are located between Stations 4 and 5 and range between 15,000 and 31,000 mg/kg dry weight (U.S. EPA/ ERT 1995). Clams from Station 4 had the third-highest and those from Station 5 had the highest chromium concentrations at the site. Clams from Station 8, where historical concentrations of chromium in the sediments are about 7,600†mg/kg dry weight, had the second highest concentration among all Tannery Bay stations.

Clams from all reference and Tannery Bay stations had significantly higher total chromium content per organism when compared with the initial content of 0.28 µg (Figure 7b; Table 5). The chromium content in Tannery Bay clams ranged from 1.19 µg at Station 10 to 8.36 µg at Station 5. Clams at the reference stations accumulated the least amount of chromium, with an average content of 0.81 µg. Clams at Tannery Bay stations 3 through 8 had significantly higher chromium contents than the average of the reference stations (Table 7). Results of the within-Tannery Bay comparison (Table 7) indicated the following statistical differences in chromium content:

Station 5 □ Stations 3, 4, 6, 7, 9, 10
Station 8 □ Stations 3, 4, 7, 9, 10
Station 10 □ Stations 3, 4, 5, 6, 7, 8.

3.3.4 Lead

Concentrations of lead in clams from the reference and Tannery Bay stations were significantly higher when compared with the average initial concentration of 0.244 mg/kg dry weight (Figure 8a; Table 4). The lead concentration in clams from Tannery Bay ranged from 0.64 to 1.68 mg/kg dry weight (Stations 3 and 5, respectively); the concentration in clams at the reference station averaged 0.89 mg/kg dry weight. Concentrations of lead in clams from Tannery Bay Stations 4, 5, 6, 8, and 10 were greater than the average of the reference stations, but these differences were not statistically significant (Table 6). Results of the within-Tannery Bay comparison indicated lead concentration in clams at Station 5 (1.68 mg/kg dry weight) was significantly higher than for clams at Station 3 (0.64 mg/kg dry weight). There were no differences in lead concentration among the other Tannery Bay stations (Table 6).

The lead content in all clams was significantly higher at the end of the study when compared with the initial content of 0.03 µg (Figure 8b; Table 5). Clams at Stations 4, 5, and 8 had the highest lead contents. Clams from all Tannery Bay stations, except Station 3, had higher lead contents than the average of the reference clams; however, the differences were not statistically significant (Table 7). Results of the within-Tannery Bay comparison indicated lead content in clams at Station 5 (0.20 µg) was significantly higher than for clams at Station 3 (0.09 µg). There were no differences in lead contents among the other Tannery Bay stations (Table 7).

3.3.5 Total Mercury

At the end of the study, all clams had a lower total mercury concentration when compared with the initial concentration of 1.26 mg/kg dry weight (Figure 9a; Table 4); the difference was statistically significant for clams from Stations 2, 6, and 7. For clams deployed in Tannery Bay, the highest mercury concentration, 1.100 mg/kg dry weight, was measured in clams at Station 9. Clams at Stations 4, 5, and 9 had mercury concentrations that were greater than the average of the reference stations (Table 4), but none of these were significantly higher than the average of the reference stations (Table 6). No significant differences in mercury concentration were detected among Tannery Bay stations when compared with one another (Table 6).

End-of-test total mercury content was not significantly different than initial content for clams at any station (Figure 9b; Table 5). Only clams at Stations 4 and 9 had final mercury contents higher than the initial content of 0.128 µg, but neither of these were significantly higher than the initial content. The lowest mercury content, 0.108 µg, was measured in clams at Station 10. Only clams at Station 4 had a mercury content that was significantly higher than the average of the clams at the reference stations (Table 7). The content value for

clams at Station 9 is not significantly greater than the average of the reference clams. This is because, although the mean content at Station 9 appears larger than Station 4 (Figure 9b), one replicate with a very large content caused the large mean and variance and skewed the distribution. When analyzing the rank-it transformed data, the other three replicates within Station 9, which lie directly around the mean of the references, were more influential in determining significance. No significant differences in mercury content were detected among Tannery Bay stations when compared with one another (Table 7).

3.3.6 Methylmercury

End-of-test concentrations of methylmercury in clams from all stations were significantly lower than the average initial concentration of 0.259 mg/kg dry weight (Figure 10a; Tables 4, 6). End-of-test methylmercury concentrations ranged from 0.102 to 0.183†mg/kg dry weight. Tissues of clams at Stations 3, 4, and 5 contained significantly higher concentrations of methyl-mercury when compared with the average of the reference clams. Clams at Stations 7, 9, and 10 had methylmercury concentrations that were slightly, but not significantly, higher than the average of the reference clams. Clams at Reference Station 2 had the lowest methylmercury concentration measured at all stations. Results of the within–Tannery Bay comparison (Table 6) indicated the following statistical differences in tissue methylmercury concentrations:

Station 8 □ Station 3, 4, 5
Station 4 □ Stations 6, 7, 8, 9, 10.

End-of-test methylmercury content in clam tissues was significantly lower than the initial content of 0.026 µg at all stations except 3 and 4 (Figure 10b; Table 5). The highest methylmercury contents, 0.023 to 0.025 µg, were found in clams from Stations 3 and 4, but these were not significantly different than the initial content. At the end of the study, clams at Stations 3, 4, 5, 6, 7, and 9 all had significantly higher methylmercury contents than the average of the reference clams (Table 7). Station 8 was the only Tannery Bay station with a methylmercury content that was below 0.015 µg, the average content of the reference clams. Results of the within–Tannery Bay comparison on methylmercury content (Table 7) indicated the following statistical differences:

Station 3 □ Station 8, 10
Station 4 □ Stations 5, 6, 7, 8, 9, 10.

3.3.7 Trace Element Bioavailability

The stations were ranked according to their relative degree of bioavailable trace elements. The increase in trace element content in clams was used as an indicator of bioavailability. For each trace element, the amount of trace element uptake was weighted by dividing the end-of-test content by the initial content. The quotients from each of the five trace elements were then summed for each station. The quotients calculated for each station are summarized in Table 8. By using this weighted ranking process, Station 5 appears to have the most bioavailable trace elements, followed by Station 8 and Station 4. The reference stations had the least amount of bioavailable trace elements, followed by Stations 10 and 9. The following ranked order, from stations with the most to the least bioavailable trace elements, resulted from this analysis:

Sta 5 > Sta 8 > Sta 4 > Sta 6 > Sta 7 > Sta 3 > Sta 9 > Sta 10 > Sta 2 > Sta 1.

3.4 Clam Growth Metrics

Two metrics were used to assess growth: whole-animal wet weight and end-of-test tissue weight. Only whole-animal wet weight was measured for each individual at both the beginning and end of the test. Therefore, the only growth rates based on changes (i.e., increase or decrease) in whole-animal wet weights could be calculated. Initial tissue weights were determined only for the T_0 clams sampled at the start of the test for chemical analysis. Because there was no statistical difference in the whole-animal weight of clams among individual cages (including the clams used for the initial tissue-weight determinations and chemical analyses) at the start of the test, it was assumed that the average tissue weight was also similar among all cages. Based on this assumption, the end-of-test tissue weights were evaluated for statistical differences; any differences observed were assumed to have occurred during the test period. Appendix E contains the actual weight measurements made during the field study.

Descriptive statistics were calculated for the various growth metrics and are summarized in Table 9. The end-of-test values are provided for each of these metrics; the absolute change after the 55-day exposure period is provided only for the whole-animal wet-weight data.

3.4.1 Whole-Animal Wet Weight

At the start of the test, whole-animal wet weights by individual ranged from 4.01 to 7.95†g; mean whole-animal wet weight by station was ~5.5 g. End-of-test whole-animal wet weights by individual ranged from 3.44 to 8.29 g. Mean end-of-test whole-animal weights by station ranged from 5.56 to 5.76 g. The lowest end-of-test whole-animal wet weights were found for clams at Reference Station 1; the highest for clams at Tannery Bay Stations 6 and 7 (Figure 11; Table 9).

The clams at Reference Stations 1 and 2 had the lowest increase in all growth metrics evaluated after the 55-day exposure. Clams at Station 1, the Waiska Bay site, had the poorest growth. The data for the two reference stations were compared statistically to determine the utility of the reference data in subsequent comparisons. The results of that comparison indicated that, based on growth rates and end-of-test tissue weights, the clams at Reference Station 1 were significantly smaller than those at Reference Station 2. However, data for both reference stations were retained as a point of comparison for clams exposed to relatively uncontaminated conditions even though clam growth was less than expected.

The end-of-test whole-animal wet-weight data were suitable for an ANOVA after log transformation. Results of the Dunnett's multiple range test indicated that clams at Stations 3, 4, 6 and 7 were, on average, significantly heavier than those at the reference stations (Figure 11; Table 10). There were no significant differences in end-of-test whole-animal wet weights among Tannery Bay stations (Table 10).

Growth rates based on whole-animal wet weight were calculated from the initial and end-of-test data. The lowest mean growth rate by station was 5.16 mg/week, measured for clams at Reference Station 1; the highest mean growth rate of 28.04 mg/week was measured for clams at Station 6 (Figure 12; Table 10). On an individual basis, the minimum growth rate was -80.15 mg/week and the maximum growth rate was 99.24 mg/week. The growth rate data required a rank-it transformation before testing with the ANOVA and Dunnett's test. Results of these analyses indicated that growth rates at Stations 3, 4, 6, 7, 8, 9, and 10 were significantly higher than those at the reference stations. Clams at Station 5 were the only animals that grew less than the average of the reference clams. Results of the within-Tannery Bay comparison (Table 10) indicated the following statistical differences in growth rates:

Station 3 ≠ Stations 4, 5, 6, 8, 9, 10
Station 4 ≠ Stations 3, 5, 6, 7, 9
Station 5 ≠ Stations 3, 4, 6, 7, 8, 9, 10
Station 6 ≠ Stations 3, 4, 5, 7, 8, 10
Station 7 ≠ Stations 4, 5, 6, 8, 9, 10
Station 8 ≠ Stations 3, 5, 6, 7, 9
Station 9 ≠ Stations 3, 4, 5, 7, 8, 10
Station 10 ≠ Stations 3, 5, 6, 7, 9.

Stations 4, 8, and 10 had similar growth rates, as did the following pairs: Stations 3 and 7, and 9 and 6. Clams at Station 5 had a significantly lower growth rate (9.57 mg/week) than clams at all other stations in Tannery Bay.

3.4.2 End-of-Test Tissue Weights

Mean tissue weight at the start of the test by station was estimated at 0.66 g wet weight. This estimate was based on the tissue weights measured for the 300 animals used for test initiation (T_0) tissue-chemistry analyses (Table 10). Mean end-of-test tissue weights by station ranged from 0.74 to 0.92 g wet weight, the overall range for individuals was 0.34 to 1.71†g wet weight (Figure 13; Table†10). The lowest mean tissue weights were measured in clams deployed at Reference Station 1 and Station 5. The end-of-test tissue-weight data were suitable for analysis with an ANOVA and Dunnett's multiple comparison without transformation. Results of these analyses indicated that the average end-of-test tissue weight for the reference stations was significantly lower than tissue weights for clams at all treatment stations, with the exception of Station 5. End-of-test tissue weights for clams at Station 5 were statistically similar to the average of the reference clams (Table 10). Results of the within-Tannery Bay comparison (Table 10) indicated the following statistical differences in tissue weights:

Station 3 ≠ Stations 4, 5, 7, 8, 9, 10
Station 4 ≠ Stations 3, 5, 10
Station 5 ≠ Stations 3, 4, 6, 7, 8, 9, 10
Station 6 ≠ Stations 5, 10
Station 7 ≠ Stations 3, 5, 10
Station 8 ≠ Stations 3, 5, 10
Station 9 ≠ Stations 3, 5, 10
Station 10 ≠ Stations 3, 4, 5, 6, 7, 8, 9.

Stations 4, 6, 7, 8, and 9 had similar tissue weights, as did stations 3 and 6.

3.4.3 Percent Lipids

Clams from all stations contained slightly higher percentages of lipids than the 1.30% found in T_0 clam tissues (Table 9). Station 9 clams had a significantly greater percentage of lipids than the average of the reference station clams (Figure 14). Clams from the other Tannery Bay stations had slightly more lipids per mass than the average of clams at the reference stations, but percentages were not statistically different. Results of the within-Tannery Bay comparison indicated no differences in percent lipids among clams at any of the stations (Table 10).

3.4.4 Percent Solids

Clams at Reference Station 2 and Tannery Bay Stations 5 and 10 had lower percentages of solids in their tissues at the end of deployment than T_0 clams (Figure 15). All the end-of-test values were significantly similar to the 15.2% solids measured in the T_0 clams (Table 9). Clams at Stations 6, 7, and 9 had significantly higher percentages of solids than the reference station clams. Only clams at Station 5 had a slightly lower percentage than the reference stations. Results of the within-Tannery Bay comparison indicated that Station 5 clams had a significantly lower percentage of solids in tissues than clams at Station 7 (Table 10).

3.5 Temperature

Water temperatures at each station were recorded at approximate 12-min intervals over the 55-day exposure period using one *in situ* computerized data logger per station (HoboTemp, Onset Instruments). Data were downloaded from the logging devices using the instruments' data-recovery software. Minimum, maximum, and mean temperatures for each station at the depth of the cages are summarized in Table 11. Reference Station 1 had a higher minimum, maximum, and mean temperature than all other stations over the deployment period, while Station 5 had the lowest minimum and mean temperature. The actual temperature profiles (Figure 16) show that the remaining eight stations follow similar patterns and seem to lie in approximately the same range.

The temperature data were statistically analyzed to determine whether the apparent differences were significant. The following two null hypotheses were tested:

1. There is no difference in daily average temperature across stations;
2. There is no difference in the range of temperatures across stations.

3.5.1 Testing for Differences in Mean Temperature

Temperatures at all stations displayed similar patterns with daily and seasonal cycles (Figure 16), although Reference Station 1 had a higher average temperature and treatment Station 5 had a lower average temperature than the other stations. The temperature series for all stations showed very strong autocorrelations (a measure of dependence between observations of the same series), requiring a non-standard analysis of mean differences. To reduce variability and autocorrelation, each series was reduced to daily mean temperatures (Figure 17), then an analysis of pairwise station differences was performed using one-sample *t*-tests (two tailed; P=0.05) to determine if there were statistical differences in daily average temperatures among stations. The

results of the *t*-tests on paired data (Table 12) show that the mean daily temperature for Reference Station 1 is significantly warmer than all study sites. The mean temperature for Reference Station 2 is significantly warmer than Station 5, and significantly colder than Stations 7, 8, and 10. Comparisons of mean daily temperature between Tannery Bay stations showed that several treatment stations also differed significantly from each other (Table 12).

3.5.2 Testing for Differences in Temperature Range

To assess the effects of temperature conditions on clam growth, temperature ranges over 1-week periods were evaluated. This time interval was selected because 7 days is a manageable time period, as opposed to comparisons based on an hourly or daily basis, and it is expected to have some biological relevance. Weekly intervals are also commonly used to measure changes in environmental conditions and growth in aquatic organisms.

The results of the one-way ANOVA performed to test for differences between temperature ranges indicate a significant difference between the average weekly temperature ranges at all stations (Table 13). The results of the Newman-Keuls Multiple Range test to determine which stations differed from which other stations indicated the weekly range in temperature at Reference Station 1 was significantly smaller than at all other stations (P=0.05). There is no evidence that the range of temperatures at Reference Station 2 is different from that at the study sites.

3.6 Sediment and Surface Water Chemistry vs. Tissue Chemistry

Results of chemical analyses performed on surface water collected by HydroQual at the beginning and end of test, and sediment samples collected at the end of the test are summarized in Tables 14 and 15. Sediments were also collected at the beginning of the test and analyzed for methyl- and total mercury.

The end-of-test (EOT) sediment chemistry values were compared with the lowest effect level (LEL) values developed by the Ontario Ministry of Environment (1993) as a means of ranking the stations for relative toxicity. For each trace element, the concentration measured in the sediment was divided by its corresponding LEL value. The quotients of the five measured trace elements (excluding methylmercury, since there was no LEL value) were summed by station and provide a relative estimate of the severity of sediment contamination (Table 16).

For example, LEL quotients <1 for a single contaminant indicate low risk from that contaminant; therefore, a sum of LEL quotients <5 would equate to low risk at the station based on the 5 trace elements measured; potential additive effects

of toxicity were not taken into account. Reference Stations 1 and 2 had the lowest Sums of Quotients, both < 5. The highest Sums (820 and 720, respectively, from Stations 3 and 4) were from sediments situated between the peninsula forming Tannery Point and the small island. Sediments in this area also have the highest amount of TOC at 11.7% and 12.4%, a potential source of binding ligands for the uncomplexed trace elements. The next highest Sums of Quotients were found for Stations 5, 6, 7, and 8, ranging between 161 and 423. The TOC concentration at each of these stations, except Station 5, was about half of that measured at Stations 3 and 4. TOC at Station 5 was similar to TOC at Stations 3 and 4. Although the Sums of Quotients from Tannery Bay were lowest at Stations 9 and 10 (40.52 and 51.96, respectively), chromium concentrations exceeded their LEL value at these stations. A TOC of <1% at Stations 9 and 10 may have reduced potential binding sites for trace elements resulting in lower concentrations at these stations. TOC at Reference Stations 1 and 2 was also <1%.

End-of-test sediment and surface-water data were compared with the tissue chemistry data, and correlation analyses (Table 17) were used to determine the strength of the relationship between these variables.

For non-detect values, one-half the detection limit was used. The strongest relationships were seen for chromium in surface water and clam tissues and methylmercury in sediment and tissue (Table 17). The concentration of chromium in clam tissues was better correlated with the chromium in surface water (r=0.62) than chromium in sediments (r=0.27). This is not surprising because the clams are filter feeders, and although placed directly on top of the sediments, they actively take in copious quantities of particulate material associated with the water column during the normal filtration process. These correlations suggest that the clams are obtaining chromium from particulates associated with the water column. The limited number of paired data points used in these analyses may alone drive a stronger correlation. The tissue and surface-water correlation used only 5 data points, and the tissue and sediment comparison used only 10.

The correlation coefficients for total mercury in water, sediment, and tissue were low (Table 17). The strongest correlation for methylmercury was for sediment and tissue (r=0.68). The correlation coefficients for arsenic, cadmium, and lead among the different media were very poor (Table 17). No correlation coefficients could be calculated for cadmium and lead for the water:sediment and water:tissue comparisons because for both cadmium and lead, the concentration in each surface-water sample collected at the four stations was reported as “less than” the detection limit, resulting in insufficient data to perform correlation analyses.

3.7 Tissue Chemistry vs. Survival and Clam Growth Metrics

The concentration of each trace element measured in clam tissue was compared with survival, whole-animal wet weight, growth rates, and end-of-test tissue weights (both wet and dry). All correlation coefficients were very low (Table 18), although there was a high degree of variability.

3.8 Temperature vs. Clam Growth

Temperature was compared with survival, whole-animal wet-weight, growth rates, and end-of-test tissue weights (both wet and dry). For each comparison, there was a high degree of variability and all correlation coefficients were very low (Table 19). Positive relationships were found for growth rates and survival; negative relationships were found for tissue weights (both wet and dry). These results suggest that none of the clam growth metrics are strongly correlated with temperature.

4.0 Discussion

The baseline biomonitoring study was successfully completed as proposed and the project-specific objectives were met. All cages were retrieved; high survival permitted assessments of chemical uptake and adverse effects. Clams at most of the Tannery Bay stations accumulated significant amounts of chromium when compared with reference clams. All clams increased in both soft-tissue weights and whole-animal wet weights after the 55-day exposure period; however, compared with reference clams, Tannery Bay clams did not demonstrate any significant growth effects due to exposure conditions. This discussion will focus on the interpretation of the tissue chemistry results when evaluated in light of the sediment and surface-water chemistry and the utility of growth metrics as indicators of effects.

4.1 Meeting the Purpose and Objectives of the Study

The purpose of the monitoring program is to document whether the selected remedy for the site is effective at reducing concentrations of bioavailable trace elements in Tannery Bay. This purpose is achieved by meeting the specific objectives of this study: 1) Determine whether chromium, total mercury, methylmercury, lead, cadmium, and arsenic in Tannery Bay sediments are available to biota residing in and/or using the Bay, and 2) determine whether exposure to bioavailable concentrations of metals may have adverse effects on local biota.

The concentrations of trace elements measured in the soft tissues of clams after the 55-day deployment provide a baseline of trace-element bioavailability for filter-feeding organisms that dwell within the surficial sediments or on top of these sediments.

4.2 Survival of Deployed Clams

Clam survival was very good at 92% which ensured sufficient tissues for the chemical analyses and sufficient individuals for assessment of effects. Although survival is usually not a very discriminating metric to evaluate adverse effects unless physical conditions (i.e., temperature, salinity, DO) are outside the normal range for the species, or toxic materials are present at extremely high concentrations, survival can provide a means of quickly identifying hot spots and prioritizing exposure conditions.

Based on mean survival by station, Station 5 appears to be the only station where exposure conditions may be deleterious. However, survival by cage within Station 5 is variable: two cages had low survival rates (77% and 81%; Table 3) and two had high survival (96% and 93%), comparable to other Tannery Bay stations. No other Tannery Bay station had such high variability in survival rates among cages at a single station. High variability in survival at Station 5 may be due to environmental heterogeneity. The American *Corbicula* has a preference for lotic conditions commonly found in shallow, well-oxygenated shore lake habitats (Aldridge & McMahon 1978, McMahon 1979). In native lotic habitats, *C. fluminea* is able to inhabit a wide variety of substrata, including bare rock, loose gravel, sand, and even silt and mud (Horne & McIntosh 1979). This species is nearly always eliminated from areas with decreasing sand, mud, or silt sediments of high organic and low oxygen content (Aldridge & McMahon 1978, Eng 1979, Fast 1971, Lenat & Weiss 1973, McMahon 1979). Station 5 was located at the furthest end of Tannery Bay in a highly vegetated area. It is possible that two of the cages were situated on top of decaying plant material, subjecting clams to high organics and low dissolved-oxygen conditions.

Percent survival in this study is comparable to survival reported for this species in other studies. For example, in a field study conducted to evaluate thermal plumes, survival of reference clams ranged from 93.5% to 99.6% (Foe & Knight 1987); survival of clams exposed to the thermal plumes ranged from 2% to 95.5%.

4.3 Tissue Chemistry

Changes in trace element concentration and content were used to assess bioavailability. The concentration data are useful for comparisons with previous or other studies. The change in trace-element content, or actual mass, in the clam is a direct measure of uptake, and provides an indication of exposure to organisms higher in the food chain. In this study, arsenic bioavailability was discovered only by analysis of the content data.

4.3.1 Tissue Concentration

The results of this study indicate that bioavailable chromium is present at all Tannery Bay stations. Although clams at Stations 9 and 10 accumulated the least amount of chromium, the end-of-test concentrations in clams at these stations were greater than initial concentrations. Clams at Stations 5 and 8 accumulated the most chromium, with an increasing gradient in tissue concentration from Stations 3 and 4 to 5.

The results for total and methylmercury are difficult to interpret due to the high concentration present in clams at the beginning of the test. *C. fluminea* collected from the Saline River in Arkansas for this study contained 1.263 µg/g dry weight (0.193 µg/g wet weight) total mercury compared with total mercury of 0.10-0.2 µg/g dry weight in *Corbicula* collected in other studies (Leland and Scudder 1990; Elder and Mattraw 1984). Unfortunately, the beginning-of-test tissue samples were frozen and not analyzed until the end-of-test. Therefore, there was no indication until the end of the study that the initial mercury concentration was high. Clams at all stations had lower end-of-test mercury concentrations when compared with initial concentrations. Although it is difficult to use the mercury tissue-chemistry data to establish true baseline conditions, they may be useful in establishing trends or ranking areas within Tannery Bay. Total mercury concentrations were highest at stations 4, 5, and 9. Methylmercury concentrations were highest at Stations 3, 4, and 5. Whether the differences noted in mercury concentrations within Tannery Bay are due to differential depuration among stations, differential uptake among stations, or some combination of these mechanisms cannot be determined from this study.

Clams at Stations 4, 5, and 8 had the highest lead concentrations. However, clams at all stations, including the reference stations, increased their lead concentration over the duration of the study. The lack of a statistically significant difference between reference and Tannery Bay stations suggests that lead contamination is not restricted to Tannery Bay.

By evaluating only the tissue-chemistry concentration data, arsenic and cadmium do not appear to be bioavailable in Tannery Bay. Except for cadmium at Station 8, end-of-test concentrations for both arsenic and cadmium were lower than those measured at the beginning of the test.

4.3.2 Tissue Content

The content data normalize the tissue chemistry with respect to clam growth, allowing comparisons of uptake unbiased by differences in tissue mass at the end of the test. The trends in the tissue content data are similar to those identified for the tissue concentration data, with one notable exception. The content data show that arsenic and cadmium were both bioavailable to clams.

Clams at Stations 3, 6, 7, and 8 accumulated significantly more arsenic than the average of the reference stations, with clams at Station 8 having the highest arsenic content. Cadmium content in clams at Stations 2 and 8 were significantly higher than the initial content. Station 8 cadmium content was significantly higher than the average of the reference stations.

Based on content, the clams at Station 3 also accumulated significant amounts of chromium compared with the average of the reference clams. For total mercury, clams at Station 4 had a statistically significant accumulation based on content. Clams at all Tannery Bay stations, except Stations 8 and 10, had significantly higher methylmercury contents compared with the average of the reference clams. However, content data for both total and methylmercury must be interpreted with the knowledge that initial values were higher than in the test area, as discussed in Section 4.3.1.

The bioavailability of arsenic and cadmium was not evident from analysis of the tissue concentration data alone. Although the clams accumulated arsenic and cadmium, they grew enough to maintain concentrations similar to, or slightly lower than, the initial concentrations, indicating that growth dilution did occur.

For predatory species, it is the content or dose (i.e., the quantifiable amount of a material introduced into an animal (Rand and Petrocelli 1985)) in food sources that is significant with respect to potential adverse effects. The toxicity of a metal is determined by the dose at the receptor site. The primary difference between concentration and content is that concentration allows for common reporting of a contaminant per unit weight of the animal, whereas content is an indication of the total amount of contaminant available within the animal. Thus, for arsenic and cadmium, there appeared to be no concern when only the tissue concentration data were examined; however, by evaluating the content data it is evident that these trace elements are available for uptake and could enter the food chain through organisms resident in Tannery Bay.

4.4 Sediment and Surface-Water Chemistry

Both sediment and surface-water samples were collected during clam deployment and retrieval. The sediment deployment samples were analyzed only for total- and methylmercury and conventional parameters (e.g., grain size, TOC, etc.). Sediment retrieval samples were analyzed for all study trace elements. These data indicate high variability in the sediment chemistry data, as well as in the composition of sediments. The area is heterogeneous, with wide fluctuations in the amount of fine-grained material and TOC present. Chromium and lead concentrations were highly correlated with TOC (r=0.94 and r=0.92, respectively). Chromium and lead concentrations also correlated with percent fines (r=0.80 and r=0.75, respectively). The association of metals with these fine organic-rich materials helps explain some of the spatial variability in sediment chemistry.

Surface waters for one reference and four Tannery Bay stations were analyzed from both the deployment and retrieval samples. Except for chromium and methylmercury, the correlation analyses indicated poor relationships between water and sediment chemistry. However, because of the small surface-water sample size, results from these correlation analyses must be used cautiously; small sample size alone may drive a stronger correlation. The correlation for chromium suggests that the unfiltered surface water over sediments has proportionate amounts of chromium, most likely associated with the particulate material within the water column.

4.5 Comparison of Bioavailability and Sediment Contamination

To assess the relative bioavailability of all five trace elements measured for clams at different stations, quotients calculated from the end-of-test tissue content divided by the initial tissue-content data were summed for five contaminants at each station (Table 8). Stations were ranked according to degree of uptake as follows:

Ranked order based on tissue quotients from greatest contaminant uptake to least uptake:

Sta 5 > Sta 8 > Sta 4 > Sta 6 > Sta 7 > Sta 3 > Sta 9 > Sta 10 > Sta 2 > Sta 1.

This ranked order is somewhat different than the station rankings calculated for sediments based on exceedance of the Ontario LEL values (Table 16).

Ranked order based on sediment LEL quotients from most contaminated to least contaminated:

Sta 3 > Sta 4 > Sta 5 > Sta 6 > Sta 7 > Sta 8 > Sta 10 > Sta 9 > Sta 1 > Sta 2.

The tissue and sediment rankings agree on the areas of lesser concern in Tannery Bay (i.e., Stations 9 and 10) and the areas of modest concern (i.e., Stations 6 and 7). There is some agreement on the most contaminated areasóthose around Stations 4 and 5. The primary differences in bioavailability and degree of sediment contamination are Stations 3 and 8. Based on tissue chemistry, Station 8 appears to be a greater concern than Station 3; sediment chemistry suggests that Station 3 is the area of greatest concern. The reason for this discrepancy is uncertain, but is probably a result of several environmental factors affecting contaminant availability discussed below. The reference stations had the lowest concentrations of contaminants and the smallest contaminant uptake.

Station 3 is characterized by sediments composed primarily of fines containing high concentrations of trace elements and TOC; bioavailability was found to be moderate. Station 8 is characterized by sediments composed primarily of sand and moderate-to-low concentrations of both trace elements and TOC; bioavailability was found to be very high. Bioavailability at Station 8 may be increased relative to sediment concentrations due to lower binding of contaminants. Another possible explanation is tied to the apparent semi-circular, northwest-to-northeast, surface-water flow in Tannery Bay. Under this scenario, Station 3 would receive more flow from the river, whereas Station 8 would receive water that had come in contact with contaminated bay sediments for a longer duration. Of all the areas monitored in Tannery Bay, Stations 3, 4, and 5 have the highest TOC levels and the highest percent fines. Although both organic carbon and fine, particulate material can serve as binding sites for labile trace elements, the high levels of trace elements measured in clam tissue at Stations 5 and 4 suggest that not all of the trace elements are bound and biologically unavailable to aquatic receptors.

Clams at Station 3 may not have accumulated trace elements in proportion to their supply in sediment due to both sediment binding and influence of water from St. Mary's River. A fair relationship was found between water and tissue chemistry (r=0.62), suggesting that biologically available trace elements are present in the water column. It is likely that the clams also accumulated chromium from the sediments, but the weakest relationship was found between these parameters (r=0.27). The tissue chemistry data and the correlation coefficients suggest that clams are integrating exposure from both the sediment and surface-water pathways, and that the contribution from each pathway is different, depending on conditions specific to the area of deployment. The moderate correlation coefficients obtained between sediment and tissues and between water and tissues are probably due to uptake from both sediment and water sources. Water circulation, and the distribution of particulate-bound trace elements, are likely a key factor in bioavailability to the filter-feeding clams. The beginning- and end-of-test surface-water chemistry (Table 15) clearly shows high variability in total trace elements. At the start of the test, the highest concentrations were found near Stations 4 and 5. Surface water was not collected at Station 8, but data for Station 9 indicate that trace elements in surface water were among the lowest at the start of the test. At the end of the test, the trace-element concentrations in surface water were similar for all locations sampled.

One unknown is the relationship between the horizon of sediment to which the clams were exposed and the horizon of sediment used in chemical analysis. Clams were probably exposed to trace element concentrations in the top 1-2 cm. It is uncertain if the sediment analyzed included deeper sediments and potentially different trace element concentrations. If surface sediments were homogenized with slightly deeper sediments, the correlation coefficients between tissue and sediment concentration could be lower as a consequence of sampling technique.

4.6 Comparison with Previous Studies

The 1997 baseline monitoring study data corroborate the presence of sediments in Tannery Bay contaminated with chromium and other trace elements. Sediment chromium concentrations measured during the 1997 baseline monitoring study are fairly consistent with data collected in 1993 (Cannelton Ind. 1995a), 1994 (US EPA/ERT 1995), and 1995 (Cannelton Ind. 1995b). The most comprehensive data set appears to be associated with the 1994 and 1995 sampling events. In all sampling events, the highest concentrations of chromium were found in sediments between the mainland and the small island in the western corner of the bay. In general, the highest concentrations are found to the west of the small island in Tannery Bay while the lowest are along the outer portion of Tannery Bay as it merges with the Saint Mary's River; mid-range concentrations are found in sediments in the eastern portion of Tannery bay. The surficial sediments from the area surrounding the 1997 baseline monitoring Station 4 historically have had the highest chromium concentrations: 18,430 mg/kg measured in 1993 (Cannelton Ind. 1995a), 30,000 mg/kg measured in 1994 (US EPA/ERT 1995), and 28,400 measured in 1995 in sediments collected from an area slightly to the southeast (Cannelton Ind. 1995b). In the 1997 baseline monitoring study, the highest chromium concentration in surficial sediments, 20,598 mg/kg, was measured in sediments collected from Station 3. In previous studies, chromium concentrations in sediments from the vicinity of Station 3 were reported as 1,871 mg/kg (Cannelton Ind. 1995a) and 8,200 mg/kg (US EPA/ERT, 1995); samples collected in 1995 from an area slightly to the east of Station 3 had a chromium concentration of 16,300 mg/kg (Cannelton Ind. 1995b). In the 1997 baseline monitoring study, the lowest chromium concentration was measured in sediments from Station 9. Historically, chromium concentrations in this area have been quite variable, reported as 3,014 mg/kg in 1993 (Cannelton Ind. 1995a), 5,800 mg/kg in 1994 (US EPA/ERT 1995), and 1,850 in 1995 (Cannelton Ind. 1995b). In the 1995 sampling event (Cannelton Ind. 1995b), subsurface sediments were collected and reported to contain chromium concentrations equal to, or higher than, those measured in the surficial sediments. It is possible that currents and ice movement in Tannery Bay and the Saint Mary's River continue to move surficial sediments, causing deeper, more contaminated sediments to become exposed. Both historical and recent data emphasize the need for continued monitoring.

The amount of chromium accumulated by crayfish in 1994 (U.S. EPA/ERT 1995) is similar to the amount accumulated by clams in this biomonitoring study. In 1994, tissues of crayfish from Tannery Bay were reported to contain between 1.4 and 9.6 mg Cr/kg tissue wet weight. One very high value of 29 mg/kg wet

weight was reported at one station from Hairball Beach (Station HB-3). The chromium concentrations in clams deployed in Tannery Bay ranged from 1.43 to 11.24 mg/kg wet weight. The concentrations of chromium in fish tissues measured in 1994 were within the ranges reported for both crayfish and clams. Tissue chemistry data were collected for the mayfly *Hexagenia* during the remedial pre-design studies (Cannelton Ind. 1995a). The concentration of chromium in mayflies collected from Tannery Bay ranged from 255 to 776 mg/kg dry weight compared with dry weights of 9.49 to 70.23 mg/kg in clams. Concentrations in mayflies are 1 to 2 orders of magnitude higher than measured in clam tissues during this baseline study (Table 4).

In contrast to the tissue:sediment correlations for the clams in this study, chromium concentrations in mayfly tissues were highly correlated with sediment concentrations measured in 1994 (r=0.987). It is unclear if the mayfly data, or even the crayfish or fish data, are directly comparable to the clam data. Concerns include their different feeding strategy as selective sediment feeders (mayflies actively feed on lighter, finer sediments containing higher amounts of organic material), their duration in the sediments (up to 2 years for mayflies), their migratory nature (none of these species remain within a specified area), and potential changes in exposure conditions between 1993 and 1997. Filter-feeding clams and sediment-feeding mayflies receive very different exposures to trace elements in the same sediments. Clams integrate exposure from two media, while the sediment- dwelling mayflies reflect a narrower source. Adding another species with a different feeding strategy (such as crayfish) to the monitoring program would improve the dataset on availability and sediment recovery. A sediment-feeding organism may have higher concentrations than the filter-feeding clams. The differences portrayed by the mayfly data support the need for a second species, particularly if information on the bioavailability of trace elements within the upper 10 cm of sediment is required.

4.7 Growth

One component of the study was to evaluate the potential for adverse effects associated with exposure to trace elements in Tannery Bay. The metrics used to evaluate growth, end-of-test whole-animal wet weight, growth rates based on whole weights, and end-of-test tissue weights did not indicate impact due to exposure in Tannery Bay when compared with the average of the reference stations. The data generated in this study should be used for baseline purposes. Limited comparison should be made to growth with respect to reference clams because of the poor growth observed in Reference Station 1 clams. Clams at Reference Station 1 had the lowest growth of all clams; the Reference Station 2 clams had slightly better whole-animal and tissue growth than those at Station 1. However, on average, the reference clams did not grow as well as the clams deployed in Tannery Bay.

The most interesting comparisons with the growth data are those among Tannery Bay stations only. The clams at Station 5 had the lowest performance for each of the growth metrics evaluated. Station 5 Replicates 3 and 4, with low survival, had very low growth (3.5 mg/week) compared with Replicates 1 and 2 (14.6 mg/week), with high survival. The replicates with high survival and growth still had lower growth rates than any of the other Tannery Bay stations. Growth rates, end-of-test tissue weights, and whole-animal wet weights all decreased along a gradient across Stations 3, 4, and 5. Although no strong relationships were found when the tissue-chemistry data were correlated with the growth data, a very strong relationship exists between these parameters for Stations 3, 4, and 5.

Although no significant differences were found in percent solids for the clams after deployment, there are some trends with solids that follow those seen with elevated tissue chemistry and reduced growth. Significant reductions in percent solids have been associated with stress and exposure to various chemicals (Belanger et al. 1986a,b; Doherty 1990). The clams at Station 5 had the lowest percent solid concentration at the end of the study when compared with the other clams. The lowest percent-solids data came from replicates 3 and 4 at Station 5. Although the percent-solid data do not distinguish between classes of contaminants or stressors, this metric responds in a negative fashion to any detrimental agent. Tissues of stressed clams will have higher percentages of water than unstressed individuals. This adds to the weight-of-evidence in evaluating the impact of exposure conditions.

These growth-effects data will be most useful in future years by providing a basis for comparison with other data. Significant differences in growth parameters compared with the baseline data may reflect changes in sediment and/or surface-water chemistry.

4.8 Temperature

Although the sites within Tannery Bay and St. Mary's River were selected to minimize temperature differences, statistically significant differences were found among stations. Separating statistical significance from ecological significance is important, but difficult. What effect, if any, do the measured temperature differences have on the observed growth results? None of the clam growth metrics were strongly correlated with temperature, as indicated by the poor correlation coefficients (i.e., $r<0.5$) obtained when each of the growth metrics were compared with temperature. Although there were some differences in temperature among stations, the overall exposure conditions are within the preferred limits (viz., 10–25°C) for this species, except at Reference Station 1 where the temperature reached 26.3°C for a very short period. Prolonged exposure to temperatures > 25°C have extensive effects on *Corbicula* biology, including depressed filtration rates (Mattice 1979), feeding rates, and

reproductive capacity. When exposed to these elevated temperatures, individuals spend most of the time with their siphons withdrawn and valves closed (McMahon 1979). It is doubtful that the brief exposure to the high temperature at Station 1 greatly affected the caged clams transplanted there, although this is one concern regarding the appropriateness of Station 1 as a reference area.

Station 5 is the only station that stands apart as having different temperatures within Tannery Bay. The mean temperature was 3.3°C lower than the means of the other Tannery Bay stations, and Station 5 had the lowest temperature, 10.5°C. Groundwater discharge occurring in the wetlands in the southwest corner of Tannery Bay possibly explains the lower water temperatures measured at this station. The temperatures measured at Station 5 are well within the clam's tolerance range, although it has been noted that low temperatures may reduce growth rates (Abbott 1979, Buttner & Heidinger 1980, Dreier & Tranquilli 1981) and inhibit veliger release (Heinsohn 1958, Aldridge 1976, Aldridge & McMahon 1978). The lower lethal temperature limit for *Corbicula* is near 2°C (Mattice & Dye 1976). Several reports of massive midwinter mortalities and/or total extinctions have been associated with ambient water temperatures near 0°C (Bickel 1966; Dreier & Tranquill 1981; Horning & Keup 1964).

4.9 Problems Encountered during the Study

The most significant problem encountered during this study was the presence of mercury in clam tissues at the beginning of the test. The problem of background contamination experienced in this and previous studies suggests that it may be very difficult to obtain freshwater bivalves that are free of mercury contamination. It may be necessary to obtain test specimens months in advance of the study to allow for depuration at a location known to be contaminant-free. The half-life of mercury depuration is approximately 90 days (N. Bloom, pers. commun., 1998); this length of time may be necessary to remove all traces of mercury from field-collected specimens. One of the most important elements of future monitoring studies should be the chemical characterization of source animals well before initiating the study.

A second problem in this study was the selection of the reference stations. The data strongly suggest that exposure conditions, excluding chemical contaminants, were dissimilar between the reference and Tannery Bay stations. The physical attributes of the reference stations must be as similar as possible to the test stations, including temperature ranges, food availability, vegetation, water depth, and currents.

5.0 Recommendations

1) NOAA recommends that studies conducted in future years retain all study parameters. Tissue chemistry, growth effects, sediment chemistry, and surface-water chemistry are required to determine the effectiveness of the remedial alternative. A minimum of three data sets must be collected to establish a trend and provide sufficient information to re-evaluate the program requirements. At that time it may be appropriate to adjust the study parameters.

2) The second round of monitoring should not occur until shore-side remedial activities are completed.

3) Further studies should be conducted at the same time of the year to allow direct comparison of tissue-chemistry and growth-effects data.

4) The initial mercury concentration in bivalves should be reduced. Either an alternative source of clams should be identified, or the clams should be collected long enough before the study commences to allow complete, or near complete, depuration of mercury.

5) Replicate data at Station 5 was quite variable. In future years, cages placed at this station should be located away from highly vegetated sediments to ensure similar conditions for all clams.

6) NOAA recommends conducting a site reconnaissance to determine if a more appropriate and representative reference station can be located to replace the Waiska Bay Reference Station 1 for use in future years' monitoring.

7) Although the clams integrate both sediment and water chemistry, it would be advantageous to add a second species (i.e., crayfish) to the study to obtain specific data on bioavailability of trace elements in the surficial sediments and to ensure sufficient characterization of chemical bioavailability to all species (i.e., filter-feeding and deposit/sediment-feeding) currently or potentially using Tannery Bay. This recommendation should be implemented to help assess food chain impacts in the event that future year sampling data reveals no decrease in contaminant bioavailability.

6.0 References

Abbott, R.T. 1979. Asiatic clam (*Corbicula fluminea*) vertical distributions in Dale Hollow Reservoir, Tennessee. Proc. First Int. *Corbicula* Symp., p. 111-118.

Aldridge, D.W. 1976. Growth, reproduction, and bioenergetics in a natural population of the Asiatic freshwater clam, *Corbicula manilensis* Philippi. Master's Thesis, Univ. Texas at Arlington.

Aldridge, W.E., & R.F. McMahon. 1978. Growth, fecundity, and bioenergetics in a natural population of the freshwater clam, *Corbicula manilensis* Philippi, from North Central Texas. J. Mol. Study 44:49-70.

Belanger, S.E., D.S. Cherry, & J. Cairns, Jr. 1986a. Uptake of chrysotile asbestos fibers alters growth and reproduction of Asiatic clams. Can. J. Fish. Aquat. Sci. 43:43-52.

Belanger, S.E., J.L. Farris, D.S. Cherry, and J. Cairns. 1986b. Growth of Asiatic clams (*Corbicula* sp.) during and after long-term zinc exposure in field-located and laboratory artificial streams. Arch. Environ. Contam. Toxicol. 15:427-434.

Belanger, S., D. Cherry, J. Cairns, Jr., and M. McGuire. 1987. Using Asiatic clams as a biomonitor for chrysotile asbestos in public water supplies. Journal AWWA - Research and Technology pp. 69-74.

Bickel, D. 1966. Ecology of *Corbicula manilensis* Philippi in the Ohio River at Louisville, Kentucky. Sterkiana 23:19-24.

Bloom, N. 1998. Personal communication, Frontier Geosciences, Inc. Seattle, March 16, 1998.

Buttner, J.K., & R.C. Heidinger. 1980. Seasonal variations in growth of the Asiatic clam, *Corbicula fluminea* (Bivalvia: Corbiculidae) in a Southern Illinois fish pond. Nautilus 94:8-10.

Cannelton Ind. 1995a. Remedial design pre-design studies. Rep. CANN 94-4 by Cannelton Industries, Inc., Sault Ste. Marie, MI. Chicago: U.S. EPA Region V.

Cannelton Ind. 1995b. Preliminary Design Report, Cannelton Industries Site, CANN 95-4, May 1995. by Cannelton Industries, Inc., Sault Ste. Marie, MI. Chicago: U.S. EPA Region V.

Cherry, D. 1998. Personal communication, Virginia Technical University, June 30, 1998.

Colombo, J., C. Bilos, M. Campanaro, and M. Presa. 1995. Bioaccumulation of polychlorinated biphenyls and chlorinated pesticides by the Asiatic clam *Corbicula fluminea*: Its use as sentinel organism in the Rio de La Plata Estuary, Argentina. Environ. Sci. Technol. 29(4):914-927.

Doherty, F.G. 1990. The Asiatic clam, *Corbicula* spp., as a biological monitor in freshwater environments. Environ. Monit. Assess. 15:143-181.

Dreier, H., & J.A. Tranquilli. 1981. Reproduction, growth, distribution, and abundance of *Corbicula* in an Illinois cooling lake. Bull. Ill. Nat. Hist. Surv. 32: 378-393.

Elder, J.G. and H.C. Mattraw. 1984. Accumulation of trace elements, pesticides, and polychlorinated biphenyls in sediments and the clam *Corbicula manilensis* of the Apalachicola River, Florida. Arch. Environ. Contam. Toxicol. 13: 453-469.

Eng, L.L. 1979. Population dynamics of the Asiatic clam, *Corbicula fluminea* (Muller), in the concrete-lined Delta–Mendota Canal of central California. Proc. First Int. *Corbicula* Symp., p. 39-68.

Farris, J., J. Van Hassel, S. Belanger, D. Cherry, and J. Cairns, Jr. 1988. Application of cellulolytic activity of Asiatic clams (*Corbicula* sp.) to in-stream monitoring of power plant effluents. Environ. Toxicol. Chem. 7:701-713.

Fast, A.W. 1971. The invasion and distribution of the Asiatic clam (*Corbicula manilensis*) in a southern California reservoir. Bull. South. Calif. Acad. Sci. 70:91-98.

Foe, C., & A. Knight. 1987. Assessment of the biological impact of point source discharges employing Asiatic clams. Arch. Environ. Contam. Toxicol. 16:39-51.

Heinsohn, G.E. 1958. Life history and ecology of the freshwater clam, *Corbicula fluminea*. Master's Thesis, Univ. Calif., Santa Barbara.

Horne, F.R., & S. McIntosh. 1979. Factors influencing distribution of mussels in the Blanco River of Central Texas. Nautilus 94:119-133.

Horning, W.B., & L. Keup. 1964. Decline of the Asiatic clam in the Ohio River. Nautilus 78:29-30.

Jones, B.R. 1996. Ecological risk management of mercury at the Cannelton Industries Superfund Site. Memo. to Rosita Clark, RPM, U.S. EPA Region V, Oct. 7, 1996.

Kracko, K. 1992. Cannelton Industries Final Report. R. F. Weston, Inc., Edison, NJ [unpag.].

Leland, H.V. and B.C. Scudder. 1990. Trace elements in *Corbicula fluminea* from the San Joaquin River, California. Sci. Total Environ. 97/98:641-672.

Lenat, D.R., & C.M. Weiss. 1973. Distribution of benthic macroinvertebrates in Lake Wylie North Carolina—South Carolina. Publ. 331, Dep. Environ. Sci. & Eng., School of Public Health, Univ. North Carolina at Chapel Hill.

Luoma, S., N. R. Dagovitz, and E. Axtmann. 1990. Temporally intensive study of trace metals in sediments and bivalves from a large river-estuarine system: Suisan Bay/Delta in San Francisco Bay. Sci. Total Environ. 97/98:685-712.

Mac, M., C. Edsall, R. HesselBerg, and R. Sayers Jr. 1984. Flow-through bioassay for measuring bioaccumulation of toxic substances from sediment. Final Report. Great Lakes National Program Office, U.S. Environmental Protection Agency, Contribution No. 616 of the Great Lakes Fishery Laboratory.

McMahon, R.F. 1979. Response to temperature and hypoxia in the oxygen consumption of the introduced Asiatic freshwater clam *Corbicula fluminea* (Muller). Comp. Biochem. Physiol. A 63:383-388.

McMahon, R.F. 1991. Mollusca: bivalvia. In: J.H. Thorp and A.P. Covich, Eds. Ecology and Classification of North American freshwater Invertebrates. San Diego: Academic Press. p 315-399.

Mattice, J.S. 1979. Interactions of *Corbicula* sp. With power plants. Proc. First Int. *Corbicula* Symp., p. 119-138.

Mattice, J.S., & L.L. Dye. 1976. Thermal tolerance of adult Asiatic clam. ERDA Symp. Ser. 40:130-135.

NOAA/EVS Consultants. 1997. Quality assurance project plan for development and implementation of bivalve monitoring study: Cannelton Industries site – Sault Ste. Marie, Michigan. Chicago: U.S. EPA Region V.

Ontario Ministry of Environment. 1993. Guidelines for the protection and management of aquatic sediment quality in Ontario. Ottawa: Ontario Ministry of Environment, August 1993.

Piegorsch, W.W., & A.J. Bailer. 1997. Statistics for environmental biology and toxicology. London: Chapman and Hall.

Rand, G. M. and S. R. Petrocelli. 1985. Fundamentals of aquatic toxicology. Hemisphere Publishing Corporation, New York. Page 653

Riisgård, H.U.T., & S. Hansen. 1990. Biomagnification of mercury in a marine grazing food-chain: Algal cells *Phaeodactylum tricornutum*, mussels *Mytilus edulis* and flounders *Platichthys flesus* studied by means of a stepwise-reduction-CVAA method. Mar. Ecol. Prog. Ser. 62:259-270.

Salazar, M.H., & S.M. Salazar. 1995. In-situ bioassays using transplanted mussels. I. Estimating chemical exposure and bioeffects with bioaccumulation and growth, p. 216-241. *In:* Hughes, J.S., G.R. Biddinger, and E. Mones (eds.), Third symposium on environmental toxicology and risk assessment. ASTM STP 1218. Philadelphia: American Society for Testing and Materials.

Tatem, H. 1986. Bioaccumulation of polychlorinated biphenyls and metals from contaminated sediment by freshwater prawns, *Macrobrachium rosenbergii* and clams, *Corbicula fluminea*. Arch. Environ. Contam. Toxicol. 15:171-183.

U.S. EPA. 1994. Cannelton Industries, Inc: Site Description, Threats and Contaminants, Cleanup Approach, and Environmental Progress. May 1994, 2 p.

U.S. EPA. 1996. Amended Record of Decision. ìCannelton Industries Siteî [unpag.]

U.S. EPA/ERT. 1995. Final Report. Ecological Risk Assessment, Cannelton Industries Site, Sault Ste. Marie, Michigan. Environmental Response Branch, Emergency Response Division, Office of Emergency and Remedial Response. January 1995, 93 p. + figs.

WW Engineering. 1991. Remedial investigation of Cannelton Industries site, Sault Ste. Marie, MI. Proj. #04002, Sept. 1991.

7.0 TABLES

Table 1. Deployment position, time, water depth, and range of depth at each station.

Station	Cage numbers	Deployment time	GPS coordinates	Water depth (ft)	Range of depth (ft)
1 (Ref 1)	13, 22, 25, 43	7/16; 2:30pm	46°26'30.60"N 84°35'54.31"W	2' 6"	2'1" - 3'6"
2 (Ref 2)	5, 15, 24, 35	7/17;10:45am	46°29'21.51"N 84°24'03.37"W	2' 5"	2' - 3'5"
3	2, 11, 30, 37	7/16; 5:50pm	46°29'34.54"N 84°23'24.33"W	3' 6"	3'1" - 4'6"
4	3, 17, 23, 34	7/16; 7:00pm	46°29'32.94"N 84°23'23.72"W	2' 7"	2'2" - 3'7"
5	4, 18, 27, 42	7/16; 7:15pm	46°29'30.74"N 84°23'23.45"W	1' 9"	1'4" - 2'9"
6	14, 19, 26, 41	7/16; 7:30pm	46°29'32.34"N 84°23'19.23"W	1' 7"	1'2" - 2'7"
7	1, 9, 20, 38	7/17; 11:07am	46°29'31.89"N 84°23'15.05"W	2' 9"	2'4" - 3'9"
8	16, 28, 33, 44	7/16; 6:20pm	46°29'36.56"N 84°23'12.14"W	4' 6"	4'1" - 5'6"
9	8, 10, 21, 39	7/17: 10:08am	46°29'35.39"N 84°23'17.62"W	3' 8"	3'3" - 4'8"
10	6, 12, 31, 40	7/17; 10:20am	46°29'37.08"N 84°23'23.45"W	3' 2"	2'7" - 4'2"
11 (Initial tissue)	7, 29, 32, 36	NA	NA	NA	NA

NA - Not applicable

Table 2. Analyte list and targeted detection limits for clam tissues.

Analyte	Method	Target detection limit*
Chromium (total)	EPA 200.9 STP-GFAA	0.01 mg/kg
Cadmium	EPA 200.9 STP-GFAA	0.005 mg/kg
Lead	EPA 200.9 STP-GFAA	0.07 mg/kg
Arsenic	EPA 200.9 STP-GFAA	0.05 mg/kg
Total Mercury	BR-0002 CVAFS	0.0001 mg/kg
Methylmercury	BR-0011 CVAFS	0.001 mg/kg
Percent Solids	BR-1501	0.1%
Percent Lipids	EPA 8290	1.0%

* Detection limits are not guaranteed due to the possibility of matrix interferences
STP-GFAA – Stabilized temperature platform-graphite furnace atomic absorption
CVAFS – Cold vapor atomic fluorescence spectrometry
BR – Brooks Rand

Table 3. End-of-test percent survival for clams deployed in Tannery Bay and at reference stations.

	Sta 1	Sta 2	Sta 3	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Replicate 1	85	93	95	96	96	93	91	95	95	96
Replicate 2	96	95	88	87	93	97	92	95	95	91
Replicate 3	95	95	88	92	77	92	87	97	92	93
Replicate 4	93	91	93	85	81	96	97	92	92	89
Mean	92	94	91	90	87	94	92	95	94	92
SD	5.0	1.9	3.6	5.0	9.2	2.4	4.1	2.1	1.7	3.0
N	277	280	273	270	261	284	275	284	280	277

Results of statistical analyses on clam survival.

Tannery Bay stations compared with the average of reference stations

	Sta 3	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Survival	NS	NS	--	NS	NS	NS	NS	NS

-- Clams from Tannery Bay station significantly less than the average of reference stations.
NS – No significant difference between Tannery Bay station and the average of reference stations.

Table 4. Mean concentration (dry and wet weights) of trace elements in clam tissues.

Dry Weight Concentration (mg/kg)

	Initial	Sta 1 & 2[a]	Sta 1	Sta 2	Sta 3	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Arsenic												
Rep 1	6.07		6.09	4.68	5.75	4.63	4.67	4.82	5.44	5.14	5.04	5.45
Rep 2	6.25		4.78	6.01	4.53	5.41	5.48	5.00	4.73	5.76	4.45	5.33
Rep 3	6.56		5.82	5.56	5.99	5.00	6.47	5.98	5.30	6.52	5.43	5.37
Rep 4	6.12		5.79	5.41	4.89	5.17	6.52	5.90	4.95	6.26	5.22	5.15
Mean	**6.25**	**5.52**	**5.62**	**5.42**	**5.29**	**5.05**	**5.79**	**5.43**	**5.11**	**5.92**	**5.04**	**5.33**
±2SE	0.22	0.53	0.58	0.55	0.69	0.33	0.88	0.60	0.32	0.61	0.42	0.13
Cadmium												
Rep 1	3.19		2.61	2.81	3.10	1.91	2.44	1.99	2.54	2.92	2.47	2.83
Rep 2	3.15		1.78	3.35	2.01	2.60	2.63	2.09	2.47	3.22	2.17	2.82
Rep 3	2.74		2.44	3.64	3.01	2.25	2.91	2.81	2.52	3.97	2.53	3.19
Rep 4	3.15		2.08	2.93	2.36	2.29	3.15	3.97	2.56	3.48	2.55	2.72
Mean	**3.06**	**2.71**	**2.23**	**3.18**	**2.62**	**2.26**	**2.78**	**2.72**	**2.52**	**3.40**	**2.43**	**2.89**
±2SE	0.21	0.62	0.37	0.38	0.52	0.28	0.31	0.91	0.04	0.44	0.18	0.21
Chromium												
Rep 1	2.38		6.51	6.31	17.80	18.10	62.20	14.50	26.20	34.30	8.83	7.92
Rep 2	2.77		4.48	4.68	20.80	32.80	79.20	17.50	16.30	19.20	12.50	7.12
Rep 3	2.92		13.00	5.69	17.50	9.10	82.20	19.60	17.60	101.00	13.30	14.70
Rep 4	2.90		8.77	6.87	13.10	40.80	57.30	22.60	17.70	45.10	24.80	8.13
Mean	**2.74**	**7.04**	**8.19**	**5.89**	**17.30**	**25.20**	**70.23**	**18.55**	**19.45**	**49.90**	**14.86**	**9.47**
±2SE	0.25	2.76	3.65	0.94	3.17	14.27	12.32	3.42	4.54	35.68	6.91	3.52
Lead												
Rep 1	0.620		0.895	1.570	0.778	0.800	1.450	0.568	0.663	0.879	0.822	0.826
Rep 2	0.026		0.460	0.887	0.426	2.770	1.730	1.460	0.872	0.779	0.702	0.973
Rep 3	0.165		0.764	0.997	0.554	0.925	2.190	0.879	0.903	2.260	0.988	1.070
Rep 4	0.165		0.625	0.920	0.807	1.050	1.360	1.170	0.698	1.530	0.994	0.805
Mean	**0.244**	**0.890**	**0.686**	**1.094**	**0.641**	**1.386**	**1.683**	**1.019**	**0.784**	**1.362**	**0.877**	**0.919**
±2SE	0.259	0.326	0.187	0.321	0.183	0.928	0.373	0.383	0.121	0.685	0.141	0.126
Mercury												
Rep 1	0.993		1.210	0.793	0.830	0.885	0.932	0.827	0.644	0.697	0.879	0.781
Rep 2	1.660		0.858	0.771	0.876	0.995	1.030	0.844	0.814	1.090	0.783	0.873
Rep 3	1.060		1.130	0.877	0.862	0.981	1.260	0.678	0.987	0.792	1.930	0.853
Rep 4	1.340		1.100	0.893	0.894	1.040	1.020	0.675	0.810	1.030	0.807	0.926
Mean	**1.263**	**0.954**	**1.075**	**0.834**	**0.866**	**0.975**	**1.061**	**0.756**	**0.814**	**0.902**	**1.100**	**0.858**
±2SE	0.304	0.167	0.152	0.060	0.027	0.065	0.140	0.092	0.140	0.188	0.555	0.060
Methylmercury												
Rep 1	0.255		0.149	0.121	0.153	0.171	0.153	0.146	0.116	0.086	0.139	0.125
Rep 2	0.243		0.105	0.077	0.162	0.180	0.124	0.143	0.146	0.097	0.141	0.135
Rep 3	0.267		0.201	0.093	0.136	0.157	0.197	0.113	0.159	0.102	0.143	0.131
Rep 4	0.269		0.185	0.105	0.176	0.223	0.151	0.100	0.103	0.123	0.137	0.134
Mean	**0.259**	**0.130**	**0.160**	**0.099**	**0.157**	**0.183**	**0.156**	**0.126**	**0.131**	**0.102**	**0.140**	**0.131**
±2SE	0.012	0.045	0.043	0.019	0.017	0.028	0.030	0.023	0.026	0.016	0.003	0.005

Table 4 (continued)

Wet Weight Concentration (mg/kg)

	Initial	Sta 1 & 2[a]	Sta 1	Sta 2	Sta 3	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Arsenic												
Rep 1	0.91		0.93	0.68	0.89	0.76	0.73	0.78	0.92	0.85	0.79	0.84
Rep 2	0.97		0.73	0.88	0.77	0.82	0.88	0.80	0.74	0.88	0.72	0.80
Rep 3	0.98		0.89	0.84	0.87	0.81	1.04	0.98	0.82	1.02	0.87	0.81
Rep 4	0.94		0.89	0.81	0.79	0.76	1.05	0.95	0.85	0.94	0.84	0.77
Mean	**0.95**	**0.83**	**0.86**	**0.80**	**0.83**	**0.79**	**0.93**	**0.88**	**0.83**	**0.92**	**0.81**	**0.80**
±2SE	0.03	0.09	0.09	0.09	0.06	0.03	0.15	0.10	0.08	0.08	0.07	0.03
Cadmium												
Rep 1	0.48		0.40	0.41	0.48	0.32	0.38	0.32	0.43	0.48	0.39	0.44
Rep 2	0.49		0.27	0.49	0.34	0.40	0.42	0.33	0.39	0.49	0.35	0.42
Rep 3	0.41		0.37	0.55	0.44	0.36	0.47	0.46	0.39	0.62	0.41	0.48
Rep 4	0.48		0.32	0.44	0.38	0.34	0.51	0.64	0.44	0.52	0.41	0.41
Mean	**0.46**	**0.41**	**0.34**	**0.47**	**0.41**	**0.35**	**0.45**	**0.44**	**0.41**	**0.53**	**0.39**	**0.44**
±2SE	0.04	0.09	0.06	0.06	0.06	0.03	0.05	0.15	0.03	0.06	0.03	0.03
Chromium												
Rep 1	0.36		1.00	0.91	2.74	2.99	9.77	2.35	4.43	5.66	1.39	1.23
Rep 2	0.43		0.69	0.69	3.52	4.99	12.75	2.80	2.54	2.94	2.01	1.07
Rep 3	0.44		1.99	0.86	2.56	1.47	13.23	3.21	2.73	15.86	2.14	2.21
Rep 4	0.44		1.34	1.02	2.11	6.00	9.23	3.64	3.04	6.77	3.99	1.21
Mean	**0.42**	**1.06**	**1.25**	**0.87**	**2.73**	**3.86**	**11.24**	**3.00**	**3.19**	**7.80**	**2.38**	**1.43**
±2SE	0.04	0.43	0.56	0.14	0.59	2.02	2.04	0.55	0.85	5.60	1.12	0.52
Lead												
Rep 1	0.09		0.14	0.23	0.12	0.13	0.23	0.09	0.11	0.15	0.13	0.13
Rep 2	0.00		0.07	0.13	0.07	0.42	0.28	0.23	0.14	0.12	0.11	0.15
Rep 3	0.05		0.12	0.15	0.08	0.15	0.35	0.14	0.14	0.35	0.16	0.16
Rep 4	0.05		0.10	0.14	0.13	0.15	0.22	0.19	0.12	0.23	0.16	0.12
Mean	**0.05**	**0.13**	**0.10**	**0.16**	**0.10**	**0.21**	**0.27**	**0.16**	**0.13**	**0.21**	**0.14**	**0.14**
±2SE	0.04	0.05	0.03	0.04	0.03	0.14	0.06	0.06	0.01	0.11	0.02	0.02
Mercury												
Rep 1	0.149		0.185	0.115	0.128	0.146	0.146	0.134	0.109	0.115	0.138	0.121
Rep 2	0.257		0.131	0.113	0.148	0.151	0.166	0.135	0.127	0.167	0.126	0.131
Rep 3	0.159		0.173	0.132	0.126	0.159	0.203	0.111	0.153	0.124	0.311	0.128
Rep 4	0.205		0.168	0.133	0.144	0.153	0.164	0.109	0.139	0.155	0.130	0.138
Mean	**0.193**	**0.144**	**0.164**	**0.123**	**0.136**	**0.152**	**0.170**	**0.122**	**0.132**	**0.140**	**0.176**	**0.129**
±2SE	0.050	0.028	0.023	0.011	0.011	0.005	0.024	0.014	0.019	0.024	0.090	0.007
Methylmercury												
Rep 1	0.038		0.023	0.018	0.024	0.028	0.024	0.024	0.020	0.014	0.022	0.019
Rep 2	0.038		0.016	0.011	0.027	0.027	0.020	0.023	0.023	0.015	0.023	0.020
Rep 3	0.040		0.031	0.014	0.020	0.025	0.032	0.019	0.025	0.016	0.023	0.020
Rep 4	0.041		0.028	0.016	0.028	0.033	0.024	0.016	0.018	0.018	0.022	0.020
Mean	**0.039**	**0.020**	**0.024**	**0.015**	**0.025**	**0.028**	**0.025**	**0.020**	**0.021**	**0.016**	**0.022**	**0.020**
±2SE	0.002	0.007	0.007	0.003	0.004	0.003	0.005	0.004	0.003	0.002	0.001	0.000

[a]Value represents average of data (n=8) for Reference Stations 1 and 2

Table 5. Mean content (µg dry weight) of trace elements in clam tissues.

	Content (µg dry weight)											
	Initial	**Sta 1 & 2[a]**	**Sta 1**	**Sta 2**	**Sta 3**	**Sta 4**	**Sta 5**	**Sta 6**	**Sta 7**	**Sta 8**	**Sta 9**	**Sta 10**
Arsenic												
Rep 1	0.62		0.62	0.58	0.79	0.67	0.58	0.72	0.82	0.77	0.72	0.70
Rep 2	0.65		0.64	0.75	0.73	0.70	0.69	0.74	0.67	0.78	0.62	0.65
Rep 3	0.66		0.60	0.69	0.81	0.74	0.73	0.87	0.71	0.92	0.77	0.67
Rep 4	0.60		0.64	0.67	0.72	0.64	0.72	0.81	0.73	0.82	0.72	0.67
Mean	**0.63**	**0.65**	**0.62**	**0.67**	**0.76**	**0.69**	**0.68**	**0.79**	**0.73**	**0.82**	**0.71**	**0.67**
±2SE	0.02	0.05	0.02	0.07	0.05	0.04	0.07	0.07	0.06	0.07	0.07	0.02
Cadmium												
Rep 1	0.33		0.27	0.35	0.43	0.27	0.30	0.30	0.38	0.44	0.35	0.36
Rep 2	0.33		0.24	0.42	0.32	0.33	0.33	0.31	0.35	0.44	0.30	0.34
Rep 3	0.27		0.25	0.45	0.41	0.33	0.33	0.41	0.34	0.56	0.36	0.40
Rep 4	0.31		0.23	0.36	0.35	0.29	0.35	0.54	0.38	0.46	0.35	0.35
Mean	**0.31**	**0.32**	**0.25**	**0.40**	**0.38**	**0.31**	**0.33**	**0.39**	**0.36**	**0.47**	**0.34**	**0.36**
±2SE	0.02	0.09	0.02	0.05	0.05	0.03	0.02	0.11	0.02	0.06	0.03	0.02
Chromium												
Rep 1	0.24		0.66	0.78	2.45	2.61	7.73	2.18	3.97	5.16	1.26	1.02
Rep 2	0.29		0.60	0.58	3.36	4.22	10.04	2.61	2.32	2.60	1.74	0.86
Rep 3	0.29		1.35	0.71	2.37	1.34	9.31	2.85	2.35	14.18	1.90	1.83
Rep 4	0.29		0.97	0.85	1.93	5.09	6.36	3.09	2.62	5.90	3.40	1.05
Mean	**0.28**	**0.81**	**0.89**	**0.73**	**2.53**	**3.31**	**8.36**	**2.68**	**2.81**	**6.96**	**2.07**	**1.19**
±2SE	0.02	0.25	0.34	0.11	0.60	1.67	1.64	0.39	0.78	5.02	0.92	0.43
Lead												
Rep 1	0.063		0.091	0.195	0.107	0.115	0.180	0.085	0.100	0.132	0.117	0.106
Rep 2	0.003		0.061	0.111	0.069	0.356	0.219	0.217	0.124	0.106	0.098	0.118
Rep 3	0.016		0.079	0.124	0.075	0.136	0.248	0.128	0.120	0.317	0.141	0.133
Rep 4	0.016		0.069	0.114	0.119	0.131	0.151	0.160	0.103	0.200	0.136	0.104
Mean	**0.03**	**0.11**	**0.08**	**0.14**	**0.09**	**0.18**	**0.20**	**0.15**	**0.11**	**0.19**	**0.12**	**0.12**
±2SE	0.027	0.043	0.013	0.040	0.024	0.115	0.043	0.056	0.012	0.094	0.020	0.013
Mercury												
Rep 1	0.102		0.124	0.099	0.114	0.127	0.116	0.124	0.098	0.105	0.125	0.101
Rep 2	0.172		0.114	0.096	0.142	0.128	0.131	0.126	0.116	0.148	0.109	0.106
Rep 3	0.106		0.117	0.109	0.117	0.145	0.143	0.099	0.132	0.111	0.275	0.106
Rep 4	0.132		0.121	0.111	0.131	0.130	0.113	0.092	0.120	0.135	0.111	0.120
Mean	**0.128**	**0.111**	**0.119**	**0.104**	**0.126**	**0.132**	**0.126**	**0.110**	**0.116**	**0.125**	**0.155**	**0.108**
±2SE	0.032	0.010	0.004	0.007	0.013	0.008	0.014	0.017	0.014	0.020	0.080	0.008
Methylmercury												
Rep 1	0.026		0.015	0.015	0.021	0.025	0.019	0.022	0.018	0.013	0.020	0.016
Rep 2	0.025		0.014	0.010	0.026	0.023	0.016	0.021	0.021	0.013	0.020	0.016
Rep 3	0.027		0.021	0.012	0.018	0.023	0.022	0.016	0.021	0.014	0.020	0.016
Rep 4	0.026		0.020	0.013	0.026	0.028	0.017	0.014	0.015	0.016	0.019	0.017
Mean	**0.026**	**0.015**	**0.018**	**0.012**	**0.023**	**0.025**	**0.018**	**0.018**	**0.019**	**0.014**	**0.020**	**0.017**
±2SE	0.001	0.004	0.003	0.002	0.004	0.002	0.003	0.004	0.003	0.001	0.001	0.001

[a]Value represents average of data (n=8) for Reference Stations 1 and 2

Table 6. Results of statistical analyses on tissue concentration data.

Tannery Bay stations compared with the average of reference stations

	Sta 3	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Arsenic	NS	NS	NS	NS	NS	NS	NS	NS
Cadmium	NS	NS	NS	NS	NS	*	NS	NS
Chromium	NS	*	*	*	*	*	NS	NS
Lead	NS	NS	NS	NS	NS	NS	NS	NS
Mercury	NS	NS	NS	NS	NS	NS	NS	NS
Methylmercury	*	*	*	NS	NS	--	NS	NS

* Concentration in clams from Tannery Bay station significantly greater than the average of reference stations.
NS – No significant difference between Tannery Bay station and the average of reference stations.
-- Concentration in clams from Tannery Bay station significantly less than the average of reference stations.

All Stations compared with the Initial (T_0) concentration

	Sta 1	Sta 2	Sta 3	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Arsenic	NS	NS	NS	--	NS	NS	--	NS	--	NS
Cadmium	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Chromium	*	NS	*	*	*	*	*	*	*	*
Lead	*	*	*	*	*	*	*	*	*	*
Mercury	NS	--	NS	NS	NS	--	--	NS	NS	NS
Methylmercury	--	--	--	--	--	--	--	--	--	--

* Concentration in clams from station significantly greater than the initial (T_0) concentration.
NS - No significant difference between station and the initial (T_0) concentration.
-- Concentration in clams from station significantly less than the initial (T_0) concentration.

Results of Student Newman-Keuls analyses on Tannery Bay stations

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

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

Table 6 (continued).

Log-transformed Chromium	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Sta 3	.846750	**.00100***	.812555	.922308	**.04041***	.476774	.098294
Sta 4		**.00166***	.834543	.670226	**.03548***	.549013	.063644
Sta 5			**.00122***	**.00113***	.093466	**.00032***	**.00015***
Sta 6				.886829	**.04532***	.606781	.103420
Sta 7					**.03528***	.688880	.113172
Sta 8						**.01085***	**.00056***
Sta 9							.162674

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

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

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

Values in **bold** face and marked with an asterisk indicate a significant difference between stations.

Table 7. Results of statistical analyses on tissue content data.

Tannery Bay Stations compared with the average of reference stations

	Sta 3	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Arsenic	*	NS	NS	*	*	*	NS	NS
Cadmium	NS	NS	NS	NS	NS	*	NS	NS
Chromium	*	*	*	*	*	*	NS	NS
Lead	NS	NS	NS	NS	NS	NS	NS	NS
Mercury	NS	*	NS	NS	NS	NS	NS	NS
Methylmercury	*	*	*	*	*	NS	*	NS

* Content in clams from Tannery Bay station significantly greater than the average of reference stations.
NS – No significant difference between Tannery Bay station and the average of reference stations.
-- Concentration in clams from Tannery Bay station significantly less than the average of reference stations.

All Stations compared with the Initial (T_0) content

	Sta 1	Sta 2	Sta 3	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Arsenic	NS	NS	*	NS	NS	*	NS	*	NS	NS
Cadmium	NS	NS	NS	NS	NS	NS	NS	*	NS	NS
Chromium	*	*	*	*	*	*	*	*	*	*
Lead	*	*	*	*	*	*	*	*	*	*
Mercury	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Methylmercury	--	--	NS	NS	--	--	--	--	--	--

* - Content in clams from station significantly greater than the initial (T_0) content.
NS - No significant difference between station and the initial (T_0) content.
--Content in clams from station significantly less than the initial (T_0) content.

Results of Student Newman-Keuls analyses on Tannery Bay stations

Arsenic	**Sta 4**	**Sta 5**	**Sta 6**	**Sta 7**	**Sta 8**	**Sta 9**	**Sta 10**
Sta 3	.246178	.294896	.567017	.479323	.329379	.356169	.232615
Sta 4		.935554	.123708	.463488	**.02674***	.608212	.924048
Sta 5			.140279	.581636	**.02906***	.820743	.768725
Sta 6				.409248	.390203	.222626	.099445
Sta 7					.159087	.501585	.522781
Sta 8						.060453	**.01858***
Sta 9							.805475

Log-transformed Cadmium	**Sta 4**	**Sta 5**	**Sta 6**	**Sta 7**	**Sta 8**	**Sta 9**	**Sta 10**
Sta 3	.271655	.623085	.883704	.935928	.052864	.732871	.750743
Sta 4		.438111	.260652	.272000	**.00216***	.479573	.352153
Sta 5			.627829	.541491	**.01082***	.703402	.695554
Sta 6				.959430	**.02906***	.762610	.886242
Sta 7					.065513	.500424	.979693
Sta 8						**.02008***	**.04653***
Sta 9							.759936

Table 7 (continued)

Log-transformed Chromium	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Sta 3	.929033	**.00375***	.802568	.931000	**.04635***	.398803	**.03103***
Sta 4		**.00395***	.933628	.808083	**.02598***	.593180	**.02991***
Sta 5			**.00485***	**.00404***	.228600	**.00072***	**.00015***
Sta 6				.915009	.053327	.516024	**.03141***
Sta 7					**.03848***	.620461	**.03736***
Sta 8						**.00914***	**.00025***
Sta 9							.075181

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

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

Methylmercury	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Sta 3	.338606	.102697	.133255	.080469	**.00140***	.092543	**.02270***
Sta 4		**.01893***	**.02323***	**.01710***	**.00027***	**.03042***	**.00305***
Sta 5			.956651	.888703	.112302	.791600	.558412
Sta 6				.979007	.074222	.892308	.333662
Sta 7					.123403	.612682	.642834
Sta 8						.058875	.199605
Sta 9							.454670

Values in **bold** face and marked with an asterisk indicate a significant difference between stations.

Table 8. Quotients derived by dividing end-of-test tissue content by initial tissue content.

	As	Cd	Cr	Pb	Hg	Sum
Sta 1	0.990	0.797	3.23	3.041	0.931	9.0
Sta 2	1.068	1.283	2.648	5.51	0.812	11.3
Sta 3	1.209	1.218	9.127	3.738	0.986	16.3
Sta 4	1.086	0.992	11.97	7.473	1.036	22.6
Sta 5	1.081	1.064	30.19	8.075	0.982	41.4
Sta 6	1.246	1.264	9.691	5.977	0.863	19.0
Sta 7	1.163	1.174	10.17	4.536	0.910	18.0
Sta 8	1.302	1.528	25.14	7.64	0.975	36.6
Sta 9	1.120	1.104	7.49	4.977	1.213	15.9
Sta 10	1.062	1.177	4.302	4.67	0.846	12.1

Table 9. Descriptive statistics on clam growth metrics.

		Initial (T_0)	Sta 1	Sta 2	Sta 3	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Initial	**Mean**	5.45	5.53	5.52	5.52	5.58	5.49	5.55	5.58	5.46	5.49	5.51
WAWW	**Min.**	4.01	4.02	4.04	4.01	4.02	4.10	4.07	4.04	4.02	4.01	4.02
(g)	**Max.**	7.79	7.90	7.93	7.92	7.95	7.79	7.89	7.91	7.75	7.75	7.85
	SD	0.83	0.84	0.84	0.88	0.88	0.79	0.83	0.88	0.80	0.85	0.82
	±2SE	0.10	0.10	0.10	0.10	0.10	0.09	0.10	0.10	0.09	0.10	0.09
End-of-test	**Mean**		5.56	5.62	5.71	5.72	5.58	5.76	5.76	5.58	5.70	5.63
WAWW	**Min.**		3.98	4.03	4.20	4.15	4.03	4.12	4.15	4.13	3.44	4.30
(g)	**Max.**		7.98	8.11	8.06	8.06	7.95	7.83	8.09	7.77	8.28	8.29
	SD		0.82	0.81	0.86	0.85	0.79	0.83	0.88	0.79	0.86	0.81
	±2SE		0.10	0.10	0.10	0.10	0.10	0.10	0.11	0.09	0.10	0.10
□ WAWW	**Mean**		0.04	0.11	0.18	0.14	0.08	0.22	0.19	0.15	0.21	0.15
(g)	**Min.**		-0.39	-0.60	-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	0.70	0.58	0.46
	SD		0.09	0.11	0.12	0.12	0.11	0.12	0.12	0.13	0.11	0.09
	±2SE		0.01	0.01	0.02	0.02	0.01	0.02	0.01	0.02	0.01	0.01
WAWW	**Mean**		5.16	14.49	22.49	17.92	9.57	28.04	24.26	19.25	27.24	18.56
Growth	**Min.**		-49.62	-76.34	-31.81	-57.25	-69.97	-22.90	-26.72	-80.15	-73.79	-19.08
(mg/wk)	**Max.**		39.44	45.80	72.52	99.24	49.62	71.25	69.97	89.06	73.79	58.52
	SD		11.80	14.17	15.31	15.49	14.63	15.56	14.77	16.40	14.51	11.18
	±2SE		1.42	1.69	1.85	1.88	1.81	1.85	1.78	1.95	1.73	1.34
End-of-test	**Mean**	0.66	0.74	0.84	0.92	0.87	0.81	0.90	0.88	0.89	0.88	0.83
Tissue	**Min.**	0.32	0.34	0.39	0.50	0.47	0.42	0.42	0.41	0.45	0.42	0.42
(g)	**Max.**	1.09	1.18	1.28	1.39	1.30	1.27	1.63	1.41	1.71	1.25	1.33
	SD	0.14	0.14	0.14	0.16	0.15	0.13	0.16	0.17	0.15	0.15	0.14
	±2SE	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
Percent	**Mean**	15.2	15.2	14.8	15.8	15.7	14.7	16.2	16.3	15.6	16.0	15.1
Solids	**Min.**	15.0	14.4	14.5	14.6	14.7	14.0	16.0	15.5	15.0	15.7	14.9
	Max.	15.5	17.4	15.1	16.9	16.5	15.6	16.4	17.2	16.5	16.1	15.5
	±2SE	0.24	1.48	0.26	0.98	0.84	0.75	0.17	0.88	0.65	0.20	0.27
Percent	**Mean**	1.30	1.36	1.35	1.56	1.39	1.40	1.50	1.48	1.43	1.72	1.37
Lipids	**Min.**	1.08	1.11	1.06	1.41	1.00	1.24	1.34	1.33	1.21	1.54	1.15
	Max.	1.46	1.65	1.91	1.70	1.82	1.72	1.84	1.66	1.69	1.93	1.54
	±2SE	0.18	0.23	0.38	0.12	0.42	0.22	0.24	0.14	0.20	0.16	0.18
	N	300	277	280	273	270	261	284	275	284	280	277

WAWW – Whole-animal wet weight.

Table 10. Results of statistical analyses on clam growth metrics.

Tannery Bay stations compared with the average of reference stations

	Sta 3	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
WAWW	*	*	NS	*	*	NS	NS	NS
WAWW Growth rate	*	*	NS	*	*	*	*	*
EOT Tissue weight	*	*	NS	*	*	*	*	*
% Solids	NS	NS	NS	*	*	NS	*	NS
% Lipids	NS	NS	NS	NS	NS	NS	*	NS

WAWW – Whole-animal wet weight.
EOT – End-of-test.
* Clams from Tannery Bay station significantly greater than the average of reference stations.
NS – No significant difference between Tannery Bay station and the average of reference stations.

Results of Student Newman-Keuls analyses on Tannery Bay stations

Log-transformed end-of-test WAWW	**Sta 4**	**Sta 5**	**Sta 6**	**Sta 7**	**Sta 8**	**Sta 9**	**Sta 10**
Sta 3	.867246	.377873	.861547	.789735	.284385	.861222	.526827
Sta 4		.365780	.810651	.625932	.293884	.937562	.597062
Sta 5			.164255	.179095	.987677	.368545	.755777
Sta 6				.896708	.137959	.873297	.424607
Sta 7					.145318	.840497	.412874
Sta 8						.244659	.485442
Sta 9							.365668

Rank- it transformed Growth Rate	**Sta 4**	**Sta 5**	**Sta 6**	**Sta 7**	**Sta 8**	**Sta 9**	**Sta 10**
Sta 3	**.00072***	**.00002***	**.00004***	.139430	**.00892***	**.00012***	**.00266***
Sta 4		**.00001***	**.00003***	**.00002***	.437565	**.00002***	.597145
Sta 5			**.00003***	**.00002***	**.00001***	**.00003***	**.00002***
Sta 6				**.00683***	**.00002***	.708783	**.00002***
Sta 7					**.00014***	**.00782***	**.00002***
Sta 8						**.00001***	.485304
Sta 9							**.00002***

Tissue Weight	**Sta 4**	**Sta 5**	**Sta 6**	**Sta 7**	**Sta 8**	**Sta 9**	**Sta 10**
Sta 3	**.00072***	**.00003***	.075583	**.01181***	**.04229***	**.00485***	**.00003***
Sta 4		**.00002***	.151994	.581178	.352838	.554438	**.00523***
Sta 5			**.00003***	**.00002***	**.00002***	**.00001***	**.03653***
Sta 6				.403761	.527323	.330604	**.00002***
Sta 7					.513972	.687648	**.00090***
Sta 8						.542322	**.00010***
Sta 9							**.00207***

Table 10 (continued)

Percent Lipids	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Sta 3	.902962	.866733	.745944	.893682	.848253	.313136	.903733
Sta 4		.950793	.953924	.937862	.974102	.405374	.901736
Sta 5			.917972	.864730	.877328	.372000	.980931
Sta 6				.901736	.879546	.378010	.959420
Sta 7					.722749	.462647	.953924
Sta 8						.373886	.985781
Sta 9							.393714

Percent Solids	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Sta 3	.834347	.225505	.646079	.654861	.962322	.601823	.526351
Sta 4		.232043	.686619	.648643	.958376	.742218	.485736
Sta 5			.067887	**.04795***	.159345	.112709	.435463
Sta 6				.793791	.771365	.714562	.242913
Sta 7					.710338	.802691	.189968
Sta 8						.856783	.277800
Sta 9							.342190

WAWW – Whole-animal wet weight.
Values in **bold** face and marked with an asterisk indicate a significant difference between stations.

Table 11. Summary of water temperature conditions during the study, by station, summer 1997.

	Min. temp. (°C)	Max. temp. (°C)	Mean temp. (°C)
Sta 1	15.9	26.3	20.2
Sta 2	13.9	23.1	18.2
Sta 3	12.4	24.0	18.2
Sta 4	12.1	24.5	17.8
Sta 5	10.5	24.1	15.1
Sta 6	11.8	24.2	18.3
Sta 7	13.4	23.7	18.7
Sta 8	14.1	23.5	18.7
Sta 9	13.2	23.2	18.5
Sta 10	13.9	24.1	18.5

Table 12. Results of statistical analyses on mean daily temperature data.

Comparison stations	Mean difference	Standard deviation	*t*-statistic	df	*p*-value
Station 1 - Station 2	1.93	0.46	4.21	10	**0.0018***
Station 1 - Station 3	1.95	0.27	7.23	10	**0.0000***
Station 1 - Station 4	2.45	0.22	11.29	10	**0.0000***
Station 1 - Station 5	5.08	0.29	17.32	10	**0.0000***
Station 1 - Station 6	1.82	0.27	6.85	10	**0.0000***
Station 1 - Station 7	1.35	0.33	4.06	10	**0.0023***
Station 1 - Station 8	1.61	0.35	4.58	10	**0.0010***
Station 1 - Station 9	1.60	0.38	4.23	10	**0.0018***
Station 1 - Station 10	1.67	0.35	4.81	10	**0.0007***
Station 2 - Station 3	0.01	0.21	0.03	10	0.9765
Station 2 - Station 4	0.49	0.28	1.72	10	0.1164
Station 2 - Station 5	3.27	0.32	10.26	10	**0.0000***
Station 2 - Station 6	0.08	0.27	0.30	10	0.7705
Station 2 - Station 7	0.51	0.18	2.91	10	0.1555
Station 2 - Station 8	0.40	0.11	3.51	10	**0.0056***
Station 2 - Station 9	0.41	0.21	2.00	10	0.0732
Station 2 - Station 10	0.29	0.07	3.91	10	**0.0029***
Station 3 - Station 4	0.31	0.10	3.29	10	**0.0081***
Station 3 - Station 5	3.28	0.25	13.07	10	**0.0000***
Station 3 - Station 6	0.05	0.18	0.28	10	0.7865
Station 3 - Station 7	0.47	0.07	6.26	10	**0.0001***
Station 3 - Station 8	0.47	0.16	2.87	10	0.0166
Station 3 - Station 9	-0.37	0.09	-4.13	10	**0.0021***
Station 3 - Station 10	0.28	0.16	1.77	10	0.1076
Station 4 - Station 5	2.72	0.22	12.38	10	**0.0000***
Station 4 - Station 6	0.47	0.08	6.01	10	**0.0001***
Station 4 - Station 7	1.16	0.19	6.20	10	**0.0001***
Station 4 - Station 8	0.93	0.27	3.41	10	**0.0067***
Station 4 - Station 9	0.68	0.16	4.32	10	**0.0015***
Station 4 - Station 10	0.78	0.25	3.16	10	0.0102
Station 5 - Station 6	3.03	0.15	19.58	10	**0.0000***
Station 5 - Station 7	3.46	0.22	15.48	10	**0.0000***
Station 5 - Station 8	3.65	0.35	10.40	10	**0.0000***
Station 5 - Station 9	3.44	0.39	8.88	10	**0.0000***
Station 5 - Station 10	3.40	0.43	7.91	10	**0.0000***
Station 6 - Station 7	0.53	0.17	3.19	10	**0.0097***
Station 6 - Station 8	0.49	0.27	1.81	10	0.0999
Station 6 - Station 9	-0.24	0.18	-1.32	10	0.2161
Station 6 - Station 10	0.20	0.24	0.83	10	0.4281
Station 7 - Station 8	0.23	0.12	1.85	10	0.0948
Station 7 - Station 9	0.28	0.12	2.28	10	0.0460
Station 7 - Station 10	0.23	0.13	1.86	10	0.0924
Station 8 - Station 9	0.11	0.10	1.05	10	0.3172
Station 8 - Station 10	0.06	0.12	0.49	10	0.6319
Station 9 - Station 10	-0.02	0.09	-0.20	10	0.8481

NOTE: *p*-values in bold with asterisk represent significant difference between comparison stations.
df–degrees of freedom.

Table 13. Differences in weekly temperature ranges across stations.

	Sta 1	Sta 2	Sta 3	Sta 4	Sta 5	Sta 6	Sta 7	Sta 8	Sta 9	Sta 10
Means of ranges	4.87	7.00	7.97	8.43	8.47	8.84	6.79	5.90	6.62	7.32

Comparison	Test statistic	# of means	*p*-value
Station 1 - Station 2	5.676	5	**<0.005***
Station 1 - Station 3	7.763	7	**<0.001***
Station 1 - Station 4	8.551	9	**<0.001***
Station 1 - Station 5	8.296	8	**<0.001***
Station 1 - Station 6	9.182	10	**<0.001***
Station 1 - Station 7	5.376	4	**<0.005***
Station 1 - Station 8	3.329	2	**<0.025***
Station 1 - Station 9	4.888	3	**<0.005***
Station 1 - Station10	6.380	6	**<0.001***
Station 2 - Station 6	3.505	6	>0.10
Station 2 - Station 8	2.348	4	>0.20

NOTE: *p*-values in bold with asterisk represent significant difference between comparison stations.

Table 14. Results of chemical analyses on sediment samples collected at the end of the study.

	THg (μg/g)	MeHg (μg/g)	As (μg/g)	Cd (μg/g)	Cr (μg/g)	Pb (μg/g)	TOC (%)	Dry wt (%)	Gravel (%)	Sand (%)	Silt (%)	Clay (%)	Porosity (%)	Dry bulk density (g/cm^3)
Sta 1	0.0896	0.000737	6.49	0.98U	27.1	16.8	0.86	23.2	0.07	91.79	6.23	1.91	48.15	1.37
Sta 2	0.0311	0.0000385	2.00U	0.98U	13.4U	13.6U	0.23	79.7	0.81	95.35	2.66	1.18	44.07	1.5
Sta 3	2.07	0.00226	12.3	5.33	20598	218	11.72	16.2	0	48.61	32.97	18.42	81.3	0.35
Sta 4	1.27	0.00648	24	13.1	17789	142	12.38	26	0	28.59	47.97	23.44	81.86	0.35
Sta 5	1.04	0.00461	14.4	14.1	10108	114	10.53	25.1	0	21.62	50.39	27.99	85.07	0.31
Sta 6	0.433	0.0032	23.8	2.75	7800	60.7	5.09	51.2	0	50.56	40.39	9.05	68.06	0.79
Sta 7	0.264	0.0016	8.36	3.67	4479	53	1.66	63.3	0	54.4	40.3	5.3	54.82	1.15
Sta 8	0.19	0.000998	10.5	2.15	3980	55.7	5.52	71	0.04	80.25	16.16	3.55	50.57	1.22
Sta 9	0.0969	0.000707	5.19	0.98U	984	15.7	0.7	69.8	0	89.06	8.22	2.71	50.87	1.28
Sta 10	0.126	0.000409	2.00U	0.98U	1291	21.5	0.67	72.7	0.54	93	4.79	1.67	49.04	1.37

Table 15. Results of chemical analyses on surface water samples collected at the beginning and end of the study.

	THg (UF) (ng/L)	THg (Dis) (ng/L)	MeHg (UF) (ng/L)	MeHg (Dis) (ng/L)	As (UF) (μg/L)	As (Dis) (μg/L)	Cd (UF) (μg/L)	Cd (Dis) (μg/L)	Cr (UF) (μg/L)	Cr (Dis) (μg/L)	Pb (UF) (μg/L)	Pb (Dis) (μg/L)	TSS (mg/L)	TOC (mg/L)	DOC (mg/L)	Hard-ness (mg/L)	NH_4 (mg N/L)	NO_2	Chl-*a* (μg/L)	Phaeo (μg/L)	pH
Deployment																					
Sta 1	2.07	1.87	0.224	0.201	0.26	0.18	0.1U	0.1U	1.70U	1.70U	0.61U	0.61U	2	10.2	11.42	46.8	0.018	NA	2.03	1.58	7.0
Sta 4	5.7	0.728	0.0939	0.0214(J)	0.18	0.11	0.1U	0.1U	45.4	3.06	0.61U	0.61U	2.63	2.13	2.12	79.7	0.015	NA	2.19	1.25	7.0
Sta 5	0.771	0.488	0.0843	0.0376	0.2	0.15	0.1U	0.1U	32.7	2.28	0.61U	0.61U	2.19	2.09	1.95	78.5	0.024	NA	1.86	0.78	7.0
Sta 9	1.35	0.315	0.0317	0.0294(J)	0.21	0.2	0.1U	0.1U	6.95	0.79J	0.61U	0.61U	2.49	1.39	1.88	51.3	0.011	NA	1.62	0.55	7.0
Sta 10	2.63	0.431	0.0173(J)	0.0279(J)	0.27	0.2	0.1U	0.1U	5.82	0.42J	0.61U	0.61U	4.38	1.86	1.73	48.7	0.008	NA	3.22	1.13	7.0
Retrieval																					
Sta 1	1.19	1.57	0.112	0.0788	< 0.05	< 0.05	< 0.05	< 0.05	< 0.20	< 0.20	< 0.41	< 0.41	0.641	3.94	3.2	40	0.005	0.0013	2.75	1.55	6.81
Sta 4	2.14	0.94	0.0478	0.0321	0.06	0.06	< 0.05	0.06	7.23	1.23	< 0.41	< 0.41	0.226	2.37	1.9	61.3	0.022	0.0034	1.99	0.76	5.99
Sta 5	1.9	0.755	0.0628	< 0.0306(U)	0.08	0.1	< 0.05	< 0.05	6.27	1.01	< 0.41	< 0.41	0.604	2.3	1.92	64.7	0.041	0.0042	1.83	0.97	6.07
Sta 9	1.93	1.12	0.0619	< 0.0310(U)	0.16	0.11	< 0.05	0.05	8.12	1.05	< 0.41	< 0.41	0.415	2.24	1.89	61.1	0.048	0.0037	1.95	0.93	6.29
Sta 10	1.32	1.08	0.0304	< 0.0307(U)	0.06	0.05	< 0.05	< 0.05	3.15	0.7	< 0.41	< 0.41	0.181	2.31	1.89	43	0.038	0.0038	2.8	1.34	6.52

J = uncertain value; U = below detection limit; UF = unfiltered; Dis = dissolved; NA = Not available
All metals in terms of total concentration

Table 16. Calculated quotients for EOT sediment concentration/LEL, and sum of quotients by station.

	THg	MeHg	As	Cd	Cr	Pb	Sum of Quotients	TOC	% fines
Sta 1	0.45	na	1.08	0.82	1.04	0.54	**3.93**	0.86	8.14
Sta 2	0.16	na	0.17	0.82	0.26	0.22	**1.62**	0.23	3.84
Sta 3	10.35	na	2.05	8.88	792.23	7.03	**820.55**	11.72	51.39
Sta 4	6.35	na	4.00	21.83	684.19	4.58	**720.96**	12.38	71.41
Sta 5	5.20	na	2.40	23.50	388.77	3.68	**423.55**	10.53	78.38
Sta 6	2.17	na	3.97	4.58	300.00	1.96	**312.67**	5.09	49.44
Sta 7	1.32	na	1.39	6.12	172.27	1.71	**182.81**	1.66	45.6
Sta 8	0.95	na	1.75	3.58	153.08	1.80	**161.16**	5.52	19.71
Sta 9	0.48	na	0.87	0.82	37.85	0.51	**40.52**	0.7	10.93
Sta 10	0.63	na	0.17	0.82	49.65	0.69	**51.96**	0.67	6.46
LEL values (µg/g)	0.2	na	6.0	0.6	26.0	31.0			

na – not available

Table 17. Correlation coefficients *(r)* for trace elements in surface water, sediment, and clam tissues.

	Cr	THg	MeHg	As	Cd	Pb
water : sediment	0.53	0.48	0.03	-0.83	na	na
water : tissue	0.62	-0.46	0.52	0.300	na	na
sediment : tissue	0.27	0.0001	0.68	-0.042	-0.3	0.12

na = not able to calculate coefficients because there was no linear spread in the data

Table 18. Correlation coefficients for tissue chemistry vs. clam growth metrics based on concentration and content.

Clam Tissue Concentration

	Cr	THg	MeHg	As	Cd	Pb
Survival	-0.251	-0.355	-0.484	-0.354	0.019	-0.253
EOT WAWW	-0.210	-0.055	0.097	-0.274	-0.284	-0.169
Growth Rate	-0.223	-0.340	-0.256	-0.477	-0.102	-0.283
Tissue Weight (wet)	0.267	-0.082	-0.238	0.115	0.089	0.109
Tissue Weight (dry)	0.342	-0.162	-0.324	0.247	0.260	0.175

Clam Tissue Content

	Cr	THg	MeHg	As	Cd	Pb
Survival	-0.172	-0.162	-0.309	0.064	0.223	-0.133
EOT WAWW	-0.175	0.190	0.351	0.238	-0.034	-0.075
Growth Rate	-0.133	0.068	0.162	0.380	0.307	-0.116
Tissue Weight (wet)	0.283	-0.031	-0.176	0.256	0.160	0.137
Tissue Weight (dry)	0.355	-0.114	-0.268	0.385	0.322	0.198

EOT WAWW – end-of-test whole-animal wet weight.

Table 19. Correlation coefficients for temperature vs. clam growth metrics.

Survival	0.363
Growth Rate	0.122
Tissue Weight (wet)	-0.196
Tissue Weight (dry)	-0.292

8.0 FIGURES

Figure 1. Location of Cannelton Industries, Inc., Sault Ste. Marie, Michigan, and clam deployment stations in Tannery Bay and at reference stations near Waiska Bay (REF-1) and Seymour Creek (REF-2).

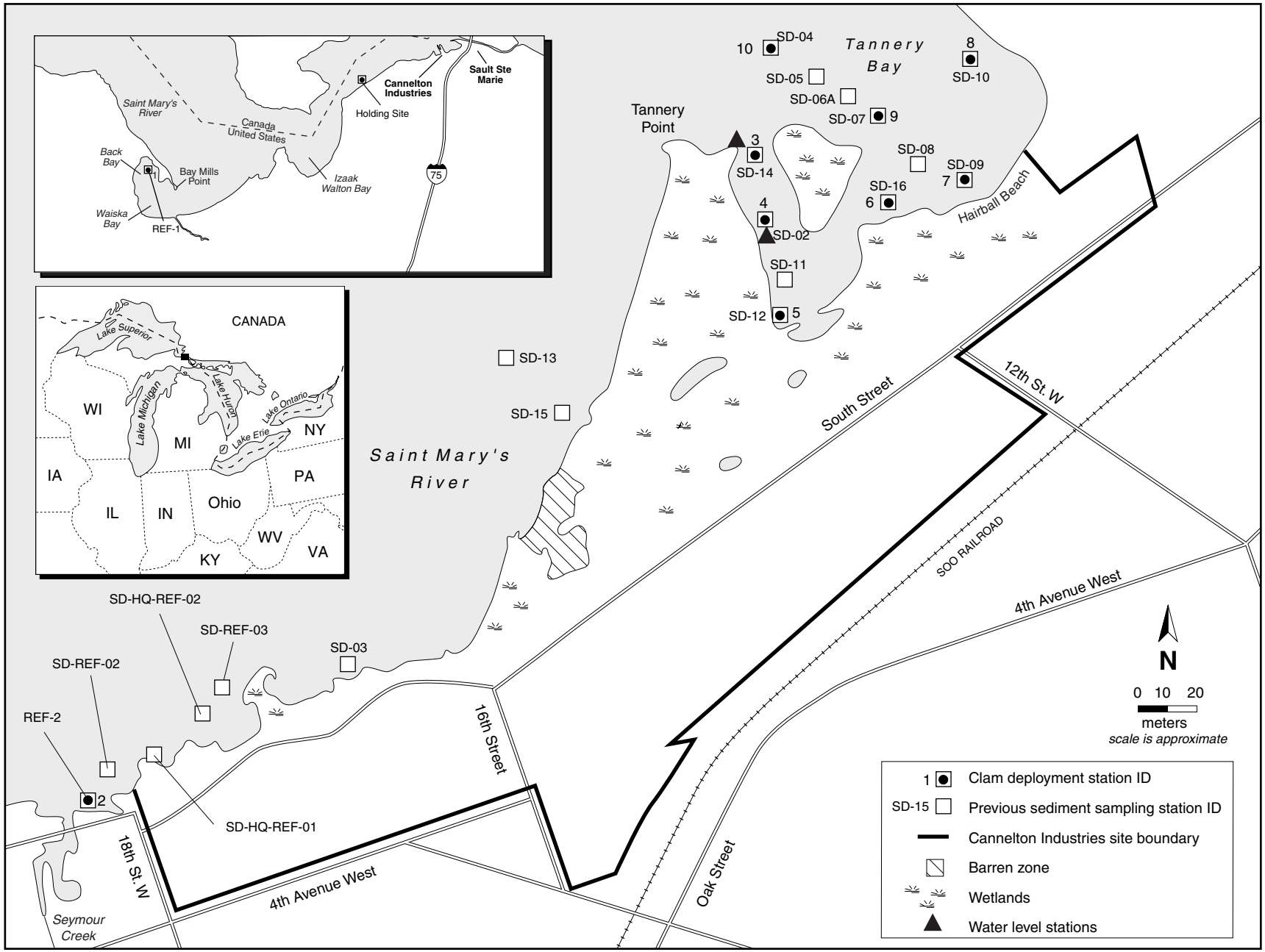
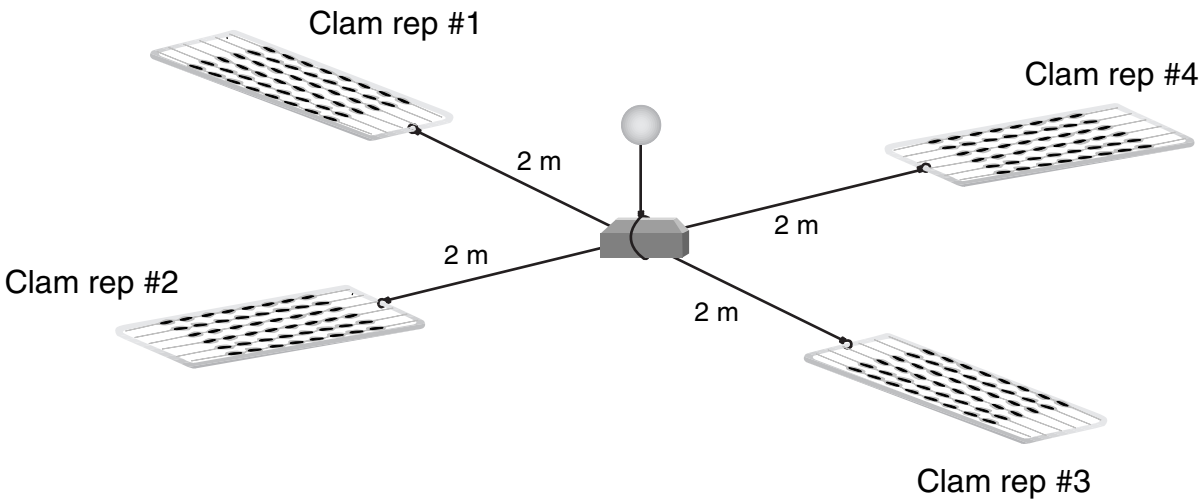


Figure 2. Deployment layout at each station.



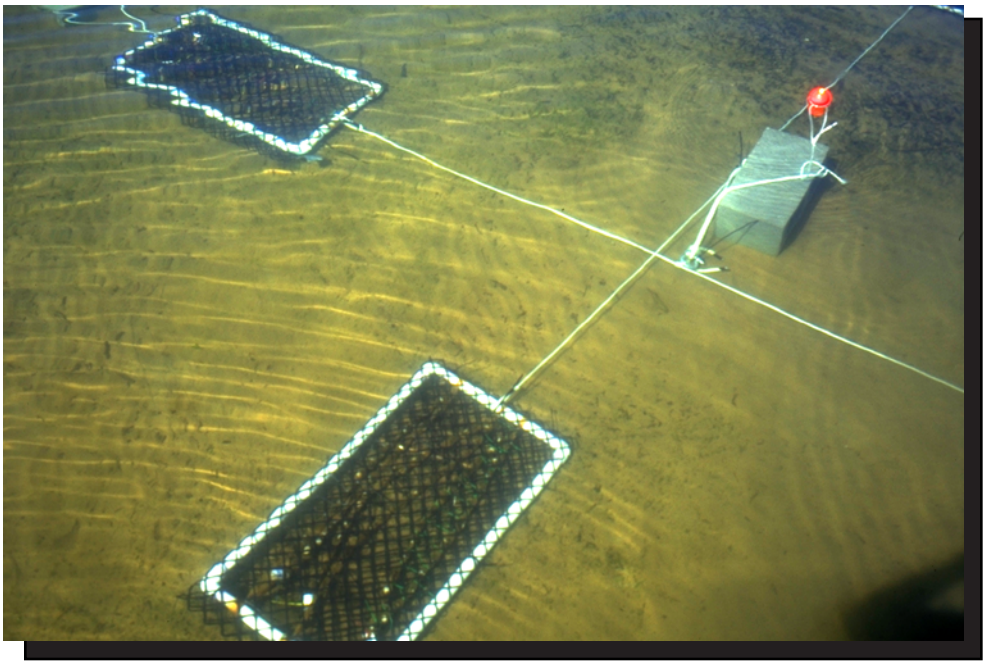
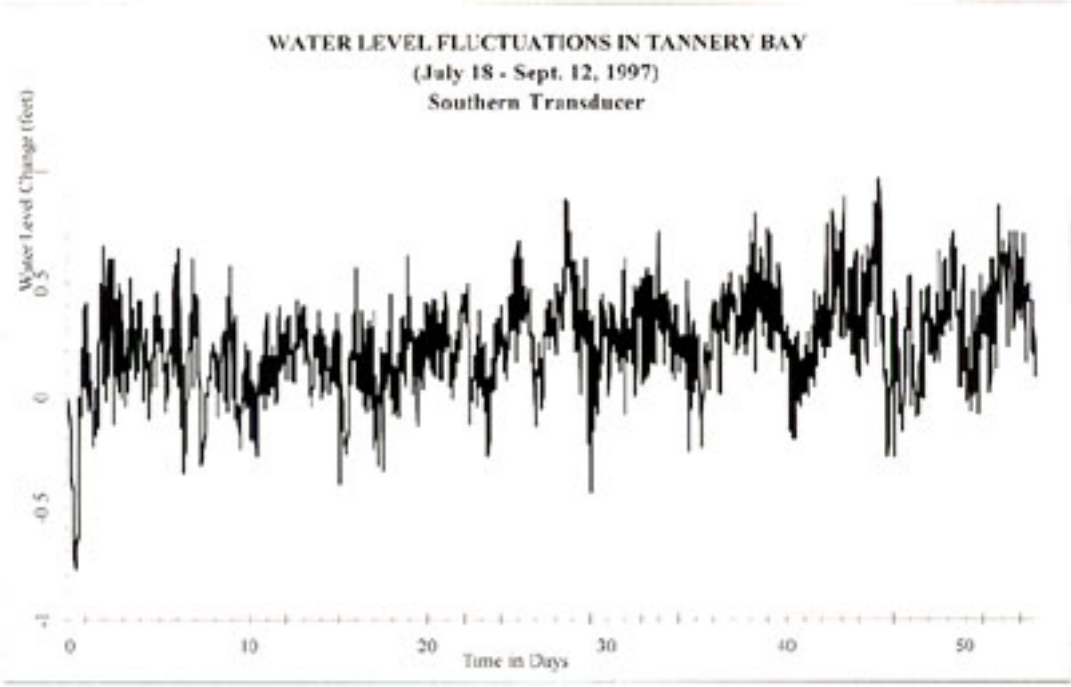


Figure 3. Water level fluctuations in Tannery Bay throughout the deployment period.



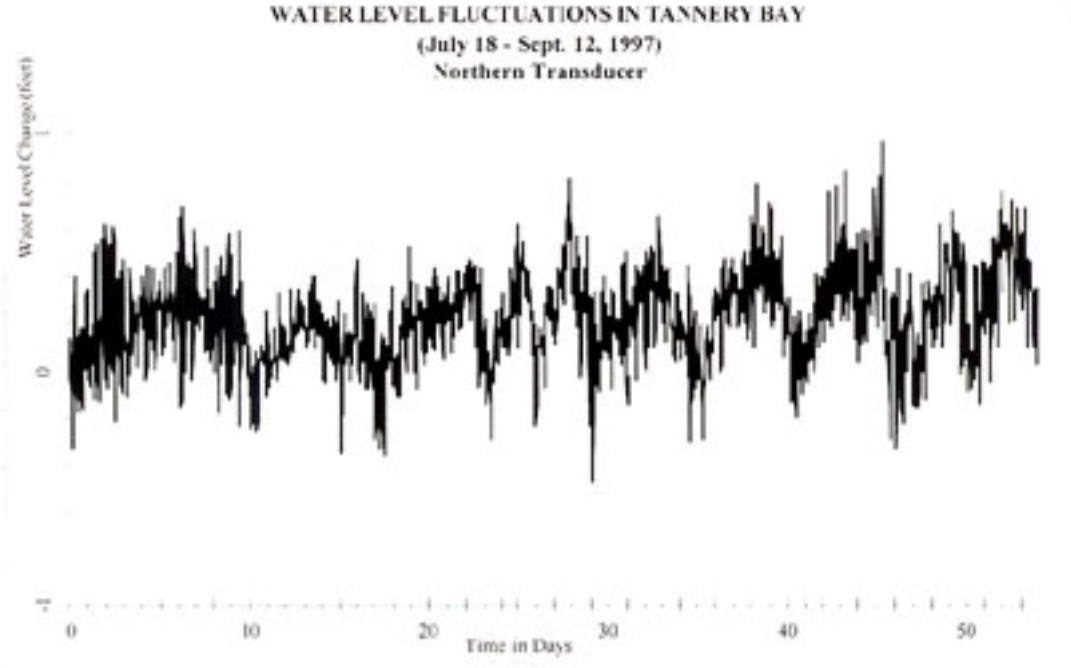
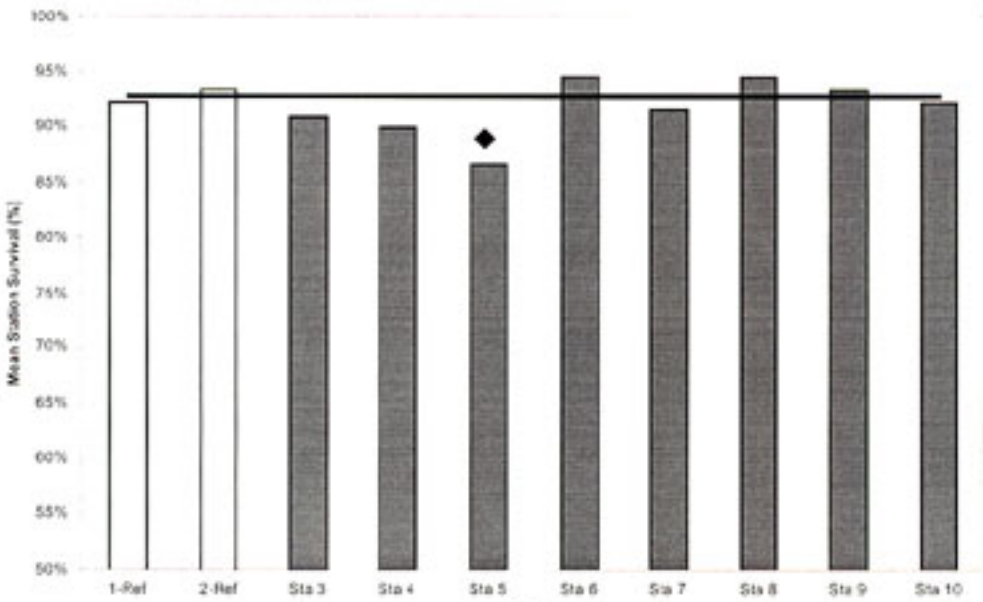


Figure 4. End-of-test percent survival for clams deployed in Tannery Bay and at reference stations.



Solid line = Average of reference stations

♦ Significantly less than average of reference stations

Figure 5a. Arsenic concentration in tissues of clams deployed in Tannery Bay and at reference stations.

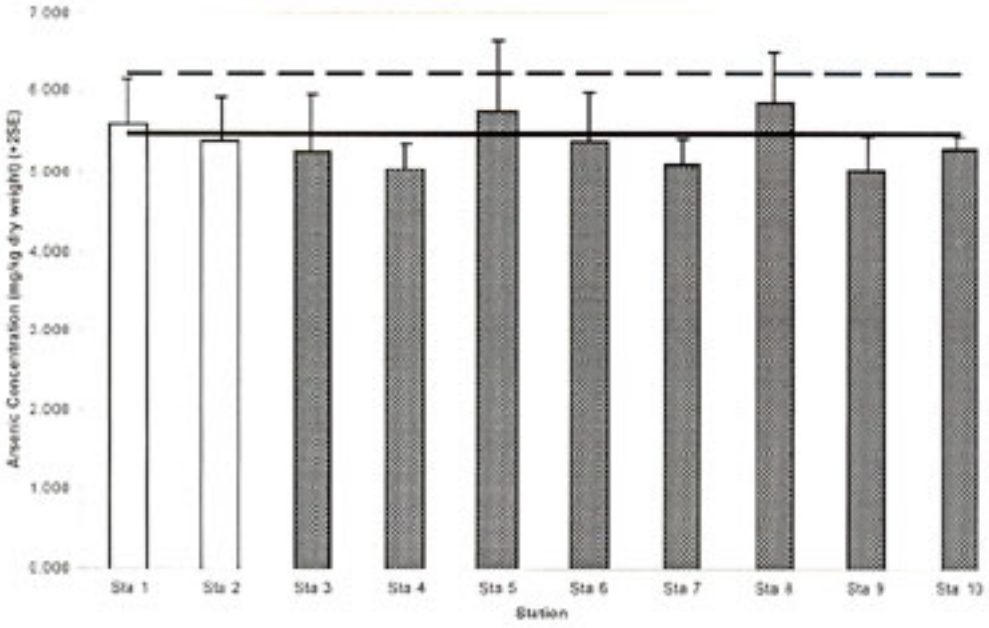
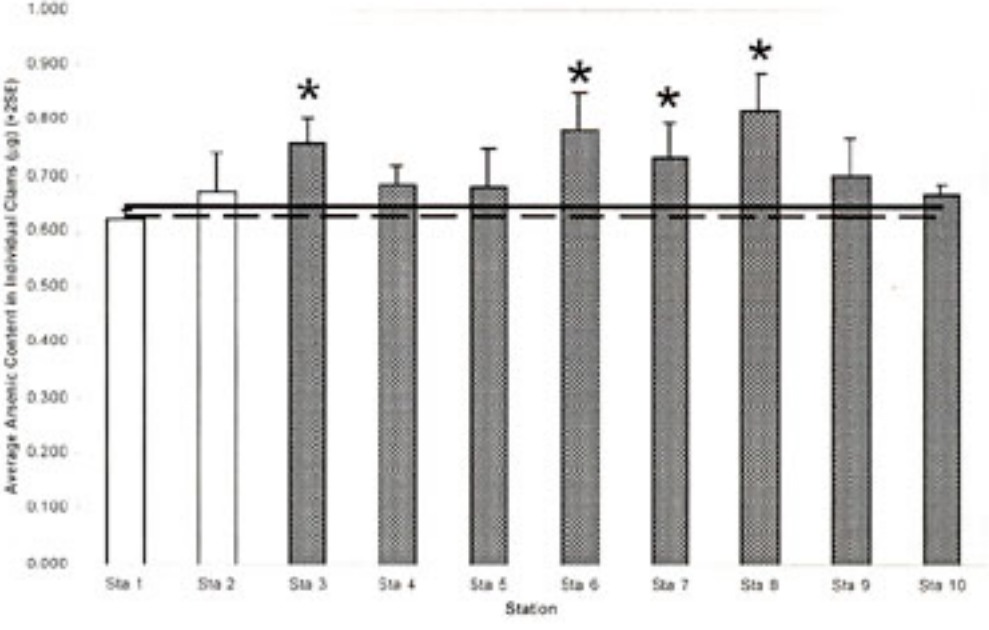


Figure 5b. Arsenic content in clams deployed in Tannery Bay and at reference stations.



Dashed line = T_0 (Initial)
Solid line = Average of reference stations
*Significantly greater than average of reference stations

Figure 6a. Cadmium concentration in tissues of clams deployed in Tannery Bay and at reference stations.

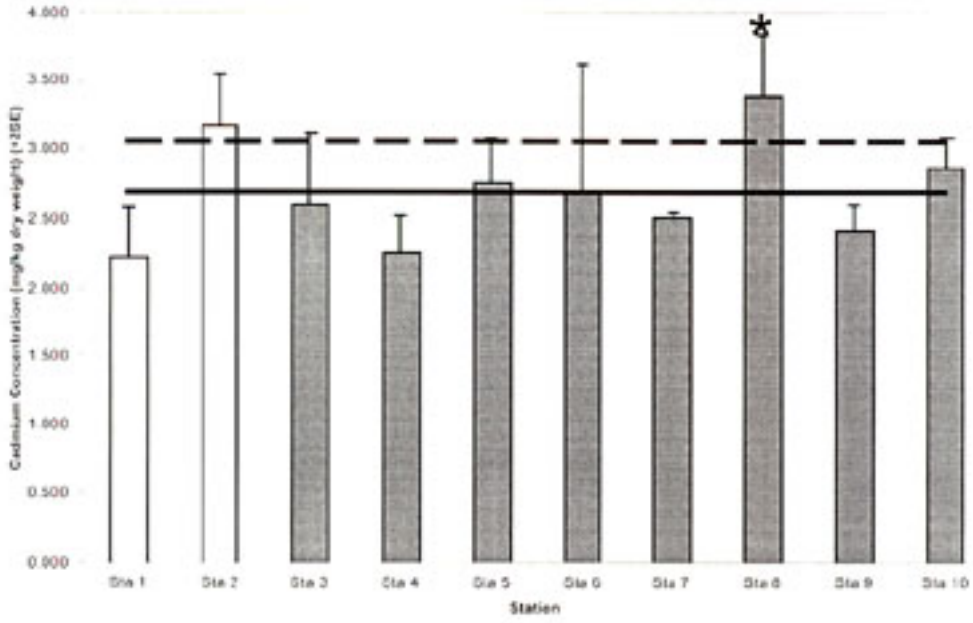
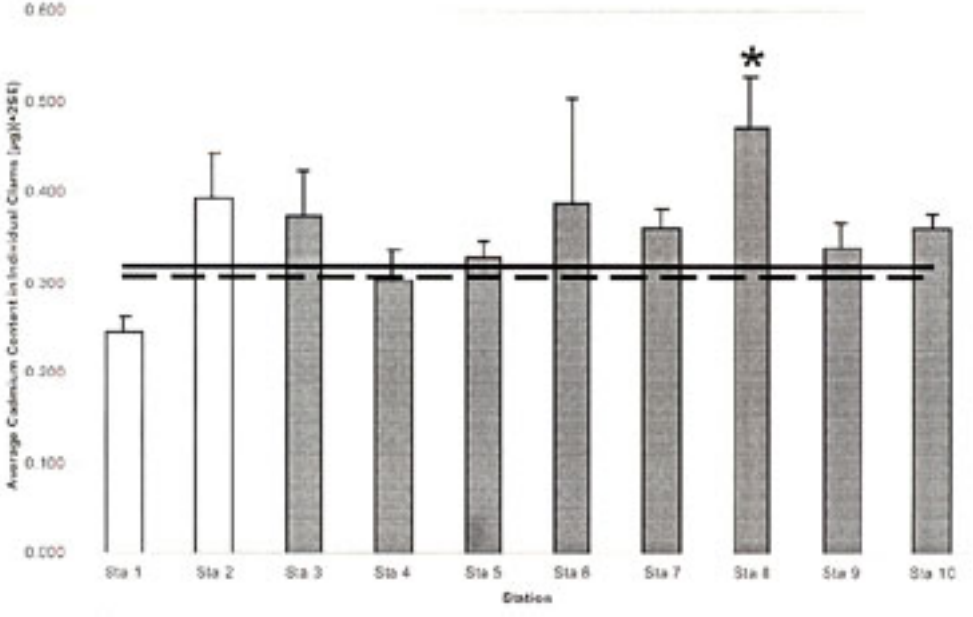


Figure 6b. Cadmium content in clams deployed in Tannery Bay and at reference stations.



Dashed line = T_0 (Initial)
Solid line = Average of reference stations
*Significantly greater than average of reference stations

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

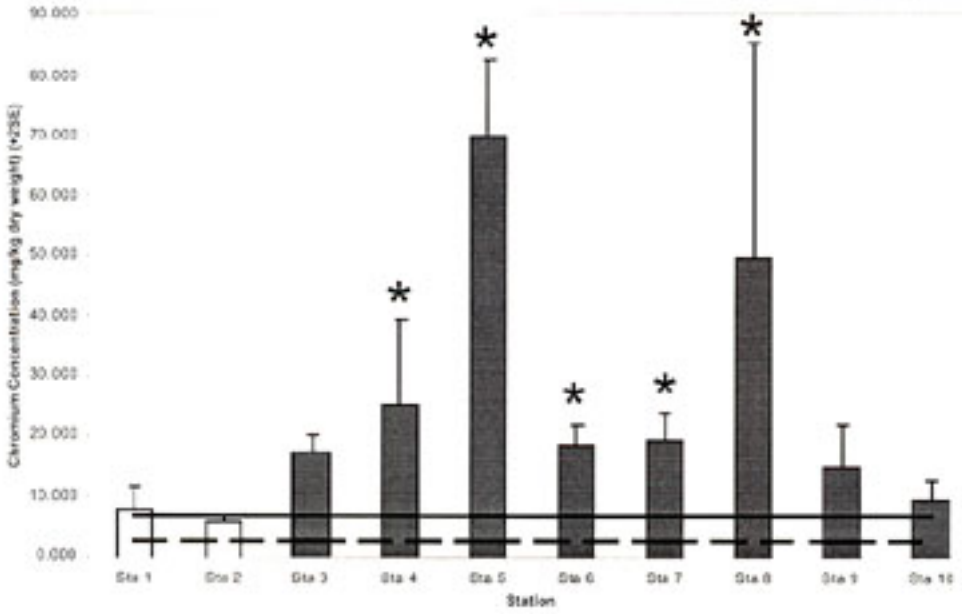
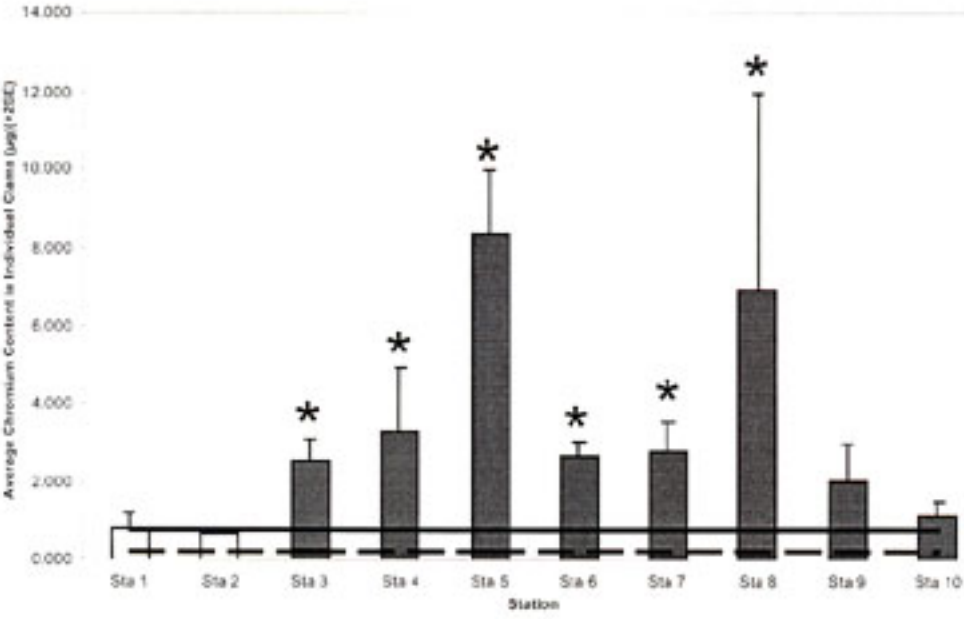


Figure 7b. Total chromium content in clams deployed in Tannery Bay and at reference stations.



Dashed line = T_0 (Initial)
Solid line = Average of reference stations
*Significantly greater than average of reference stations

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

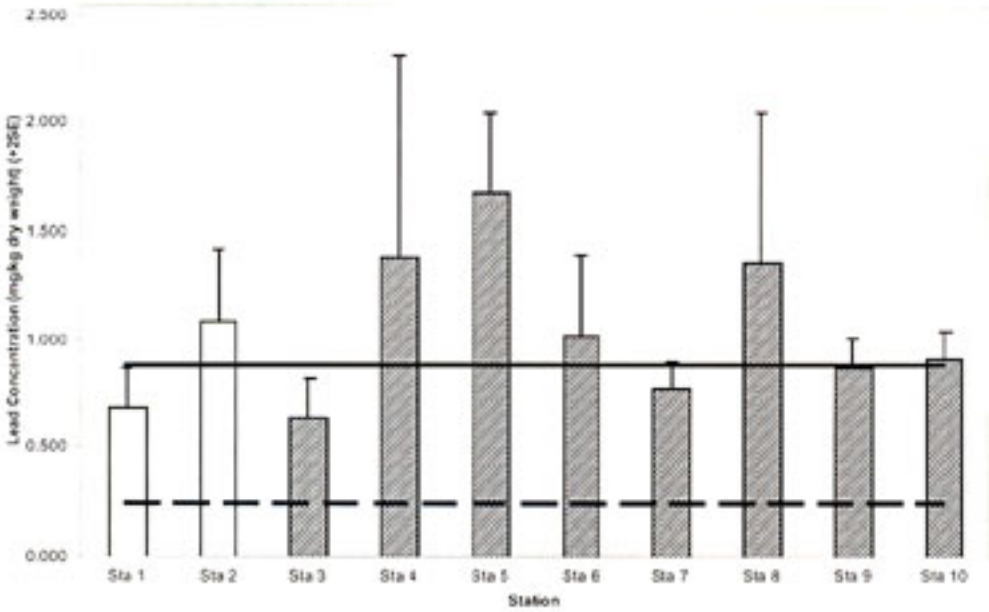
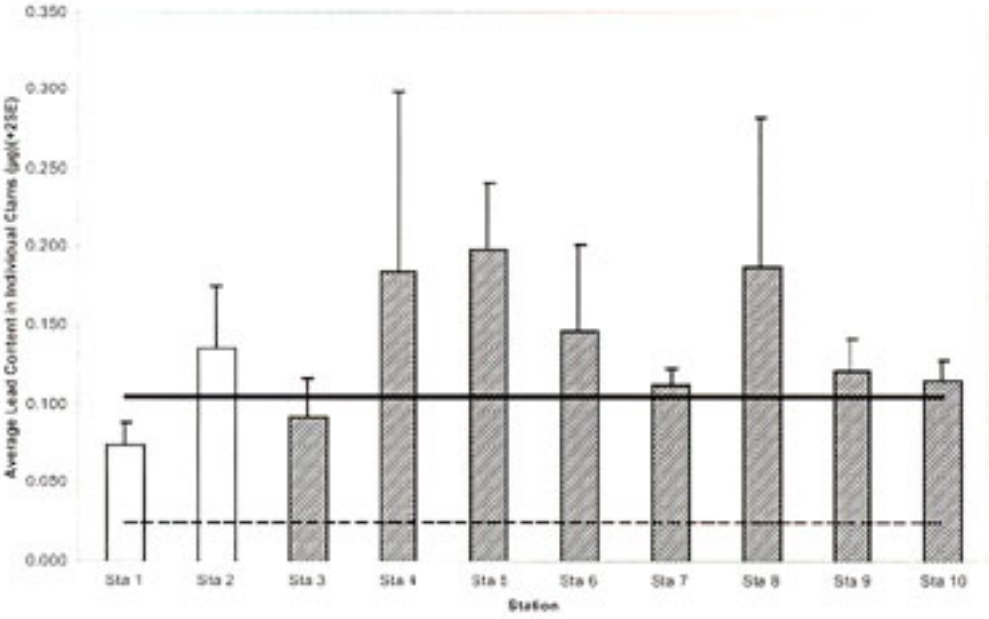


Figure 8b. Lead content in clams deployed in Tannery Bay and at reference stations



Dashed line = T_0 (Initial)
Solid line = Average of reference stations

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

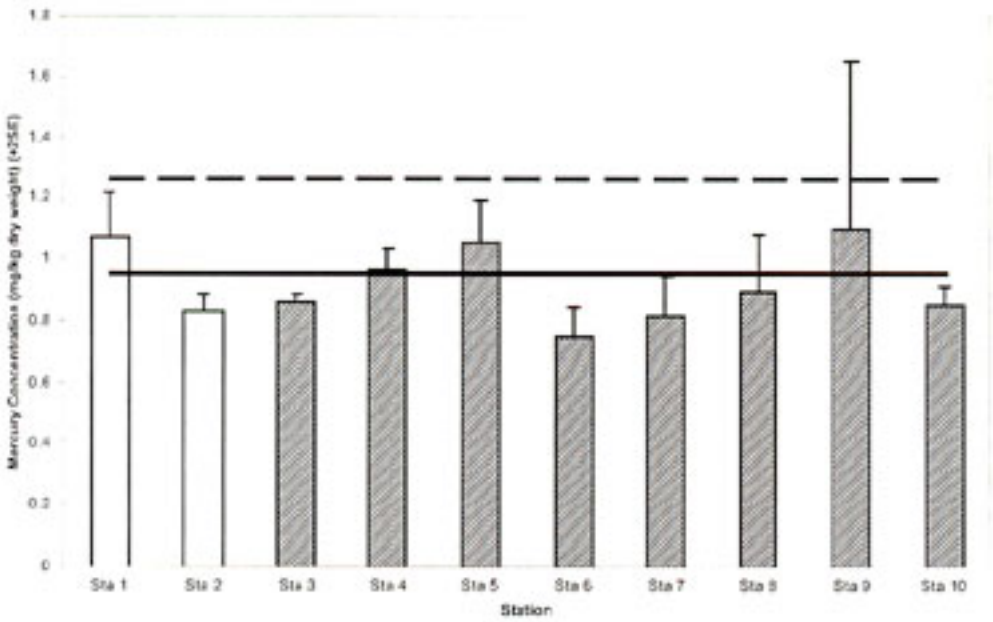
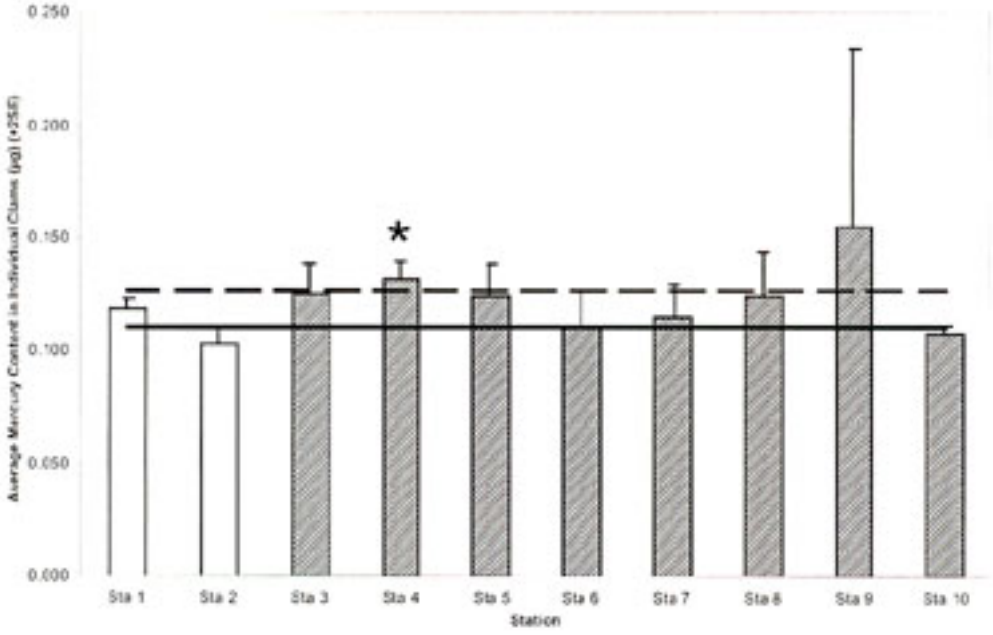


Figure 9b. Total mercury content in tissues of clams deployed in Tannery Bay and at reference Stations.



Dashed line = T_0 (Initial)
Solid line = Average of reference stations
*Significantly greater than average of reference stations

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

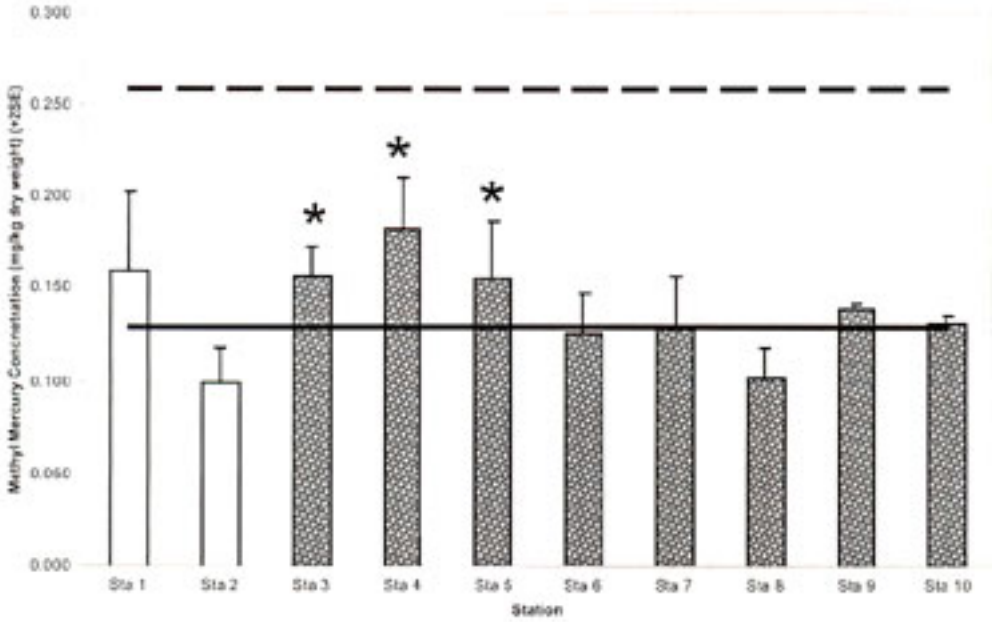
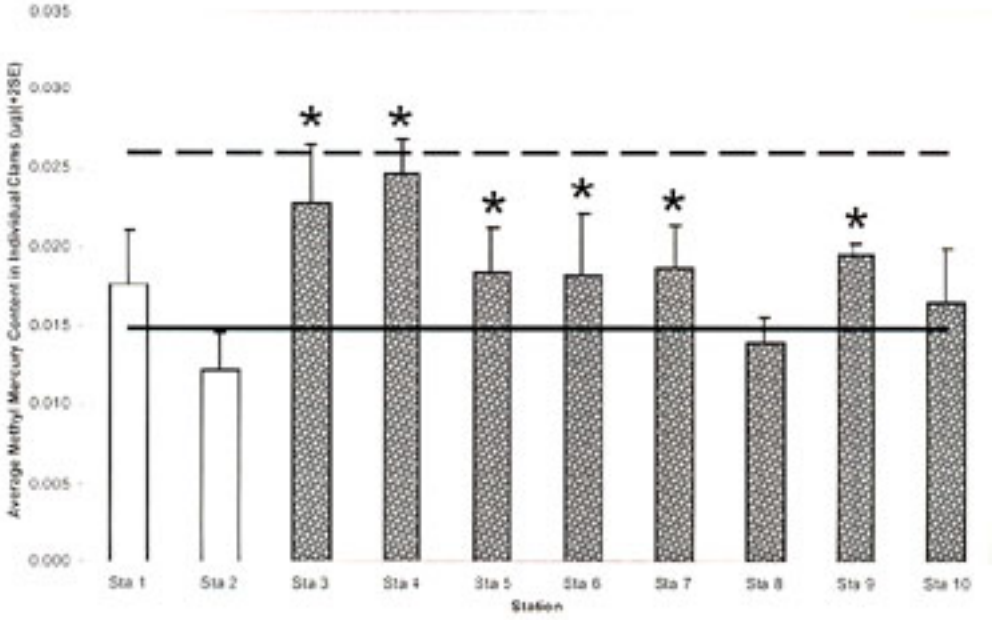


Figure 10b. Methylmercury content in tissues of clams deployed in Tannery Bay and at reference stations.



Dashed line = $\bar{T}_0$ (Initial)
Solid line = Average of reference stations
*Significantly greater than average of reference stations

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

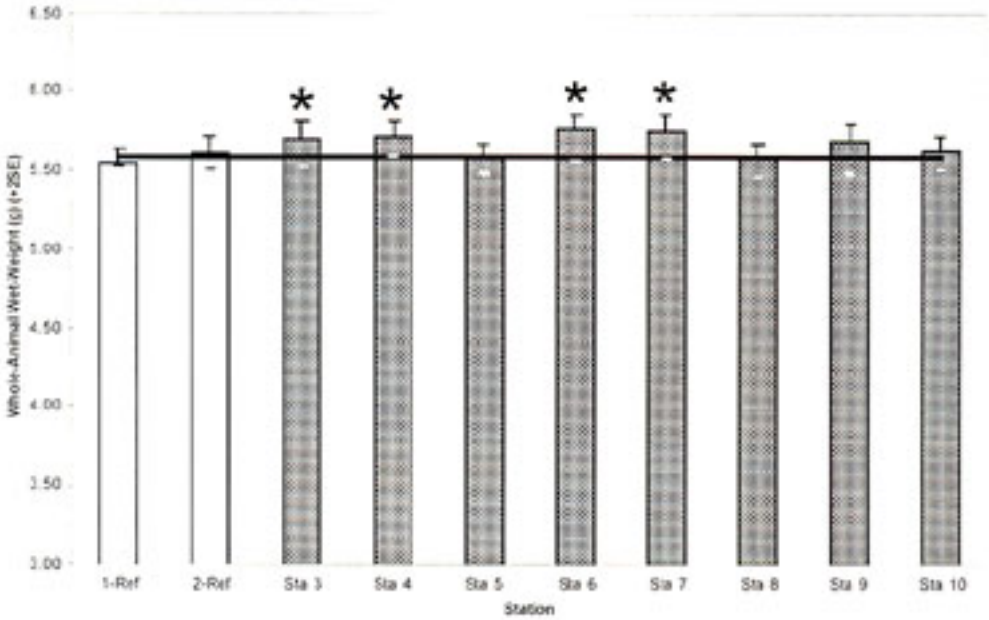
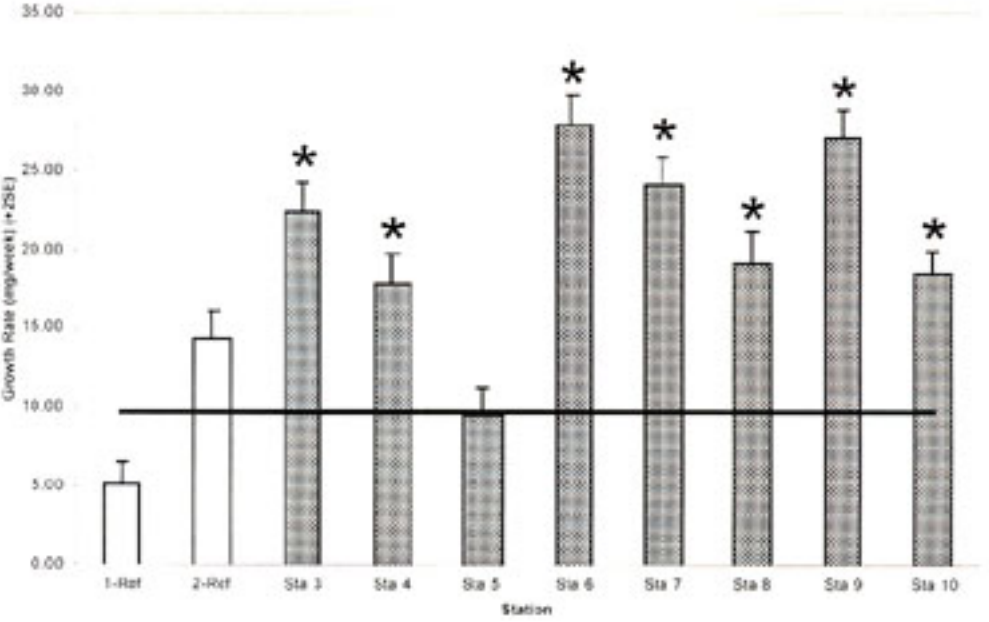


Figure 12. Whole-animal wet-weight growth rates for clams deployed in Tannery Bay and at reference stations.



Dashed line = T_0 (Initial)
Solid line = Average of reference stations
*Significantly greater than average of reference stations

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

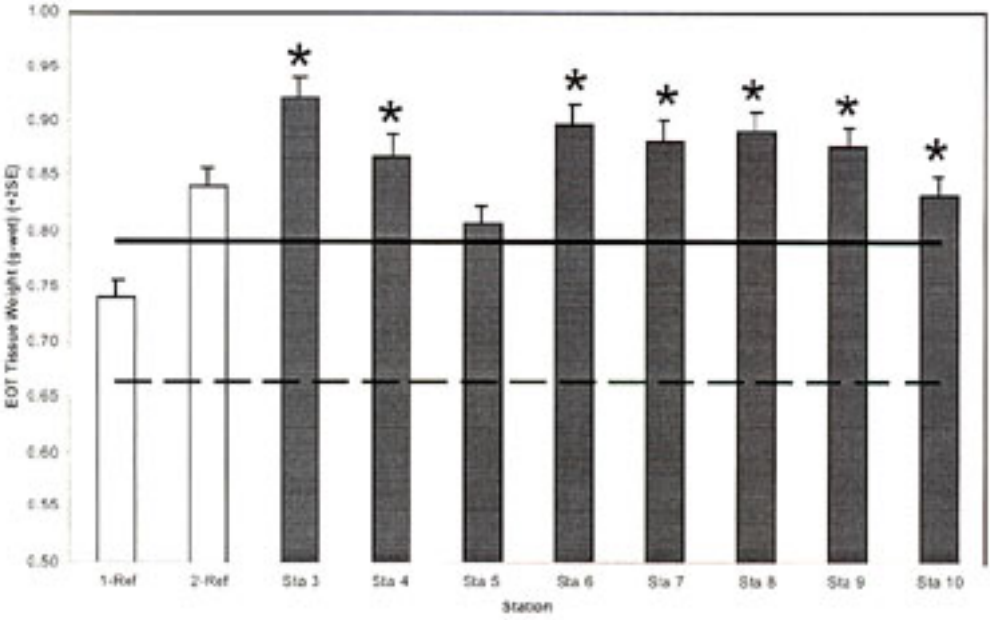
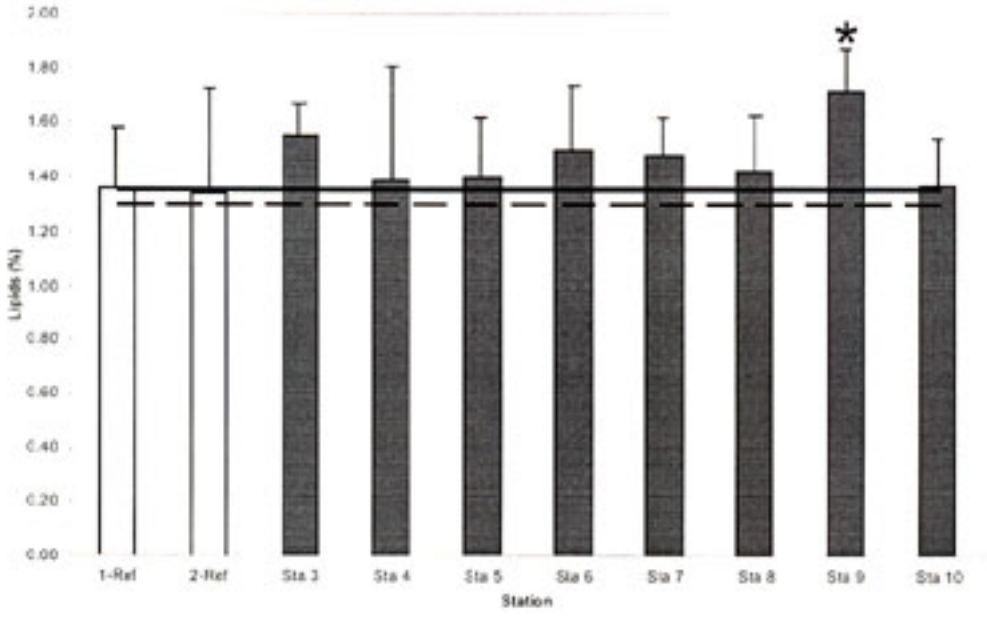


Figure 14. Percent lipids for clams deployed in Tannery Bay and at reference stations.



Dashed line = T_0 (Initial)
Solid line = Average of reference stations
*Significantly greater than average of reference stations

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

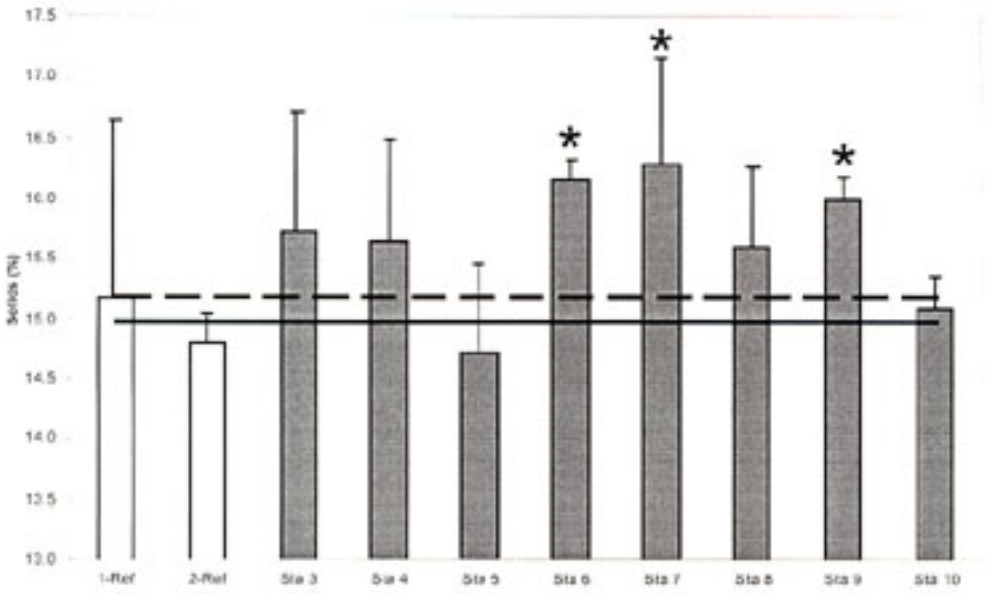
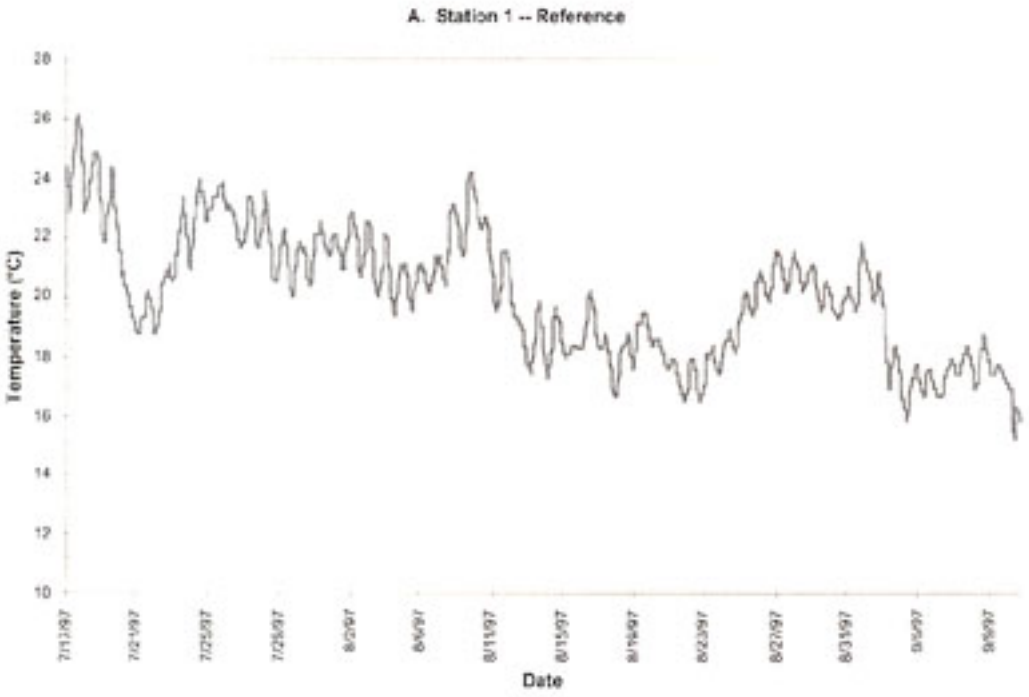


Figure 16. Water temperatures in Tannery Bay and at reference stations.



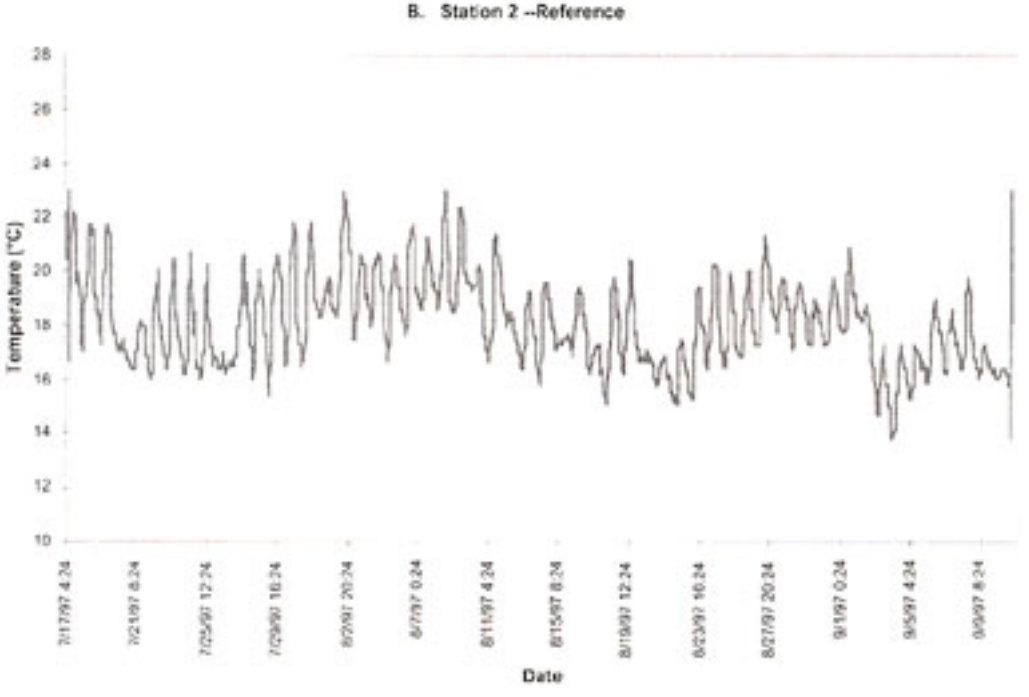
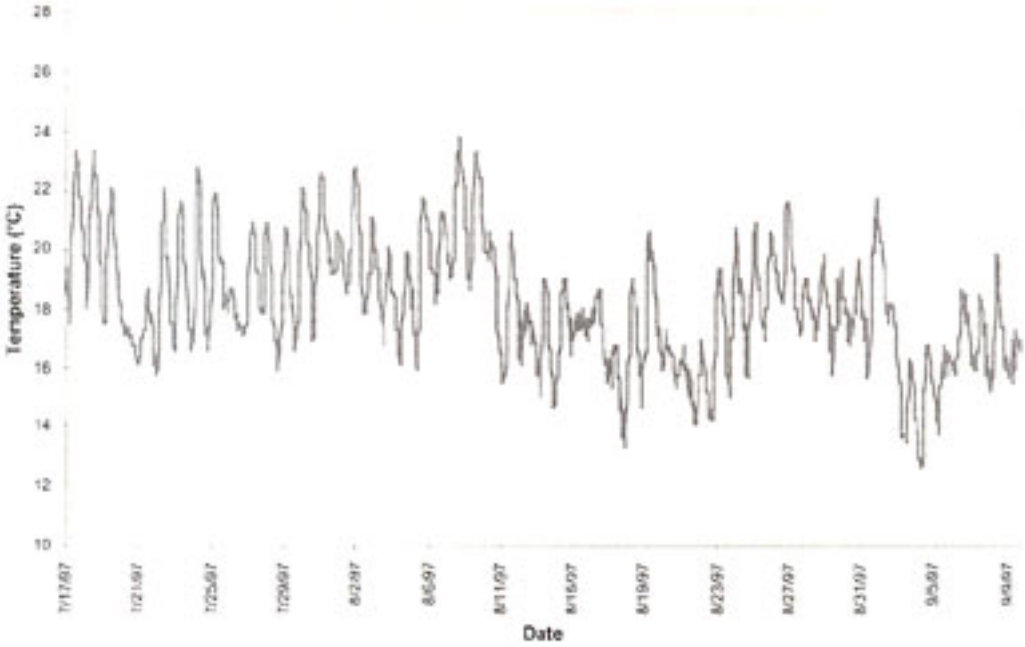


Figure 16 cont.

C. Station 3



D. Station 4

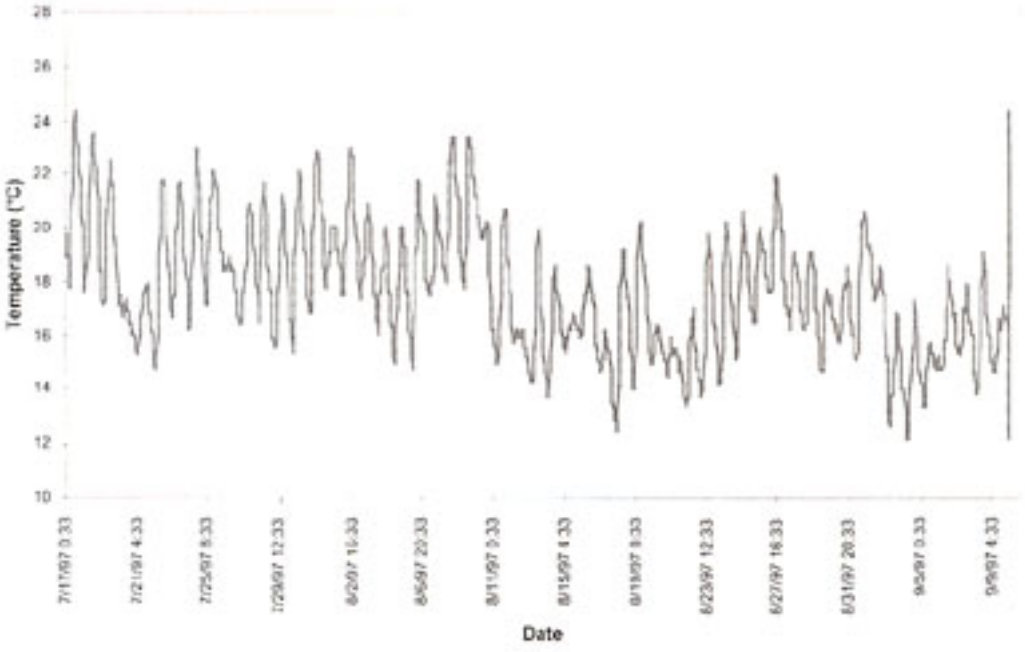
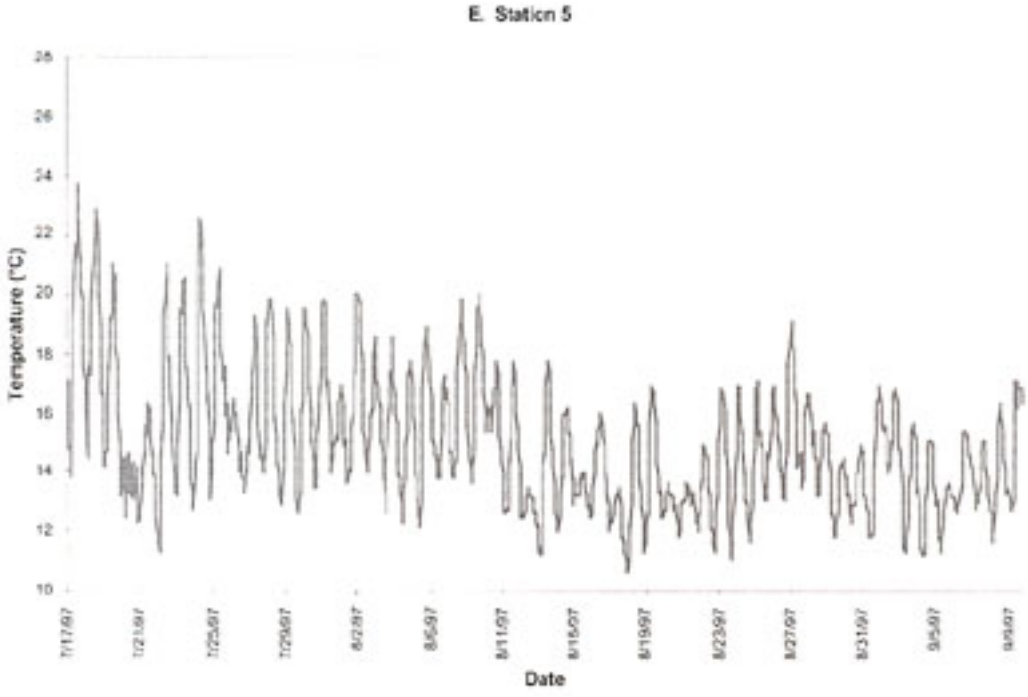


Figure 16 cont.



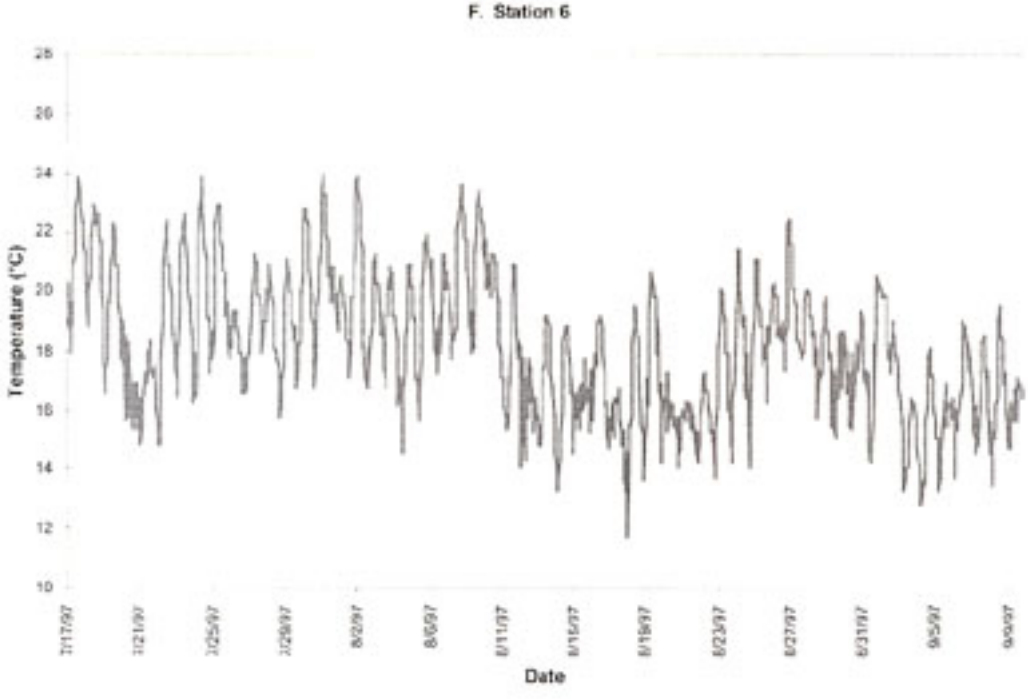
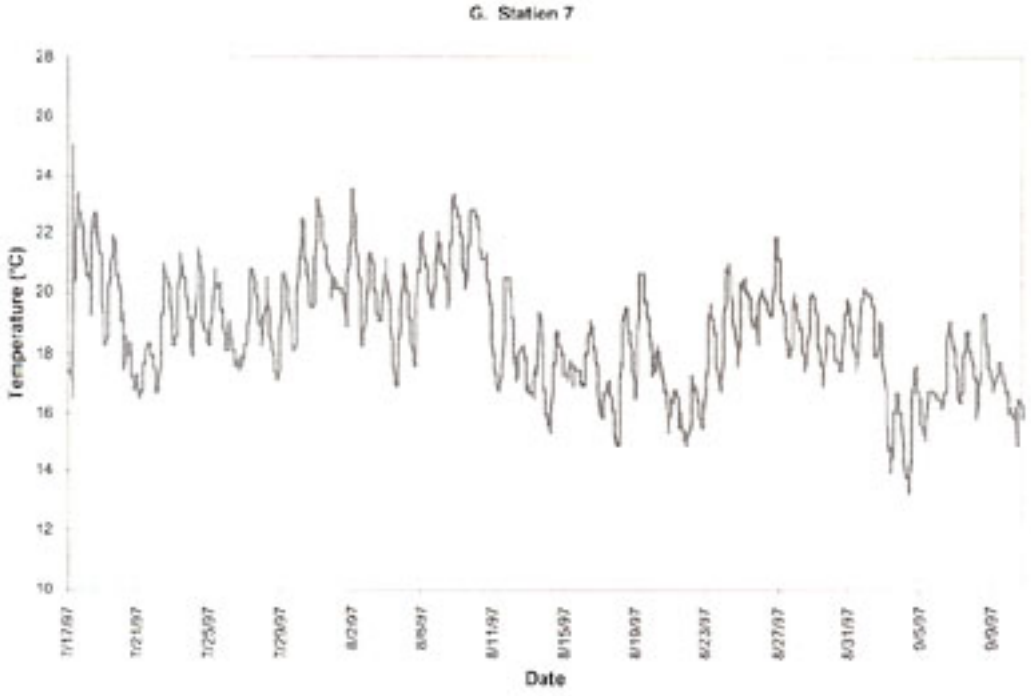


Figure 16 cont.



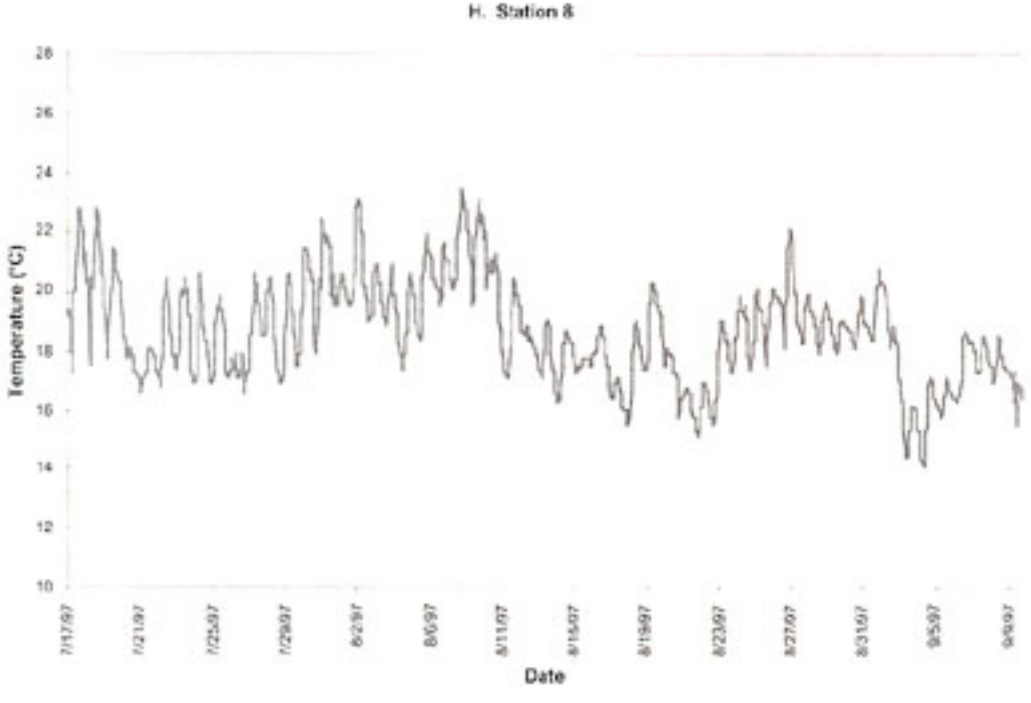
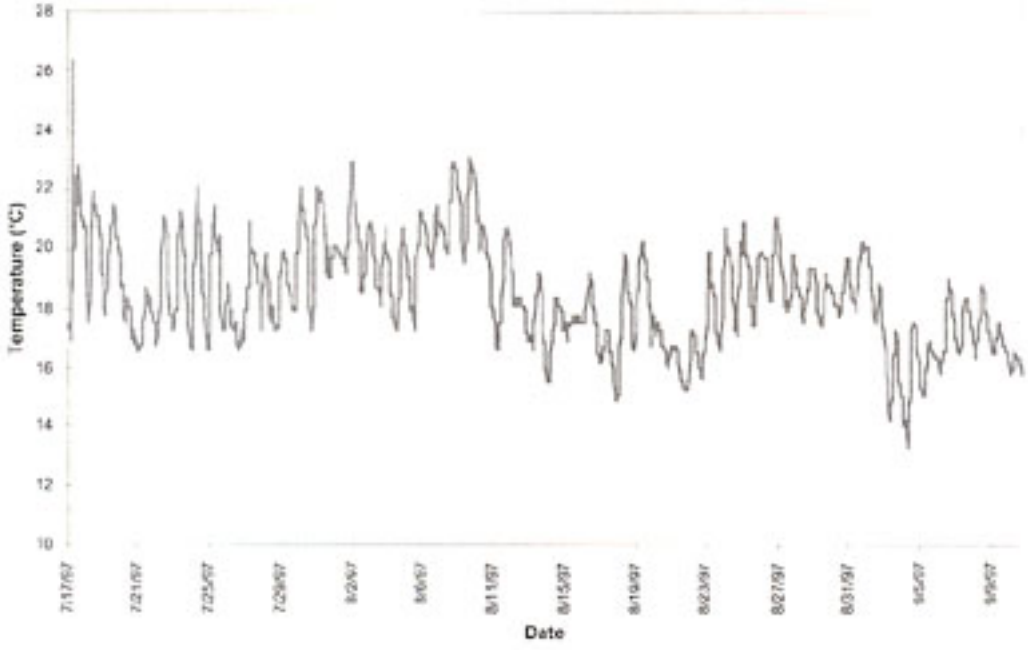


Figure 16 cont.

I. Station 9



J. Station 10

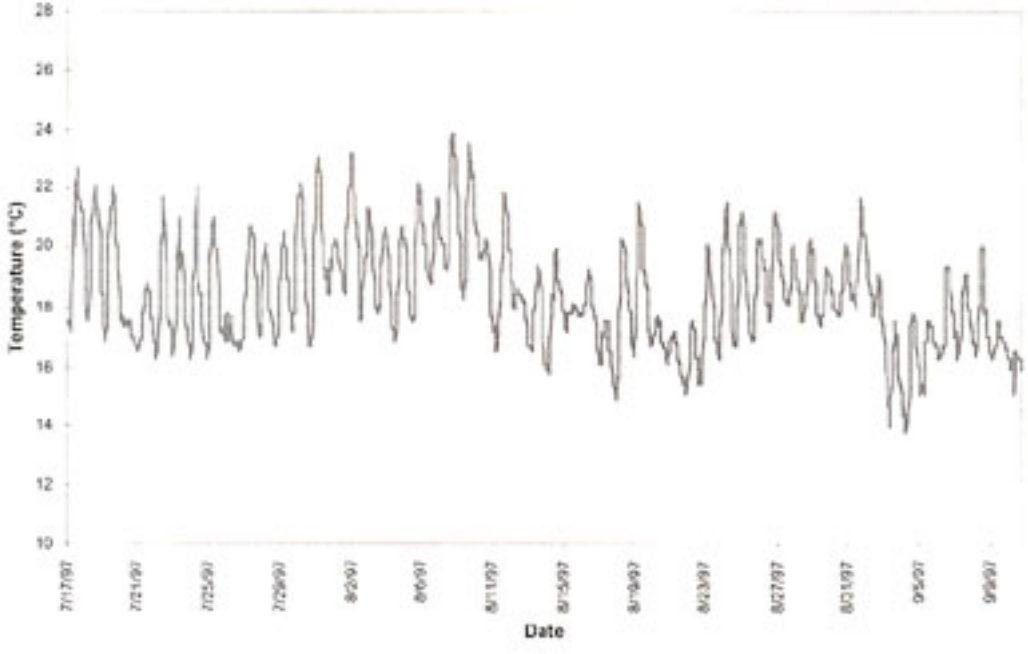
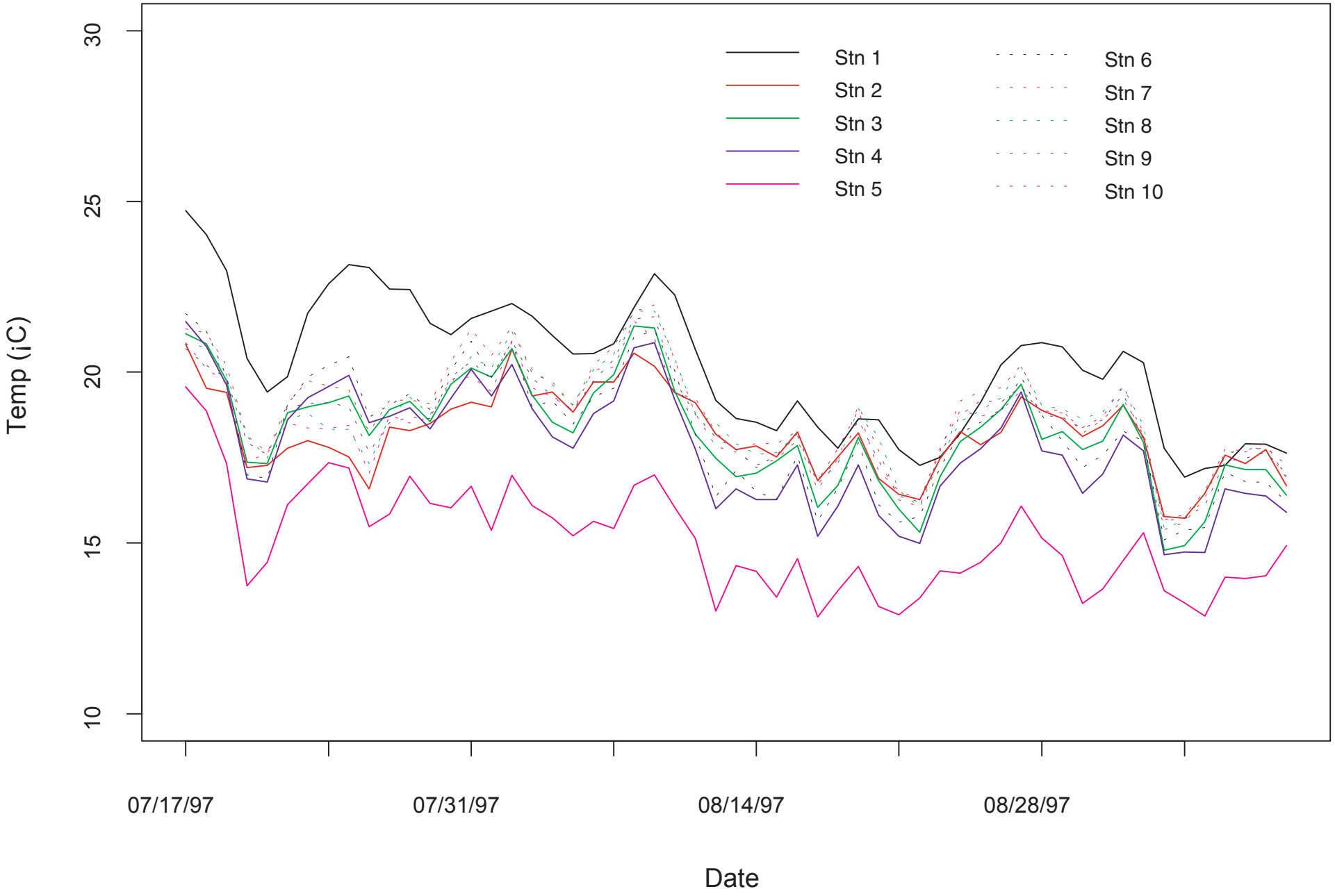


Figure 17. Average daily temperatures inTannery Bay and at reference stations.



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 by 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., μg/g), mass of chemical per animal (e.g., μg/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 of 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 (μg/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 (μg/g) is increasing

3.10. chemical concentration - mass of chemical per tissue mass (e.g., μg/g)

3.11. chemical content - mass of chemical per whole animal (e.g., μg/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_o. 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_o. 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_o 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 is 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 cages 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, Dunnetts 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 an 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. It 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 ranged 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

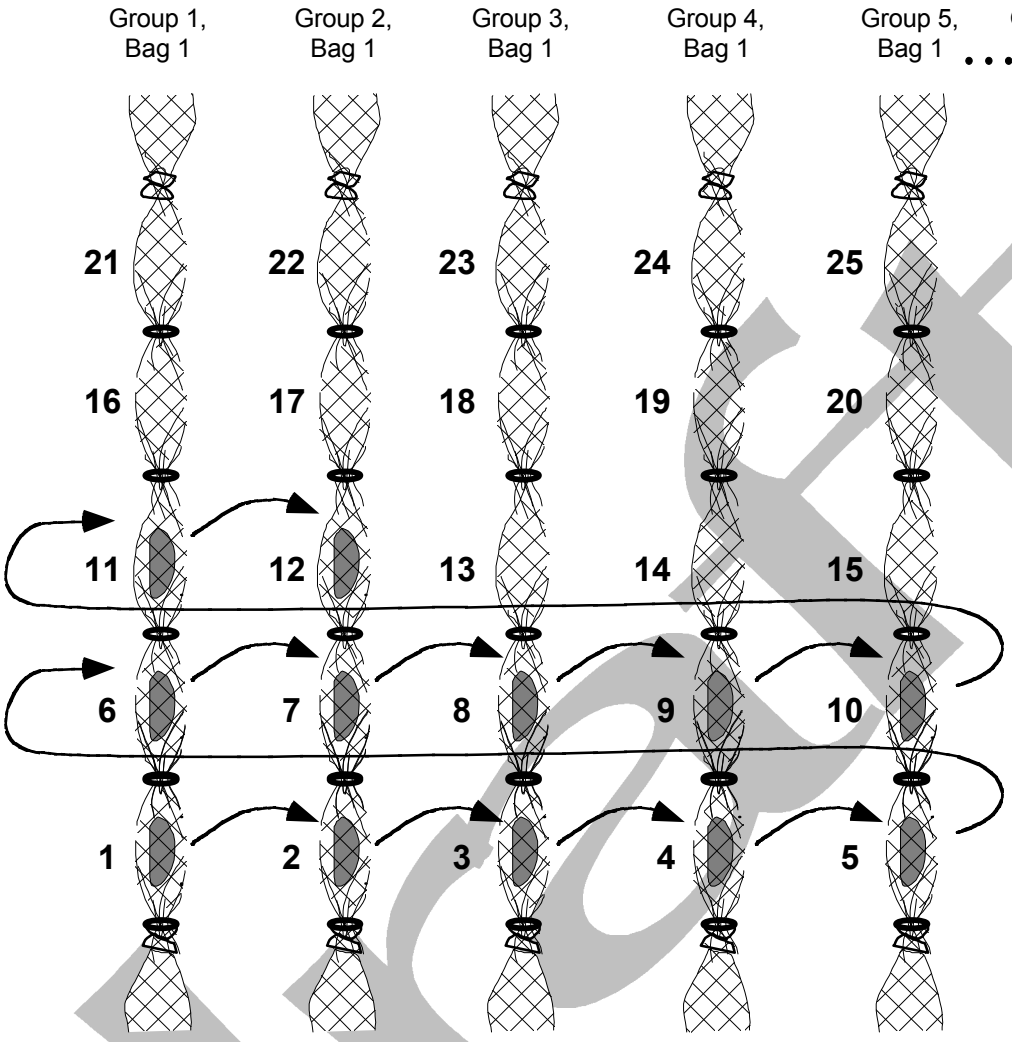


Figure 1. Distribution process used to ensure similar sizes of bivalves among treatments.

APPENDIX B
TISSUE CHEMISTRY LABORATORY REPORTS

TOTAL MERCURY

BR ID Number	Station	Replicate	Cage No.
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

BRL Data Summary

Batch #: 97-258

Analyte: Hg
Matrix: biota, filter — Prep. Date: 9/30/97
Method: BR-0002 — Analysis Date: 10/2/97

QA RESULTS

Calibration Data

Initial Calibration

pg	PA
100	178
500	841
2500	4177
7500	12284

Corr. Coef.: 0.9999
Calib. Coef.: 0.5990
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: 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
2500	4177
7500	12284

Corr. Coef.: 0.9999
Calib. Coef.: 0.5990
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
2500	4306
8000	13278

Corr. Coef.: 0.9999
Calib. Coef.: 0.5857
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%

BRL Data Summary

Batch #: 97-260

Analyte: Hg
Matrix: biota, filter — Prep. Date: 10/7/97
Method: BR-0002 — 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
100	178
500	870
2500	4179
7500	12501

Corr. Coef.: 1.0000
Calib. Coef.: 0.5893
RSD: 2.0%

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%

BRL Data Summary

Batch #: 97-261

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
2500	4045
8000	13128

low std. recovery: 107%
Calib. Coef.: 0.6023
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

BRL Data Summary

Batch #: 97-247

25753800l — 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
5	33
10	57
50	247
100	525
500	2987

Corr. Coef.: 0.9996
Calib. Coef.: 0.1798
RSD: 10.1%

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	15.5%	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
50	289
100	553
500	3142
1000	6089

Corr. Coef.: 0.9998
Calib. Coef.: 0.1733
RSD: 6.8%

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	

BRL Data Summary

Batch #: 97-256

Analyte: MMHg
Matrix: biota
Method: BR-0011

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

QA RESULTS

Calibration Data

Initial Calibration

pg	PA
10	58
50	283
100	555
500	2760
1000	5900

Corr. Coef.: 0.9995
Calib. Coef.: 0.1819
RSD: 4.9%

Calibration Verification

known pg	meas. pg	% recovery
50	54.8	109.5%
50	53.3	106.6%
50	50.9	101.9%

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%

BRL Data Summary

Batch #: 97-257

Analyte: MMHg
Matrix: biota — Prep. Date: 9/22/97
Method: BR-0011 — 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	
97BR185-36	0.0192	17.4%	0.111	D
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%	0.0968	

QA RESULTS

Calibration Data

Initial Calibration

pg	PA
5	32
10	57
50	288
100	531
500	2850
1000	4690

Corr. Coef.: 0.9950
Calib. Coef.: 0.1844
RSD: 8.6%

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
10	54
50	263
500	2829
1000	6118

Corr. Coef.: 0.9993
Calib. Coef.: 0.178
RSD: 7.0%

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

BRL Data Summary

Batch #: 97-273

Analyte: Pb
Matrix: biota
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
10	0.027
25	0.060
50	0.118
100	0.228

Corr. Coef.: 0.99977
Slope: 0.0023
Intercept: 0.002

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%	0.988	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

BRL Data Summary

Batch #: 97-274

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
10	0.025
25	0.063
50	0.124
100	0.243

Corr. Coef.: 0.99995
Slope: 0.0024
Intercept: 0.001

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%

BRL Data Summary

Batch #: 97-275

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

BRL Data Summary

Batch #: 97-275

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
10	0.022
25	0.055
50	0.106
100	0.206

Corr. Coef.: 0.99969
Slope: 0.0021
Intercept: 0.002

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	14.6%	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	

BRL Data Summary

Batch #: 97-276

Analyte: Cr
Matrix: biota — Prep. Date: 9/25/97
Method: EPA 200.9 — Analysis Date: 10/15/97

QA RESULTS

Calibration Data

Initial Calibration

ug/L	Absorbance
0	0.000
1	0.013
5	0.068
10	0.137
25	0.334
50	0.626

Corr. Coef.: 0.99941
Slope: 0.0126
Intercept: 0.000

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
0	-0.009
1	0.011
5	0.063
10	0.123
25	0.313
50	0.606

Corr. Coef.: 0.99986
Slope: 0.0122
Intercept: 0.001

Calibration Verification

Known ug/L	meas. ug/L	% recovery
20	19.86	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
5	0.051
10	0.105
25	0.268
50	0.516

Corr. Coef.: 0.9998
Slope: 0.0104
Intercept: 0.000

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 — Prep. Date: 10/9/97
Method: EPA 200.9 — 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 — Prep. Date: 10/9/97
Method: EPA 200.9 — Analysis Date: 10/13/97

QA RESULTS

Calibration Data

Initial Calibration

ug/L	Absorbance
0	-0.026
1	0.006
5	0.053
10	0.115
25	0.310
50	0.612

Corr. Coef.: 0.99986
Slope: 0.0124
Intercept: -0.005

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 %
97BR185-36	0.779	0.809	0.794	3.8%

CADMIUM

BRL Data Summary

Batch #: 97-279a

2575380001
Disk 16

Analyte: Cd
Matrix: biota
Method: EPA 200.9

Prep. 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
0.00	-0.001
0.50	0.013
1.00	0.027
2.00	0.053
5.00	0.122
10.00	0.218

Corr. Coef.: 0.9981
Slope: 0.0217
Intercept: 0.005

Calibration Verification

Known ug/L	meas. ug/L	% recovery
4.00	4.10	102.5%
4.00	4.00	100.0%
4.00	3.90	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
1.00	0.023
2.00	0.047
5.00	0.104

Corr. Coef.: 0.99854
Slope: 0.0206
Intercept: 0.002

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	26.3	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%

BRL Data Summary

Batch #: 97-280

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	

BRL Data Summary

Batch #: 97-280

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
1	0.028
2	0.057
5	0.131
10	0.223

Corr. Coef.: 0.99601
Slope: 0.0224
Intercept: 0.007

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

BRL Data Summary

Batch #: 97-281

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%

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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
10	0.024
25	0.064
50	0.123
100	0.232

Corr. Coef.: 0.99933
Slope: 0.0023
Intercept: 0.003

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%

BRL Data Summary

Batch #: 97-283

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	0.768	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	

BRL Data Summary

Batch #: 97-283

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
10	0.037
25	0.088
50	0.176
100	0.334

Corr. Coef.: 0.99958
Slope: 0.0033
Intercept: 0.003

Calibration Verification

Known ug/L	meas. ug/L	% recovery
40	36.51	91.3%
40	37.18	93.0%
40	36.64	91.6%
40	36.06	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
97BR165-16MS	ug/g	2.45	2.01	81.9%

Method Duplicate

ID	Native ug/g (wet)	Duplicate ug/g (wet)	Average ug/g (wet)	RPD %
97BR165-16	0.839	0.806	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
10	0.033
25	0.079
50	0.154
100	0.296

Corr. Coef.: 0.99975
Slope: 0.003
Intercept: 0.003

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	76.0	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

BRL Data Summary

Batch #: 97-268a

2575380001 — Disk 160

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	1.46%	
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	0.9364	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%

BRL Data Summary

Batch #: 97-268b

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

	Native		Duplicate	Average	RPD
ID	% lipids	from Batch #	% lipids	% lipids	%
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%

BRL Data Summary

Batch #: 97-266

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%	
97BR185-19	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	16.1%	
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%

BRL Data Summary

Batch #: 97-267

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 _____
_____
_____
_____

President	Date: 8/23/95
Lab Director	Date: 8/23/95
Senior Scientist	Date: 8/23/95

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

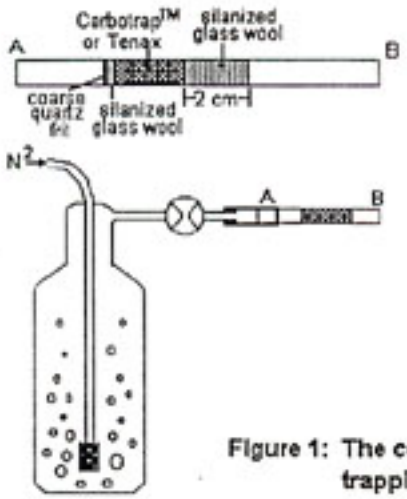


Figure 1: The construction of trapping column and its connection with a reaction vessel

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 CH_3HgCl (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 $mL \cdot min^{-1}$ 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)

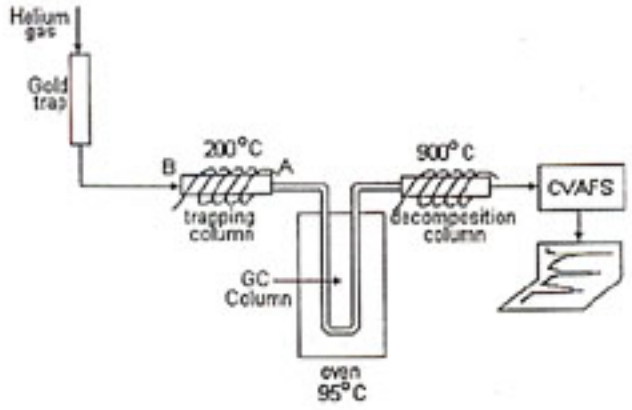


FIGURE 2: A schematic diagram of isothermal gas chromatograph system

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)

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

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:

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 ± 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% $NH_2OH\cdot HCl$

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 Stoeppler, 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 $mL\cdot min^{-1}$ 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% $NH_2OH{\cdot}HCl$ 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 $mL{\cdot}min^{-1}$ 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 + CH_3COOH) silicon tubing. Beware that once cleaned, silicon tubing quickly absorbs Hg from the air The other method involves high-volume pumping (i.e.; 50 $L \cdot min^{-1}$) 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 $ng \cdot L^{-1}$ LEVEL.

7.1.3. Samples may be preserved by adding 8 $mL \cdot L^{-1}$ 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 Hg^0.

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°C (standard freezer on coldest setting) until use. A holding time of 1 year at <-10°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 determine 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.

REFERENCES

Liang, L.; Bloom, N.S.; and Horvat, M. (1994) "Simultaneous Determination of Mercury Speciation in Biological Materials by GC/CVAFS After Ethylation and Room-Temperature Precollection." *Clin. Chem.* 40/4: 602-607.

Bloom, N.S. (1989) "Determination of Picogram Levels of Methylmercury by Aqueous Phase Ethylation, Followed by Cryogenic Gas Chromatography with Cold Vapor Atomic Fluorescence Detection." *Canadian Journal of Fisheries and Aquatic Sciences.*

Long, S.J.; Scott, D.R.; and Thompson, R.J. (1973) "Atomic Absorption Determination of Elemental Mercury Collected from Ambient Air on Silver Wool." *Anal Chem.* 45: 2227-2233.

Horvat, M.; Liang, L.; and Bloom, N. (1993) "Comparison of Distillation with Other Current Isolation Methods for the Determination of Mercury Compounds in Low Level Environmental Samples., Part II: Waters." *Analytica Chimica Acta* 282:153-168.

Horvat, M.; May, K.; Stoeppler, M.; and Byrne, A.R. (1988) *Appl. Organomet. Chem.* 2: 515.

Horvat, M.; Bloom, N.; and Liang, L. (1993) "A Comparison of Distillation with Other Current Isolation Methods for the Determination of Mercury Compounds in Low Level Environmental Samples, Part I: Sediments." *Analytica Chimica Acta* 281:135-152.

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 _____
_____
_____
_____

_____ 12/5/94
President Date

_____ 12/2/94
Lab Director Date

_____ 12.02.94
Senior Scientist 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 $ng \cdot g^{-1}$ 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° 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 $mL \cdot min^{-1}$.

4.2. Flow meter/needle valve: Capable of controlling and measuring gas flow to the purge vessel at 200-500 $mL \cdot min^{-1}$.

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 N_2 at 100 $mL \cdot min^{-1}$.

4.5. Cold vapor generator: A 250 mL or 125 mL florence flask with standard taper 24/40 neck, fitted with a spurging 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. Pipetters: All plastic pneumatic fixed volume and variable pipetters in the range of 10 µL 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 µM 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 $SnCl_2 \cdot 2H_2O$ and 200 mL concentrated HCl is brought to 1.0 L with high purity water. This solution is purged overnight with mercury-free N_2 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 $KBrO_3$ are slowly added to the acid with stirring.

Caution: This process generates copious quantities of free Cl_2 which are released from the bottle. Add the $KBrO_3$ 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 $KBrO_3$ 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 $mg \cdot L^{-1}$ 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 $\mu g \cdot mL^{-1}$ 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 $ng \cdot mL^{-1}$ working solution. Also, a 1.00 $ng \cdot mL^{-1}$ 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° C (standard freezer on coldest setting) until use. A maximum holding time of 1 year at <-10° 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 2-3 mL of high purity water may be used to rinse the sample down to the bottom. 10.0 mL of the HNO_3/H_2SO_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 $SnCl_2$ solution added. The bubbler is purged with N_2 at 300 $mL \cdot min^{-1}$ 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 $SnCl_2$ 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 $SnCl_2$. 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 Hg^0, 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.

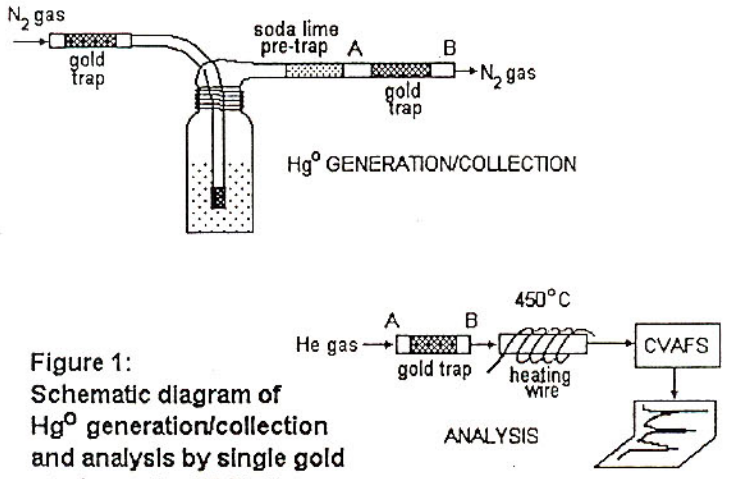


Figure 1: Schematic diagram of Hg^0 generation/collection and analysis by single gold amalgamation/CVAFS

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:

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

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:

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

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:

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

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:

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

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 determine 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 Subanogram 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.

Exhibit A

Dry Weight Determination

Tag No.	Dish No.	Tare Wt.	Wet Wt. (Net)	Dry Wt. (Gross)	Dry Wt. (Net)	Dry Wt. (%)

Scale_____
Oven_____

Time/date in_____
Time/date out_____

_____
Customer/Project

_____
Performed by

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

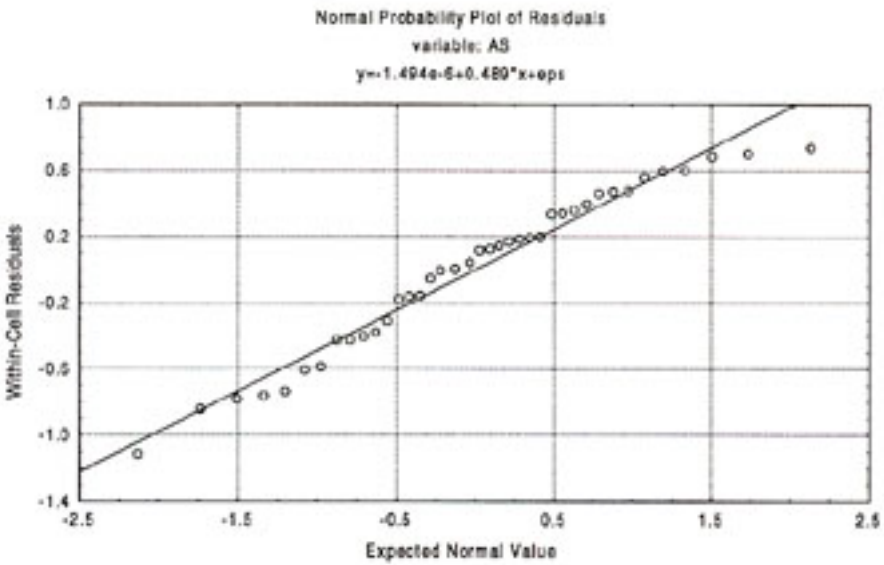
STATISTICAL RESULTS
TISSUE CHEMISTRY CONCENTRATION DATA
INCLUDING REFERENCE STATIONS 1 AND 2

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

Means

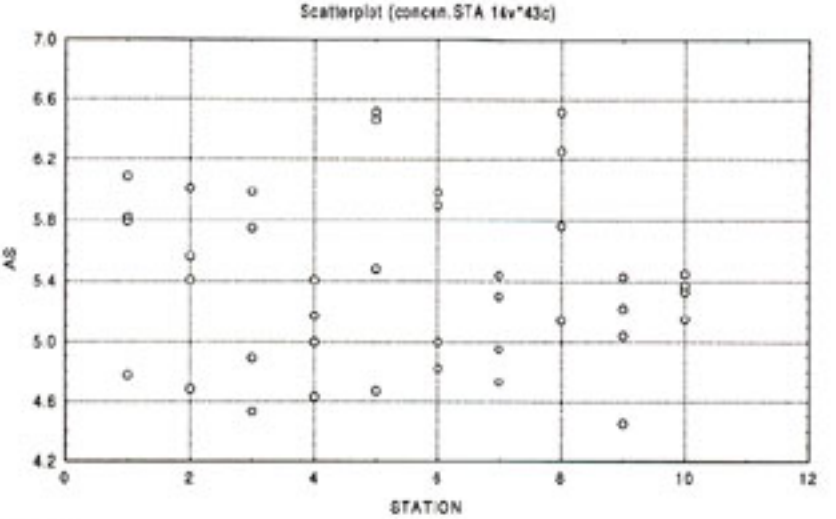
	AS	CD	CR	PB	HG	MEHG
1	5.620000	2.227500	8.19000	.686000	1.074500	.160000
2	5.415000	3.182500	5.88750	1.093500	.833500	.099025
3	5.290000	2.620000	17.30000	.641250	.865500	.156750
4	5.052500	2.262500	25.20000	1.386250	.975250	.182750
5	5.785000	2.782500	70.22500	1.682500	1.060500	.156250
6	5.425000	2.715000	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



Correlation

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



ANOVA

	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
Refs 1 and 2 vs:	
3	-0.6743861
4	-1.3784156
5	0.7929595
6	-0.2742009
7	-1.222768
8	1.1931446
9	-1.4302914
10	-0.5706344

critical value = 1.697

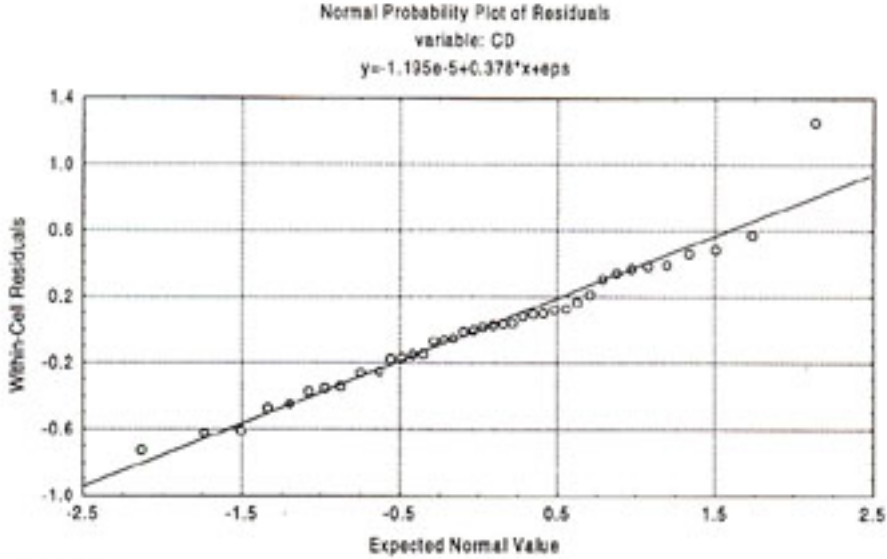
Newman-Keuls test - arsenic

	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.

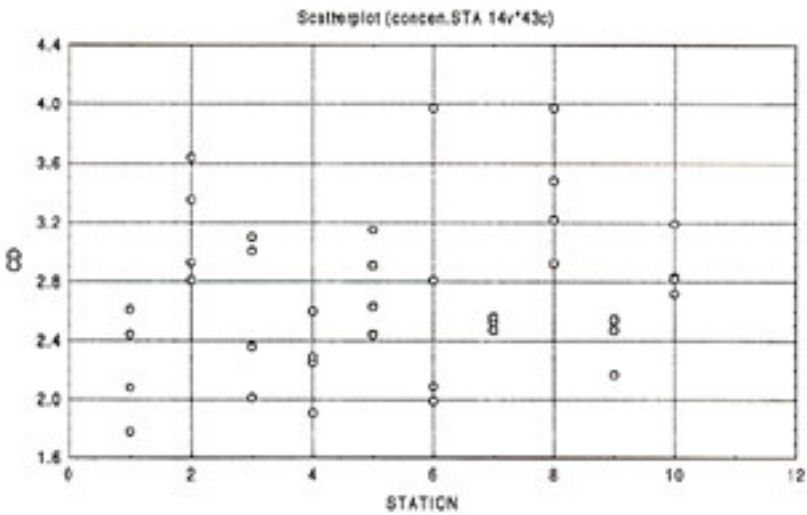
Comparison	Mean Difference	q	P value
Initial vs Station 1	0.630	1.683	ns P>0.05
Initial vs Station 2	0.835	2.230	ns P>0.05
Initial vs Station 3	0.960	2.564	ns P>0.05
Initial vs Station 4	1.198	3.199	* P<0.05
Initial vs Station 5	0.465	1.242	ns P>0.05
Initial vs Station 6	0.825	2.204	ns P>0.05
Initial 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



Correlation

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



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	0.7038776

critical value = 1.697

Newman-Keuls test - cadmium

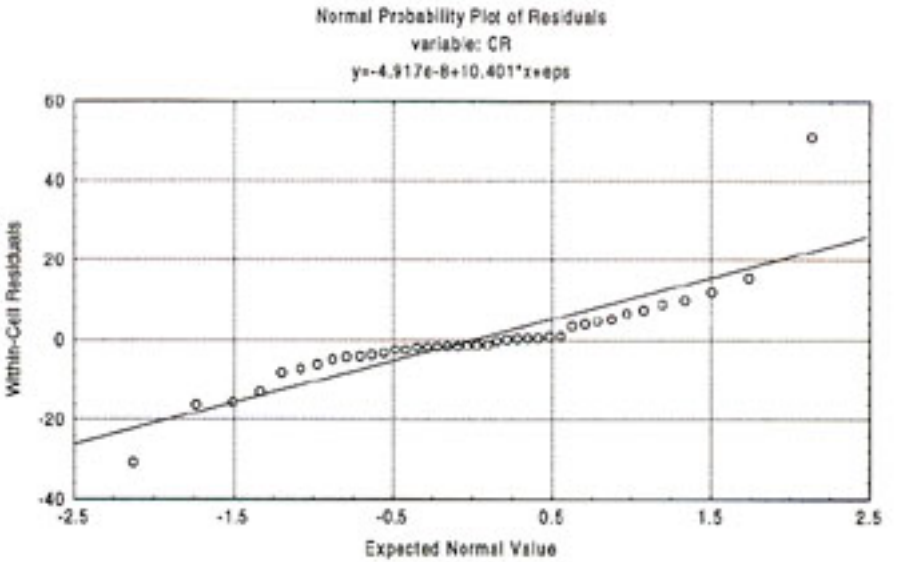
	3	4	5	6	7	8	9	10
3		.665661	.862052	.763521	.757503	.126046	.816730	.822549
4	.665661		.565403	.602881	.686484	**.02436***	.596451	.433798
5	.862052	.565403		.830683	.838204	.141291	.789479	.733573
6	.763521	.602881	.830683		.812403	.155535	.797992	.841996
7	.757503	.686484	.838204	.812403		.091184	.769555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

Durnett'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

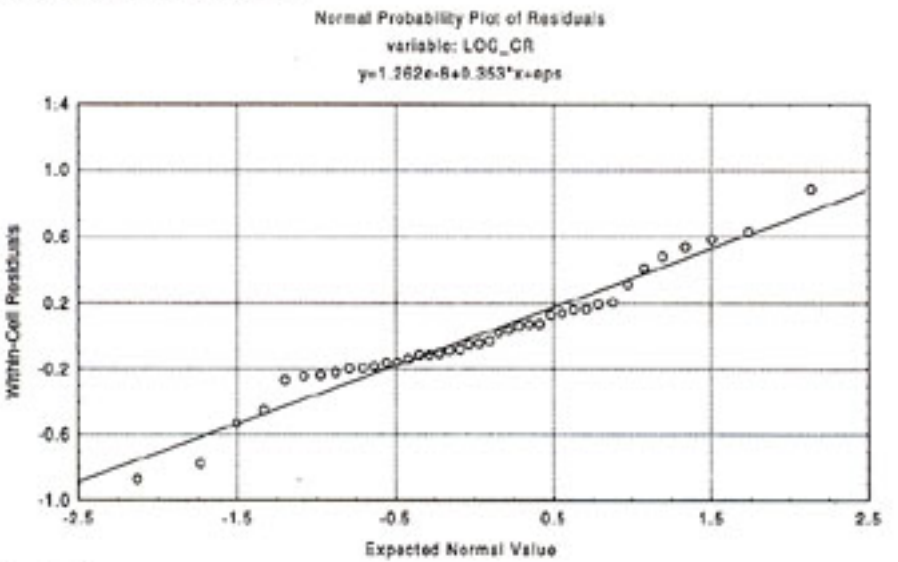
Chromium



Correlation

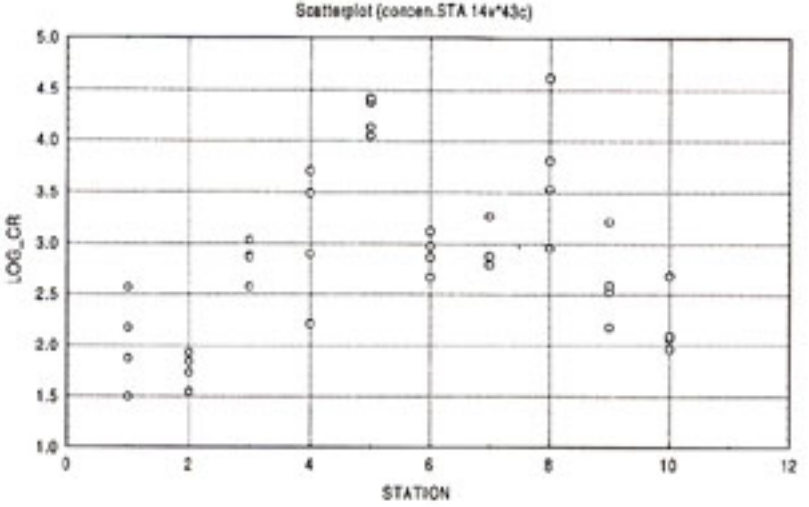
	CR_X	CR_Y	
CR_X	1.000000	.872784	**- not normal**
CR_Y	.872784	1.000000	

Log-transformed Chromium



Correlation

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



ANOVA

	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	**3.2469011**
9	1.2945549
10	0.5473012

critical value = 1.697

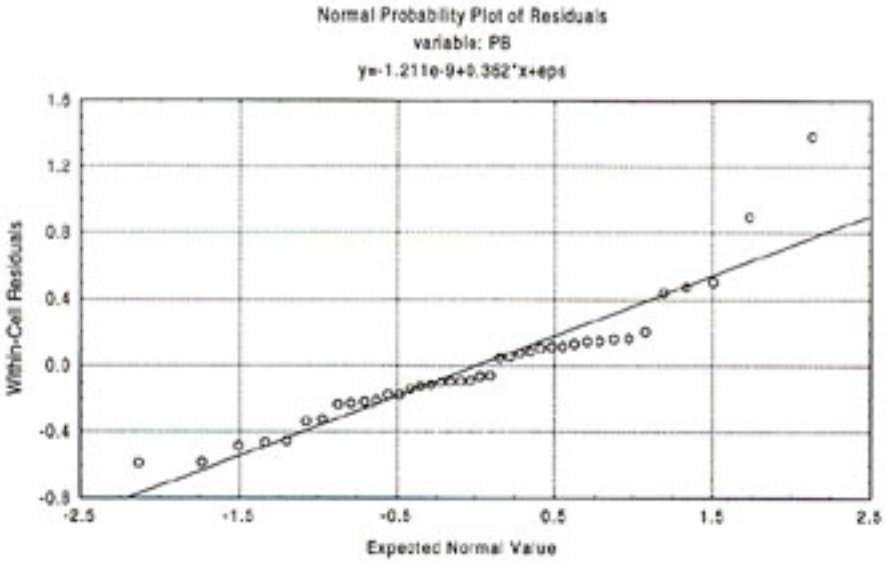
Newman-Keuls test - log chromium

	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	

Dunnett'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

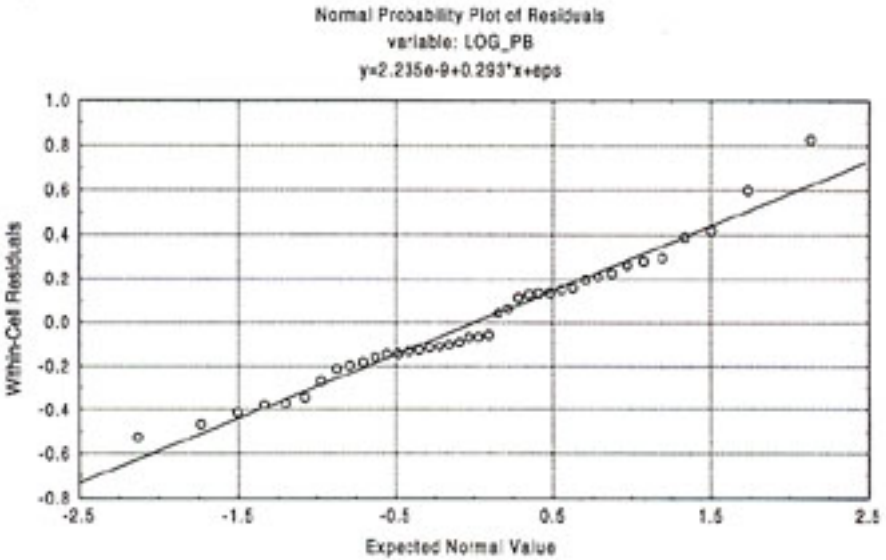
Lead



Correlation

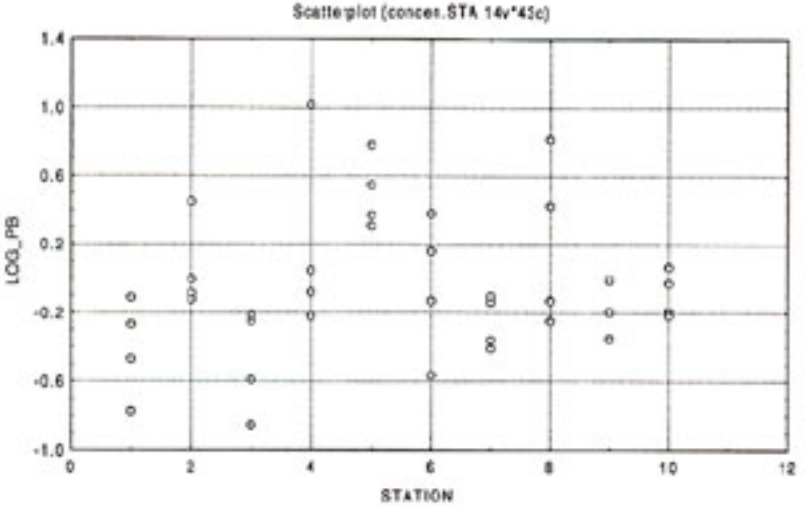
	PB_X	PB_Y	
PB_X	1.000000	.937043	**- not normal**
PB_Y	.937043	1.000000	

Log-transformed Lead



Correlation

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



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	0.2857627
7	-0.1712093
8	0.8345283
9	0.0661068
10	0.173666

critical value = 1.697

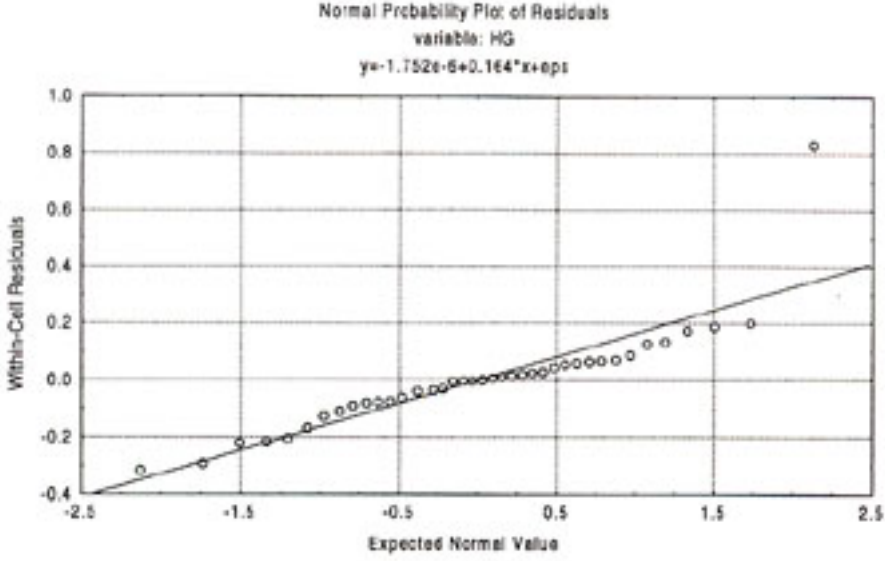
Newman-Keuls test - log lead

	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	

Dunnett'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 Difference	q	P value
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

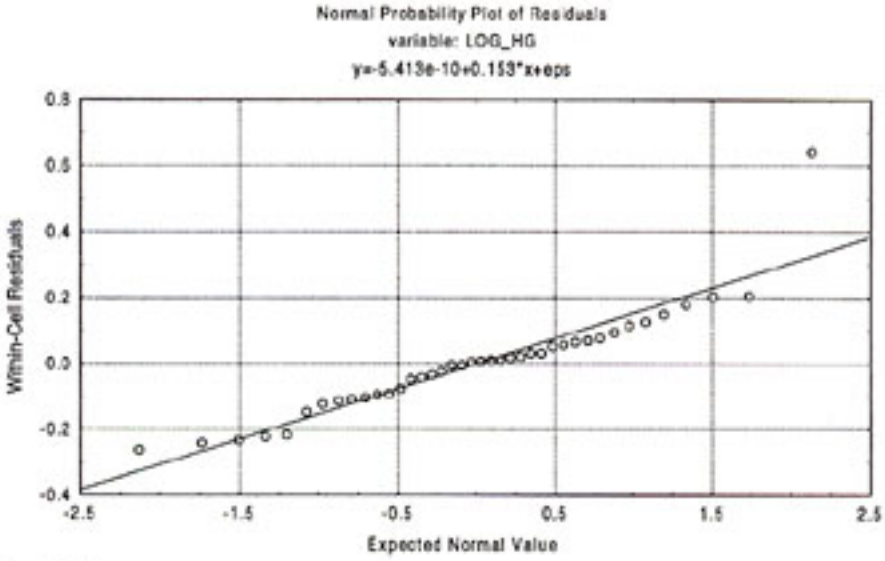
Mercury



Correlation

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

Log-transformed Mercury



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

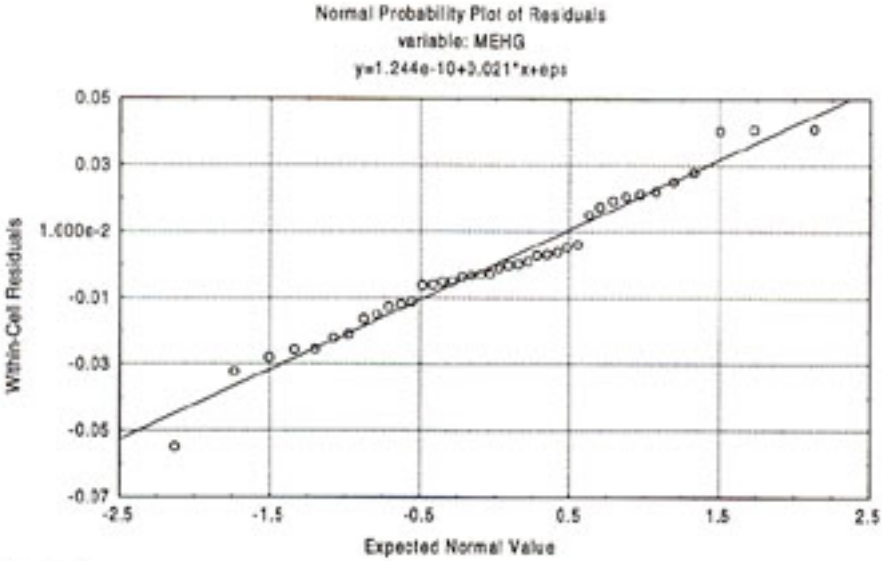
Newman-Keuls test - ranked mercury

	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	

Dunnett'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.

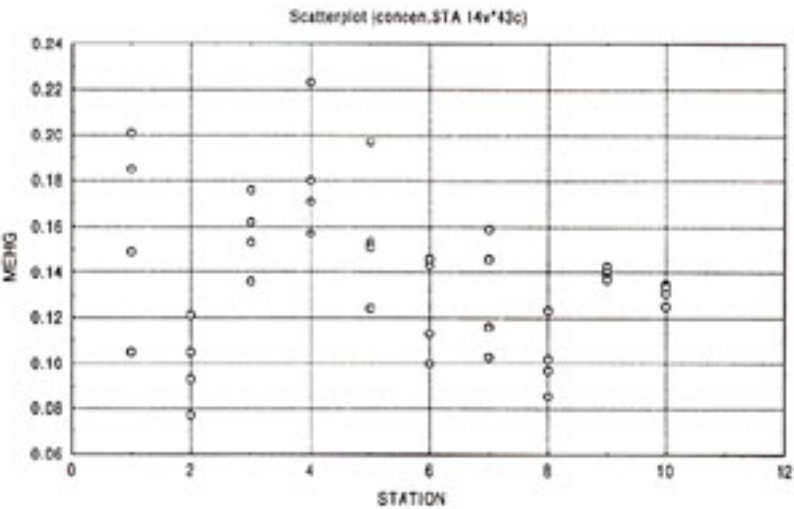
Comparison	Mean Difference	q	P value
Initial vs Station 1	0.383	0.672	ns P>0.05
Initial vs Station 2	1.691	2.967	* P<0.05
Initial vs Station 3	1.352	2.372	ns P>0.05
Initial vs Station 4	0.755	1.325	ns P>0.05
Initial vs Station 5	0.440	0.773	ns P>0.05
Initial vs Station 6	2.251	3.950	** P<0.01
Initial 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



Correlation

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



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 Difference	q	P value
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

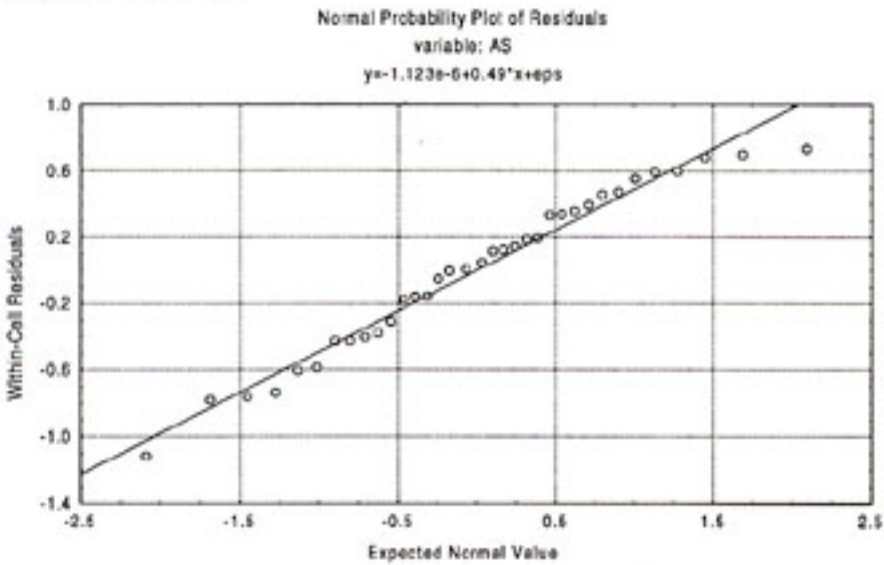
STATISTICAL RESULTS
TISSUE CHEMISTRY CONCENTRATION DATA
EXCLUDING REFERENCE STATION 1

Tissue Chemistry Concentration Statistical Results (excluding Reference Station 1)

Means

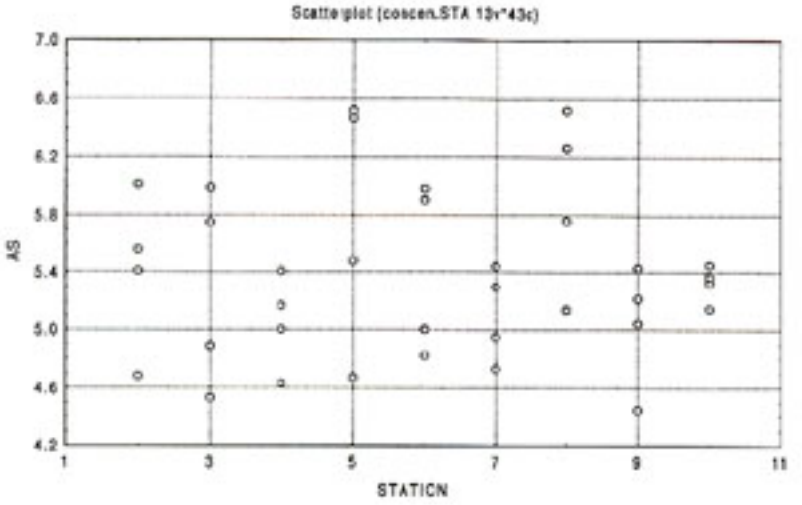
	ARSENIC	CADMIUM	CHROMIUM	LEAD	MERCURY	METHMERC
2	5.415000	3.182500	5.88750	1.093500	.833500	.099025
3	5.290000	2.620000	17.30000	.641250	.865500	.156750
4	5.052500	2.262500	25.20000	1.386250	.975250	.182750
5	5.785000	2.782500	70.22500	1.682500	1.060500	.156250
6	5.425000	2.715000	18.55000	1.019250	.756000	.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



Correlation

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



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

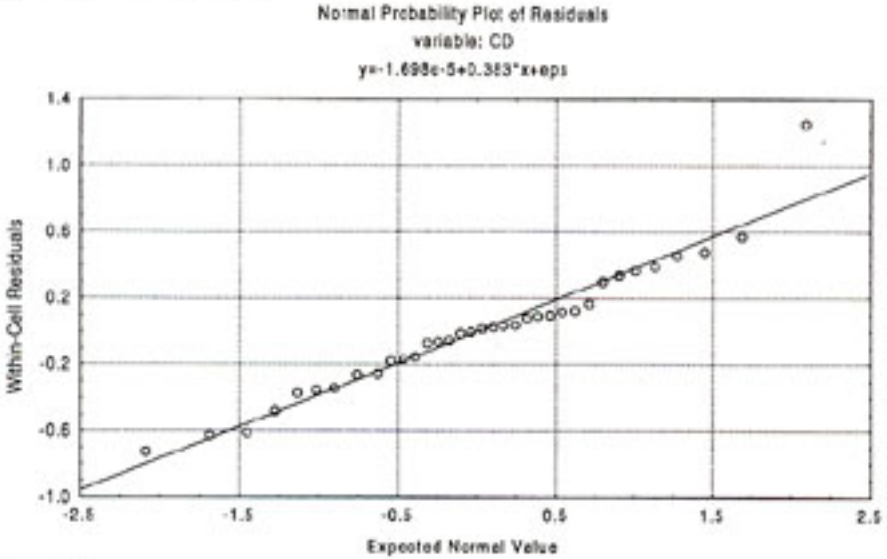
Newman-Keuls test - arsenic

	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.

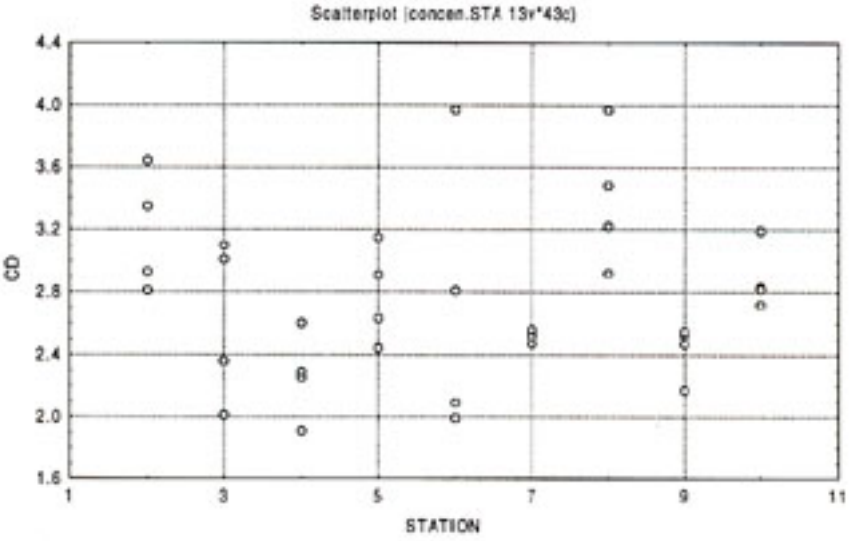
Comparison	Mean Difference	q	P value
Initial vs Station 2	0.835	2.251	ns P>0.05
Initial vs Station 3	0.960	2.588	ns P>0.05
Initial vs Station 4	1.198	3.229	* P<0.05
Initial vs Station 5	0.465	1.254	ns P>0.05
Initial vs Station 6	0.825	2.224	ns P>0.05
Initial vs Station 7	1.145	3.087	* P<0.05
Initial 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



Correlation

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



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 Difference	q	P value
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

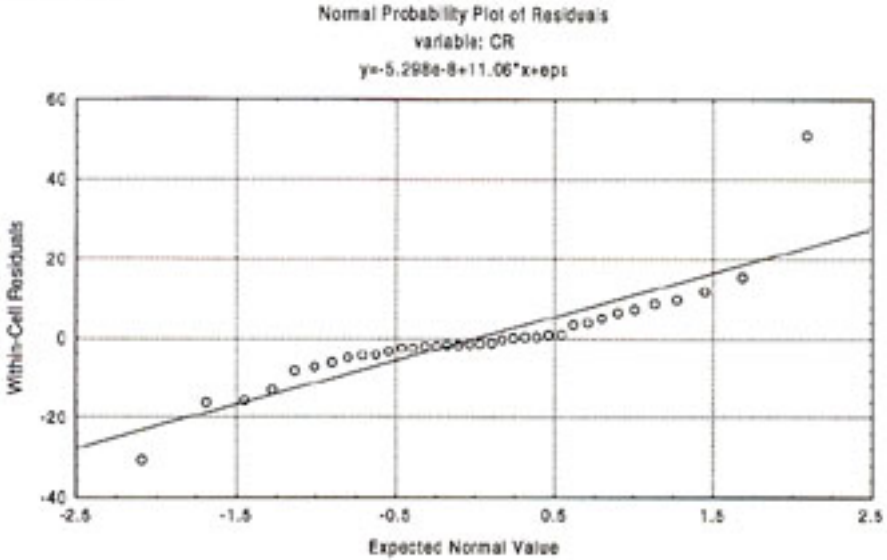
Newman-Keuls test - cadmium

	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 Difference	q	P value
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

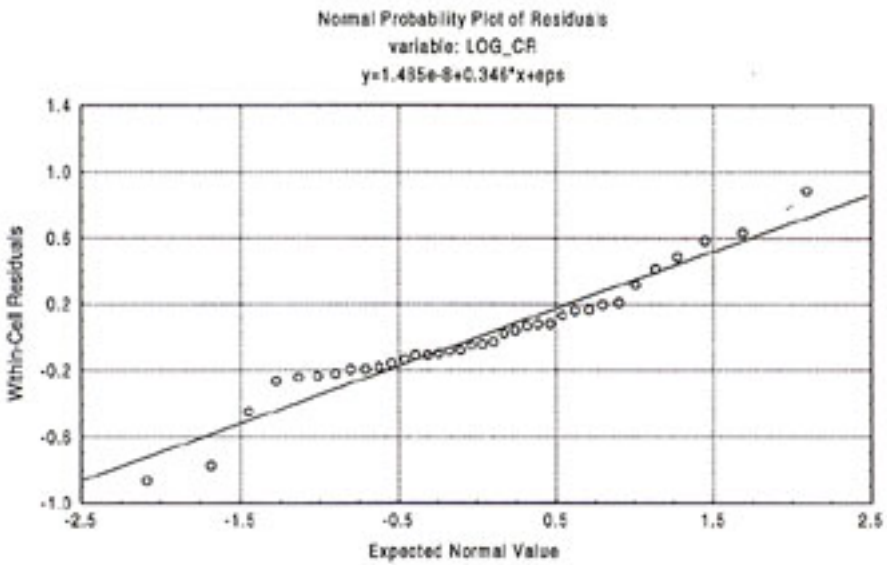
Chromium



Correlation

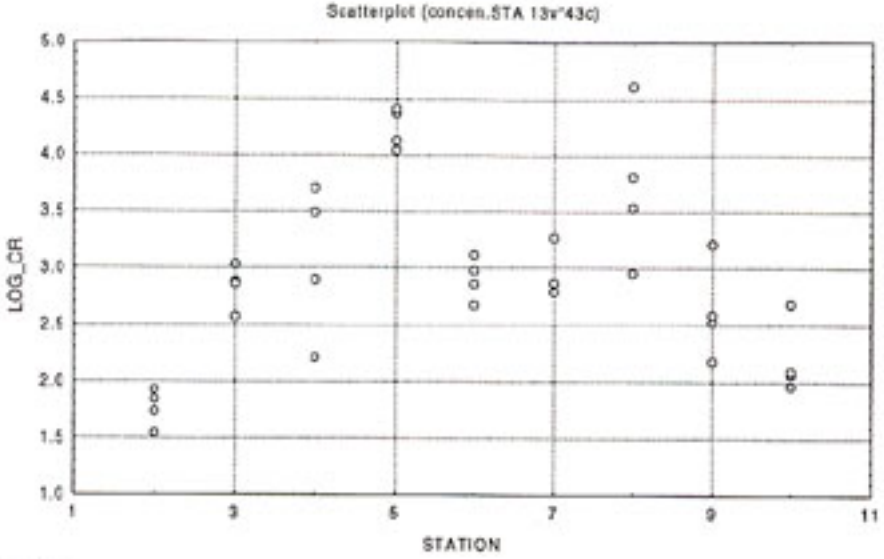
	CHROM_X	CHROM_Y	
CHROM_X	1.000000	.823525	**- not normal**
CHROM_Y	.823525	1.000000	

Log-transformed Chromium



Correlation

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



ANOVA

	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 chro
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

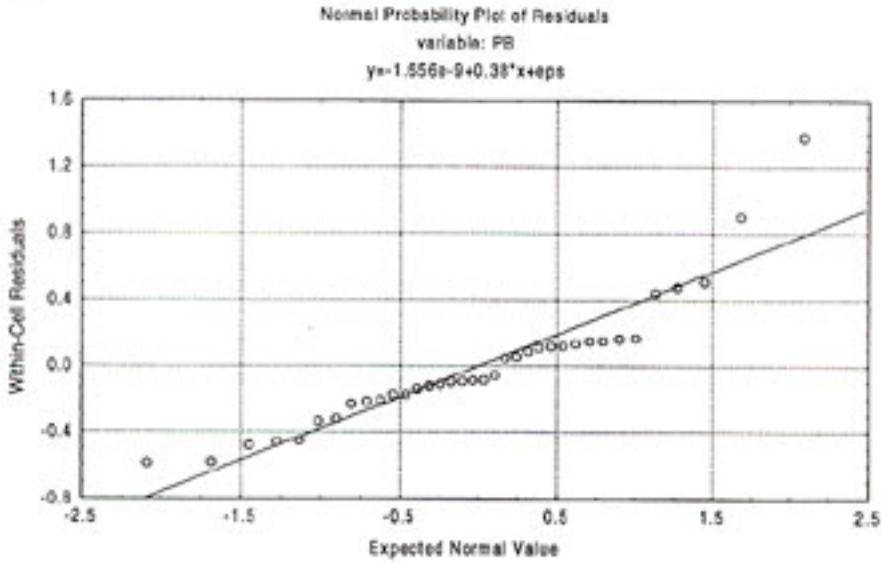
	3	4	5	6	7	8	9	10
3		.846750	**.00100***	.812555	.922308	**.04041***	.476774	.098294
4	.846750		**.00166***	.834543	.670226	**.03548***	.549013	.063544
5	.001002	.001664		**.00122***	**.00113***	.093466	**.00032***	**.00015***
6	.812555	.834543	.001225		.886829	**.04532***	.606781	.103420
7	.922308	.670226	.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	

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

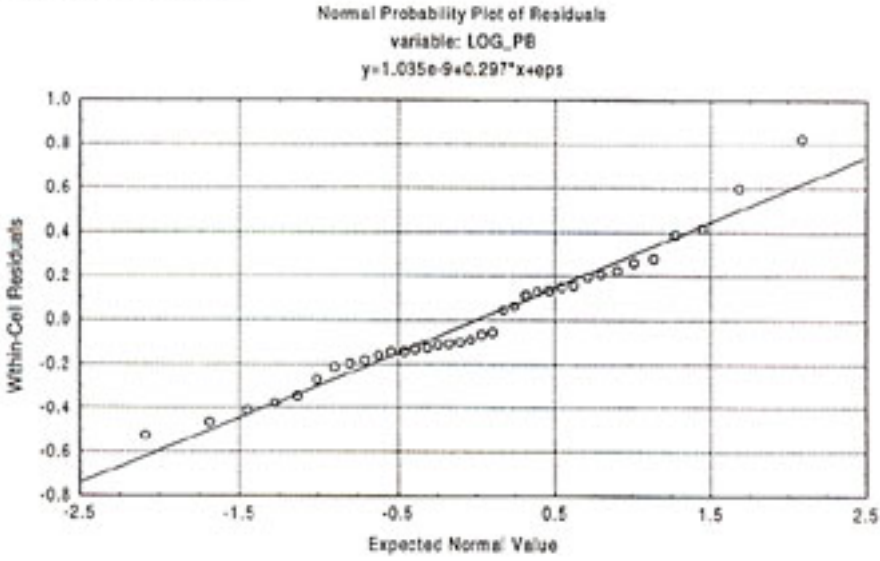
Lead



Correlation

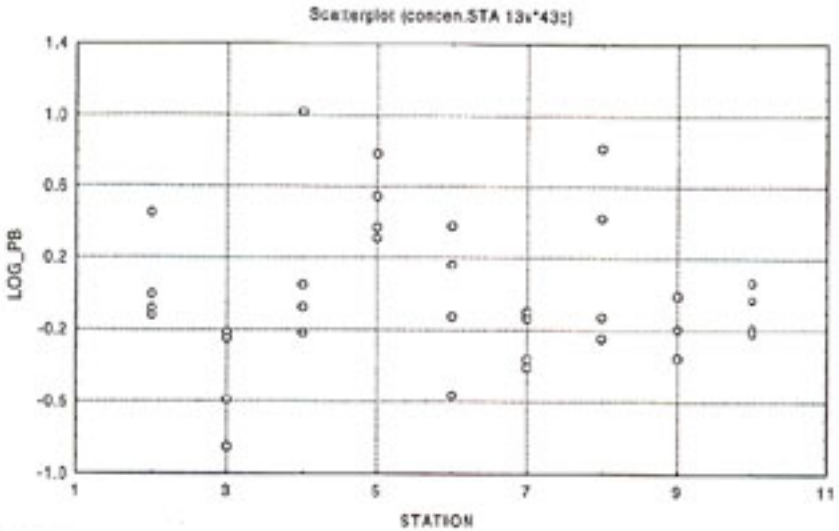
	LEAD_X	LEAD_Y	
LEAD_X	1.000000	.928758	**- not normal**
LEAD_Y	.928758	1.000000	

Log-transformed Lead



Correlation

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



ANOVA

	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

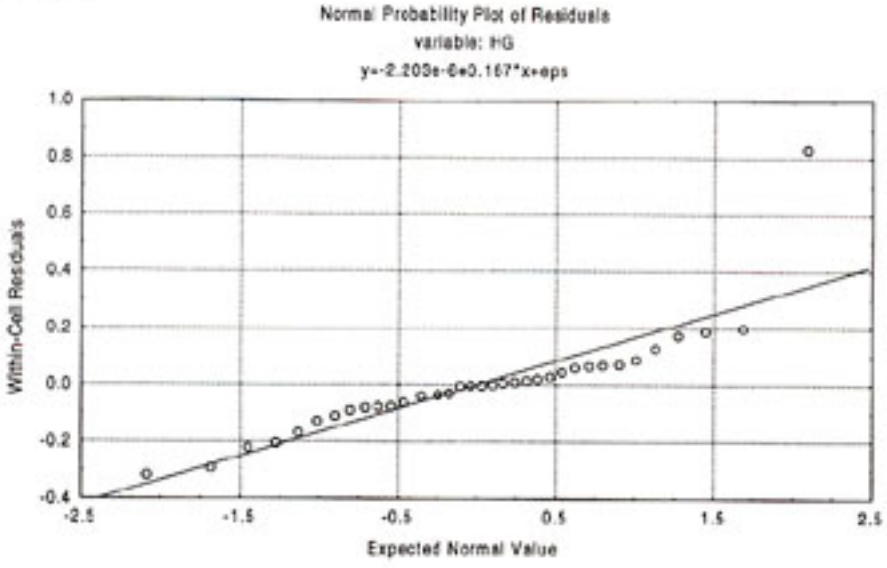
	3	4	5	6	7	8	9	10
3		.098554	**.00935***	.391874	.361751	.102810	.363678	.401195
4	.098554		.416405	.348370	.377600	.922398	.523952	.480659
5	.009350	.416405		.140419	.060593	.246678	.119946	.134218
6	.391874	.348370	.140419		.815750	.550275	.906747	.831228
7	.361751	.377600	.060593	.815750		.407054	.652333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

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

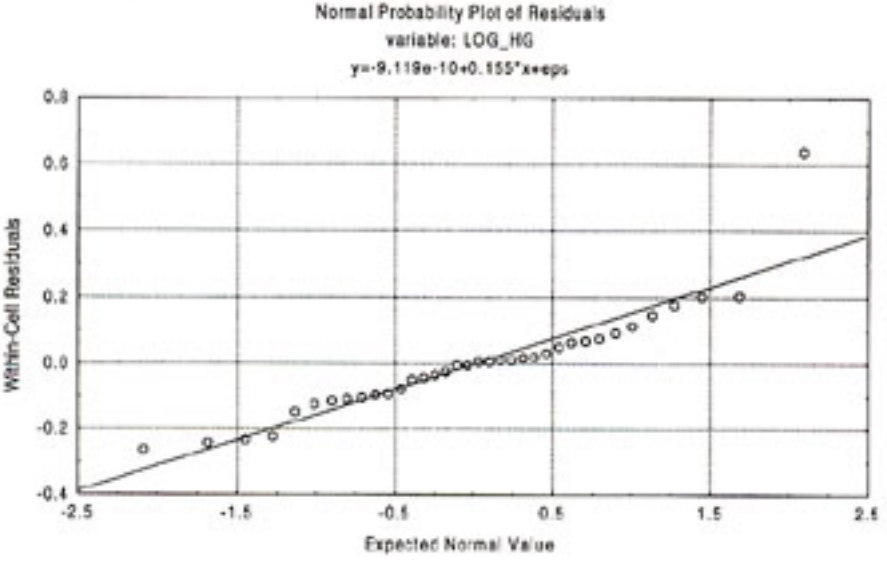
Mercury



Correlation

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

Log-transformed Mercury



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 m

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

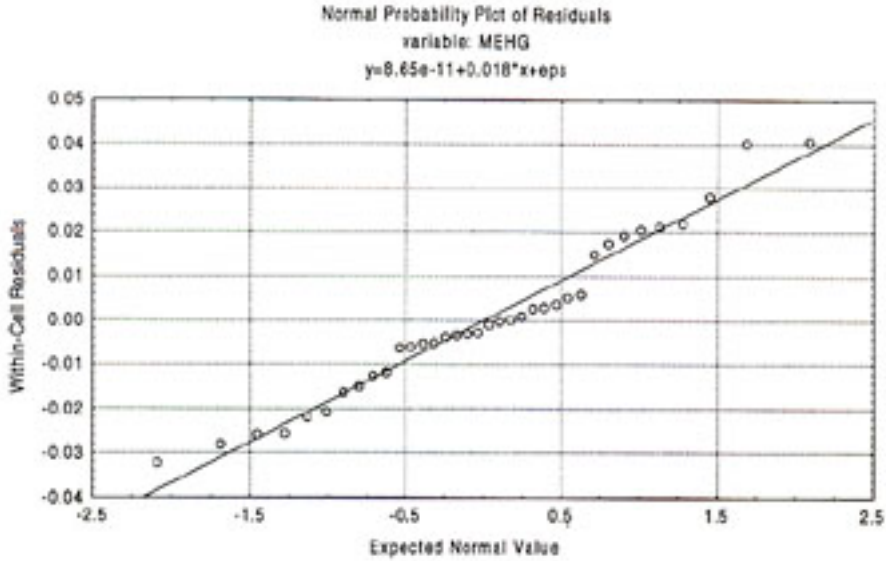
	3	4	5	6	7	8	9	10
3		.728777	.494554	.438258	.585298	.994971	.932098	.752391
4	.728777		.560977	.181286	.352135	.564255	.502584	.658985
5	.494554	.560977		.069875	.162117	.385769	.424959	.399499
6	.438258	.181286	.069875		.602263	.552391	.435239	.460747
7	.585298	.352135	.162117	.602263		.748399	.660360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

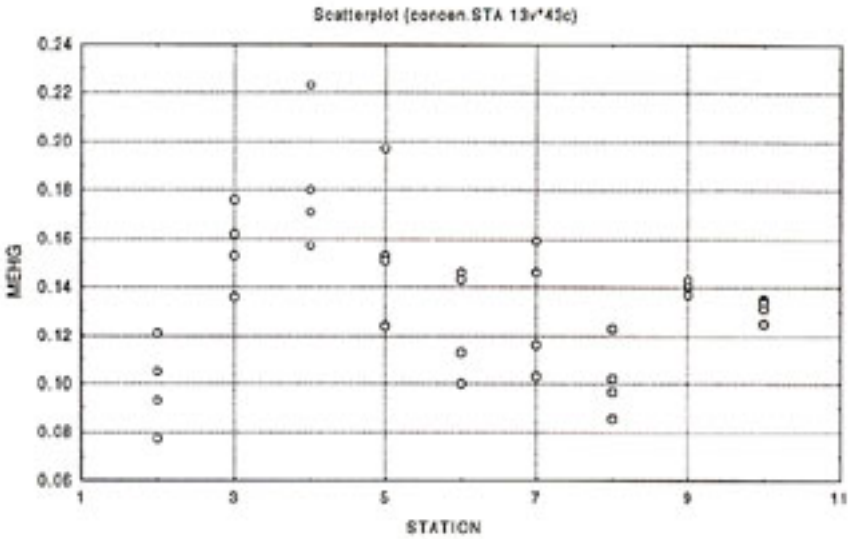
Comparison	Mean Difference	q	P value
Initial vs Station 2	1.691	2.943	* P<0.05
Initial vs Station 3	1.352	2.353	ns P>0.05
Initial vs Station 4	0.755	1.314	ns P>0.05
Initial vs Station 5	0.440	0.7664	ns P>0.05
Initial vs Station 6	2.251	3.917	** P<0.01
Initial vs Station 7	1.952	3.396	* P<0.05
Initial 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



Correlation

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



ANOVA

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

Dunnett'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 Difference	q	P value
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	

Dunnett'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 Difference	q	P value
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

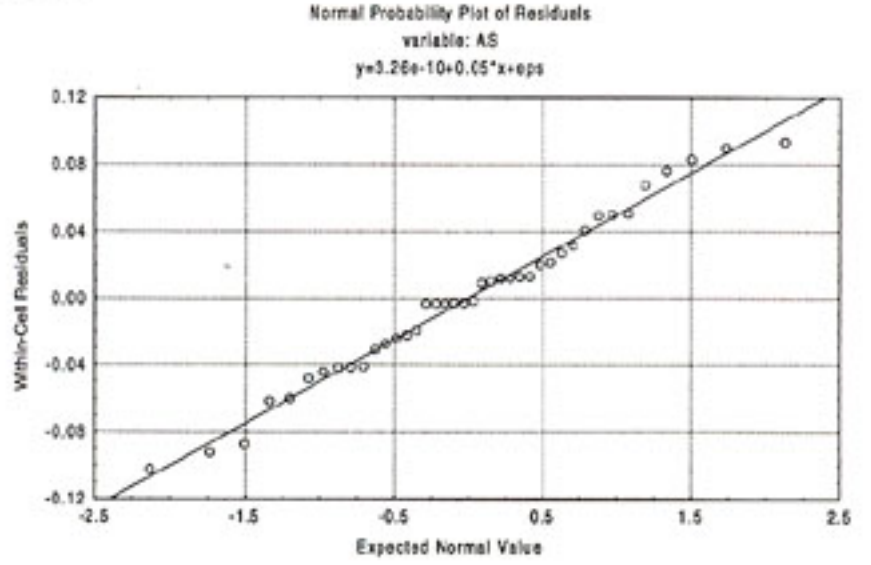
STATISTICAL RESULTS
TISSUE CHEMISTRY CONTENT DATA
INCLUDING REFERENCE STATIONS 1 AND 2

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

Means

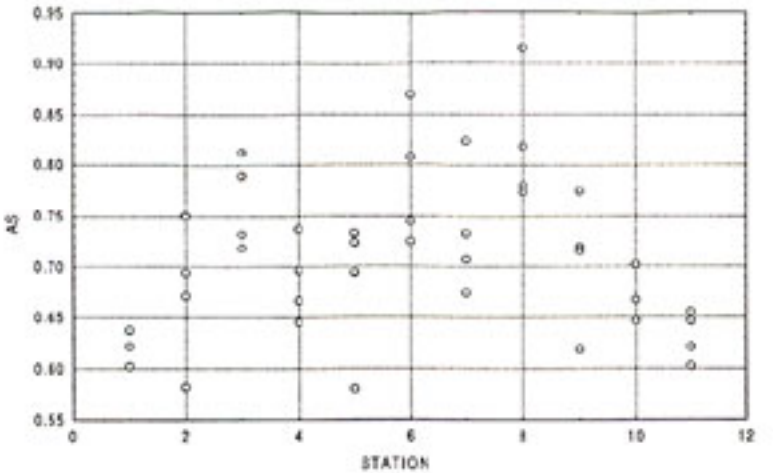
	AS	CD	CR	PB	HG	MEHG
1	.624777	.246354	.893316	.075154	.119008	.017597
2	.674566	.396493	.733056	.136177	.103809	.012330
3	.763298	.376461	2.526446	.092369	.125976	.022878
4	.685925	.306608	3.313383	.184683	.132399	.024677
5	.682629	.328843	8.356944	.199552	.125534	.018445
6	.786685	.390658	2.682702	.147712	.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



Correlation

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



ANOVA

	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	1.0607329
5	0.9642981
6	**4.0068396**
7	**2.4774195**
8	**5.0404705**
9	1.6730882
10	0.6136364

critical value = 1.697

Newman-Keuls test - arsenic

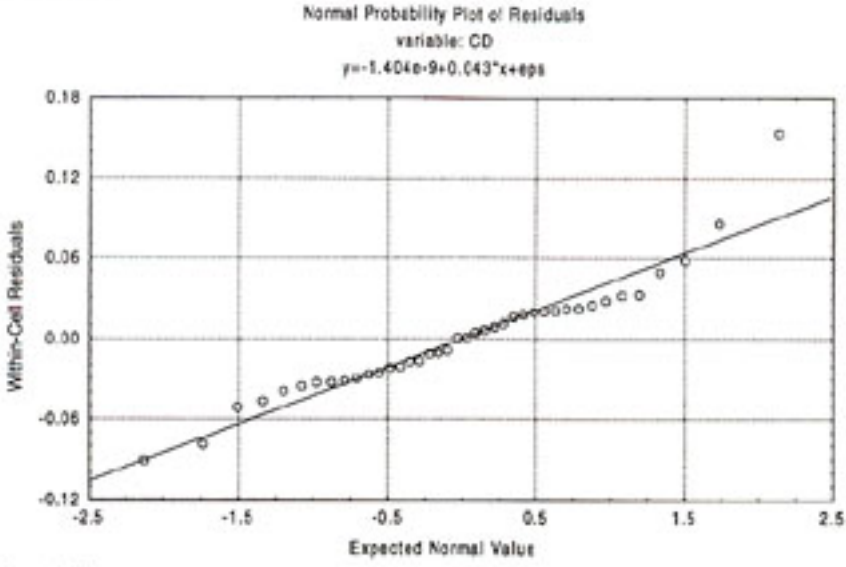
	3	4	5	6	7	8	9	10
3		.246178	.294896	.567017	.479323	.329379	.356169	.232615
4	.246178		.935554	.123708	.463488	**.02673***	.608212	.924048
5	.294896	.935554		.140279	.581636	**.02905***	.820743	.768725
6	.567017	.123708	.140279		.409248	.390203	.222626	.099445
7	.479323	.463488	.581636	.409248		.159087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

Dunnett'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 Difference	q	P value
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

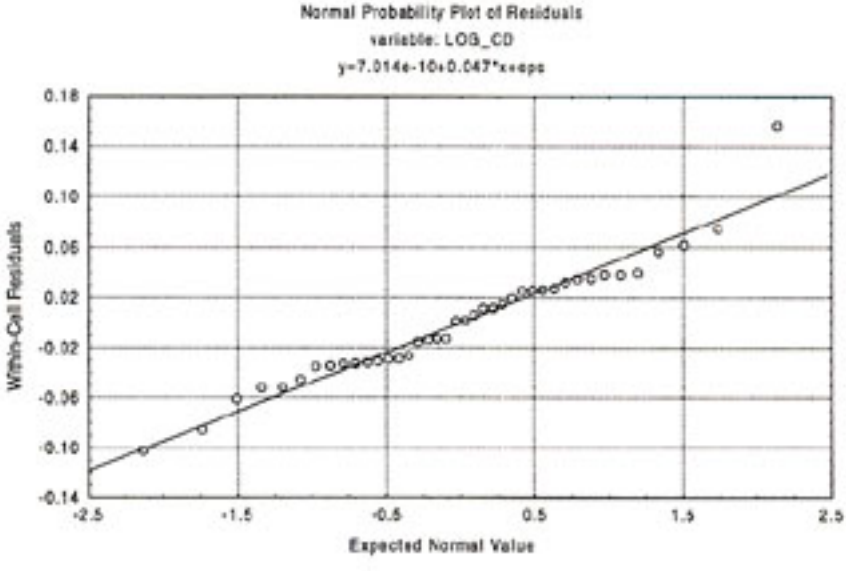
Cadmium



Correlation

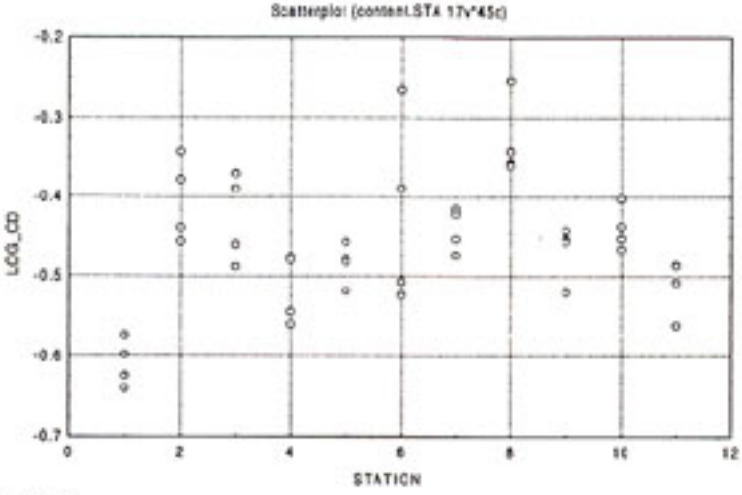
	CD_X	CD_Y	
CD_X	1.000000	.958236	**- not normal**
CD_Y	.958236	1.000000	

Log-transformed Cadmium Content



Correlation

	LGCD_X	LGCD_Y
LGCD_X	1.000000	.972382
LGCD_Y	.972382	1.000000



ANOVA

	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	0.3035288
6	1.1240911
7	0.8644192
8	**2.3423149**
9	0.5056177
10	0.8779706

critical value = 1.697

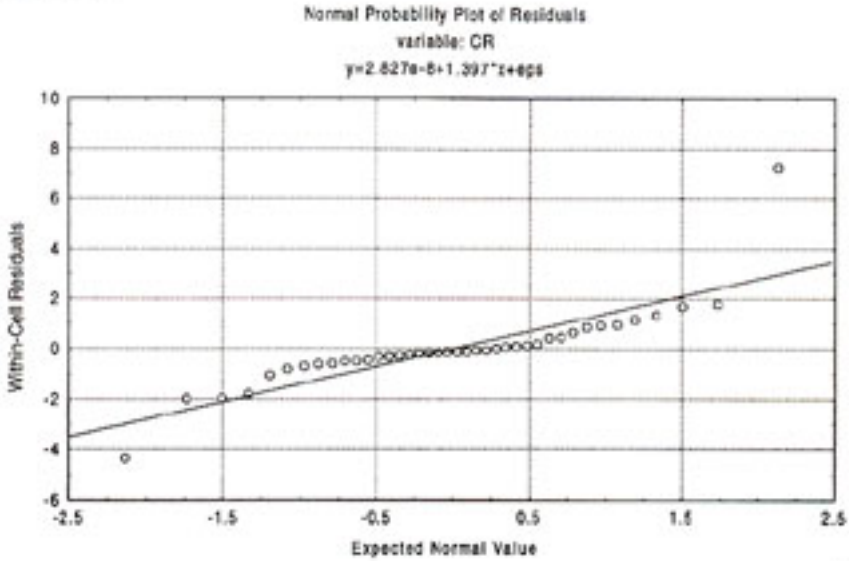
Newman-Keuls test – log-transformed cadmium

	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	

Dunnett'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 Difference	q	P value
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

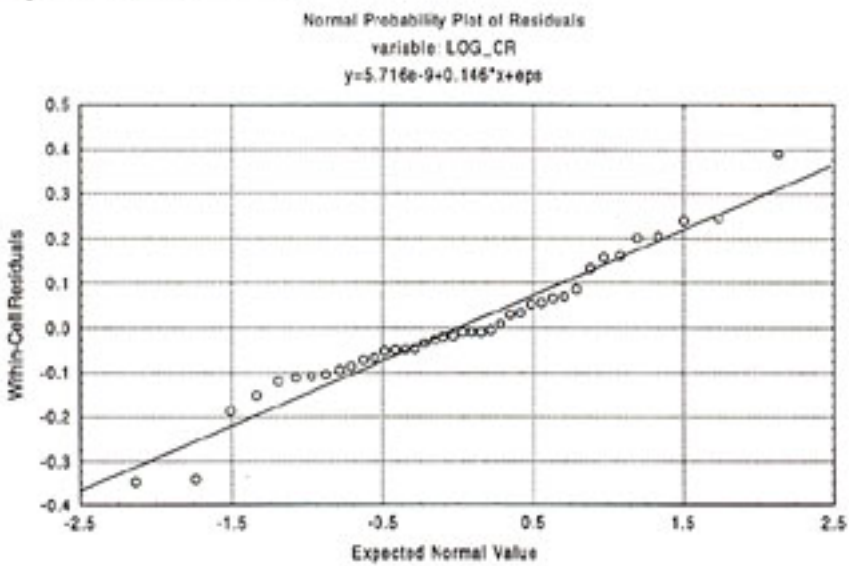
Chromium



Correlation

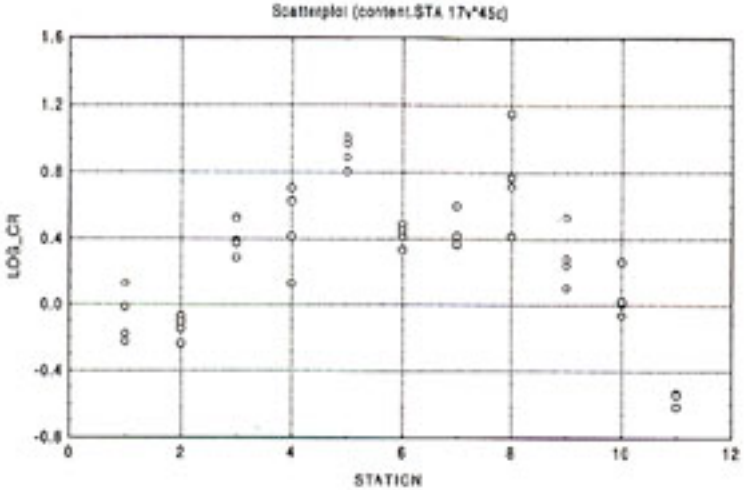
	CR_X	CR_Y	
CR_X	1.000000	.852850	**- not normal**
CR_Y	.852850	1.000000	

Log-transformed Chromium



Correlation

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



ANOVA

	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	**2.4526644**
5	**4.3606848**
6	**2.2057771**
7	**2.3228278**
8	**3.7077536**
9	1.6780957
10	0.6948919

critical value = 1.697

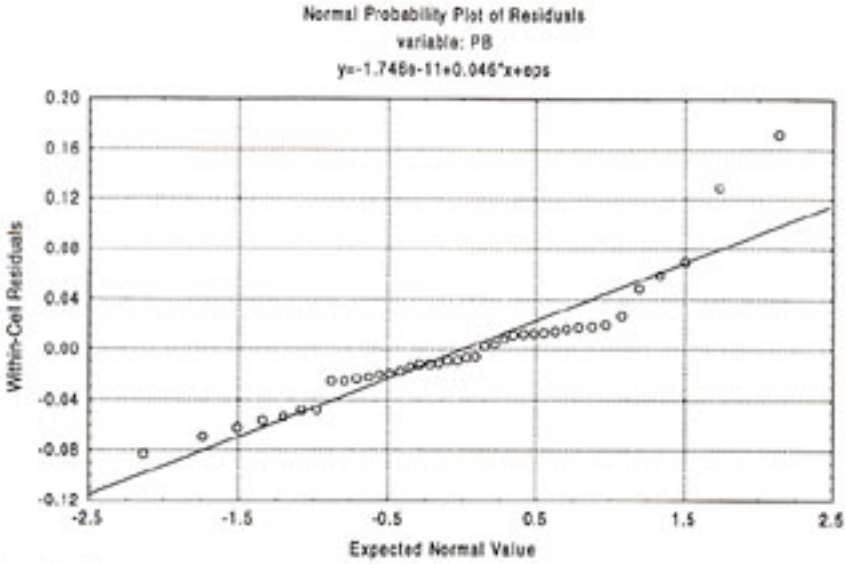
Newman-Keuls test - log chromium

	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	

Dunnett'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

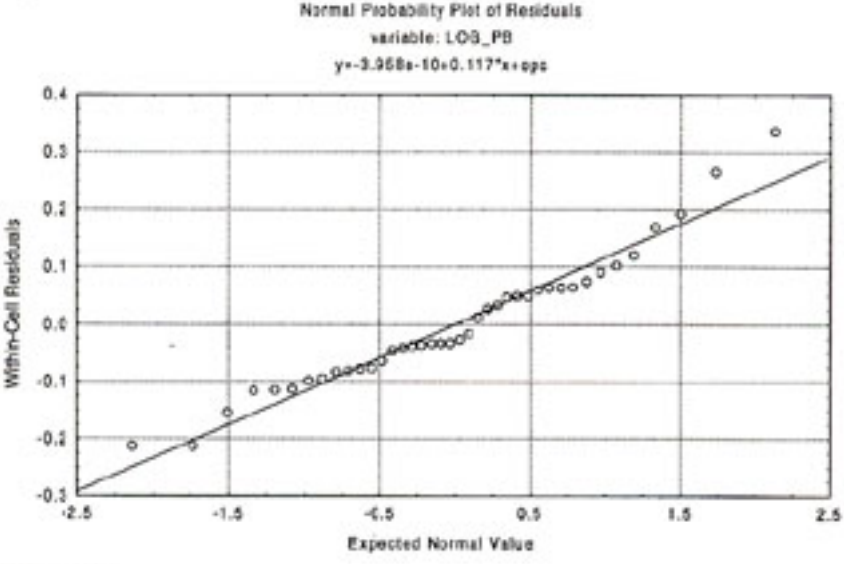
Lead



Correlation

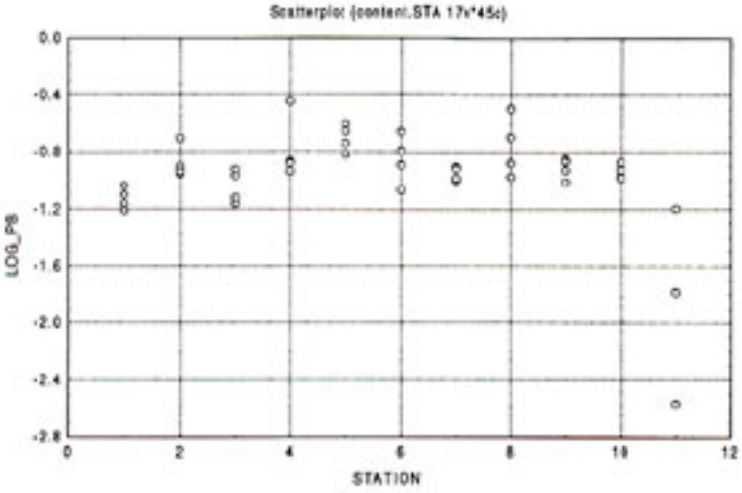
	PB_X	PB_Y	
PB_X	1.000000	.931464	**- not normal**
PB_Y	.931464	1.000000	

Log-transformed Lead



Correlation

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



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	-0.2256136
4	1.1761614
5	1.5844088
6	0.7952211
7	0.2743369
8	1.2871453
9	0.47626
10	0.3407437

critical value = 1.697

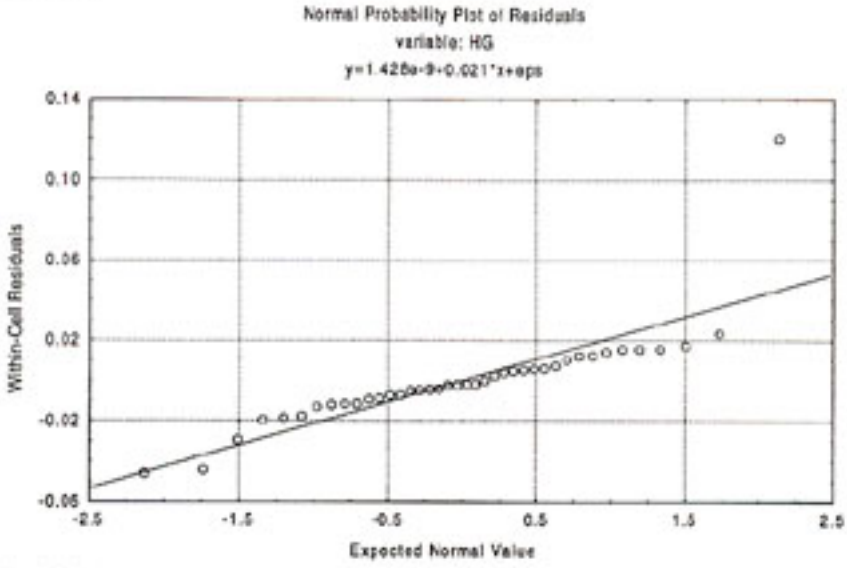
Newman-Keuls test - log lead

	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	

Dunnett'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

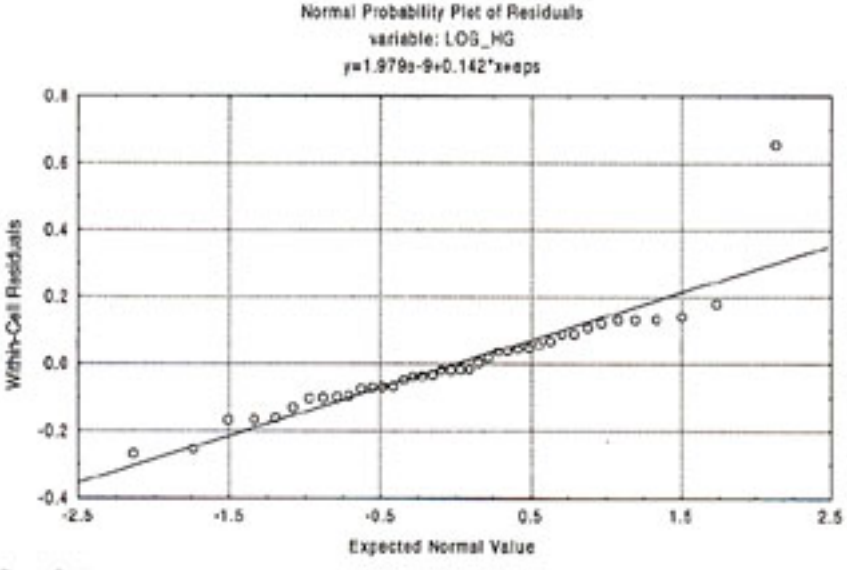
Mercury



Correlation

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

Log-transformed Mercury



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)

Refs 1 and 2 vs:	rank-it Hg
3	1.6496871
4	**2.3949827**
5	1.5866748
6	-0.3568936
7	0.6063342
8	1.5002635
9	1.4419601
10	-0.3274251

critical value = 1.697

Newman-Keuls test - ranked mercury

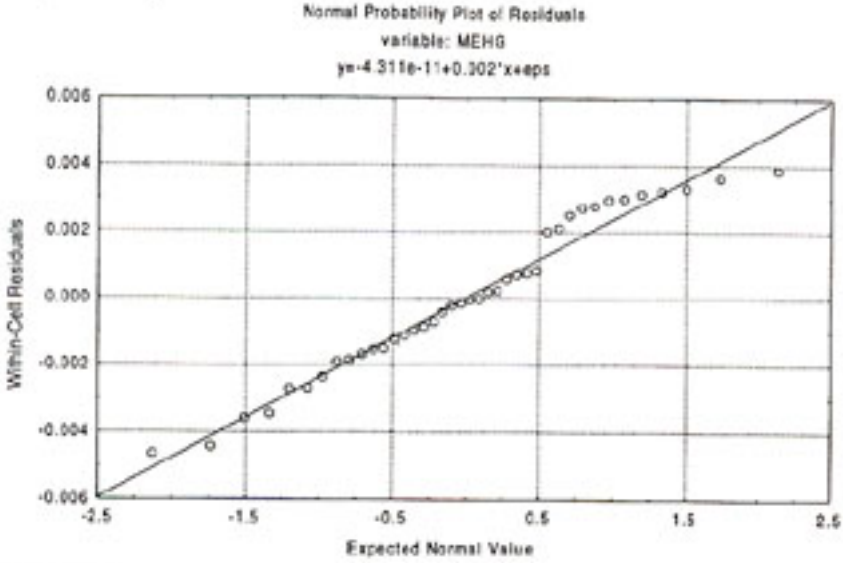
	3	4	5	6	7	8	9	10
3		.592114	.961570	.647329	.905831	.999189	.997012	.630697
4	.592114		.825743	.384487	.720227	.959687	.925465	.382022
5	.961570	.825743		.599712	.844918	.996174	.979763	.565254
6	.647329	.384487	.599712		.711649	.438136	.520619	.921914
7	.905831	.720227	.844918	.711649		.469784	.710685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

Dunnett'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.

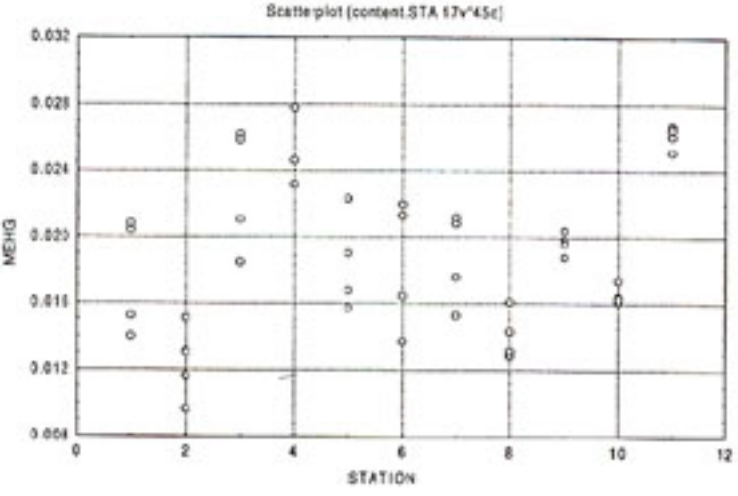
Comparison	Mean Difference	q	P value
Initial vs Station 1	0.1577	0.239	ns P>0.05
Initial vs Station 2	1.242	1.887	ns P>0.05
Initial vs Station 3	-0.1795	0.273	ns P>0.05
Initial vs Station 4	-0.5449	0.828	ns P>0.05
Initial vs Station 5	-0.1466	0.223	ns P>0.05
Initial vs Station 6	0.9369	1.423	ns P>0.05
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



Correlation

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



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	**2.6928054**
10	0.9643596

critical value = 1.697

Newman-Keuls test - methylmercury

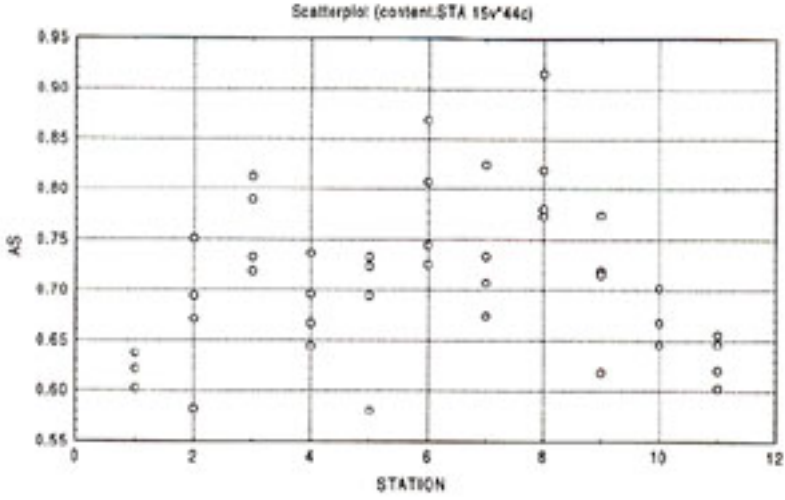
	3	4	5	6	7	8	9	10
3		.338606	.102697	.133255	.080469	**.00140***	.092543	**.02270***
4	.338606		**.01893***	**.02323***	**.01710***	**.00027***	**.03042***	**.00305***
5	.102697	.018931		.956651	.888703	.112302	.791600	.558412
6	.133255	.023231	.956651		.979007	.074222	.892308	.333662
7	.080469	.017105	.888703	.979007		.123403	.612682	.642834
8	.001397	.000274	.112302	.074222	.123403		.058875	.199505
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



ANOVA

	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

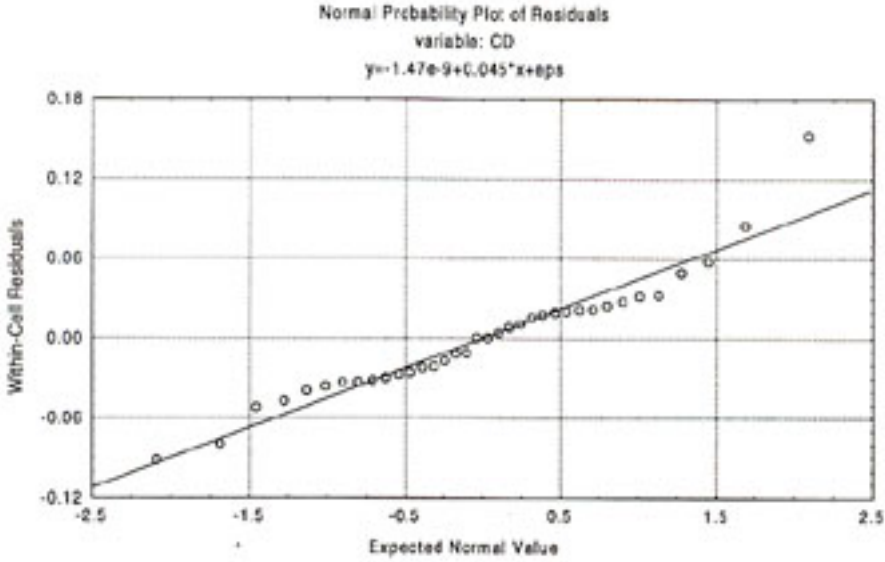
Newman-Keuls test - arsenic content

	3	4	5	6	7	8	9	10
3		.246178	.294896	.567017	.479323	.329379	.356169	.232615
4	.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	

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

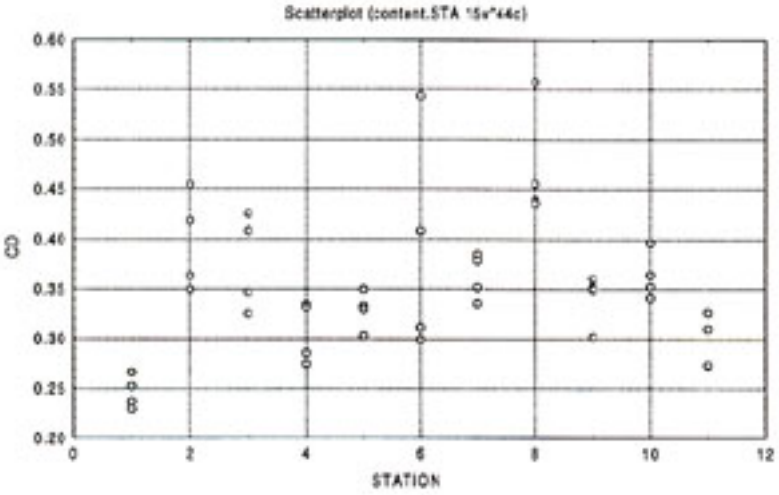
Comparison	Mean Difference	q	P value
Initial vs Station 2	-0.0432	1.090	ns P>0.05
Initial vs Station 3	-0.1319	3.327	* P<0.05
Initial vs Station 4	-0.0546	1.376	ns P>0.05
Initial vs Station 5	-0.0513	1.293	ns P>0.05
Initial vs Station 6	-0.1553	3.917	** P<0.01
Initial vs Station 7	-0.1030	2.597	ns P>0.05
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



Correlation N=36

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



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

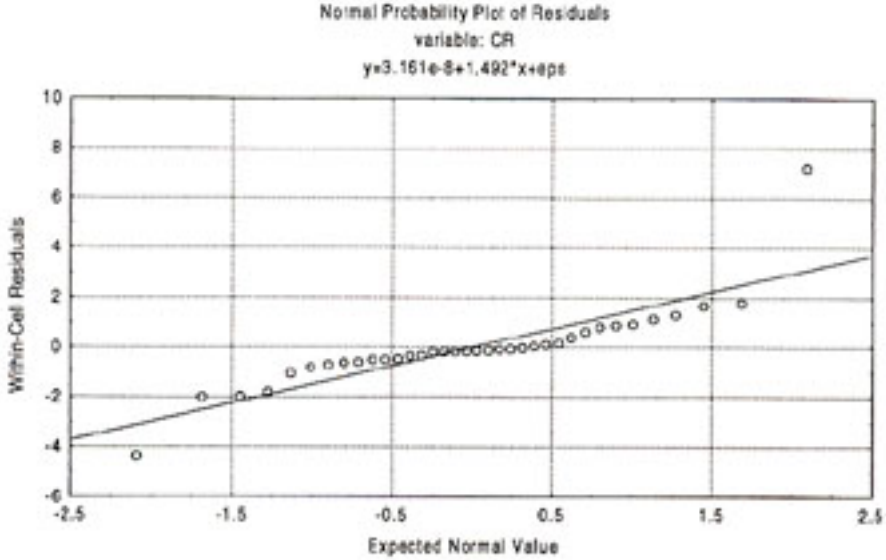
Newman-Keuls test - cadmium content

	3	4	5	6	7	8	9	10
3		.423938	.694952	.702284	.927837	**.03987***	.770663	.732849
4	.423938		.550284	.288414	.433541	**.00319***	.621133	.536677
5	.694952	.550284		.554067	.627993	**.01048***	.741698	.777155
6	.702284	.288414	.554067		.873089	**.03642***	.663062	.746933
7	.927837	.433541	.627993	.873089		**.04716***	.557576	.981203
8	.039873	.003189	.010481	.036422	.047165		**.01725***	**.03305***
9	.770663	.621133	.741698	.663062	.557576	.017254		.811352
10	.732849	.536677	.777155	.746933	.981203	.033048	.811352	

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

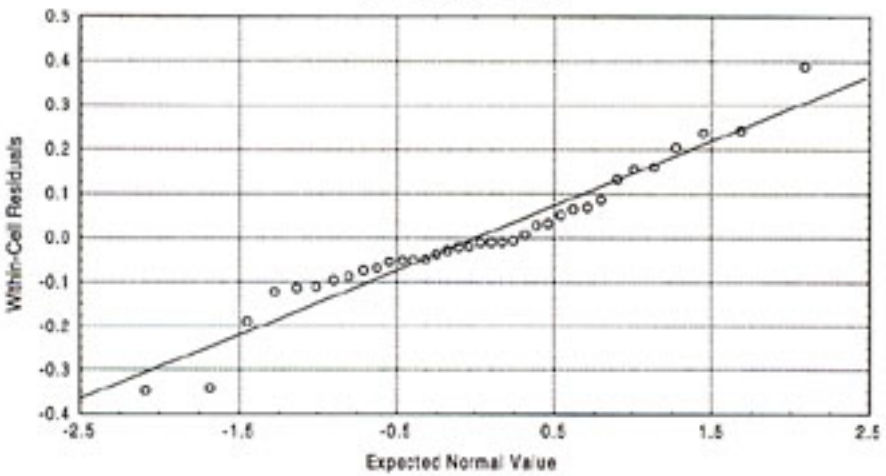
Chromium Content



Correlation N=36

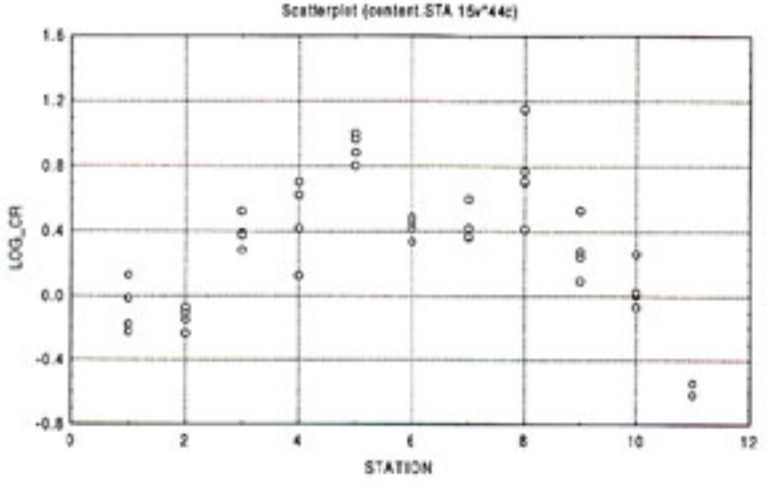
	CR_X	CR_Y	
CR_X	1.000000	.862783	**- not normal**
CR_Y	.862783	1.000000	

Log-transformed Chromium Content



Correlation N=36

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



ANOVA

	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

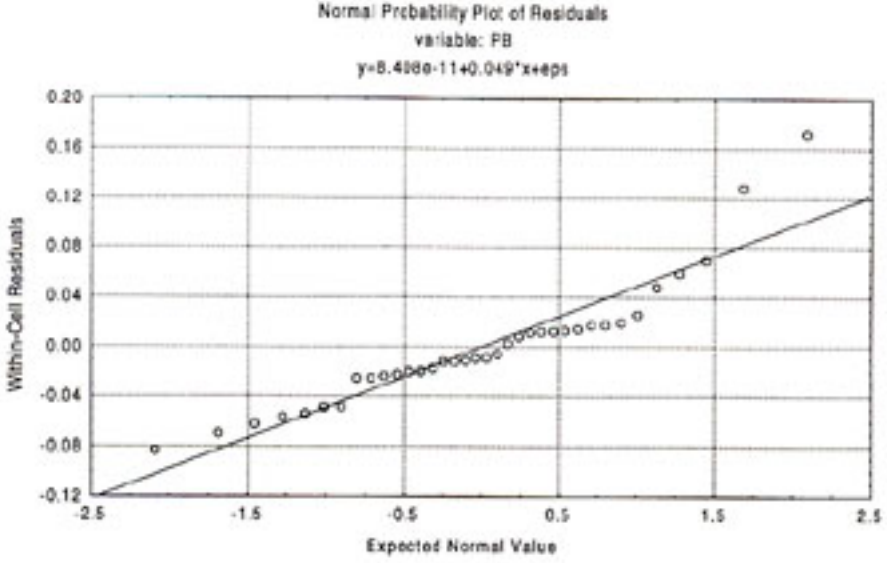
	3	4	5	6	7	8	9	10
3		.929033	**.00375***	.802568	.931000	**.04635***	.398803	**.03103***
4	.929033		**.00395***	.933628	.808083	**.02598***	.593180	**.02991***
5	.003750	.003950		**.00485***	**.00404***	.228600	**.00072***	**.00015***
6	.802568	.933628	.004854		.915009	.053327	.516024	**.03141***
7	.931000	.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	

Dunnett'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

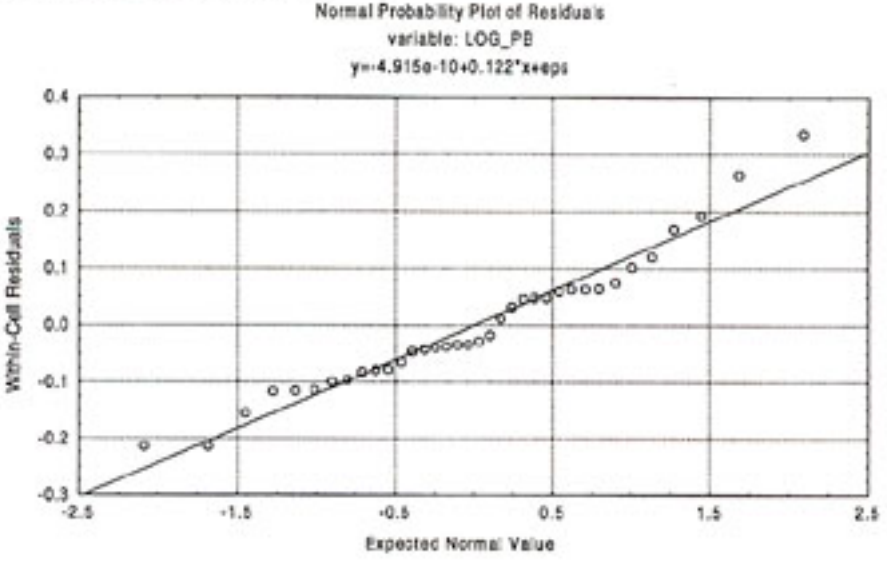
Lead Content



Correlation N=36

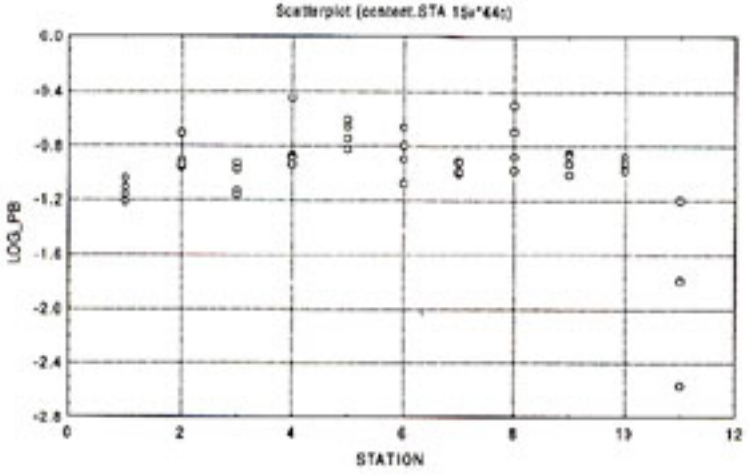
	PB_X	PB_Y	
PB_X	1.000000	.937261	**- not normal**
PB_Y	.937261	1.000000	

Log-transformed Lead Content



Correlation N=36

	LGPB_X	LGPB_Y	
LGPB_X	1.000000	.977419	**- normal**
LGPB_Y	.977419	1.000000	



ANOVA

	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

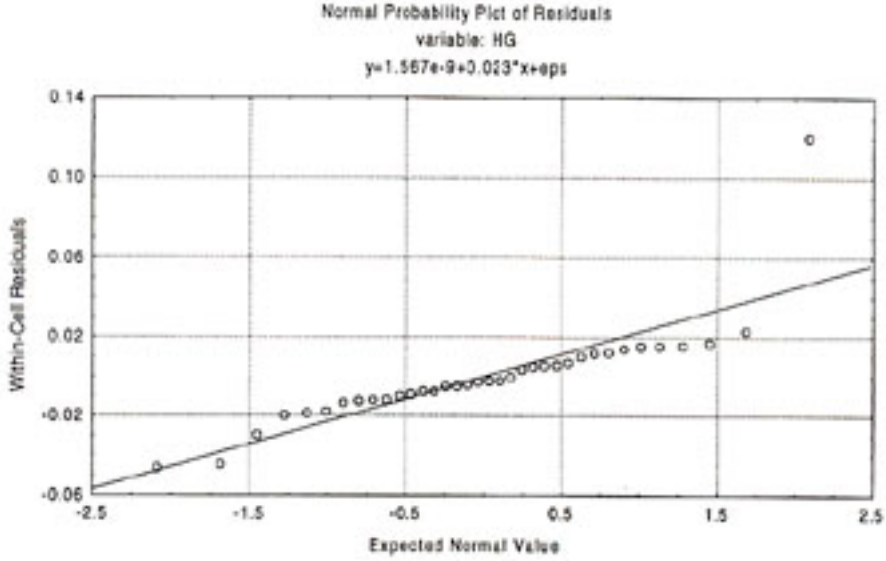
	3	4	5	6	7	8	9	10
3		.124241	**.03979***	.330186	.354026	.104362	.555812	.540986
4	.124241		.724440	.479289	.451652	.835989	.397792	.410296
5	.039790	.724440		.459243	.213493	.580128	.256272	.214819
6	.330186	.479289	.459243		.760396	.628120	.552991	.671570
7	.354026	.451652	.213493	.760396		.419832	.923403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

Dunnett'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

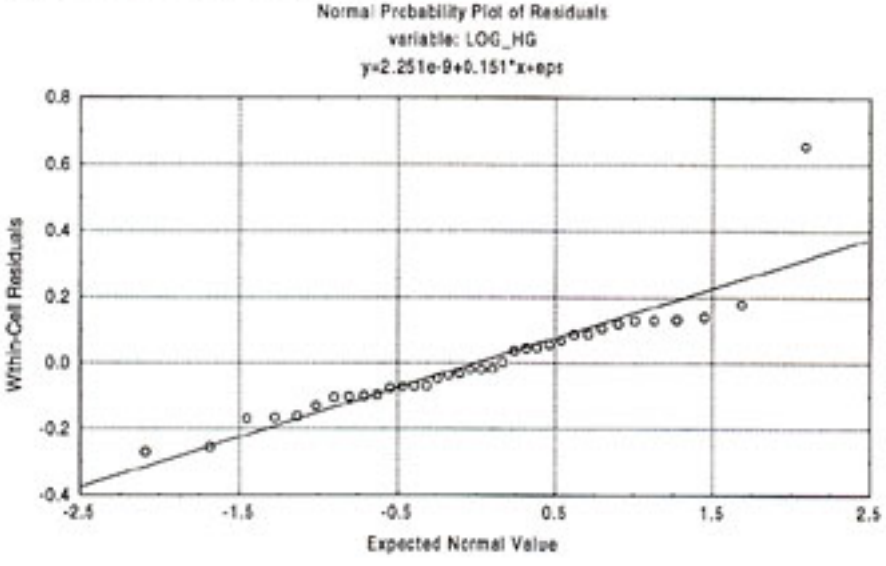
Mercury Content



Correlation N=36

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

Log-transformed Mercury Content



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

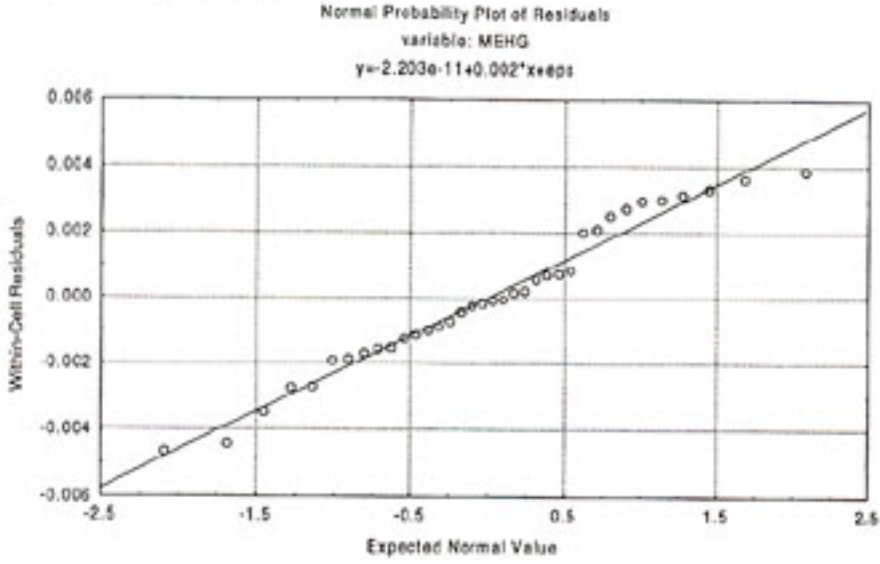
	3	4	5	6	7	8	9	10
3		.592114	.961570	.647329	.905831	.999189	.997012	.630697
4	.592114		.825743	.384487	.720227	.959687	.925465	.382022
5	.961570	.825743		.599712	.844918	.996174	.979763	.565254
6	.647329	.384487	.599712		.711649	.438136	.520619	.921914
7	.905831	.720227	.844918	.711649		.469784	.710685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

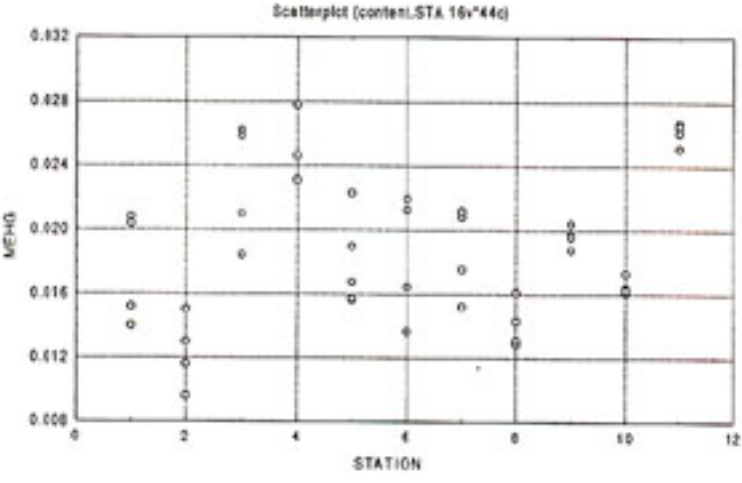
Comparison	Mean Difference	q	P value
Initial vs Station 2	1.245	1.768	ns P>0.05
Initial vs Station 3	-0.2122	0.301	ns P>0.05
Initial vs Station 4	-0.6232	0.885	ns P>0.05
Initial vs Station 5	-0.1773	0.252	ns P>0.05
Initial vs Station 6	0.8946	1.270	ns P>0.05
Initial vs Station 7	0.3634	0.516	ns P>0.05
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



Correlation N=36

	MEHG_X	MEHG_Y
MEHG_X	1.000000	.988075
MEHG_Y	.988075	1.000000



ANOVA

	Sum of Squares	df	Mean Square	F	p-level
Effect	.000480	8	.000060	9.077078	.000006
Error	.000178	27	.000007		

Dunnett'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 Difference	q	P value
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	

Dunnett'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 Difference	q	P value
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: Siagle Factor

SUMMARY

Groups	Count	Sum	Average	Variance
Cage 1	75	417.23	5.563067	0.847773
Cage 2	75	409.12	5.454933	0.736993
Cage 3	75	402.09	5.3612	0.623873
Cage 4	75	412.55	5.500667	0.724885
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	5.577867	0.733698
Cage 10	75	406.05	5.400667	0.773068
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	0.767865
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	0.799187
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	0.702087
Cage 26	75	419.7	5.596	0.634727
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	0.637219
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	0.666034
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	0.606776
Cage 43	75	418.09	5.574533	0.717449
Cage 44	75	395.11	5.268133	0.570978

ANOVA Results

H_0: 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	0.70386
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	0.616086
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	0.666571
Initial (TC)	300	1634.55	5.4485	0.685942

ANOVA Results

H_0: 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	0.598455	1.833573
Within Groups	2315.347	3289	0.703967			
Total	2321.199	3299				

Binomial Multiple Comparison Worksheet for Percent Survival

Number of Sites:		10								
Station	1	2	3	4	5	6	7	8	9	10
P	0.92	0.93	0.91	0.9	0.87	0.95	0.92	0.95	0.94	0.93
denom	0.000266	0.000233	0.0003	0.000333	0.000433	0.000167	0.000268	0.000167	0.000201	0.000235
N	277	280	273	270	261	284	275	284	280	277

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	0.036364	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	0	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	0.866703	0.3861	29	0.026364	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	0.6548	37	0.033636	FAIL TO REJECT
2 v. 8	1.000308	0.3172	24	0.021818	FAIL TO REJECT
2 v. 9	0.480055	0.6312	34	0.030909	FAIL TO REJECT
2 v. 10	0	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	0.006364	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	2.778368	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	0.478668	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 sqr Effect	Mean sqr Error	F	p-level
TISSUES	3.173694	.021693	146.3025	0.000000

Reference stations 1 & 2 vs Station 4

	Mean sqr Effect	Mean sqr Error	F	p-level
TISSUES	1.147089	.021693	52.87908	.000000

Reference stations 1 & 2 vs Station 5

	Mean sqr Effect	Mean sqr Error	F	p-level
TISSUES	.049802	.021693	2.295793	.129828

Reference stations 1 & 2 vs Station 6

	Mean sqr Effect	Mean sqr Error	F	p-level
TISSUES	2.220723	.021693	102.3720	.000000

Reference stations 1 & 2 vs Station 7

	Mean sqr Effect	Mean sqr Error	F	p-level
TISSUES	1.563956	.021693	72.09605	.000000

Reference stations 1 & 2 vs Station 8

	Mean sqr Effect	Mean sqr Error	F	p-level
TISSUES	1.905976	.021693	87.86263	.000000

Reference stations 1 & 2 vs Station 9

	Mean sqr Effect	Mean sqr Error	F	p-level
TISSUES	1.410672	.021693	65.02986	.000000

Reference stations 1 & 2 vs Station 10

	Mean sqr Effect	Mean sqr Error	F	p-level
TISSUES	.351251	.021693	16.19213	.000059

Reference stations 1 & 2 vs Initial Measurements

	Mean sqr Effect	Mean sqr 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

	EOT_WAWW
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 Difference	q		P value
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	8.235	**	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	.000725		**.00001***	**.00003***	**.00002***	.437565	**.00002***	.597145
5	.000017	.000009		**.00003***	**.00002***	**.00001***	**.00003***	**.00002***
6	.000044	.000026	.000032		**.00683***	**.00002***	.708783	**.00002***
7	.139430	.000018	.000020	.006829		**.00014***	**.00782***	**.00002***
8	.008924	.437565	.000008	.000017	.000143		**.00001***	.485304
9	.000122	.000020	.000026	.708783	.007822	.000008		**.00002***
10	.002662	.597145	.000022	.000020	.000017	.485304	.000017	

Rank-it transformed Growth Rate

Means

	GROWTH
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

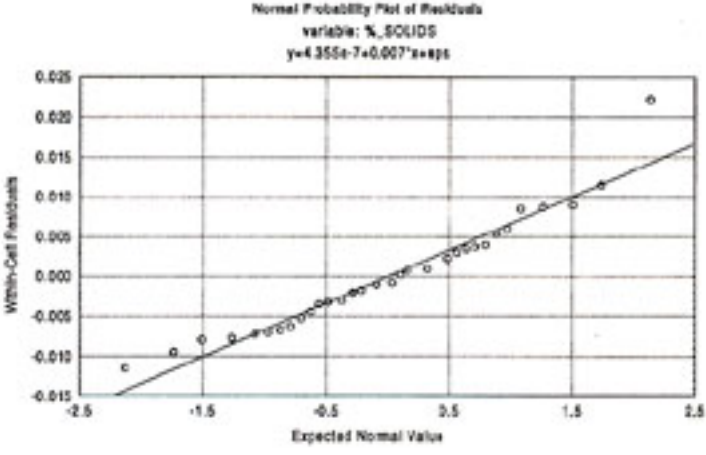
	3	4	5	6	7	8	9	10
3		.867246	.377873	.861547	.789735	.284385	.861222	.526827
4	.867246		.365780	.810651	.625932	.293884	.937562	.597062
5	.377873	.365780		.164255	.179095	.987677	.368545	.755777
6	.861547	.810651	.164255		.896708	.137959	.873297	.424607
7	.789735	.625932	.179095	.896708		.145318	.840497	.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

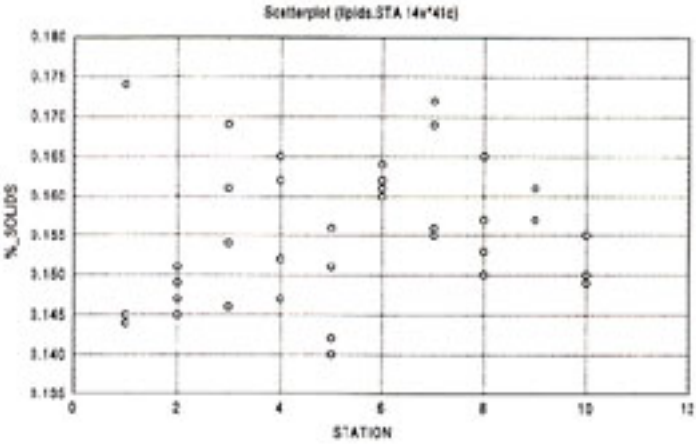
	% SOLIDS	% LIPIDS
1	.151750	1.360000
2	.148000	1.350000
3	.157500	1.555000
4	.156500	1.390000
5	.147250	1.400000
6	.161750	1.502500
7	.163000	1.482500
8	.156250	1.425000
9	.160000	1.720000
10	.151000	1.370000

Percent Solids



Correlation N=40

	SOLID_X	SOLID_Y	
SOLID_X	1.000000	.971485	- **normal**
SOLID_Y	.971485	1.000000	



ANOVA

	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)

Refs 1 and 2 vs:	% Solids
3	1.6349716
4	1.4206491
5	-0.5026591
6	**2.5462673**
7	**2.8142054**
8	**1.3669435**
9	**2.1710279**
10	0.2412253

critical value = 1.697

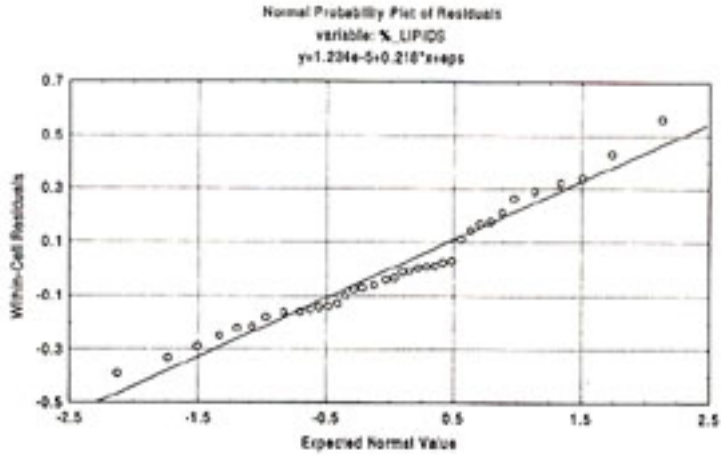
Newman-Keuls test - Percent Solids

	3	4	5	6	7	8	9	10
3		.834347	.225505	.646079	.654861	.962322	.601823	.526351
4	.834347		.232043	.686619	.648643	.958376	.742218	.485736
5	.225505	.232043		.067887	**.04795***	.159345	.112709	.435463
6	.646079	.686619	.067887		.793791	.771365	.714562	.242913
7	.654861	.648643	.047946	.793791		.710338	.802691	.189968
8	.962322	.958376	.159345	.771365	.710338		.856783	.277800
9	.601823	.742218	.112709	.714562	.802691	.856783		.342190
10	.526351	.485736	.435463	.242913	.189968	.277800	.342190	

Dunnett'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.

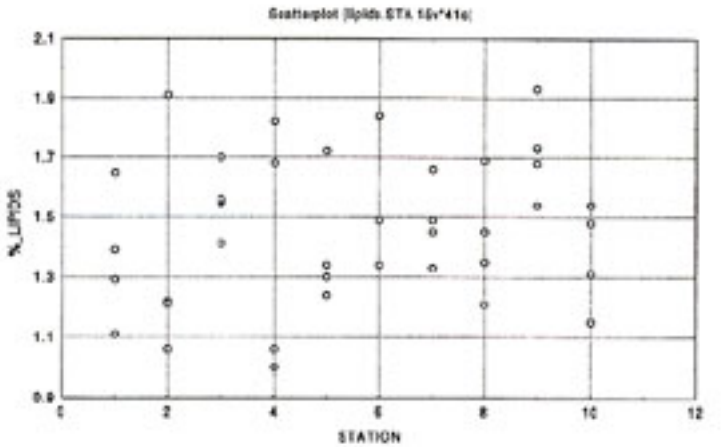
Comparison	Mean Difference	q	P value
Initial vs Station 1	0.00025	0.048	ns P>0.05
Initial vs Station 2	0.00400	0.772	ns P>0.05
Initial vs Station 3	-0.00550	1.062	ns P>0.05
Initial vs Station 4	-0.00450	0.869	ns P>0.05
Initial vs Station 5	0.00475	0.917	ns P>0.05
Initial vs Station 6	-0.00975	1.882	ns 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



Correlation N=40

	LIPID_X	LIPID_Y
LIPID_X	1.000000	.981625
LIPID_Y	.981625	1.000000



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	0.4644848
9	**2.4219567**
10	0.0995325

critical value = 1.697

Newman-Keuls test - Percent Lipids

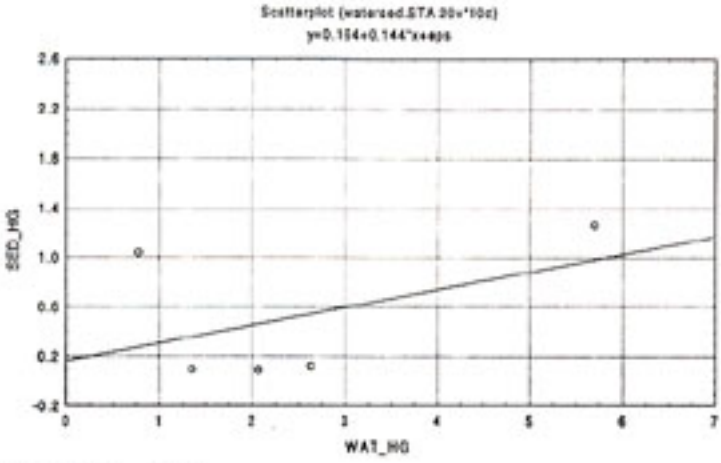
	3	4	5	6	7	8	9	10
3		.902962	.866733	.745944	.893682	.848253	.313136	.903733
4	.902962		.950793	.953924	.937862	.974102	.405374	.901736
5	.866733	.950793		.917972	.864730	.877328	.372000	.980931
6	.745944	.953924	.917972		.901736	.879546	.378010	.959420
7	.893682	.937862	.864730	.901736		.722749	.462647	.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	

Dunnett'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.

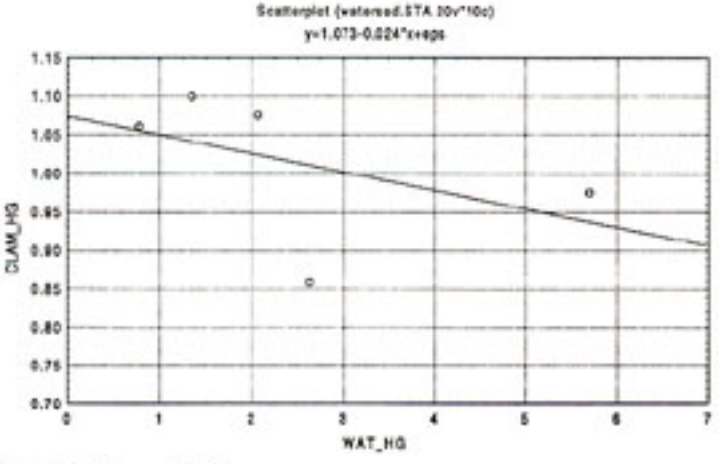
Comparison	Mean Difference	q	P value
Initial vs Station 1	-0.0625	0.367	ns P>0.05
Initial vs Station 2	-0.0525	0.309	ns P>0.05
Initial vs Station 3	-0.2575	1.514	ns P>0.05
Initial vs Station 4	-0.0925	0.544	ns P>0.05
Initial vs Station 5	-0.1025	0.602	ns P>0.05
Initial vs Station 6	-0.2050	1.205	ns P>0.05
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:



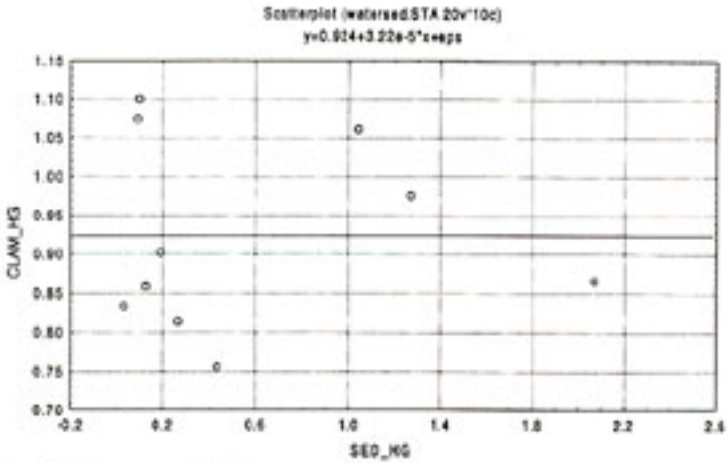
Correlation N=5

	WAT_HG	SED_HG
WAT_HG	1.000000	.474903
SED_HG	.474903	1.000000



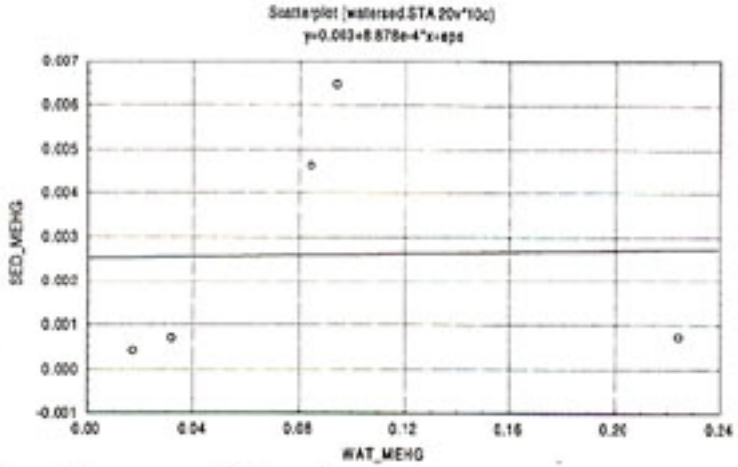
Correlation N=5

	WAT_HG	CLAM_HG
WAT_HG	1.000000	-.462263
CLAM_HG	-.462263	1.000000



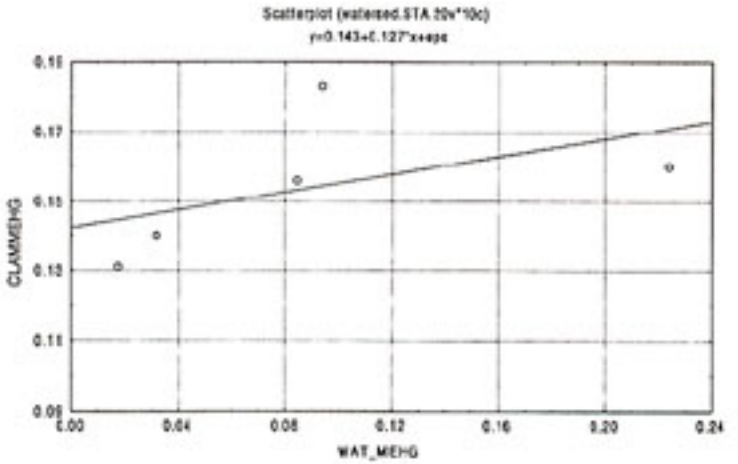
Correlation N=10

	SED_HG	CLAM_HG
SED_HG	1.000000	.000181
CLAM_HG	.000181	1.000000



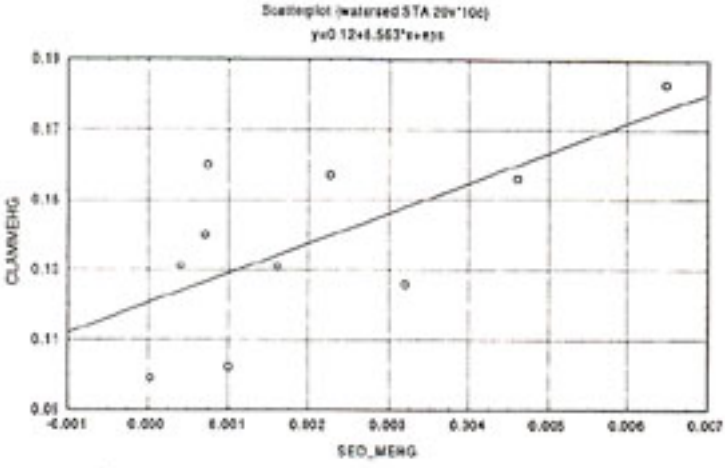
Correlation N=5

	WAT_MEHG	SED_MEHG
WAT_MEHG	1.000000	.026072
SED_MEHG	.026072	1.000000



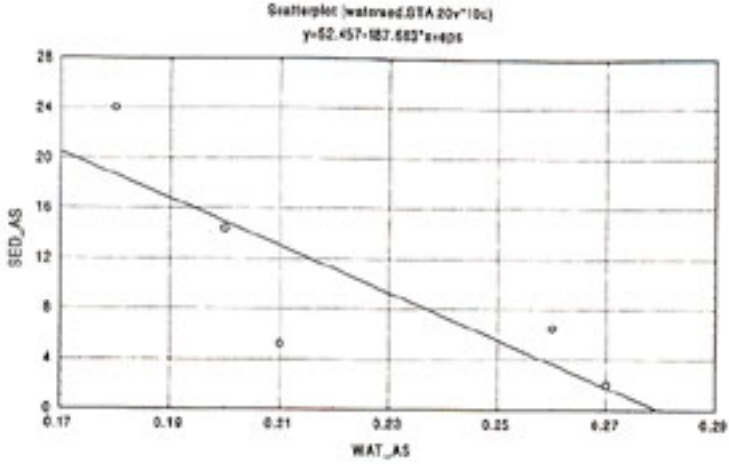
Correlation N=5

	WAT_MEHG	CLAMMEHG
WAT_MEHG	1.000000	.518423
CLAMMEHG	.518423	1.000000

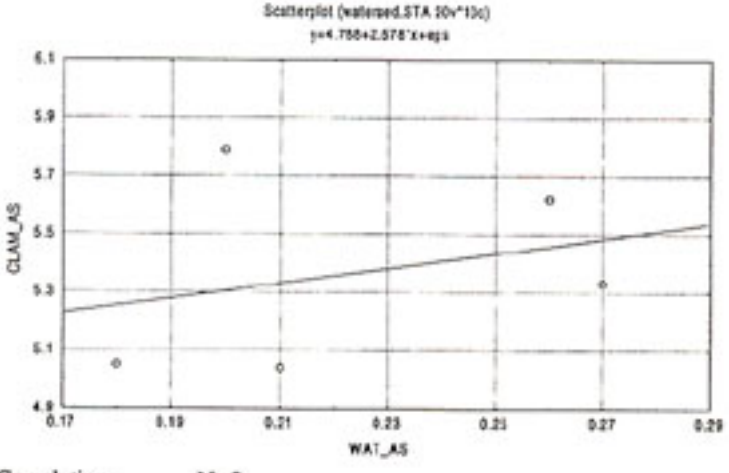


Correlation N=10

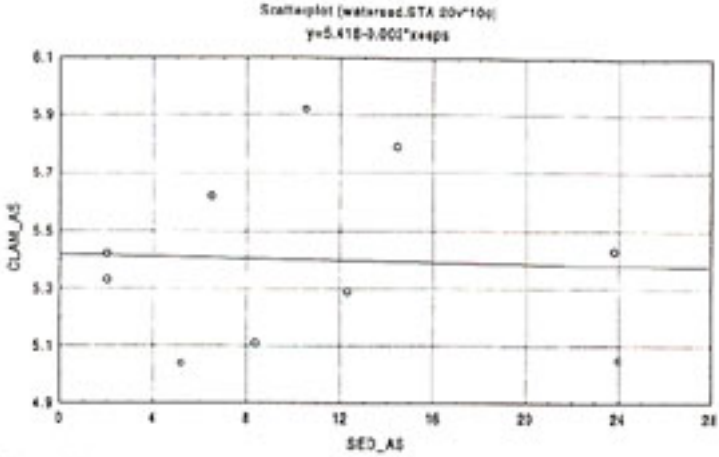
	SED_MEHG	CLAMMEHG
SED_MEHG	1.000000	.676960
CLAMMEHG	.676960	1.000000



Correlation	N=5	
	WAT_AS	SED_AS
WAT_AS	1.000000	-.828647
SED_AS	-.828647	1.000000

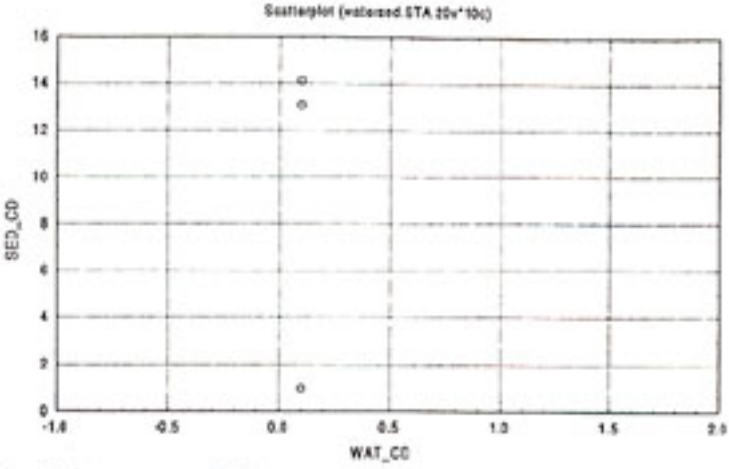


Correlation	N=5	
	WAT_AS	CLAM_AS
WAT_AS	1.000000	.300121
CLAM_AS	.300121	1.000000

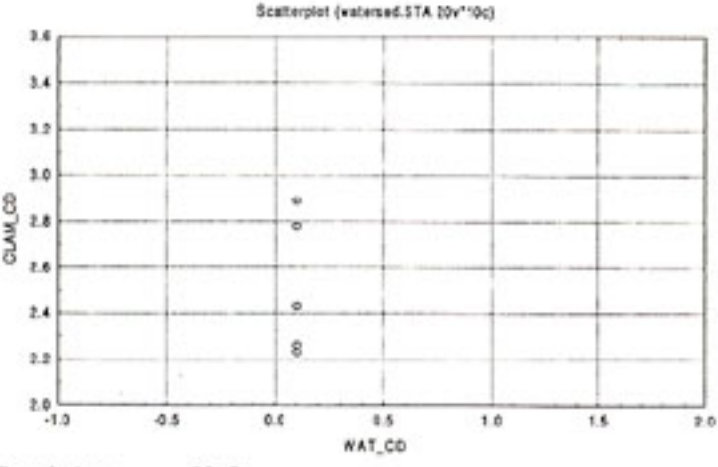


Correlation N=10

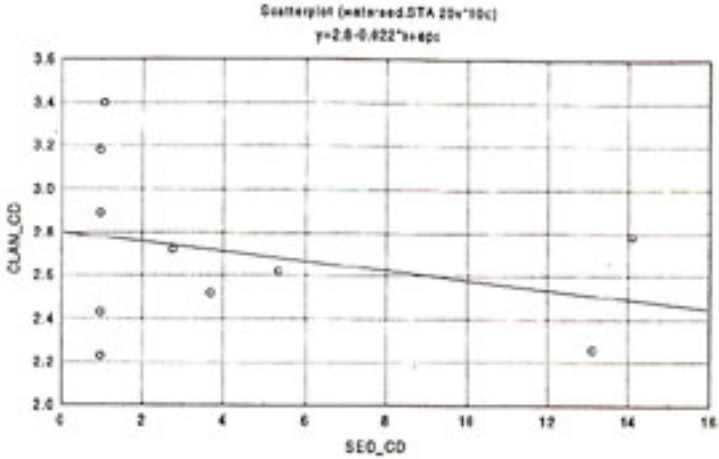
	SED_AS	CLAM_AS
SED_AS	1.000000	-.042809
CLAM_AS	-.042809	1.000000



Correlation	N=5	
	WAT_CD	SED_CD
WAT_CD	1.000000	--
SED_CD	--	1.000000

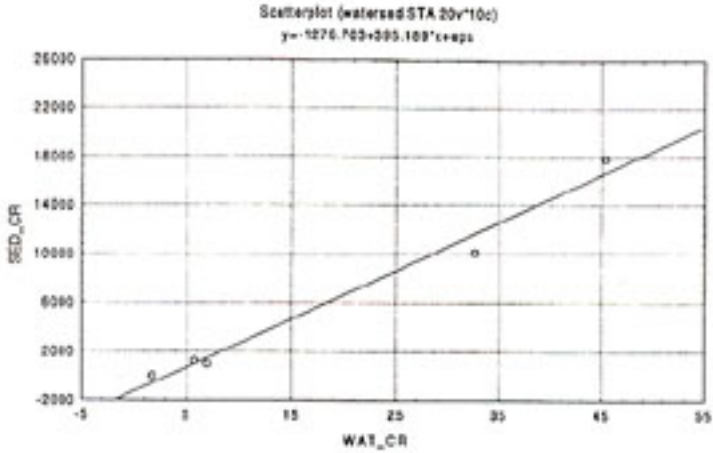


Correlation	N=5	
	WAT_CD	CLAM_CD
WAT_CD	1.000000	--
CLAM_CD	--	1.000000



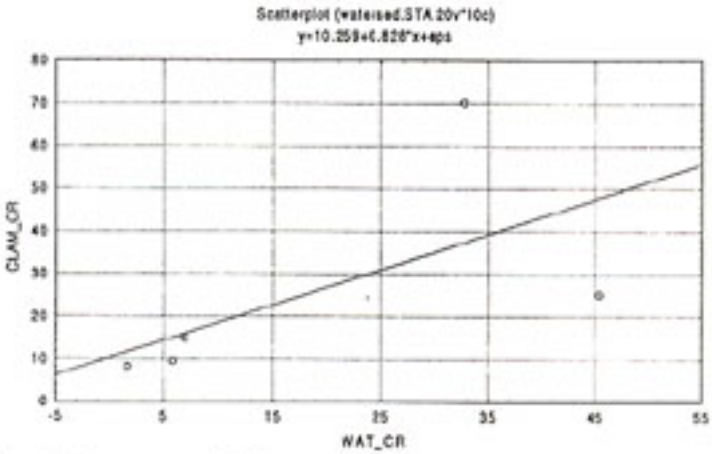
Correlation N=10

	SED_CD	CLAM_CD
SED_CD	1.000000	-.296137
CLAM_CD	-.296137	1.000000



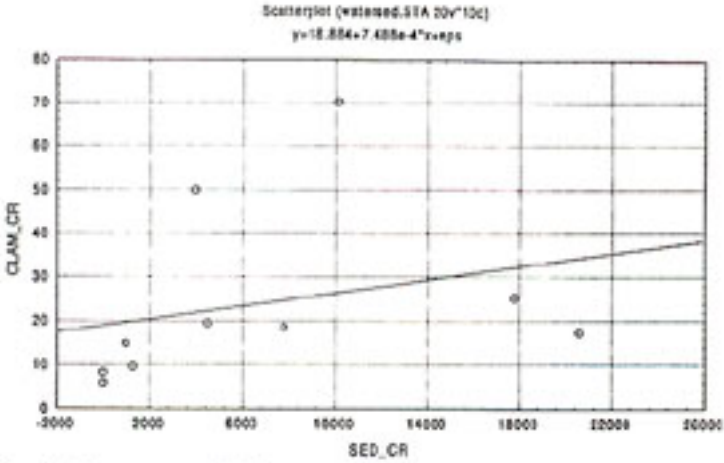
Correlation N=5

	WAT_CR	SED_CR
WAT_CR	1.000000	.990882
SED_CR	.990882	1.000000



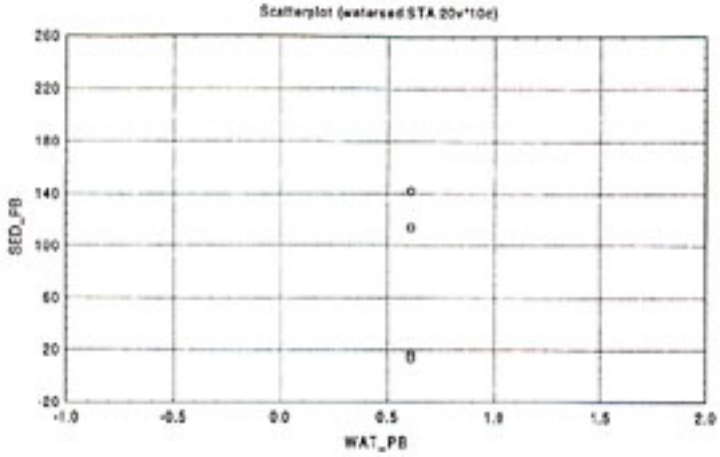
Correlation N=5

	WAT_CR	CLAM_CR
WAT_CR	1.000000	.621165
CLAM_CR	.621165	1.000000

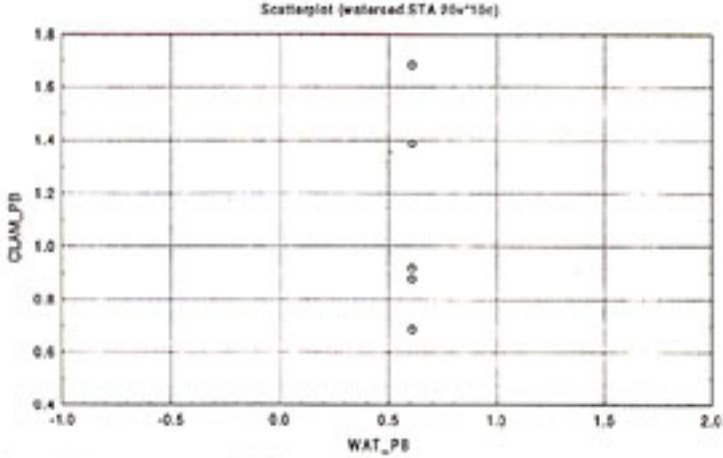


Correlation N=10

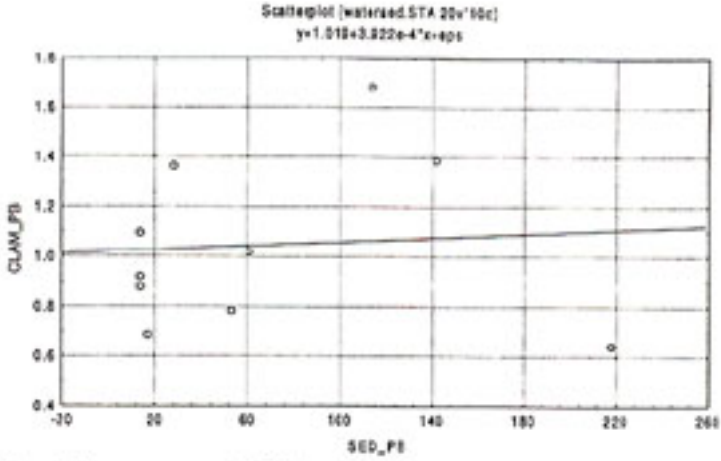
	SED_CR	CLAM_CR
SED_CR	1.000000	.270382
CLAM_CR	.270382	1.000000



Correlation	N=5	
	WAT_PB	SED_PB
WAT_PB	1.000000	--
SED_PB	--	1.000000



Correlation	N=5	
	WAT_PB	CLAM_PB
WAT_PB	1.000000	--
CLAM_PB	--	1.000000



Correlation N=10

	SED_PB	CLAM_PB
SED_PB	1.000000	.080533
CLAM_PB	.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
	Sta 1	**Sta 2**	**Sta 3**	**Sta 4**	**Sta 5**	**Sta 6**	**Sta 7**	**Sta 8**	**Sta 9**	**Sta 10**	**Initial (T0)**
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

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 1	2	4.70	5.52	5.23	4.48	5.12	6.31	5.88	5.70	6.96	4.91	5.29
	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

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

Initial Whole-Animal Wet-Weights (g) by Station

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

Initial Whole-Animal Wet-Weights (g) by Station

	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	5.25
	2	4.58	4.90	4.34	4.88	5.43	4.82	4.36	5.17	4.30	6.16	5.42
	3	6.69	6.58	5.19	4.91	5.72	4.83	4.47	4.02	4.14	5.66	5.24
	4	4.74	5.88	4.33	6.13	4.44	4.39	4.60	5.31	5.28	4.94	5.62
	5	6.52	4.98	4.77	6.36	5.17	5.52	4.08	4.98	5.80	4.82	4.61
	6	6.25	5.09	5.70	4.86	5.29	4.66	6.23	6.33	4.83	4.43	5.67
	7	5.29	4.44	4.33	4.72	6.25	4.88	5.42	6.08	6.47	5.30	4.39
	8	4.39	5.26	5.76	4.02	5.62	6.00	5.60	4.03	5.23	6.23	4.70
	9	5.71	6.56	5.20	5.00	4.81	5.33	7.64	5.37	6.06	4.28	4.05
	10	7.59	5.93	4.31	5.02	4.76	5.19	4.67	6.73	4.13	5.44	5.82
	11	4.80	4.55	5.15	5.24	6.18	5.67	5.42	5.09	4.72	4.53	4.64
	12	6.05	5.94	6.20	5.10	4.84	4.48	4.50	4.76	4.08	5.99	5.02
	13	5.09	5.36	4.79	4.07	5.53	5.08	6.05	5.55	6.95	5.49	5.21
	14	5.58	4.73	5.75	4.61	5.67	4.53	4.96	4.31	4.82	4.14	5.38
	15	6.01	4.49	4.29	5.21	4.55	5.22	6.44	4.51	5.43	5.14	6.84
	16	4.29	4.87	7.45	4.57	4.13	5.45	5.03	4.31	4.20	4.72	5.99
	17	5.71	5.95	7.40	4.51	4.27	5.63	5.00	5.04	5.98	4.62	5.45
	18	5.55	4.96	4.73	4.36	4.52	5.66	6.47	5.54	4.77	6.55	5.07
	19	5.49	4.41	5.98	5.42	5.01	4.30	5.63	4.02	5.95	6.01	4.24
	20	5.10	4.97	5.41	4.77	6.25	4.79	4.31	4.12	4.31	5.78	6.66
	21	5.07	5.87	5.21	5.99	6.71	5.86	4.40	4.34	6.16	5.29	7.16
	22	5.70	4.78	6.38	5.83	5.84	5.61	4.91	4.57	4.92	4.46	4.92
	23	6.41	5.33	5.91	6.41	6.24	6.30	4.39	5.51	4.62	4.34	5.84
	24	4.65	4.93	4.84	5.20	5.46	4.08	5.54	4.88	5.02	5.06	4.83
	25	5.44	5.67	5.46	6.39	5.61	4.81	5.95	4.61	4.72	7.70	5.03
	26	6.46	6.72	5.52	5.73	5.62	4.81	5.00	5.68	5.15	5.18	5.14
	27	5.01	5.72	4.96	5.29	5.76	5.24	5.96	5.52	4.83	7.28	5.87
	28	4.18	6.54	4.66	5.57	4.21	5.04	5.25	5.08	6.38	6.28	4.35
	29	4.98	5.73	6.67	4.40	7.05	4.64	5.64	6.08	6.42	6.13	5.58
	30	4.20	4.94	6.76	5.86	5.11	5.62	4.67	5.54	6.09	6.56	6.08
	31	5.91	5.55	4.80	4.80	5.19	5.75	6.81	5.92	5.49	6.02	4.94
	32	5.95	5.79	5.54	6.41	6.79	4.35	5.33	5.24	4.76	4.76	6.26
	33	6.60	5.43	5.23	6.54	5.33	6.94	7.28	5.06	5.47	5.21	5.56
	34	6.51	4.63	6.37	5.87	4.20	4.93	5.49	4.31	5.14	5.00	5.94
	35	5.29	5.89	4.71	5.63	6.28	4.11	4.62	6.38	5.63	5.18	4.63
	36	4.98	5.95	4.22	5.96	4.23	5.31	5.13	5.73	4.92	5.43	4.59
	37	5.51	4.97	4.46	5.21	5.67	4.17	5.67	4.55	4.52	5.91	5.52
	38	5.58	6.45	6.55	6.63	5.37	6.45	7.84	6.30	6.88	5.88	6.50
	39	4.83	4.47	5.27	5.03	6.41	6.51	4.53	4.90	6.81	5.43	4.60
	40	5.20	4.32	6.61	4.33	5.58	6.30	5.20	5.27	6.38	6.99	4.54
	41	5.30	4.05	4.63	5.90	5.59	5.46	5.68	6.65	4.60	5.84	4.94
	42	4.40	4.26	5.43	5.87	5.07	4.70	4.32	5.89	4.56	7.22	5.93
	43	5.86	6.93	7.73	6.79	5.65	5.94	5.00	5.05	5.39	5.88	5.34
	44	5.41	7.18	5.90	6.48	5.76	4.70	5.98	4.98	5.59	4.47	4.08

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Initial Whole-Animal Wet-Weights (g) by Station

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
	Sta 1	**Sta 2**	**Sta 3**	**Sta 4**	**Sta 5**	**Sta 6**	**Sta 7**	**Sta 8**	**Sta 9**	**Sta 10**
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	

End-of-Test Whole-Animal Wet-Weights (g) by Station

	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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End-of-Test Whole-Animal Wet-Weights (g) by Station

	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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End-of-Test Whole-Animal Wet-Weights (g) by Station

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	

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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

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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
	Sta 1	**Sta 2**	**Sta 3**	**Sta 4**	**Sta 5**	**Sta 6**	**Sta 7**	**Sta 8**	**Sta 9**	**Sta 10**
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

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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

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Change in Whole-Animal Wet-Weight (g) by Station

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

1997 Cannelton Clam Biomonitoring Study

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
		Sta 1	**Sta 2**	**Sta 3**	**Sta 4**	**Sta 5**	**Sta 6**	**Sta 7**	**Sta 8**	**Sta 9**	**Sta 10**
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

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 1	3	-	-1.27	8.91		31.81	-48.35	5.09		-5.09	15.27	0.00
		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

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
		Sta 1	**Sta 2**	**Sta 3**	**Sta 4**	**Sta 5**	**Sta 6**	**Sta 7**	**Sta 8**	**Sta 9**	**Sta 10**	**Initial (To)**
Rep 1 - 1		0.61	0.86		0.98	1.07	0.96	0.95	0.79	0.87	0.95	0.67
	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

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

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

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

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 1	4-	0.54	1.03		0.81	0.85	0.77	0.70	1.03	0.82	0.47	0.63
	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

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

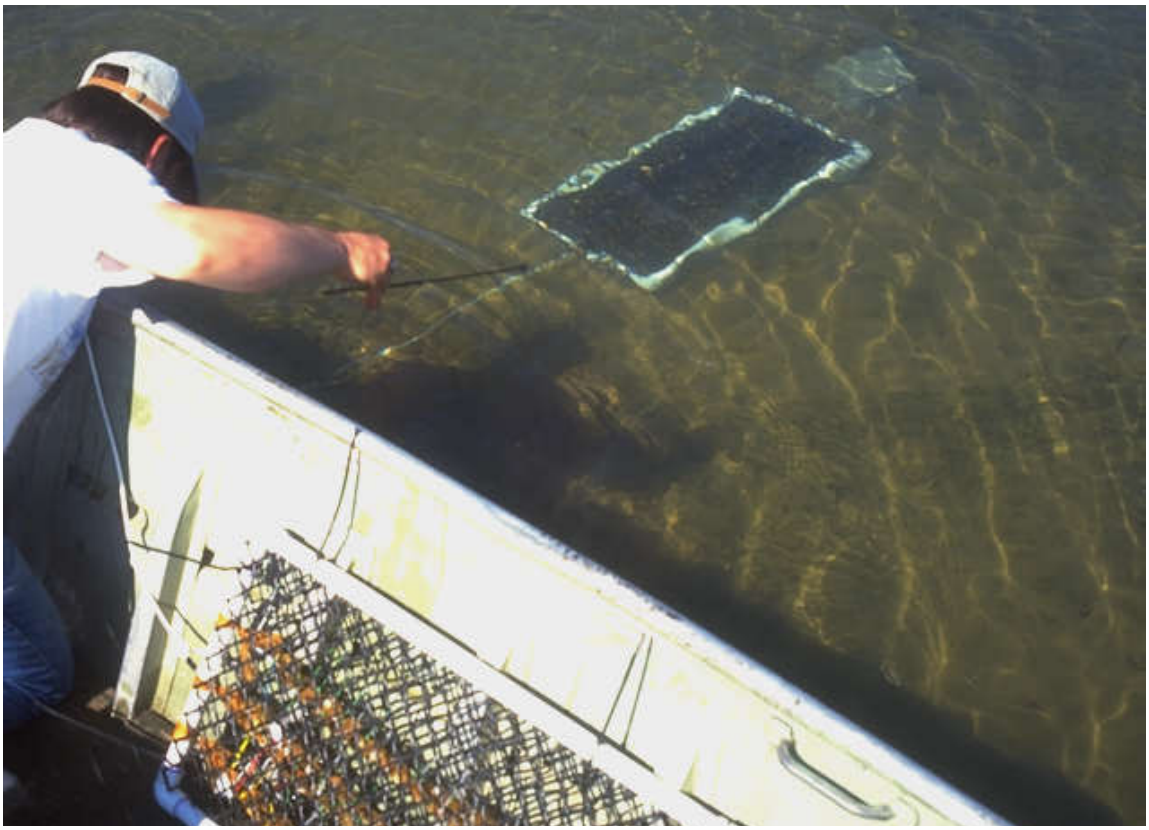
5. PVC cages containing clams prior to deployment

6. Attaching predator mesh

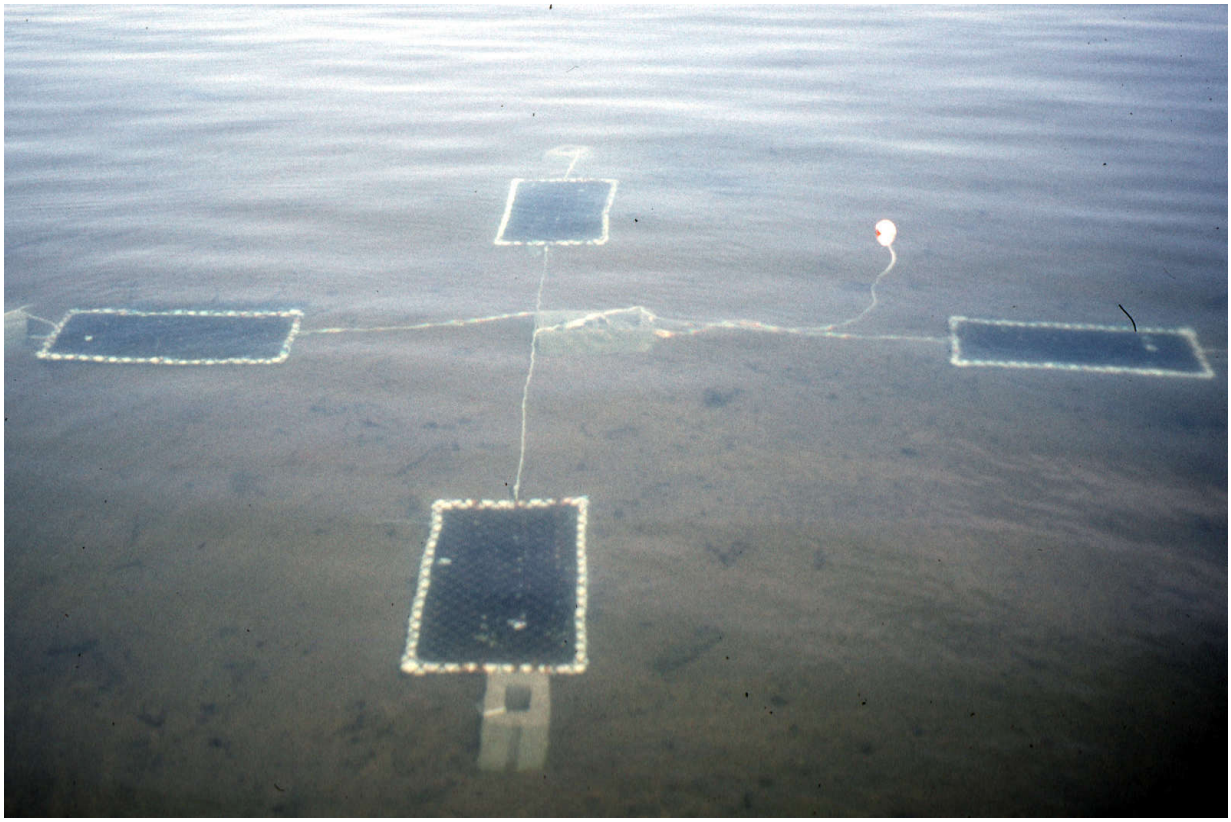
7. Deploying a clams at the holding site

8. Retrieving clams at the holding site

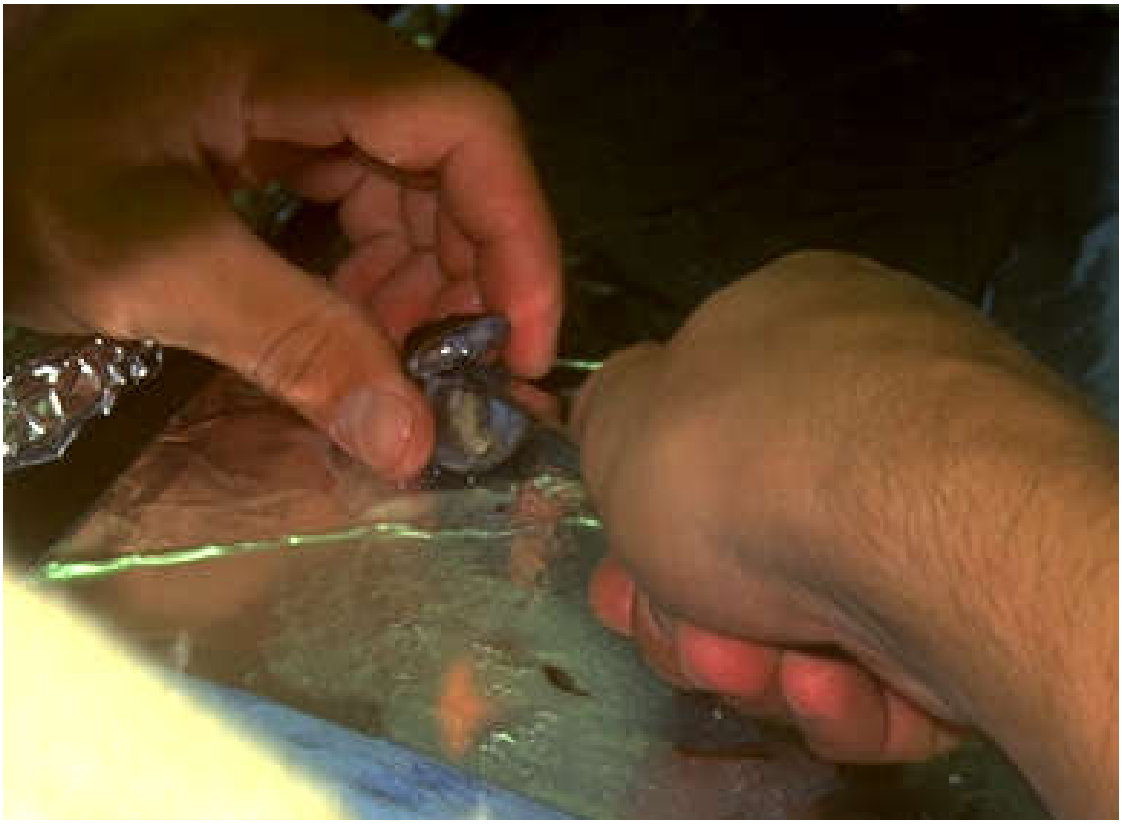
9. Preparing cages for deployment. For each station, caged clams, surrounded with predator-protection mesh, are tethered together and attached to a cement block



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